DNA replication in the context of development: Tissue-specific remodeling of the DNA replication fork and dynamic R-loop signatures across embryogenesis

By

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Dissertation

Submitted to the Faculty of the

Graduate School of Vanderbilt University

In partial fulfillment of the requirements

for the degree of

DOCTOR OF PHILOSOPHY

In

BIOLOGICAL SCIENCES

June 30th, 2022

Nashville, Tennessee

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Dedicated to Rachel, the light of my life, without whom this thesis would not exist.

ACKNOWLEDGEMENTS

I knew graduate school would be challenging, but I still underestimated how difficult it would be. Without the help of several people playing different but essential roles, I would not be here today. I thank Jared Nordman, my advisor. I wasn't an easy student to mentor, especially for a brand-new PI. He handled everything with aplomb and grace, and I think together we have laid the foundations for a great laboratory.

I thank my mom, Kathy, and sister, Amanda. They have given me emotional and psychological support over my entire life. Rachel's family, in particular her mom, Cathy, have also supported me and encouraged me to go back to graduate school and fulfill this dream.

I thank my committee members Kendal Broadie, Dave Cortez, Jim Patton, and my chair Kathy Friedman. They have given invaluable feedback and support on my science. Kathy especially supported the more emotionally taxing aspects of being a graduate student.

I have been lucky to have several people who encouraged me to go back to graduate school and believed in me even before I believed in myself. Some of the most important of these people are Laura Hover, Ty Abel, Michael Cooper, Hal Moses, Phil Owens, and Gerardo Valadez.

I've been lucky to work with a number of great people in my immediate lab. I thank Saumya Patel, Souradip Das, Dongsheng Han, Reyhaneh Tirgar, and Logan Richards, Jack Rong, and Amanda Sun. Mentoring Amanda was a wonderful experience, and I'm very proud of her own graduate career now. House parties at Logan's played a pivotal role in maintaining my mental health.

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CHAPTER I: INTRODUCTION

OVERVIEW

“But our manner of knowing is so weak that no philosopher could perfectly investigate the nature of even one little fly” - Thomas Aquinas.

DNA replication is a fundamental challenge of life. In order to proliferate, every organism must be able to replicate and divide its DNA into daughter cells. DNA is the unit of inheritance that that underlies evolution and is the bedrock of the central dogma of biology: DNA is transcribed into RNA, which is in turn translated into proteins. Defects in DNA replication can cause in mutations that can result in loss of function or defects in proteins and functional RNAs. These errors ultimately drive cellular dysfunction and disease. Since DNA is copied to daughter cells, every error that occurs is passed on to daughter cells and can propagate throughout the organism or tissue. Catastrophic DNA damage can even cause cellular death. DNA replication is meticulously regulated to ensure accurate transmission of genetic and epigenetic data. Therefore, the timely and accurate replication of DNA is of utmost importance to every life form. DNA replication must also overcome a multitude of challenges each and every time a genome is copied.

Challenges in DNA replication can range from conflicts between replication and transcription, limiting nucleotide pools, DNA secondary structures and many others (Zeman and Cimprich, 2014). In addition, epigenetic information must be accurately copied from one parent strand to the daughter strands to maintain chromatin organization and transcription programs (Alabert and Groth 2012). In multicellular organisms, DNA replication occurring in the context of development can pose unique challenges due to atypical cell cycles and unusual chromatin environments (Nordman

and Orr-Weaver, 2012). All these obstacles must be overcome to ensure the accurate and timely replication of the genome to maintain life.

In this introduction, I will review what has previously been discovered about DNA replication, focusing on the macromolecular machine that orchestrates DNA replication: the replication fork. DNA replication in the context of development will be detailed, focusing specifically on work in the fruit fly, *Drosophila melanogaster*, which has been an invaluable tool for studying DNA for over a century. Finally, I will detail R-loops, a nucleic acid structure that forms when nascent transcripts reanneals to the template DNA. R-loops have been shown to be a multifaceted factor in epigenetic regulation, a driver of genome instability and yet plays essential roles in DNA repair and replication (Skourti-Stathaki and Proudfoot, 2014). Understanding how R-loop dynamics change during development, influence establishment of the chromatin environment, and serve as triggers of the DNA damage response has been a focus of my thesis research. These ideas are essential to the research I conducted, which has focused on the central question of how DNA replication and the chromatin environment are regulated during the confines of development. More specifically, (1) if the replication fork itself can be remodeled during development to accommodate for cell-type specific replication programs and (2) how R-loop position and abundance changes during development. This work has furthered our understanding of DNA dynamics during development and moves us closer to fully understanding the nature of ‘one little fly’.

The fundamentals of DNA replication

DNA replication occurs in multiple steps across the cell cycle, beginning in late mitosis and across G1. In eukaryotes, the six-member Origin Recognition Complex (ORC) binds to hundreds to thousands of sites across the genome, depending on the size of the organism's genome (Fig. 1-1) (Sun and Kong, 2010). These sites are termed origins of replication. In yeast, these sites are highly sequence specific, but in metazoans where ORC binds is not completely understood. While ORC binding is sequence independent in metazoans, origins of replications are enriched at open chromatin such as that found in promoters and enhancer regions of DNA (Hutchins et al. 2016). The local chromatin environment may also play a role in ORC binding, as histone acetylation and H4K20 methylation may contribute either directly or indirectly to ORC binding (MacAlpine et al. 2010).

The initial steps of helicase loading have been most well established in budding yeast. While highly conserved, the increasing complexity of metazoan helicase loading may be more intricately regulated. Helicase loading also requires Cdc6 and Cdt1 to act cooperatively and sequentially to load two heterohexameric MCM2-7 complexes head-to-head at a replication origin (Ticau et al. 2015). Singe molecule studies have demonstrated that Cdc6 binds to ORC and recruits the first MCM complex that is bound to Cdt1 (Ticau et al. 2015). After loading of the initial MCM hexamer, ORC recruits a second MCM through similar interactions with Cdc6 and Cdt1. At this point, Cdt1, Cdc6, and ORC can all dissociate from the DNA leaving the two bound MCM complexes. Importantly, once loaded but before activation of the helicases, the two MCM molecules

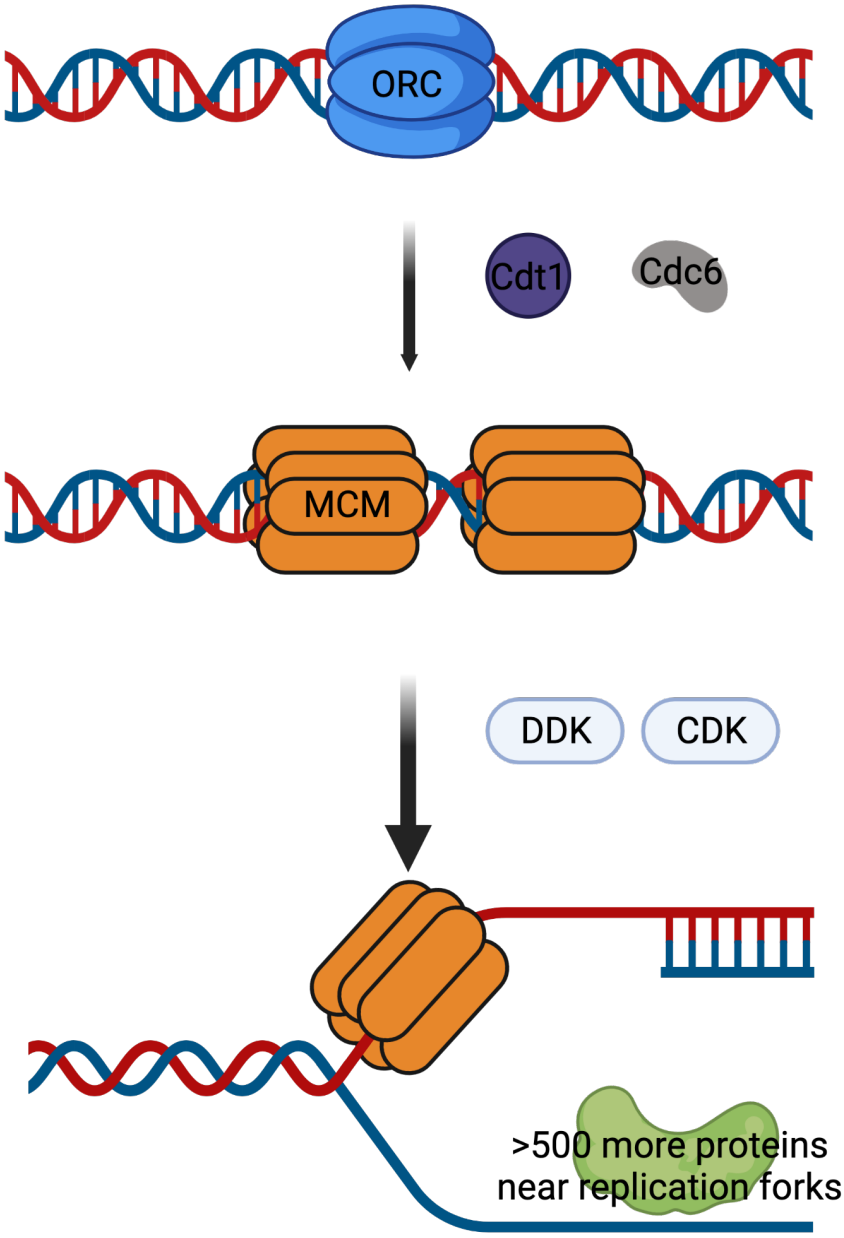


Figure 1-1: **The replicative helicases of the replication fork are loaded at ORC binding sites.** Orc binds to potential origins across the genome during late mitosis and G1. Through the activity of Cdt1 and Cdc6, 2 MCM helicases are loaded at these sites. During S Phase, the activity of the DDK and S-CDK kinases phosphorylate the helicases. Through the recruitment of hundreds more proteins, the replication forks form.

can ‘slide’ around the double-stranded DNA but are constrained by local chromatin

(Remus et al. 2009). The two MCM complexes are the core helicases in the final

replication fork. Importantly, the activity and protein levels of ORC, Cdc6 and Cdt1 are regulated across the cell cycle to prevent reloading of MCM hexamers during S phase and the unintentional reduplication of the genome (Mimura et al. 2004; Pozo and Cook, 2017; DePamphilis, 2004).

At the beginning of S phase, the helicases are activated by Dbf4-Dependent Kinase or DDK. Both DDK and the S phase CDK (S-CDK) are required for the additional recruitment of the remaining essential firing factors (Sld2, Dpb11, GINS, Mcm10 and pol ε) and the initial unwinding of DNA (Douglas et al. 2018). Mcm10 promotes further unwinding of DNA and Replication Protein A (RPA) binds to the newly available single-strand DNA (ssDNA) (Douglas et al. 2018). Dozens of new proteins are ultimately recruited, including the remainder of the DNA polymerases (Sirbu et al. 2011). This final macromolecular machine is termed the replication fork or replisome and is capable of replicating both the genetic and epigenetic information.

In addition to simply unwinding and copying the DNA, the replication fork must also be able to unpack DNA from nucleosomes and repackage newly synthesized DNA after replication. To properly extricate and re-add nucleosomes, histone chaperones and chromatin remodeling complexes are required. FACT, Asf1, and Nhp6 are histone chaperones that work to disrupt the nucleosomes ahead of the replication fork (Alabert and Groth, 2012). FACT seems to be the most essential of these and associates with polymerase α and MCM2 (Zhang et al. 2020). Multiple chromatin remodeling complexes such as Acf1-Iswi and Ino80 seem to be required to replicate efficiently through chromatin, particularly in more tightly packaged heterochromatin (Alabert and Groth, 2012).

While the essential components of the replication fork have been defined *in vitro*, the composition of the replication fork *in vivo* is much more complex (Baris et al. 2022). In the past decade, new purification strategies coupled with mass spectrometry developed by the Cortez and Groth laboratories have vastly increased our understanding of the complex proteome associated with the replication fork. By purifying proteins associated with newly synthesized DNA, hundreds of additional proteins have been shown to associate with at least a subset of replication forks (Alabert et al. 2014; Sirbu et al. 2013). Combining purification strategies with replication stressors shows that the composition of replication forks is highly dynamic (Dungrawala et al. 2015).

The protein composition of the replisome can vary in response to a variety of replication stresses such as lack of nucleotides, DNA lesions, misincorporation of ribonucleotides, replication-transcription conflicts, repetitive DNA, or DNA secondary structure (Zeman and Cimprich, 2013). Eukaryotes have conserved DNA damage response proteins to resolve damage due to these sources. Ataxia telangiectasia and Rad3 related (ATR) is an essential protein in mammals that acts at stalled replication forks (Saldivar et al. 2017). After activation, ATR activates a cascade of signaling events to prevent the replication fork from collapsing and remodel the cell cycle. Origin firing is modulated, the replisome itself is stabilized, and recruitment of fork repair proteins occurs (Saldivar et al. 2017). Though replication stress can be caused by exogenous sources, many of these impediments arise naturally as part of the normal replication program. For example, TERF2 is recruited to heterochromatin topological barriers in response to ATM for the replication fork to proceed (Mendez-Bermudez et al.

2018). Understanding how cells deal with endogenous replication stress can guide the diagnosis and treatment of human diseases that result from defects in this process.

The unique challenges of development

Development from the single zygote to a developed organism is a monumental challenge. After zygotic genome formation, embryogenesis begins and altered cell cycles may occur. At the most extreme example, common in egg laying species such as Drosophila, an entire cell cycle can occur in less than ten minutes and happens without any gap phases (Farrell and O'Farrell, 2014). These early fast cycles are hypothesized to take advantage of maternally deposited resources and speed development to avoid predators (Yuan et al. 2016). In contrast, mammalian embryonic development proceeds much more slowly but still maintain cell cycle heterogeneity. The first cleavage cycle in mouse embryos occurs 36 hours post-fertilization, while the next four cell cycles take 12 hours each (Hogan et al. 1994). Later in development, the cell cycle can be completed within 2.5 hours (Mac Auley et al. 1993).

The altered cell cycle timing is not the only challenge the DNA replication program most overcome during embryogenesis. In Drosophila, the early embryo lacks most histone modifications found in mature tissue, and there are frequently developmental-specific histone variants (Hamm and Harrison, 2018; Loppin and Berger 2020). As the embryo develops and begins to form defined cell lineages, histone modifications that are critical for gene regulation and cell differentiation must be added. Initially, Drosophila embryos rely upon maternally deposited RNA and protein and do not make *de novo* transcripts (Tadros and Lipshitz, 2009). At some point, every embryo

undergoes a maternal-to-zygotic (MZT) transition whereupon the zygotic genome is activated, and maternally deposited RNA is degraded (Hamm and Harrison, 2018). In flies, there is a minor wave of zygotic genome activation (ZGA) at cell cycle 9, and the major wave at cell cycle 14 (Tadros and Lipshitz, 2009). Mammalian embryos undergo a similar stepwise activation, with the first wave of ZGA occurring at cell cycle 2, and the major wave at cell cycle 4 (Jukam et al. 2017). Finally, DNA replication itself may regulate cellular differentiation. Recent studies of mouse embryonic stem cells demonstrated that totipotent cells have much slower replication fork speeds and use many more origins to compensate (Nakatani et al. 2022). Artificially slowing replication fork speed and altering replication timing was sufficient to change the totipotency and differentiation of the tissue (Nakatani et al. 2022). This highlights the interplay between DNA replication and development.

Proteomic studies of replication forks in embryonic stem cells have identified proteins at replication forks that aren't present in fully differentiated cells (Aranda et al. 2014; Zhao et al. 2018). Many of these proteins are hypothesized to aid with the short cell cycle or are involved with epigenetic inheritance (Aranda et al. 2014). For example, the NuRD-HDAC was found to be at replication forks and had separately been shown to be required for early embryonic development in zebrafish (Aranda et al. 2014; Christov et al. 2018). Separate research identified a Filia-Floped protein complex at replication forks in mouse embryonic stem cells which seemed to aid activation of ATR signaling and provide more robust fork restarting (Zhao et al. 2018).

In addition to the challenges of rapid embryonic cycles, unique DNA replication programs exist across development. Polyploidy, wherein cells undergo repeated rounds

of DNA replication without mitosis and cytokinesis, is common in metazoans. Polyploidy is found within repairing kidney, bladder, and liver tissue in mammals (Bailey et al. 2021). Furthermore, many different tissues in Drosophila contain polyploid cells (Fox et al. 2020; Nandakumar et al. 2020; Unhavaithaya and Orr-Weaver, 2012). The function of polyploidy is not completely understood, but the increased genomic content may allow cells to increase transcriptional output, withstand environmental stresses, and allow specialized function by large cells (Calvi et al. 1998; Orr-Weaver 2015; Van de Peer et al. 2020). Polyploidy can also arise through wound healing due to cell fusions (Losick et al. 2013).

Programmed gene amplification and underreplication of specific genomic loci may also occur in polyploid cells (Spradling and Orr-Weaver, 1988). For example, in the follicle cells of the Drosophila ovary, specific regions of the genome go through repeated round of DNA replication to increase gene copy number (Spradling and Mahowald, 1980; Griffin-Shea et al. 1982). The increased gene copy number provides additional capacity to create transcripts associated with chorion (eggshell) production in a short developmental time (Calvi et al. 1998). Many polyploid cells in Drosophila also have regions of underreplication, where specific loci have fewer copies of the chromosome in comparison to the rest of the genome (Spradling and Orr-Weaver, 1987). Importantly for human health, both gene amplification and underreplication have also been observed in the giant trophoblast cells of the placenta (Hannibal and Baker, 2016).

R-loops play multifaceted roles in the cell

R-loops are a three-stranded nucleic acid structure canonically formed when nascent RNA from transcription reanneals to the template DNA strand, resulting in a displaced single strand of DNA (Fig. 1-2) (Aguilera and García-Muse 2012). Sequences that could form R-loops to their transcribed loci were identified at the highly transcribed *18S* and *28S* sequences within the rDNA locus of *Drosophila melanogaster* (White and Hogness 1977; Glover and Hogness 1977). In high heat and formamide-containing conditions, the abundant RNA could anneal back to the duplex DNA and cause the characteristic displacement of a single strand of DNA (Birnstiel et al. 1972). A decade later, R-loop formation *in vivo* was shown to occur in the context of *E. coli* plasmids (Dasgupta et al. 1987). Persistent R-loops were shown to form at the plasmid origin of replication as a result of nearby transcription (Dasgupta et al. 1987). R-loops

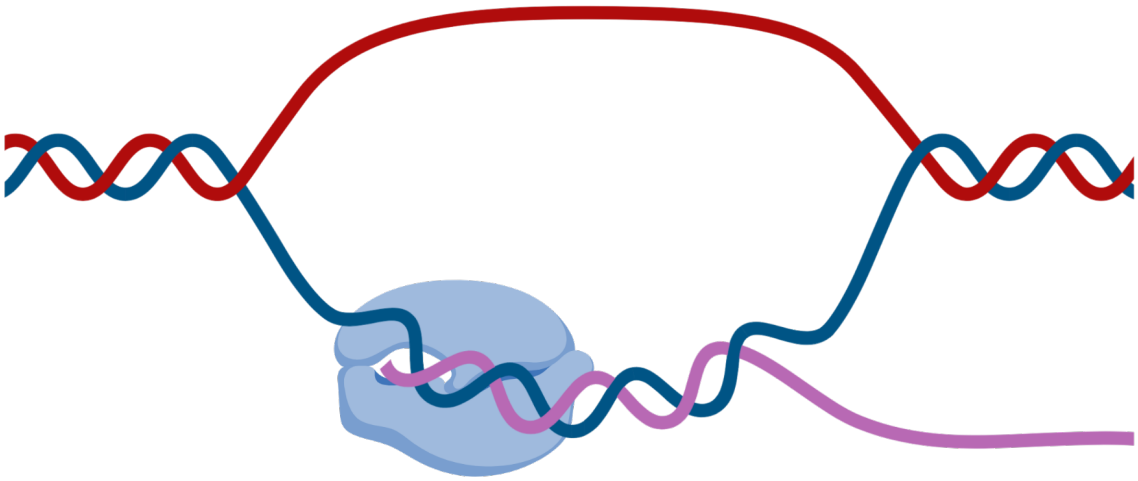


Figure 1-2: **Representation of a *cis* R-loop.** RNA is indicated by the purple strand. R-loops can also form in *trans*, in which case the polymerase would be absent.

spur initiation of DNA replication in this context through two methods (Fig. 1-3A). First, the RNA of the R-loop serves as the primer for DNA polymerase. The RNA moiety of the R-loop serves as the primer for normal DNA replication after cleavage by RNase H makes the 3' end accessible to DNA polymerase (Itoh and Tomizawa, 1980). Secondly, the displaced single-strand of DNA is available to the helicase and primase, where they can go on to initiate replication (Masukata et al. 1987). The formation of this R-loop is required for the plasmid to replicate. The most stable R-loop forms at a sequence of repeated deoxycytidine and guanisine (Masakata and Tomizawa, 1990). Other research during this era highlighted the complexity of R-loop. Changes in the rate of transcription altered the efficiency of the RNA:DNA hybrid formation, giving the first hint as to the complexity of R-loop formation (Masakata and Tomizawa, 1990).

R-loop formation also occurs in the context of phage T4 infection and in the replication of mitochondrial DNA. At least two different origins of replication within the T4 genome form R-loops in *cis* and perform similar functions as they do in the plasmid (Carlies-Kinch and Kreuzer, 1997). Transcription initiates from the promoter upstream of the R-loop forming region (Carlies-Kinch and Kreuzer, 1997). Interestingly, the R-loop structure in T4 permits the transcription of RNA from the single-stranded, non-template strand that can also serve as the primer for DNA synthesis (Belanger and Kreuzer, 1998). In mitochondria from yeast to mammals, R-loops form in *cis* via transcription of the mtRNA polymerase near GC-rich cluster (Lee and Clayton, 1998). This R-loop likely acts as the primer for DNA replication, similar to plasmids in *E. coli* (Lee and Clayton, 1998). Surprisingly, *in vitro* studies suggest that widescale incorporation of mitochondrial transcripts can be incorporated in *trans* into the mitochondrial genome during replication

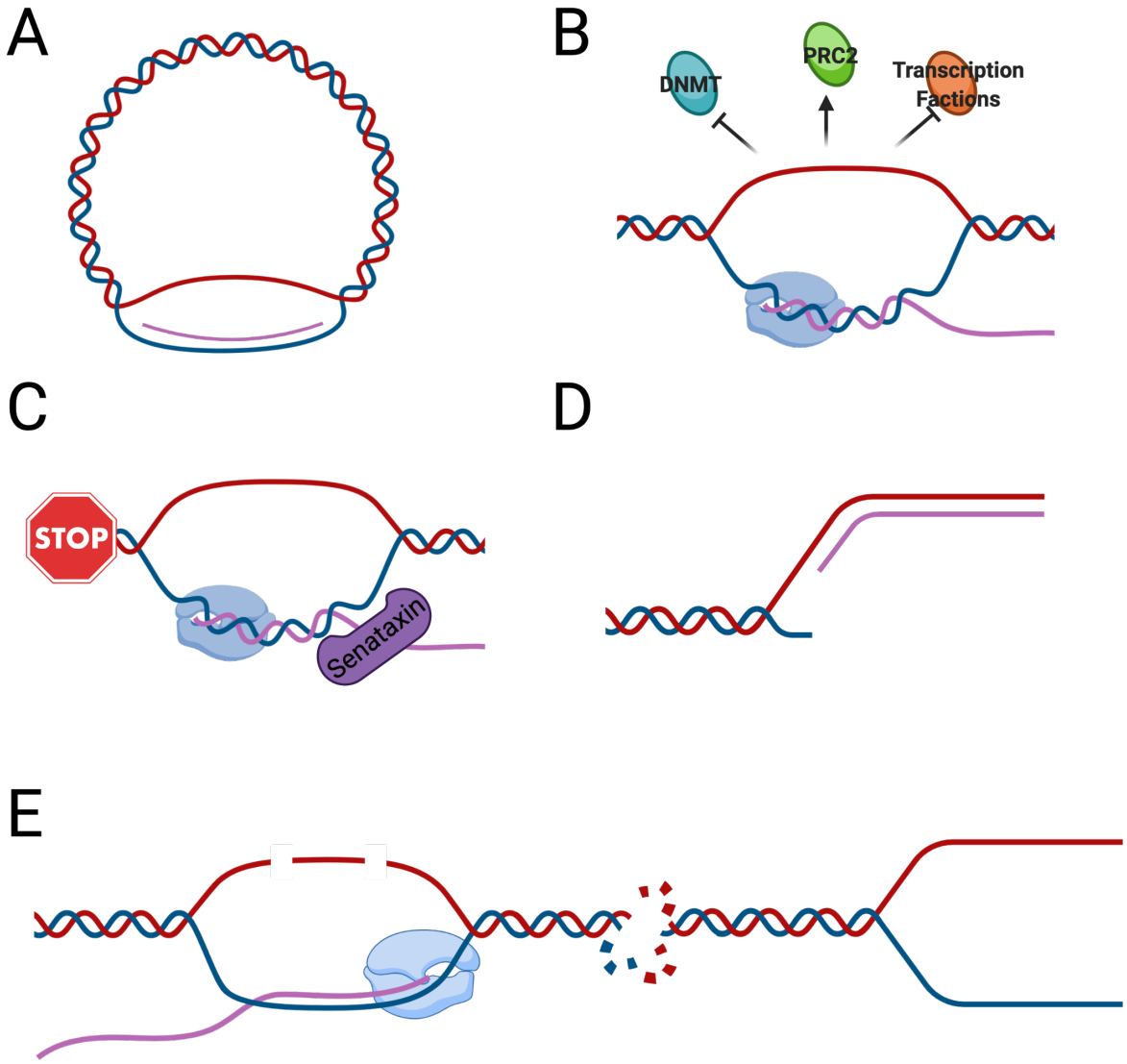


Figure 1-3: **Summary of the *in vivo* functions of R-loop. (A)** An R-loop in plasmids and mitochondria DNA to form initiation of replication. **(B)** R-loops recruit some chromatin modifying proteins, such as PRC2, and can block the recruitment of other factors such as DNMT and transcription factors. **(C)** R-loops at transcription termination sites work to halt the RNA polymerase and can recruit proteins such as Senataxin. **(D)** R-loops form at double-strand breaks to guide repair machinery and prevent excessive resection. **(E)** R-loops may also be a source of DNA damage. This can occur through damage at the displaced single-strand of DNA or when colliding with the replication fork machinery.

(Reyes et al. 2013). These early studies highlight two important aspects of R-loop biology. Though R-loops primarily form co-transcriptionally, they can form in *trans*. Second, there is a throughline linking R-loop biology to initiation of DNA replication.

In eukaryotic nuclear genomes, the link between R-loops and initiation of DNA replication failed to be established. Instead, the first study demonstrating that R-loops can form in the eukaryotic genome and serve an important physiological function came from work in B cells. This research coupled bisulfite-treatment with PCR sequencing to demonstrate that R-loops form *in vivo* (Yu et al. 2003). Importantly, the formation of R-loops across the immunoglobulin class switch locus in cultured spleen cells was dependent upon activation with LPS, demonstrating that R-loops formed specifically as a response to transcription (Yu et al. 2003). In addition to demonstrating that R-loops form in cells and could serve a function at the immunoglobulin class switch region, this study highlights two additional aspects of R-loop biology. The bisulfite treatment to specifically mark the displaced stand of DNA has been repeatedly used to confirm, and more accurately map, the extent of R-loops. In addition, later research would show that the targeting of the class switch recombination machinery was due to extensive deamination along the exposed single-strand of DNA and subsequent formation of double-stranded breaks (Chaudhuri et al. 2003; Nambu et al. 2003). The link between R-loop formation and DNA damage would soon come to greater attention. Li and Manley published their seminal work demonstrating that loss of the spicing factor protein ASF/SF2 resulted in cell death and quiescence (Li and Manley, 2005). This phenotype was due to high levels of DNA damage that they linked to formation of R-loops (Li and Manley, 2005). Overexpression of RNase H1 was able to suppress this phenotype (Li and Manley, 2005). This work was bolstered by the previous observation that THO complex mutants in yeast resulted in DNA damage (Huertas and Aguilera, 2003).

These works demonstrated important biology behind R-loop formation. In *trans*, R-loop formation is thought to occur more easily in underwound DNA, where the RNA molecule can invade and displace the two strands of DNA (Toriumi et al. 2013). In *cis*, where cotranscriptional R-loops form, R-loop formation is slightly more complicated. Transient RNA:DNA hybrids form at the site of active transcription within the RNA polymerases (Nudler et al. 1997; Daube and von Hippel 1994). However, work in bacteria and T4 systems had previously demonstrated that extensive R-loop formation occurs after the nascent transcript has exited the polymerase where it reanneals back to still accessible single-stranded DNA (Roy and Lieber 2009). This is referred to as a *cis* R-loop. The propensity of RNA processing and splicing factors to suppress R-loop formation is thought to be a result of these factors ability to bind the nascent transcript and prevent it from reannealing to the DNA (Sollier and Cimprich, 2015). Separately, the nucleotide sequence of the displaced strand also impacts the propensity to form R-loops. For example, transcription from the sense but not the antisense direction of the class-switch region forms R-loops *in vitro* (Yu et al. 2003). The ability of the displaced single strand of DNA to form secondary structures strongly impacts R-loop formation (Belotserkovskii et al. 2010, 2017). If the non-template strand at the transcription bubble forms a G-quadruplex, a common DNA secondary structure formed by repetitive guanines, it can be stabilized and fail to quickly reform duplex DNA (de Magis et al. 2019). This exposes the template strand and allows the RNA to reanneal, forming an R-loop.

With the advent of next generation sequencing, it has become apparent that many diseases and cancers have recurrent mutations in RNA processing factors (Dvinge et al. 2016). The recent fascination with R-loops as a potential driver for oncogenesis and

genome instability arises partially from these findings. However, the question of how R-loops cause such dramatic DNA damage has not been completely defined, though recent research has provided valuable insight. There are thought to be two main types of DNA damage that result from R-loop formation (Fig. 1-3E). The major type has been found to be S phase dependent and seems to occur where a replication fork and R-loop meet (Gan et al. 2011). By combining estrogen-inducible transcription with flow cytometry to determine the cell cycle, widescale R-loop induced damage only occurred during S phase when replication forks would be active (Stork et al. 2016). Extensive work in bacteria and metazoan systems has linked how precisely the interplay between replication and transcription and how it can cause DNA damage.

The less severe class of genomic instability arises solely from the existence of the R-loop and potentially damage to the displaced single-strand of DNA (Beletskii and Bhagwat, 1996; Kim and Jinks-Robertson, 2012). This can be the result of deamination of the cytosine in cells that express cytosine deaminase or endogenous factors that react with single-strand DNA (Conticello 2008). This results in a specific mutational signature of cytosine to thymidine transitions and other point mutations (Beletskii and Bhagwat, 1996). However, there is compelling research to show that in some cases, this damage can be more extensive. In hyperactive R-loop forming mutants, the activity of transcription-coupled nucleotide excision repair (TC-NER) repair proteins such as XPF and XPG can cause double-strand breaks at R-loop forming sites (Sollier et al. 2014). The mechanism of this activity is thought to be from cleavage of the single-strand DNA at the edges of the R-loop (Sollier et al. 2014). Coupled with breaks in the displaced strand,

this can result in double-strand breaks. However, it is unclear if this phenomenon is coupled to replication or not (Crstini et al. 2019).

The orientation of both the replication fork and the transcription complex in R-loop driven DNA damage is important. Conflicts between replication and transcription can occur both co-directionally, in which the replication fork progresses in the same direction as the transcription complex, or head-on where the two complexes collide. Work in bacteria engineered to transcribe ribosomal RNA either codirectionally or in the head-on orientation with respect to the origin of replication demonstrated that only transcription in the head-on orientation resulted in a delay of the replication fork (French 1992). Bacterial genomes are generally arranged to minimize head-on conflicts between transcription and replication, though there are exceptions such as genes associated with stress survival (Rocha, 2008, Merrikh 2017). It is hypothesized that the head-on orientation for transcription associated with these loci is to encourage DNA damage and therefore increased mutagenesis to promote adaption to stress (Merrikh and Merrikh, 2018). Additional work by the Merrikh lab linked the formation of R-loops specifically with head-on conflicts (Lang et al. 2017). Importantly, expression of RNase H III allowed for these conflicts to be resolved, as measured by lack of DNA damage and normal gene expression indicating that the R-loop, not the transcription machinery is responsible for the damage (Lang et al. 2017). One thing that is not clear is how R-loop formation occurs in these conflicts. Presumably, a stalled RNA polymerase allows for a permissive environment for R-loop formation. Active transcription is known to cause positive DNA supercoiling in front of the polymerase, and negative supercoiling behind it (Liu and Wang, 1987; Wu et al. 1988). The unwinding of DNA during replication also generates

positive supercoiling in front of the replication fork (Vos et al. 2011). This torsional stress could alter the dynamics at both the stalled replication fork and RNA polymerase machinery, allowing a more permissive environment for R-loops to form and change the stability of replication and transcription proteins on DNA. In this scenario, the resolution of R-loops would be required to allow the proper release of torsional stress. This model is supported by multiple lines of evidence demonstrating that topoisomerases are associated with R-loop formation and resolution (Lang and Merrikh, 2021; Manzo et al. 2018; Promonet et al. 2020).

The evidence for DNA damage due to replication-transcription conflicts in metazoans is also compelling. Common fragile sites are loci that frequently exhibit chromosomal instability (Debatisse et al. 2012). This damage is frequently transcription dependent (Debatisse et al. 2012). Common fragile sites are frequently found at long and/or highly transcribed genes, where transcription of a single gene may take an entire cell cycle (Helmrich et al. 2011). It has become apparent that directionality also plays an important role in metazoans. In yeast, plasmids undergo recombination when transcription occurs only in the head-on direction (Prado and Aguilera, 2005). Using an episomal system, Hamperl et al. demonstrated that head-on but not codirectional conflicts resulted in increased R-loop levels (Hamperl et al. 2017). By combining R-loop mapping data and Okazaki fragment sequencing data (OK-seq), which allows one to determine the directionality of the replication fork, R-loops were found to occur more frequently in head-on collisions. Importantly, greater R-loop-dependent DNA damage occurs by perturbing the normal replication program (Hamperl et al. 2017). Head-on collisions also activate the ATR DNA damage checkpoint, which often occurs at slowed or stalled replication forks.

It is important to note that not all codirectional conflicts are without damage. In bacteria with deficient transcript termination and translation, codirectional conflicts are also capable of forming double-strand breaks (Dutta et al. 2011). In eukaryotes, codirectional conflicts results in elevated activation of ATM, a DNA damage marker normally associated with double-strand breaks (Hamperl et al. 2017; Lee and Paull 2021). This activation may be due to very rare but damaging codirectional conflicts. It is not clear if this is the case or what factor(s) may precipitate these events if they do occur. Alternatively, it has been hypothesized that activation of ATM results in alternative splicing and transcription of DNA damage response genes and/or spliceosome components in order to help resolve R-loops (Tresini et al. 2016). In summary, conflicts between replication and transcription are an important source of genome instability. When they occur in the head-on orientation, they result in increased R-loop formation and DNA damage. Codirectional conflicts frequently, though not always, result in decreased R-loop levels and little to no DNA damage.

In addition to their roles in causing DNA damage, RNA:DNA hybrids also function to sense DNA damage and repair it. Work by the Zou group has demonstrated that RPA, a single-stranded DNA binding protein, is capable of binding the displaced DNA strand of an R-loop (Nguyen et al. 2017). This interaction is important for the recruitment of RNase H1 to resolve R-loops (Nguyen et al. 2017). The Zou group also showed that the ATR pathway can be activated during mitosis and this activation is dependent on R-loops (Kabeche et al. 2018). R-loop-dependent activation of ATR is dependent on Aurora A kinase, but how precisely ATR is activated by R-loops is still unknown. It appears to be via a separate mechanism than how ATR is normally activated, which normally occurs

via binding of RPA to single-stranded DNA and recruitment of the Rad9-Hus1-Rad1 complex to resected 3' DNA ends (Saldivar et al. 2017).

R-loops also serve important roles in the repair of double-stranded breaks (Fig. 1-3D) (DSB). The role of small non-coding RNAs generated by the DROSHA and DICER pathways had been previously linked to repair of DSB and activation of the DNA damage response (Francia et al. 2012). DRIP-ChIP and yeast genetics were combined with an inducible DSB system to probe whether R-loops form at DSBs. R-loops were shown to form at the induced site and manipulation of RNase H levels to stabilize or degrade R-loops resulted in repair defects (Ohle et al. 2016). Overexpression of RNase H led to excessive resection at DSBs, while loss of RNase H led to impaired RPA binding, slower repair, and increased chromosomal recombination (Keskin et al. 2014; Ohle et al. 2016). Later work suggested a role for R-loops in stimulating homologous recombination at DSBs in mitosis and meiosis (Ouyang et al. 2021; Yang et al. 2021). It has been hypothesized that, in addition to controlling recruitment of RPA and resection at DSBs, R-loops may play a role in guiding DSB repair factors to DSBs (D'Alessandro et al. 2018). R-loops that form at DSBs appear to form in *cis* via permissive transcription of the ssDNA, and RNA polymerase II is found at these sites (Ohle et al. 2016). However, both human and yeast Rad52, an important protein involved with DSB repair and homologous recombination, has been shown to catalyze formation of RNA:DNA hybrids *in vitro* (Keskin et al. 2014). It is therefore unclear if the R-loops at DSBs form in *cis, trans*, or some combination thereof. More research will be necessary to understand how, precisely, R-loops promote effective DSB repair, but it is clear they serve an important function.

R-loops have been linked to numerous human pathologies. The tumor suppressors BRCA1 and BRCA2 have been implicated in R-loop resolution (Racca et al. 2021; Bhatia et al. 2014). Components of the Fanconi-Anemia complex have also been linked to R-loop resolution (García-Rubio et al. 2015). Beyond tumorigenesis and genome stability, R-loops have been linked to a variety of neurodegenerative disorders. In cell lines derived from Friedreich's ataxia patients, R-loops have been shown to form at trinucleotide repeats and cause transcriptional silencing (Groh et al. 2014). Similarly, R-loops have been found at the promoter regions of FMR1 and may also cause gene silencing (Colak et al. 2014). Senataxin mutants have been an important tool to study R-loops as it was one of the first proteins found to unwind R-loops (Skourti-Stathaki et al. 2011). These mutations are also found in patients with oculomotor apraxia type 2 (AOA2) and amyotrophic lateral sclerosis type 4 (ALS4) (Groh et al. 2017). The recurrent findings of R-loops associated with human disease underscores the importance of understanding R-loops.

The advent of next-generation sequencing and the rediscovery of the S9.6 antibody, which specifically binds to the RNA:DNA moiety in an R-loop, recontextualized R-loop formation and abundance in the eukaryotic genome. Work done by the Chédin lab established DNA:RNA immunoprecipitation sequencing (DRIP-seq) and demonstrated that instead of being a rare byproduct of transcription, R-loops form at thousands of sites across the mammalian genome, occupying over 5% of the genome (Ginno et al. 2012). In the years since, R-loop mapping studies in bacteria, yeast, plants, insects and mammals demonstrated consistently high levels of R-loop formation, ranging from 5-10% of the mappable genome (Santos-Pereira and Aguilera, 2015; Dumelie and Jaffrey 2018;

Wahba and Koshland et al. 2016; Fang and Zhang et al. 2019; Xu and Sun et al. 2017; Yan and Liu et al. 2020; Zeller and Gasser et al. 2016; Chen and Fu et al. 2017; Chen and Fazzio et al. 2015; Crossley and Cimprich et al. 2020; Ginno and Chédin et al. 2012; Tan-Wong and Proudfoot et al. 2019; Chan and Hieter et al. 2014; Liu and Han et al. 2021). The presence of R-loops in all these species led to a new and deeper understanding of the regulatory functions of R-loops across the genome and where R-loops are prone to forming.

R-loops are most frequently found at the promoter, the 5'UTR, TSS, TTS and 3' UTR of genes (Sanz et al. 2016). Though they seem more likely to form in highly transcribed genes, especially the ribosomal DNA locus, high transcription is not a requirement (Sanz et al. 2016). R-loops are frequently found from the beginning of the 5' UTR and up to the first intron of genes (Sanz et al. 2016). They can also form across entire gene bodies in highly transcribed genes without introns (Sanz et al. 2016). In fact, insertion of introns into R-loop forming genes showed that recruitment of the splicing machinery reduced overall R-loop levels (Bonnet et al. 2017). R-loops also seem to form at sites of repetitive DNA such as centromeres and satellite DNA (Sanz et al. 2016; Zeng et al. 2021). This finding seemed surprising, as these sites are often thought of as transcriptionally repressed, and the function of R-loops at these sites is not well understood.

Though R-loops form throughout the genome, why they form and what their function is at each site varies. Since R-loops were first mapped in mammalian cells, their properties and genome-wide positions have been best characterized in mammals (Ginno et al. 2012). Perhaps the most well understood sites of R-loop formation is at promoters

and transcription start sites, where the CpG skew provides an ideal environment for stabilization of the displaced ssDNA due to secondary structures and reinvasion of the RNA to form R-loops (Fig. 1-3B) (Ginno et al. 2013). R-loops at these sites fall into two main types: TSS anchored that form across the promoter and through the TSS, and R-loop anchored that begin downstream of the transcription start site (TSS) in the exon and extend to the first intron (Chédin 2016). TSS anchored R-loops are characterized by chromatin that is highly accessible, histone modifications associated with active transcription such as H3K4me2/3, H3K9ac, and H3K27ac, and tend to have unmethylated promoters (Chédin 2016). At R-loop anchored regions, pausing of the RNA polymerase is more common and histone modifications are enriched for H3K36me and H3K4me1 (Chédin 2016). In contrast, R-loops at transcription termination sites (TTS) are enriched for repressive histone modifications such as H3K9me2 (Skourti-Stathaki et al. 2014). At TTS, R-loops seem to play a role in halting the RNA polymerase and causing transcript termination as well (Fig. 1-3C) (Skourti-Stathaki et al. 2011; Proudfoot 2016). Similarly, R-loops at repetitive elements are also associated with repressive histone modification (Nadel et al. 2015). The question of whether R-loops are more likely to form at sites of these chromatin markers and certain chromatin associated factors or whether they help establish the epigenetic environment around them is a question of vital importance to the field.

At promoters, R-loops prevent methylation of DNA. *In vitro* studies examining the binding of DNMT1 and DNMT3a/b, the maintenance and *de novo* DNA methyltransferases, respectively, demonstrated that they cannot efficiently bind to R-loops (Ross et al. 2010). Later work examining *Senataxin* hyperactive mutants that

decrease R-loops genome-wide had increased DNA methylation at hundreds of genes with concomitant gene silencing (Grunseich et al. 2018). Even in this seemingly clearcut case, however, there may be interplay between R-loop formation and the epigenetic landscape. Loss of the TET family of the enzymes, responsible for demethylating DNA, causes decreased R-loop formation without changes in transcription (Sabino et al. 2022). Conversely, tethering of a TET enzyme to a specific locus increases R-loop formation (Sabino et al. 2022). The authors hypothesize that 5hmC, an intermediate of the demethylation of cytosine (5mC), may promote R-loop formation and lend credence to this idea with *in vitro* assays (Sabino et al. 2022). This dynamic exchange between R-loop formation and DNA methylation, where a seemingly simple blockage of a protein by an R-loop becomes more complex with further investigation, highlights the difficulty in interpreting the causative role of R-loops in establishing the epigenetic landscape.

What is the evidence that R-loops modify the chromatin in their environment? Degradation of R-loops directly impacts the binding of PRC2 and Tip60-p400 and alters the histone markers at specifically at R-loop sites (Chen et al. 2015). Both proteins have biochemical evidence that they can interact with the nascent RNA of an R-loop (Guttman et al. 2011; Alecki et al. 2020). Additionally, a screen using histone mutants in yeast linked R-loop formation to H3S10P and chromatin compaction (Castellano-Pozo et al. 2013).

However, other evidence is much more corollary. H3K4me3 is enriched at promoters and the H3K4me3 methyltransferase SET1/COMPASS can theoretically bind to the single strand of an R-loop (Krajewski et al. 2005). Binding for PAF1 and LSD1, a histone methyltransferase and demethylase, respectively, are enriched at R-loops (Sanz et al. 2016; Pinter et al. 2021). A combination of mining of deposited ChIP-seq data and

new mass spectrometry screens for R-loop interacting proteins has revealed a plethora of potential candidates that could be recruited to R-loops and modify the chromatin (Sanz et al. 2016; Cristini et al. 2018; Wang et al. 2018; Mosler et al. 2021). While many of these interactions will be validated, there will undoubtedly be false positives. In addition, how the correct histone modifying proteins are recruited to R-loops at different regions despite their similar structure is entirely unknown.

It is also not fully understood which aspects of R-loop formation are universal or species specific. For example, yeast are much more likely to form R-loops over polyA tracts than other species (Wahba et al. 2016). In plants, antisense R-loops are more common and have been studied as important determinant of gene repression (Xu et al. 2017). For example, formation of R-loops at the promoter of COOLAIR causes transcriptional repression (Sun et al. 2013). In maize, extensive R-loop formation occurs at centromeres (Liu et al. 2021). R-loops formed from circular RNA help establish chromatin loops and cause deposition of CENH3, the centromeric H3 variant (Liu et al. 2020). While R-loops may serve similar functions in other species, as of now it is unknown.

In my thesis, I have conducted research examining how DNA replication is alternatively regulated during development. I identified a new function for the Rif1 protein controlling replication fork progression during underreplication and gene amplification. Quantitative mass spectrometry was performed of replication forks during Drosophila embryogenesis to identify their components. Finally, I adapted a technique to map R-loops during Drosophila embryogenesis. This work expanded our knowledge of the factors associated with R-loops formation and how they change during development.

Chapter II: Rif1 inhibits replication fork progression and controls DNA copy number in Drosophila

Abstract

Control of DNA copy number is essential to maintain genome stability and ensure proper cell and tissue function. In *Drosophila* polyploid cells, the SNF2-domain-containing SUUR protein inhibits replication fork progression within specific regions of the genome to promote DNA underreplication. While dissecting the function of SUUR's SNF2 domain, we identified an interaction between SUUR and Rif1. Rif1 has many roles in DNA metabolism and regulates the replication timing program. We demonstrate that repression of DNA replication is dependent on Rif1. Rif1 localizes to active replication forks in a partially SUUR-dependent manner and directly regulates replication fork progression. Importantly, SUUR associates with replication forks in the absence of Rif1, indicating that Rif1 acts downstream of SUUR to inhibit fork progression. Our findings uncover an unrecognized function of the Rif1 protein as a regulator of replication fork progression.

* This chapter has been published as Munden, A., Rong, Z., Sun, A., Gangula, R., Mallal, S. & Nordman, J. T. Rif1 inhibits replication fork progression and controls DNA copy number in Drosophila. *Elife* **7,** e39140 (2018).

Introduction

Accurate duplication of a cell's genetic information is essential to maintain genome stability. Proper regulation of DNA replication is necessary to prevent mutations and other chromosome aberrations that are associated with cancer and developmental abnormalities (Jackson et al., 2014). DNA replication begins at thousands of cis-acting sites termed origins of replication. The Origin Recognition Complex (ORC) binds to replication origins where, together with Cdt1 and Cdc6, it loads an inactive form of the MCM2-7 replicative helicase (Bell and Labib, 2016). Inactive helicases are phosphorylated by two key kinases, S-CDK and Dbf4-dependent kinase (DDK), which results in the activation of the helicase and recruitment of additional factors to form a pair of bi-directional replication forks emanating outward from the origin of replication (Siddiqui et al., 2013). Although many layers of regulation control the initiation of DNA replication, much less is known about how replication fork progression is regulated.

In metazoans, replication origins are not sequence specific and are likely specified by a combination of epigenetic and structural features (Aggarwal and Calvi, 2004; Cayrou et al., 2011; Eaton et al., 2011; Mesner et al., 2011; Miotto et al., 2016; Remus et al., 2004). Furthermore, replication origins are not uniformly distributed throughout the genome. The result of non-uniform origin distribution is that, in origin-poor regions of the genome, a single replication fork must travel great distances to complete replication. If a replication fork encounters an impediment within a large origin-less region of the genome, then replication will be incomplete, resulting in genome instability (Newman et al., 2013). In fact, origin-poor regions of the genome are known to be associated with chromosome fragility and genome instability (Debatisse et al., 2012; Durkin and Glover, 2007; Letessier

et al., 2011; Norio et al., 2005). This highlights the need to regulate both the initiation and elongation phases of DNA replication to maintain genome stability.

DNA replication is also regulated in a temporal manner where specific DNA sequences replicate at precise times during S phase, a process known as the DNA replication timing program. While euchromatin replicates in the early part of S phase, heterochromatin and other repressive chromatin types replicate in the latter portion of S phase (Gilbert, 2002; Rhind and Gilbert, 2013). Although the process of replication timing has been appreciated for many years, the underlying molecular mechanisms controlling timing have remained elusive. The discovery of factors that regulate the DNA replication timing program, however, demonstrate that replication timing is an actively regulated process.

One factor that regulates replication timing from yeast to humans is Rif1 (Rap1-interacting factor 1). Rif1 was initially identified as a regulator of telomere length in budding yeast (Hardy et al., 1992), but this function of Rif1 appears to be specific to yeast (Xu et al., 2004). Subsequently, Rif1 has been shown to regulate multiple aspects of DNA replication and repair. In mammalian cells, Rif1 has been shown to regulate DNA repair pathway choice by preventing resection of double-strand breaks and favoring non-homologous end joining (NHEJ) over homologous recombination (Chapman et al., 2013; Di Virgilio et al., 2013; Zimmermann et al., 2013). Rif1 from multiple organisms contains a Protein Phosphatase 1 (PP1) interaction motif and Rif1 is able to recruit PP1 to DDK-activated helicases to inactive them and prevent initiation of replication (Davé et al., 2014; Hiraga et al., 2014; Hiraga et al., 2017).

In yeasts, flies and mammalian cells, Rif1 has been shown to regulate the replication timing program (Cornacchia et al., 2012; Hayano et al., 2012; Peace et al., 2014; Sreesankar et al., 2015; Yamazaki et al., 2012). The precise mechanism(s) through which Rif1 functions to control replication timing are not fully understood. For example, Rif1 has been shown to interact with Lamin and is thought to tether specific regions of the genome to the nuclear periphery (Foti et al., 2016). How this activity is related to Rif1's ability to inactivate helicases together with PP1 in controlling the timing program remains obscure.

Studying DNA replication in the context of development provides a powerful method to understand how DNA replication is regulated both spatially and temporally. Although DNA replication is a highly ordered process, it must be flexible enough to accommodate the changes in S phase length and cell cycle parameters that occur as cells differentiate (Matson et al., 2017). For example, during *Drosophila* development the length of S phase can vary from ~8 hr in a differentiated mitotic cell to 3 – 4 min during early embryonic cell cycles (Blumenthal et al., 1974; Spradling and Orr-Weaver, 1987). Additionally, many tissues and cell types in *Drosophila* are polyploid, having multiple copies of the genome in a single cell (Edgar and Orr-Weaver, 2001; Lilly and Duronio, 2005; Zielke et al., 2013).

In polyploid cells, copy number is not always uniform throughout the genome (Rudkin, 1969; Hua and Orr-Weaver, 2017; Spradling and Orr-Weaver, 1987). Both heterochromatin and several euchromatic regions of the genome have reduced DNA copy number relative to overall ploidy (Nordman et al., 2011). Underreplicated euchromatic regions of the genome share key features with common fragile sites in that they are

devoid of replication origins, late replicating, display DNA damage and are tissue-specific (Andreyeva et al., 2008; Nordman et al., 2014; Sher et al., 2012; Yarosh and Spradling, 2014). The presence of underreplication is conserved in mammalian cells, but the mechanism(s) mammalian cells use to promote underreplication is unknown (Hannibal et al., 2014). In *Drosophila*, underreplication is an active process that is largely dependent on the distribution of ORC and on the Suppressor of Underreplication protein, SUUR (Hua et al., 2018; Makunin et al., 2002; Nordman and Orr-Weaver, 2015).

Understanding how the SUUR protein functions will significantly increase our understanding of the developmental control of DNA replication. The SUUR protein has a recognizable SNF2-like chromatin remodeling domain at its N-terminus, but based on sequence analysis, this domain is predicted to be defective for ATP binding and hydrolysis (Makunin et al., 2002; Nordman and Orr-Weaver, 2015). Outside of the SNF2 domain, SUUR has no recognizable motifs or domains, which has hampered a mechanistic understanding of how SUUR promotes underreplication. Recently, however, SUUR was shown to control copy number by directly reducing replication fork progression (Nordman et al., 2014). SUUR associates with active replication forks and while loss of SUUR function results in increased replication fork progression, overexpression of SUUR drastically inhibits fork progression without affecting origin firing (Nordman et al., 2014; Sher et al., 2012). These findings, together with previous work showing that loss of SUUR function has no influence on ORC binding (Sher et al., 2012) and that SUUR associates with euchromatin in an S phase-dependent manner (Kolesnikova et al., 2013), further supports SUUR as a direct inhibitor of replication fork progression within specific regions

of the genome. The mechanism through which SUUR is recruited to replication forks and how it inhibits their progression remains poorly understood.

Here we investigate how SUUR is recruited to replication forks and how it inhibits fork progression. We show that localization of SUUR to replication forks, but not heterochromatin, is dependent on its SNF2 domain. We identify an interaction between SUUR and the conserved replication factor Rif1, indicating they are in the same protein complex. Importantly, we demonstrate that underreplication is dependent on *Rif1*. Critically, we have shown that Rif1 localizes to replication forks in an SUUR-dependent manner, where it acts downstream of SUUR to control replication fork progression. Our findings provide mechanistic insight into the process of underreplication and define a new function for Rif1 in replication control.

Results

The SNF2 domain is essential for SUUR function and replication fork localization

As a first step in understanding the mechanism of SUUR function, we wanted to define how it is localized to replication forks. SUUR has only one conserved domain: a SNF2-like domain in its N-terminal region that is predicted to be defective for ATP binding and hydrolysis (Makunin et al., 2002; Nordman and Orr-Weaver, 2015). To study the function of SUUR's SNF2 domain, we generated a mutant in which the SNF2 domain was deleted and the resulting mutant protein was expressed under the control of the endogenous *SuUR* promoter. This mutant, $SuUR^{\Delta SNF}$, was then crossed to an *SuUR* null mutant so that it was the only form of the SUUR protein present (Figure 2-1A). We tested the function of the $SuUR^{\Delta SNF}$ mutant protein by assessing its ability to promote

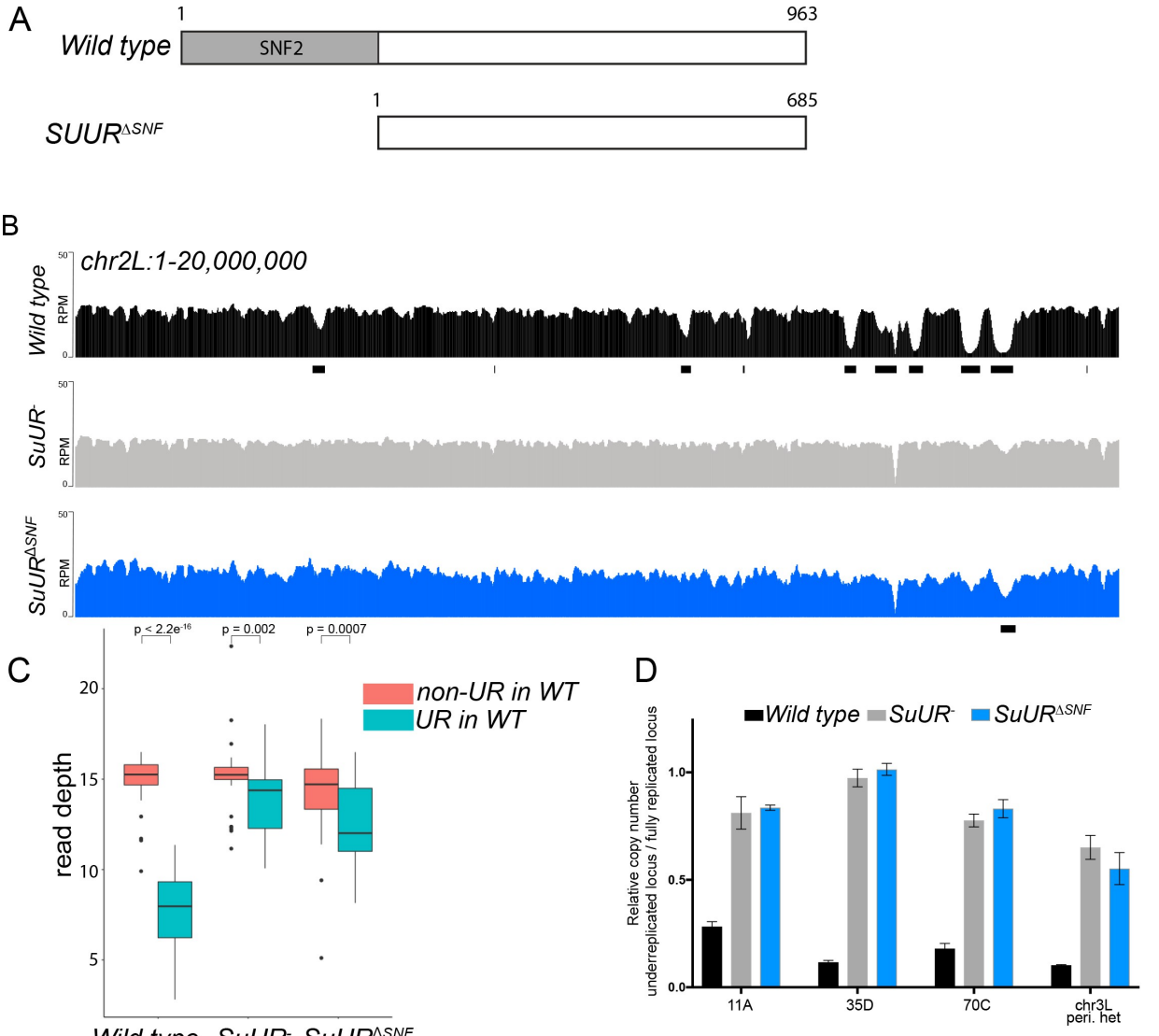

A
Wild type
1
963
SNF2
SUUR^ΔSNF
1
685
B
chr2L:1-20,000,000
Wild type
SuUR-
SuUR^ΔSNF
RPM
C
p < 2.2e-16
p = 0.002
p = 0.0007
non-UR in WT
UR in WT
read depth
Wild type
SuUR-
SuUR^ΔSNF
D
Wild type
SuUR-
SuUR^ΔSNF
Relative copy number
underreplicated locus / fully replicated locus
11A
35D
70C
chr3L
peri. het
E
DAPI
anti-SUUR
EdU
MERGE
Wild type
SuUR^ΔSNF

Figure 2-1: **The SNF2 domain is essential for SUUR function and replication fork localization.** (**A**) Schematic representation of the SUUR and SUUR$^{\Delta SNF}$ proteins. (**B**) Illumina-based copy number profiles (Reads Per Million; RPM) of *chr2L* 1 – 20,000,000 from larval salivary glands. Black bars below each profile represent underreplicated regions identified by CNVnator. (**C**) Average read depth in regions of euchromatic underreplication domains called in wild-type salivary glands vs. the fully replicated regions of the genome. A Welch Two Sample t-test was used to determine p values. (**D**) Quantitative droplet-digital PCR (ddPCR) copy number assay for multiple underreplicated regions. Each bar is the average enrichment relative to a fully replicated control region for three biological replicates. Error bars are the SEM. (**E**) Localization of SUUR in wild-type and *SuUR*$^{\Delta SNF}$ mutant follicle cells. A single representative stage 13 follicle cell nucleus is shown. Arrowheads indicate sites of amplification. Asterisk marks the chromocenter (heterochromatin). Scale bars are 2 μm. DAPI = blue, SUUR = green, EdU = red. Contributions: Analysis and visualization of data in B and C.

underreplication in the larval salivary gland. We purified genomic DNA from larval salivary glands isolated from wandering third instar larvae and generated genome-wide copy number profiles using Illumina-based sequencing. We compared the results we obtained from the *SuUR*$^{\Delta SNF}$ mutant to copy number profiles from wild-type (WT) and *SuUR* null mutant salivary glands. To identify underreplicated domains, we used CNVnator, which identifies copy number variants (CNVs) based on a statistical analysis of read depth (Abyzov et al., 2011). To be called as underreplicated, regions must not be called as underreplicated in 0 – 2 hr embryo samples that have uniform copy number and must be larger than 10 kb.

The effect of deleting the SNF2 domain was qualitatively and quantitatively similar to the *SuUR* null mutant. Qualitatively, underreplication was suppressed in the *SuUR*$^{\Delta SNF}$ mutant and the copy number profile was similar to the *SuUR* null mutant (Figure 2-1B, Supplemental Figure 2-1). Quantitatively, out of the 90 underreplicated sites identified in

WT salivary glands, 59 were not detected in the *SuUR*$^{\Delta SNF}$ mutant (Supplementary Table 2-1) and copy number was significantly increased in the euchromatic underreplicated domains similar to the *SuUR* null mutant (Figure 2-1C). We validated our deep-sequencing findings using quantitative droplet digital PCR (ddPCR) at four underreplicated domains (Figure 2-1D). Our findings show that the SNF2-like domain of SUUR is necessary to promote underreplication.

To determine if the SuUR$^{\Delta SNF}$ protein was still able to associate with chromatin, we localized SuUR and the SuUR$^{\Delta SNF}$ mutant proteins in ovarian follicle cells. During follicle cell development, these cells undergo programmed changes in their cell cycle and DNA replication programs (Claycomb and Orr-Weaver, 2005; Hua and Orr-Weaver, 2017). At a precise time in their differentiation program, follicle cells cease genomic replication and amplify six defined sites of their genome through a re-replication-based mechanism. Early in this gene amplification process, both initiation and elongation phases of replication are coupled. Later in the process, however, initiation no longer occurs and active replication forks can be visualized by pulsing amplifying follicle cells with 5-ethynyl-2'-deoxyuridine (EdU) (Claycomb et al., 2002). Active replication forks resolve into a double-bar structure, where each bar represents a series of active replication forks travelling away from the origin of replication (Claycomb and Orr-Weaver, 2005). By monitoring SuUR localization in amplifying follicle cells, we can unambiguously determine if SuUR associates with active replication forks.

SuUR has two distinct modes of chromatin association during the endo cycle. It constitutively localizes to heterochromatin and dynamically associates with replication forks (Kolesnikova et al., 2013; Nordman et al., 2014; Swenson et al., 2016). In agreement

with previous studies, SUUR localized to both replication forks and heterochromatin in amplifying follicle cells (Figure 2-1E) (Nordman et al., 2014). In contrast, the SuUR$^{\Delta SNF}$ mutant localized to heterochromatin, but its recruitment to active replication forks was severely reduced (Figure 2-1E; Supplemental Figure 2-2). Together, these results demonstrate that the SNF2 domain is important for SUUR recruitment to replication forks and is essential for SUUR-mediated underreplication.

SUUR associates with Rif1

Interestingly, overexpression of the SNF2 domain and C-terminal portion of SUUR have different underreplication phenotypes. Whereas overexpression of the C-terminal two-thirds of SUUR promotes underreplication (Kolesnikova et al., 2005), overexpression of the SNF2 domain suppresses underreplication in the presence of endogenous SUUR (Kolesnikova et al., 2005). The C-terminal region of SUUR, however, has no detectable homology or conserved domains (Makunin et al., 2002). These observations, together with our own results demonstrating that the SNF2 domain of SUUR is responsible for its localization to replication forks, led us to hypothesize that SUUR is recruited to replication forks through its SNF2 domain where it could recruit an additional factor(s) through its C-terminus to inhibit replication fork progression.

To test the hypothesis that a critical factor interacts with the C-terminal region of SUUR to promote underreplication, we used immunoprecipitation mass spectrometry studies to identify SUUR-interacting proteins. We generated flies that expressed FLAG-tagged full-length SUUR or the SNF2 domain of SUUR under control of the *hsp70* promoter, induced and immunoprecipitated these constructs and identified associated

proteins through mass spectrometry. We verified that both full-length SUUR and the SNF2 domain were expressed equally (Supplemental Figure 2-3B). If SUUR recruits a factor to replication forks outside of its SNF2 domain, then we would expect this factor to be present only in full-length purifications and not in the SNF2 domain purification. A single protein fulfilled this criteria: Rif1 (Figure 2-2A). This result raises the possibility Rif1 works together with SUUR to inhibit replication fork progression.

To ensure that the association between SUUR and Rif1 was not bridged by chromatin, we used NP40 to extract chromatin proteins and treated the extract with Benzonase to digest DNA. We then immunoprecipitated FLAG-SUUR and used Western blotting to determine if Rif1 could co-IP using a highly specific anti-Rif1 antibody (Supplemental Figure 2-4). Even in these conditions, SUUR was able to co-IP Rif1 (Figure 2-2B; Supplemental Figure 2-3A). We conclude that SUUR and Rif1 exist in the same protein complex and the interaction between SUUR and Rif1 is independent of chromatin bridging.

Underreplication is dependent on Rif1

If SUUR recruits Rif1 to replication forks to promote underreplication, then underreplication should be dependent on *Rif1*. To test this hypothesis, we used CRISPR-based mutagenesis to generate *Rif1* null mutants in *Drosophila* (Bassett et al., 2013; Gratz et al., 2013) (Figure 2-3A). Western blot analysis of ovary extracts from two deletion mutants, $Rif1^{1}$ and $Rif1^{2}$, show no detectable Rif1 protein (Supplemental Figure 2-4A). Also, no signal was detected in the $Rif1^{1}/Rif1^{2}$ mutant by immunofluorescence (Supplemental Figure 2-4B). The $Rif1^{1}/Rif1^{2}$ null mutant was viable and fertile showing

A

	Full length SUUR			SNF2 domain			negative control		
	Repl. #1	Repl. #2	Repl. #3	Repl. #1	Repl. #2	Repl. #3	Repl. #1	Repl. #2	Repl. #3
SUUR	36	48	26	21	18	10	1	1	2
Rif1(CG30085)	29	24	14	1	0	0	0	0	0

Comparison of Rif1 abundance*	
Full length vs. SNF2	$p < 0.00010$
Full length vs. neg. ctrl	$p < 0.00010$

*Fisher's Exact Test

B

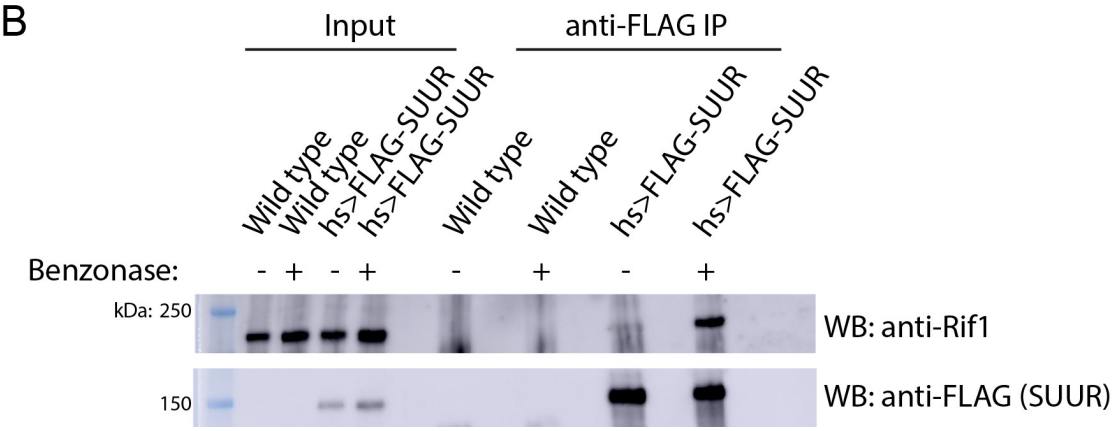


Figure 2-2: **SUUR associates with Rif1.** (**A**) Total spectrum counts of FLAG-SUUR, FLAG-SNF2 and Oregon R (no FLAG control) for three independent IP-mass spectrometry experiments (biological replicates). A Fisher's Exact test of spectrum counts was used to determine significance. (**B**) Immunoprecipitation of FLAG-SUUR and no FLAG control (wild-type) from 0 to 24 hr embryos extracted with NP40 lysis buffer with or without Benzonase treatment. Membranes were probed with anti-Rif1 and anti-FLAG antibodies to monitor Rif1 and SUUR, respectively. Contributions: None.

only a modest defect in embryonic hatch rate relative to wild-type flies with a 92% hatch rate for wild-type embryos vs. 88% for the $Rif1^{1}/Rif^{2}$ mutant embryos (Supplemental Figure 2-4C). This is in contrast to a previous study reporting *Rif1* is essential in *Drosophila* (Sreesankar et al., 2015) and consistent with a recent study that generated an independent *Rif1* null mutant using CRISPR-based mutagenesis (Seller and O'Farrell, 2018). Rif1's essentiality, however, was based on RNAi and not a mutation of the *Rif1*

gene (Sreesankar et al., 2015). The most likely explanation for this discrepancy is that the lethality in the RNAi experiments was due to an off-target effect.

To determine if *Rif1* is necessary for underreplication, we dissected salivary glands from $Rif1^{1}/Rif1^{2}$ (herein referred to as $Rif1^{-}$) heterozygous larvae and extracted genomic DNA for Illumina-based sequencing to measure changes in DNA copy number. Strikingly, underreplication is abolished upon loss of Rif1 function (Figure 2-3B,C; Supplemental Figure 2-5). We validated our sequence-based copy number assays with quantitative PCR at a subset of underreplicated regions using ddPCR (Figure 2-3D). Furthermore, we determined the read density at all euchromatic sites of underreplication called in our wild-type samples, which quantitatively demonstrates that Rif1 is essential for underreplication (Figure 2-3C). These results demonstrate that underreplication is dependent on *Rif1*.

It is possible that the *Rif1* mutant indirectly influences underreplication through changes in replication timing. Underreplicated domains, both euchromatic and heterochromatic, tend to be late replicating regions of the genome (Belyaeva et al., 2012; Makunin et al., 2002). Therefore, if these regions replicated earlier in S phase in a *Rif1* mutant, then this change could prevent their underreplication. In fact, SUUR associates with late replicating regions of the genome (Filion et al., 2010; Pindyurin et al., 2007). Due to their large polyploid nature, salivary gland cells cannot be sorted to perform genome-wide replication timing experiments. Because heterochromatin replicates exclusively in late S phase, however, late replication can be visualized when EdU is incorporated exclusively in regions of heterochromatin. To assess if *Rif1* mutants have a clear pattern of late replication in larval salivary glands, we isolated salivary glands from early 3rd instar larvae, which are actively undergoing endo cycles. We pulsed these salivary glands with

EdU to visualize sites of replication and co-stained with an anti-HP1 antibody to mark heterochromatin. In wild-type salivary glands, only rarely (1 of 238 EdU+ cells; 0.4%) did we detect EdU incorporation in regions of heterochromatin (Supplemental Figure 2-6). This is consistent with the lack of heterochromatin replication due to underreplication. In contrast, in both *SuUR* and *Rif1* mutants, we could readily detect cells that were solely incorporating EdU within regions of heterochromatin (32 of 327 EdU+ cells; 9.8% for *SuUR* and 70 of 385 EdU+ cells; 18.2% for *Rif1*) (Supplemental Figure 2-6). Therefore, we conclude that *Rif1* mutants still have a clear pattern of late replication. Given that heterochromatin underreplication is suppressed in a *Rif1* mutant, although it is still late replicating, indicates that replication timing cannot solely explain the lack of underreplication associated with loss of Rif1 function.

While characterizing Rif1's role in underreplication and patterns of DNA replication in endo cycling cells, we did observe differences in the heterochromatic regions of *SuUR* and *Rif1* mutants. First, although underreplication is suppressed in both mutants (Figure 2-3 and Supplemental Figure 2-5), the chromocenters were abnormally large in the *Rif1* mutant relative to an *SuUR* mutant as observed by DAPI staining consistent with the 'fluffy' enlarged chromocenters seen in Rif1 mutant mouse cells (Supplemental Figure 2-7) (Cornacchia et al., 2012). Although, this phenotype was present in all endo cycling cells, it was especially dramatic in the ovarian nurse cells (Supplemental Figure 2-7). Second, Illumina-based copy number profiles revealed an increase in copy number in some pericentric heterochromatin regions in the *Rif1* mutant relative to the *SuUR* mutant (Supplemental Figure 2-5). Collectively, these results suggest that heterochromatin is partially, but not fully replicated in SuUR mutant endo cycling cells, consistent with

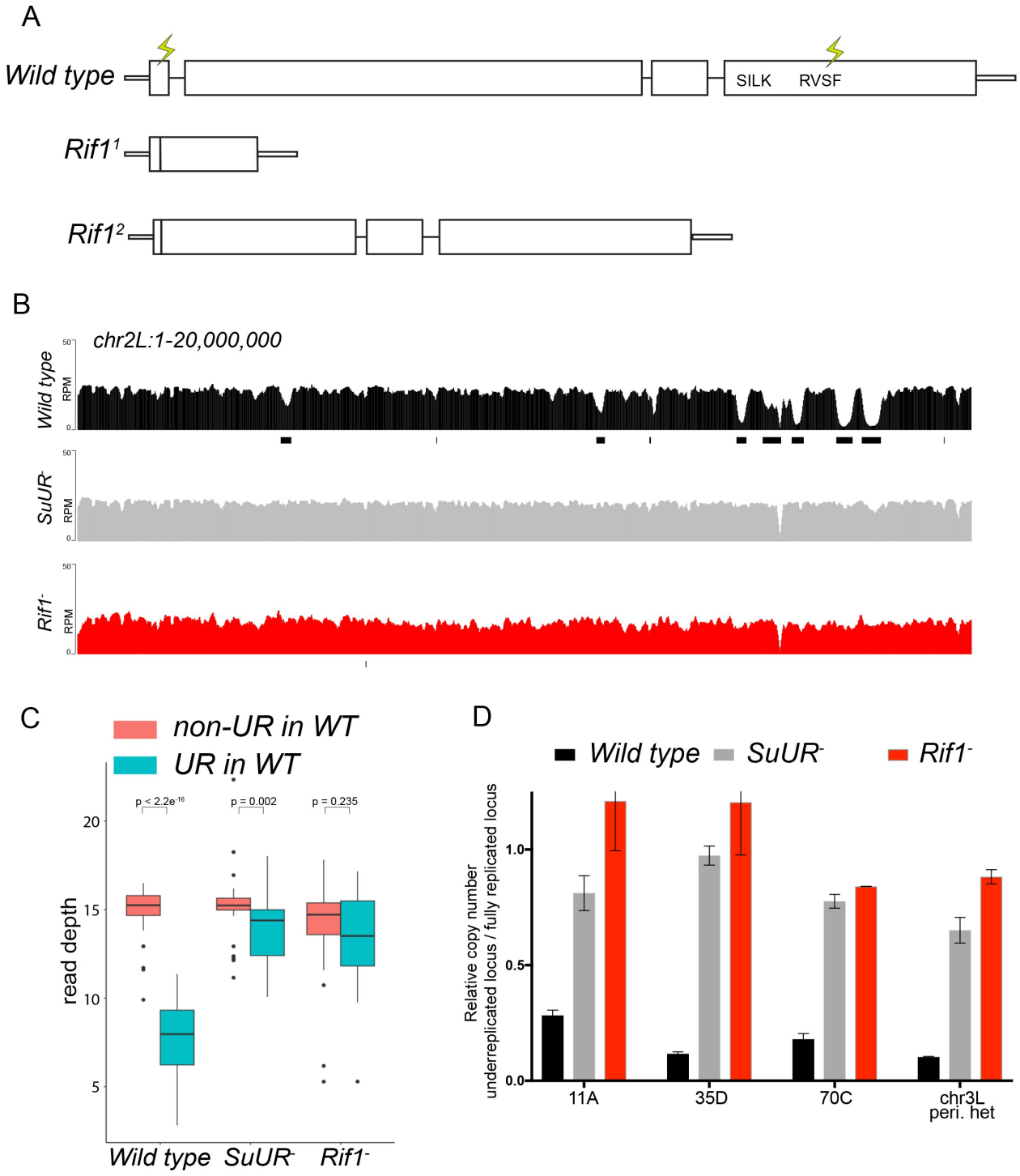


Figure 2-3: **Rif1 is required for underreplication.** (**A**) Schematic representation of the *Rif1* gene and CRISPR-induced *Rif1* mutants. Lightning bolts represent the 5' and 3' gRNA positions. (**B**) Illumina-based copy number profiles of the *chr2L* from larval salivary glands. Black bars below each profile represent underreplicated regions identified by CNVnator. The wild-type and *SuUR* profiles are the same as in Figure 1b. (**C**) Average read depth in regions of euchromatic underreplication domains called in wild-type salivary glands vs. the fully replicated regions of the genome. A Welch Two Sample t-test was used to determine p values. (**D**) Quantitative droplet-digital PCR (ddPCR) copy number assay for multiple underreplicated regions. Each bar is the average enrichment relative to a fully replicated control region for

three biological replicates. Error bars are the SEM. Contributions: Data analysis and visualization for B and C.

previous cytological analysis (Demakova et al., 2007). In contrast, loss of Rif1 function appears to completely restore heterochromatic replication in endo cycling cells.

Rif1 affects replication fork progression

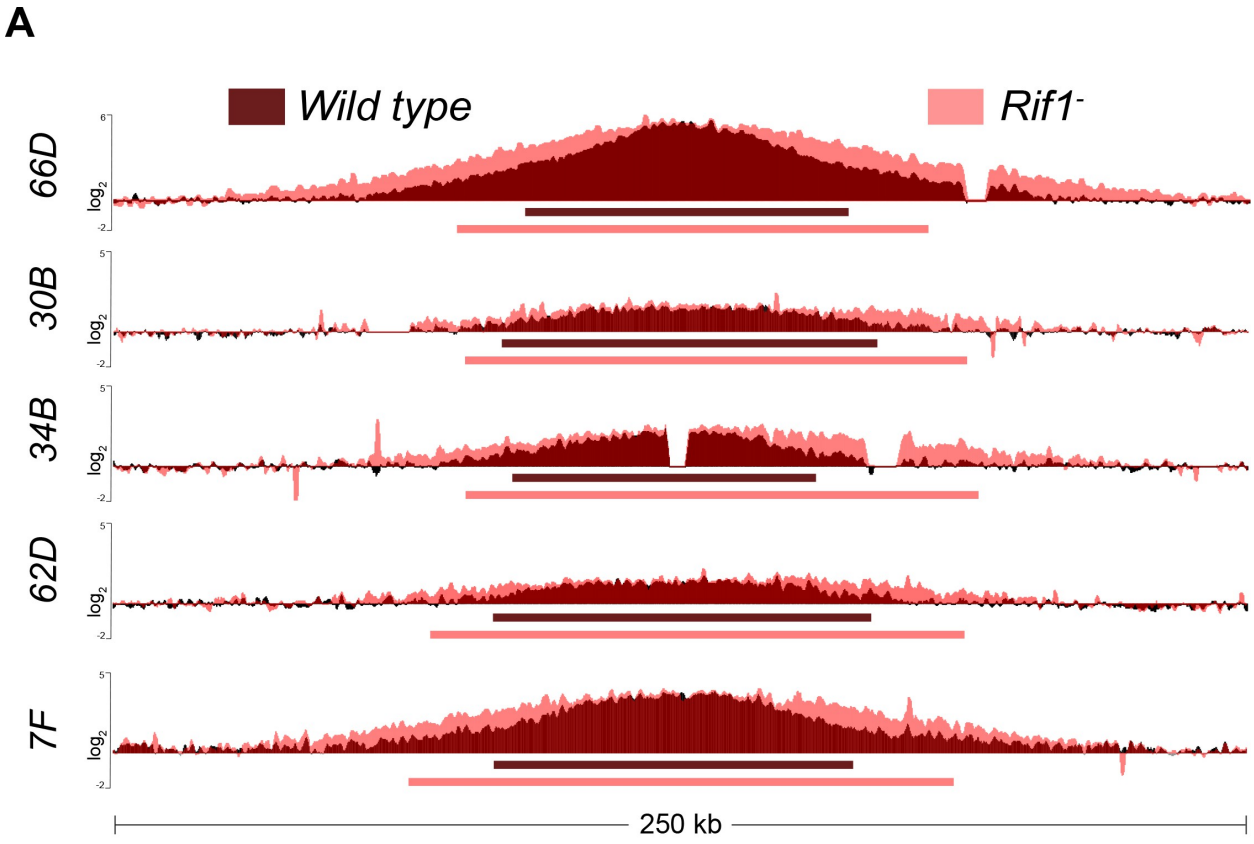
SUUR-mediated underreplication occurs through inhibition of replication fork progression (Nordman et al., 2014; Sher et al., 2012). If SUUR acts together with Rif1 to promote underreplication, then Rif1 is expected to control replication fork progression. DNA combing assays in human and mouse cells from multiple groups have come to different conclusions as to whether Rif1 affects replication fork progression (Alver et al., 2017; Cornacchia et al., 2012; Hiraga et al., 2017; Yamazaki et al., 2012). Rif1, however, has been shown to be associated with replication forks through nascent chromatin capture, an iPOND-like technique used to isolate proteins associated with active replication forks (Alabert et al., 2014). To determine directly if Rif1 controls replication fork progression, we performed copy number assays on amplifying follicle cells.

Gene amplification in ovarian follicle cells occurs at six discrete sites in the genome through a re-replication based mechanism. Copy number profiling of these amplified domains provides a quantitative assessment of the number of rounds of origin firing and the distance replication forks have travelled during the amplification process, allowing us to disentangle the initiation and elongation phases of DNA replication. To determine if Rif1 affects origin firing and/or replication fork progression, we isolated wild-type and *Rif1* mutant stage 13 egg chambers, which represent the end point of the amplification process, and made quantitative DNA copy number measurements. Loss of Rif1 function

resulted in an increase in replication fork progression without significantly affecting copy number at the origin of replication at all sites of amplification (Figure 2-4A). The increase in fork progression observed in the *Rif1* mutant was not due to a lengthening of the developmental time window for gene amplification, as there was no significant difference in egg chamber distribution between wild-type and *Rif1* mutant ovaries (Supplemental Figure 2-8).

To quantify the changes in fork progression we observed at sites of amplification, we computationally determined the peak of amplification and the region on each arm of the amplified domain that represents one half of the copy number at the highest point of the amplicon (Nordman et al., 2014). This quantitative analysis of origin firing and replication fork progression revealed that origin firing was not affected in the *Rif1* mutant, as no major change in copy number was detected at the origin of replication when comparing wild type and *Rif1* mutant stage 13 follicle cells (Supplementary Table 2-2). In contrast, the width of each replication gradient, which represents the rate of fork progression, was significantly increased at all sites of amplification (Figure 2-4A; Supplementary Table 2-2). Based on the observation that the *Rif1* mutant does not affect origin firing, but specifically affects the distance replication forks travel during the gene amplification process, and there was no change in the developmental window of gene amplification in the *Rif1* mutant, we conclude that Rif1 regulates replication fork progression.

Given that the *Rif1* mutant phenocopies an *SuUR* mutant with respect to replication fork progression, we next wanted to determine the cause of increased replication fork progression at amplified loci upon loss of Rif1 function. Previously, it was shown that a


A
Wild type
Rif1-
66D
30B
34B
62D
7F
log2
250 kb

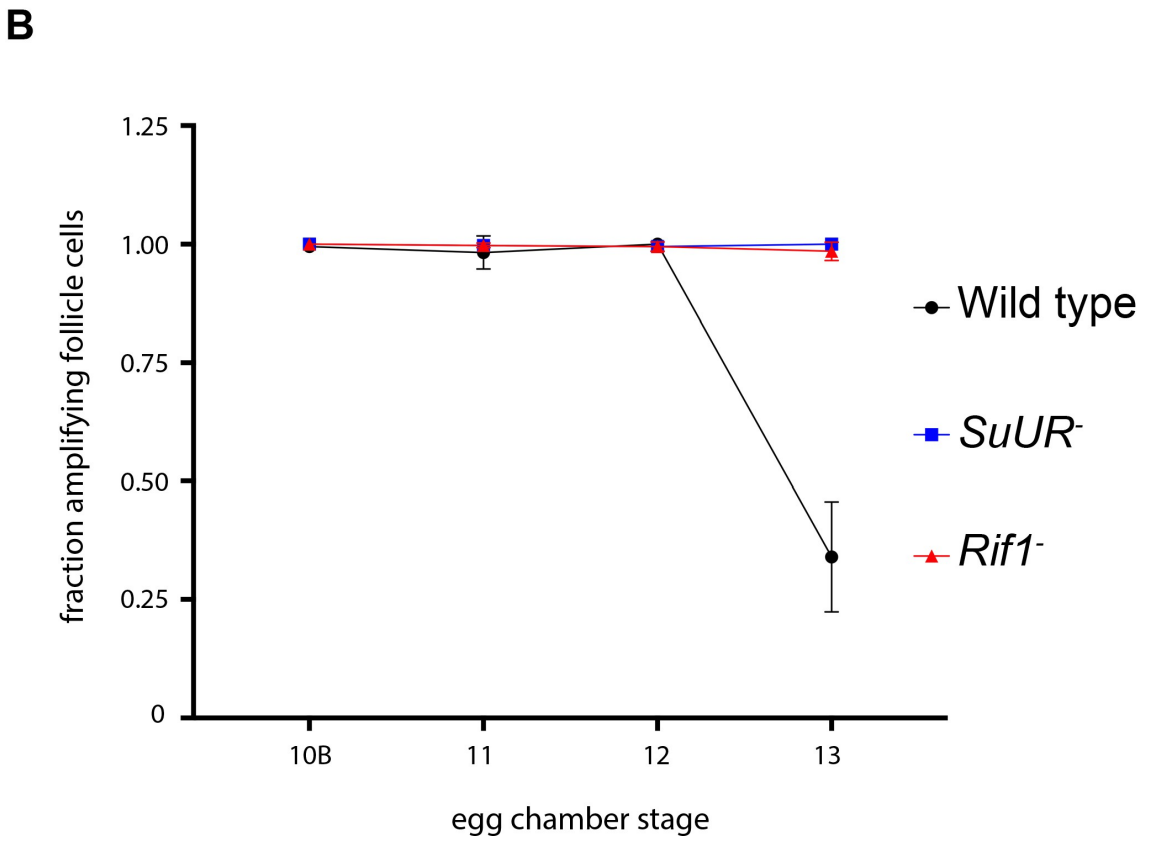

B
fraction amplifying follicle cells
1.25
1.00
0.75
0.50
0.25
0
10B
11
12
13
egg chamber stage
Wild type
SuUR-
Rif1-

Figure 2-4: **Rif1 regulates replication fork progression.** (**A**) Illumina-based copy number profile of sites of follicle cell gene amplification. DNA was extracted from wild type and *Rif1* mutant stage 13 egg chambers and compared to DNA extracted from 0 to 2 hr embryos. The resulting graphs are the $\log_2$-transformed ratios of egg chamber relative to embryonic DNA. Bars below the graphs represent the distance between the half-maximum copy number on each side of the replication origin. (**B**) Fraction of cells that display visible amplification foci in each stage of gene amplification. Average of two biological replicates in which two egg chambers from each stage were used per biological replicate. 100 – 300 follicle cells were counted per genotype. Error bars are the SEM. Contributions: Analysis and visualization for A.

prolonged period of EdU incorporation in the *SuUR* mutant, within the 7.5 hr span of gene amplification, gives rise to the extended replication gradient at sites of amplification (Nordman et al., 2014). Gene amplification starts synchronously in all follicle cells at stage 10B of egg chamber development (Calvi et al., 1998). By the end of gene amplification, however, only a subset of follicle cells display visual amplification foci as judged by EdU incorporation, likely representing a stochastic end to the gene amplification process (Nordman et al., 2014). To determine if Rif1 controls replication fork progression by increasing the period of EdU incorporation within the 7.5 hr time window of gene amplification, comparable to an *SuUR* mutant, we quantified the fraction of stage 13 follicle cells that were EdU positive. Similar to an *SuUR* mutant, loss of Rif1 function also resulted in a prolonged period of EdU incorporation with 34% of follicle cells visibly incorporating EdU in wild-type follicle cells, 100% in an *SuUR* mutant and 98.5% in the *Rif1* mutant (Figure 2-4B). This result suggests that Rif1 has a destabilizing effect on replication forks, resulting in a premature cessation of replication fork progression.

Rif1 acts downstream of SUUR

Rif1 could control SUUR activity and underreplication by at least two different mechanisms. Rif1 could act upstream of SUUR and directly or indirectly regulate SUUR's ability to associate with chromatin. For example, Histone H1 and HP1 affect

underreplication by influencing SUUR's ability to associate with chromatin (Andreyeva et al., 2017; Pindyurin et al., 2008). Alternatively, Rif1 could act downstream of SUUR to control replication fork progression. We sought to distinguish between these possibilities by determining whether SUUR could still associate with replication forks in the absence of Rif1 function.

To monitor SUUR's association with heterochromatin and replication forks in the same cell type, we localized SUUR in amplifying follicle cells where replication forks (double bars) and heterochromatin (chromocenter) can be visualized unambiguously, in the presence and absence of Rif1. SUUR localized to both replication forks and heterochromatin in the absence of Rif1 function (Figure 2-5; Supplemental Figure 2-9). Therefore, we conclude that Rif1 acts downstream of SUUR to inhibit fork progression and that SUUR lacks the ability to inhibit replication fork progression in the absence of Rif1.

Rif1 localizes to active replication forks

Although our genetic data indicate that Rif1 affects replication fork progression, we wanted to determine if Rif1 controls replication fork progression through a direct or indirect mechanism. If Rif1 directly influences replication fork progression and/or stability, then it should localize to active replication forks. To assess this possibility, we visualized Rif1 localization during gene amplification in follicle cells using a Rif1-specific antibody (Supplemental Figure 2-3).

Rif1 localization pattern was strikingly similar to that of SUUR. First, Rif1 is localized to heterochromatin in all stages of amplifying follicle cells (Figure 2-6). Second,

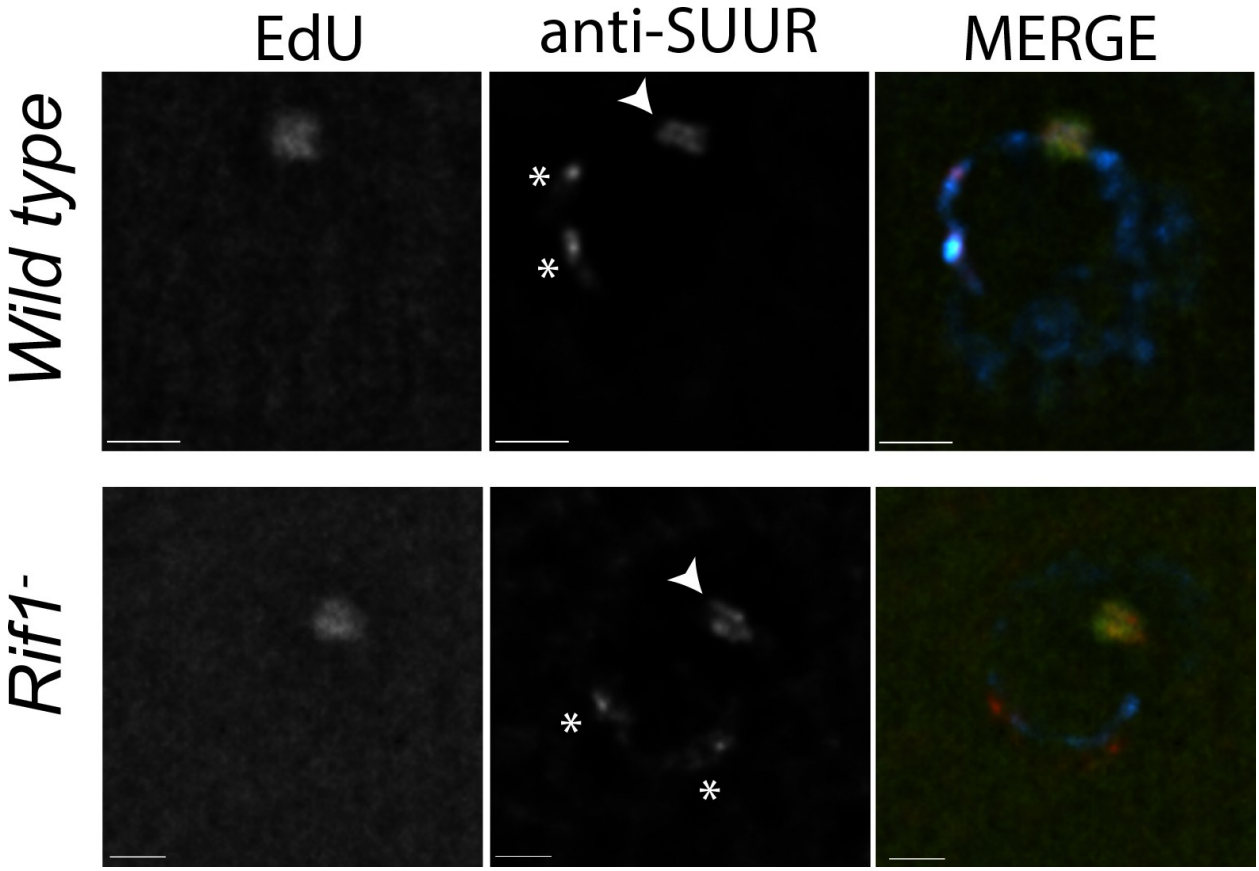


Figure 2-5: **Rif1 acts downstream of SUUR.** Localization of replication forks (EdU) and SUUR in a wild-type and *Rif1* mutant follicle cell nuclei. A single representative stage 13 follicle cell nucleus is shown. Scale bars are 2 μm. Arrowheads indicate sites of amplification. Asterisks marks the chromocenter (heterochromatin). DAPI = blue, SUUR = green, EdU = red. Contributions: None.

Rif1 localized to sites of amplification even prior to the formation of double bar structures (Supplemental Figure 2-9). Third, in the later stages of gene amplification Rif1 was localized to active replication forks. Taken together, these results demonstrate that Rif1 dynamically associates with replication forks to regulate their progression.

To verify that Rif1 associates with replication forks in a context other than the gene amplification, we used iPOND to determine if Rif1 is associated with replication forks in cultured *Drosophila* S2 cells. Briefly, cells were pulsed with EdU and immediately fixed in formaldehyde or chased with thymidine prior to fixation. Proteins associated with newly synthesized DNA (replication forks) can be identified based on their enrichment in pulse

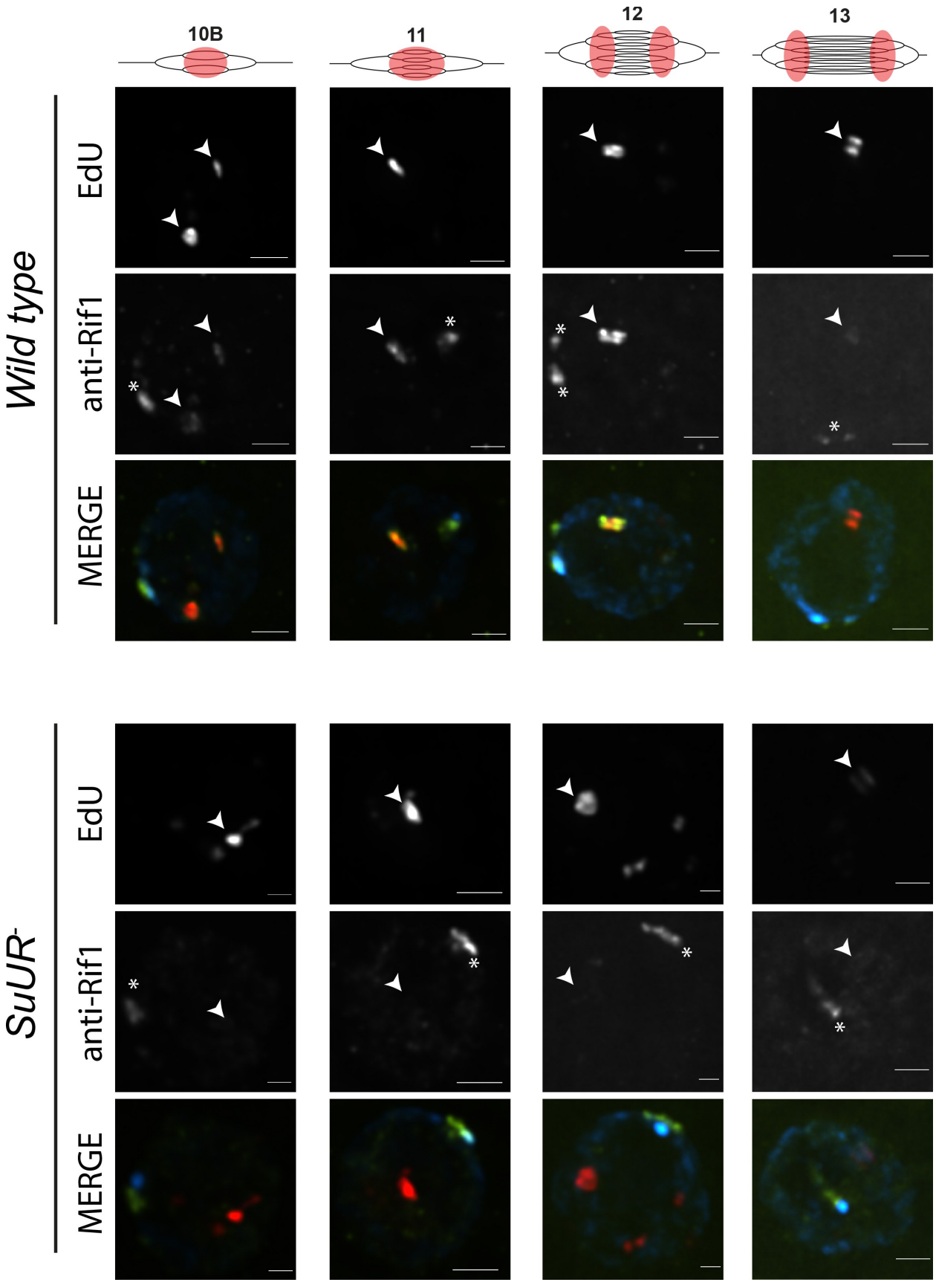

10B
11
12
13
Wild type
EdU
anti-Rif1
MERGE
SuUR-
EdU
anti-Rif1
MERGE

Figure 2-6: **SUUR is necessary to retain Rif1 at replication forks.** Localization of active replication forks (EdU) and Rif1 in a wild-type and *SuUR* mutant follicle cell nuclei. Single representative follicle cell nuclei are shown for each stage. Scale bars are 2 μm. Arrowheads indicate sites of amplification. Asterisk marks the chromocenter (heterochromatin). Contributions: None.

samples relative to chase samples (Dungrawala and Cortez, 2014; Sirbu et al., 2011). We used mass spectrometry to quantify Rif1 protein abundance in EdU pulse and chase samples (Sirbu et al., 2013). Consistent with Rif1 association with replication forks in amplifying follicle cells, Rif1 was enriched in EdU pulse samples relative to chase samples in cultured cells (Supplemental Figure 2-11A). Although this enrichment was not as abundant as our PCNA-positive control, this is expected for a protein that associates with a subset of replication forks.

To independently verify that Rif1 is localized to replication forks in cultured cells, we performed a proximity ligation assay (PLA)-based approach with nascent DNA (Roy et al., 2018; Taglialatela et al., 2017). *Drosophila* S2 cells were pulsed with EdU, fixed and EdU was subsequently biotinylated. A PLA assay was then performed using two different anti-biotin antibodies as a positive control, or an anti-biotin antibody together with an anti-Rif1 antibody. As a negative control, the same PLA assays were performed using cells that were not pulsed with EdU. Consistent with our iPOND mass-spec results, PLA foci were generated using anti-Rif1 and anti-biotin antibodies only when cells were pulsed with EdU (Supplemental Figure 2-11B). Together, these results indicate that Rif1 is associated with replication forks in amplifying follicle cells and cultured cells.

SUUR is required to retain Rif1 at replication forks

Based on our observations that SUUR and Rif1 are part of the same protein complex, and that a *Rif1* mutant phenocopies an *SuUR* mutant, we hypothesized that

SUUR recruits a Rif1/PP1 complex to replication forks. If true, then Rif1 association with replication forks should be at least partially dependent on SUUR. To test this hypothesis, we monitored the localization of Rif1 in *SuUR* mutant amplifying follicle cells. We found that Rif1's association with replication forks was largely dependent on SUUR, as the Rif1 signal was lost in late-stage amplifying follicle cells in an *SuUR* mutant (Supplemental Figure 2-10). Rif1's recruitment to replication foci, however, was not completely dependent on SUUR. In a subset of stage 10B and 11 egg chambers, when both initiation of replication and fork progression are still coupled, we observed Rif1 localization to amplification foci in a subset of follicle cells (Supplemental Figure 2-10). Rif1 staining was lost, however, in stage 12 and 13 egg chambers. We conclude that while the initial recruitment of Rif1 to sites of amplification is not completely dependent on SUUR, SUUR is necessary to retain Rif1 at replication forks.

The PP1-interacting motif of Rif1 is necessary for underreplication

Because Rif1 is known to recruit PP1 to replication origins to regulate initiation, this led us to ask if the same interaction between Rif1 and PP1 is important for Rif1's regulation of replication fork progression. Rif1 associates with Protein Phosphatase 1 (PP1) through a conserved interaction motif, thereby recruiting PP1 to MCM complexes and inactivating them (Davé et al., 2014; Hiraga et al., 2017; Hiraga et al., 2014). PP1 has also been shown to associate with Rif1 in Drosophila (Seller and O'Farrell, 2018; Sreesankar et al., 2015). Based on this model of Rif1 function, we wanted to determine if Rif1's PP1 interaction motif was necessary for Rif1-mediated underreplication. We used CRISPR-based mutagenesis to mutate the conserved SILK/RSVF PP1 interaction motif

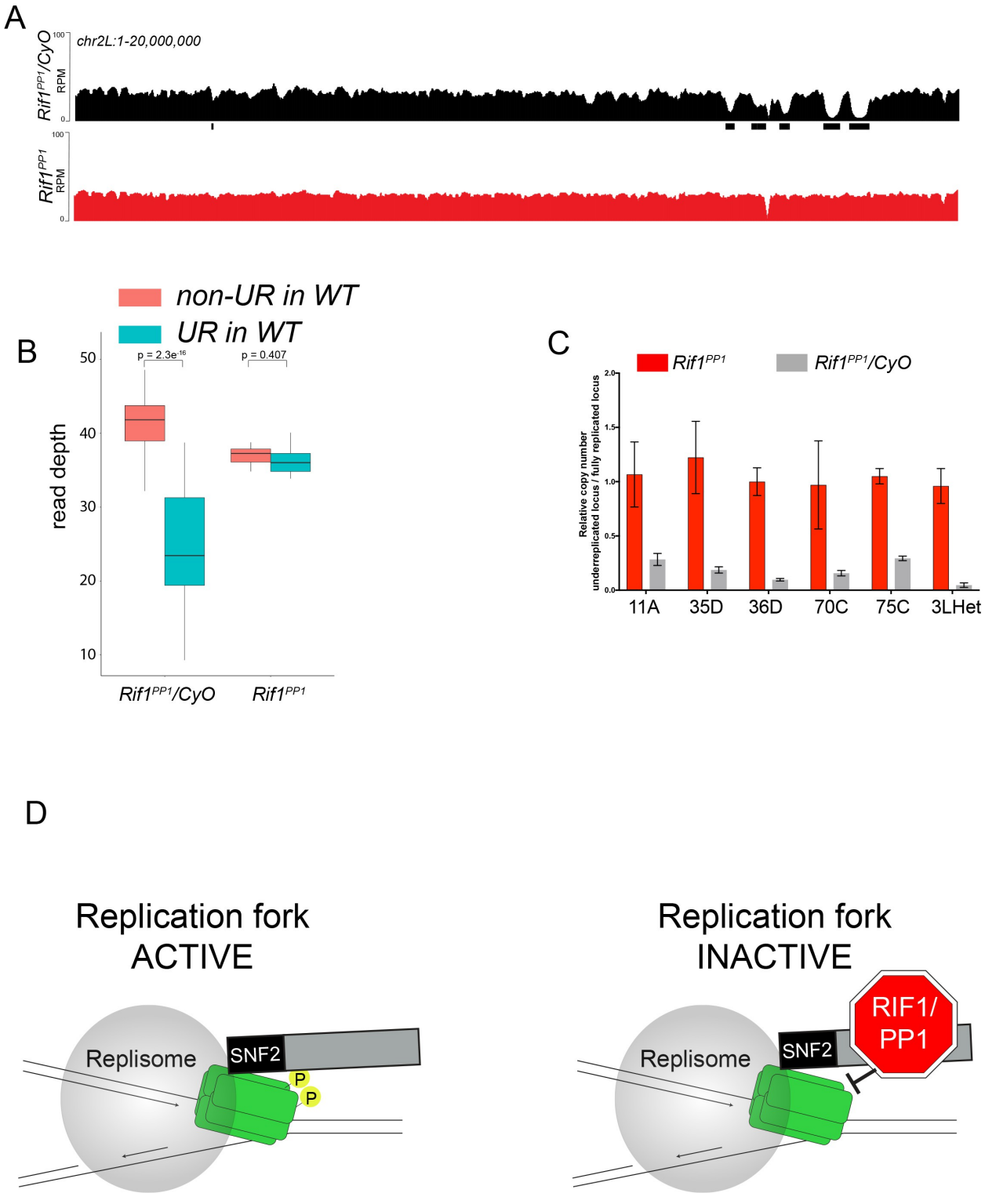


Figure 2-7: **The Rif1 PP1 interaction motif is necessary to promote underreplication.** (**A**) Illumina-based copy number profiles of *chr2L 1 - 20,000,000* from larval salivary glands. Black bars below each profile represent underreplicated regions identified by CNVnator. *Rif1^{PP1}/CyO* was used as the wild-type control. (**B**) Average read depth in regions of euchromatic underreplication domains called in wild-type salivary glands vs. the fully replicated regions of the genome. A Welch two-sample t-test was used to

determine p values. (**C**) Quantitative droplet-digital PCR (ddPCR) copy number assay for multiple underreplicated regions. Each bar is the average enrichment relative to a fully replicated control region for three biological replicates. Error bars are the SEM. (**D**) A new model for SUUR-mediated underreplication. In this model, SUUR serves as a scaffold to recruit a Rif1/PP1 complex to replication forks where Rif1/PP1 inhibits replication fork progression through dephosphorylation of a component of the replisome. Contributions: Analysis and visualization of A and B.

to SAAK/RASA. Western blot analysis showed that mutation of the SILK/RSVF motif did not affect protein stability (Supplemental Figure 2-12). Mutation of this motif has been shown to disrupt the Rif1/ PP1 interaction in organisms from yeast to humans (Alver et al., 2017; Davé et al., 2014; Hiraga et al., 2017; Hiraga et al., 2014; Mattarocci et al., 2014; Sreesankar et al., 2015; Sukackaite et al., 2017). We isolated salivary glands from wandering 3rd instar larvae of the *Rif1*^{PP1} mutant and *Rif1*$^{PP1/+}$ heterozygous animals as a wild-type control. We then extracted DNA and generated genome-wide copy number profiles by Illumina sequencing. Similar to the Rif1 mutant, underreplication was largely abolished in the *Rif1*^{PP1} mutant (Figure 2-7A-C; Supplemental Table 2-1). Thus, Rif1's PP1-interaction motif is necessary to promote underreplication, suggesting that PP1 is a mediator of underreplication. It still remains possible, however, that an additional protein(s) could interact with this motif to promote underreplication.

Discussion

The SUUR protein is responsible for promoting underreplication of heterochromatin and many euchromatin regions of the genome. Although SUUR was recently shown to promote underreplication through inhibition of replication fork progression, the underlying molecular mechanism has remained unclear. Through biochemical, genetic, genomic and cytological approaches, we have found that SUUR recruits Rif1 to replication forks and that Rif1 is responsible for underreplication. This

model is supported by several independent lines of evidence. First, SUUR associates with Rif1, and SUUR and Rif1 co-localize at sites of replication. Second, underreplication is dependent on Rif1, although *Rif1* mutants have a clear pattern of late replication in endo cycling cells. Third, SUUR localizes to replication forks and heterochromatin in a *Rif1* mutant, however, it is unable to inhibit replication fork progression in the absence of Rif1. Fourth, Rif1 controls replication fork progression and phenocopies the effect loss of SUUR function has on replication fork progression. Fifth, SUUR is required for Rif1 localization to replication forks. Critically, using the gene amplification model to separate initiation and elongation of replication, we have shown that Rif1 can affect fork progression without altering the extent of initiation. Based on these observations, we have defined a new function of Rif1 as a regulator of replication fork progression.

SNF2 domain and fork localization

Our work suggests that the SNF2 domain of SUUR is critical for its ability to localize to replication forks. This is based on the observation that deletion of this domain results in a protein that is unable to localize to replication forks, but still localizes to heterochromatin. SUUR has previously been shown to dynamically localize to replication forks during S phase, but constitutively binds to heterochromatin (Kolesnikova et al., 2013; Nordman et al., 2014). SUUR associates with HP1 and this interaction occurs between the central region of SUUR and HP1 (Pindyurin et al., 2008). Therefore, we speculate that the interaction between SUUR and HP1 is responsible for constitutive SUUR localization to heterochromatin, while a different interaction between the SNF2

domain and a yet to be defined component of the replisome, or replication fork structure itself, recruits SUUR to active replication forks during S phase.

Uncoupling of SUUR's ability to associate with replication forks and heterochromatin also provides a new level of mechanistic understanding of underreplication. Overexpression of the C-terminal two-thirds of SUUR is capable of inducing ectopic sites of underreplication. In contrast, overexpression of the SUUR's SNF2 domain, in the presence of endogenous SUUR, suppresses SUUR-mediated underreplication (Kolesnikova et al., 2005). Together with the data presented here, we suggest that overexpression of the SNF2 domain interferes with recruitment of full-length SUUR to replication forks, by saturating potential SUUR binding sites at the replication fork. Although the C-terminal region of SUUR is necessary to induce underreplication (Kolesnikova et al., 2005), the C-terminal portion of SUUR remains associated with heterochromatin in the $SuUR^{\Delta SNF}$ construct, but this protein is not sufficient to induce underreplication. We suggest that at physiological levels, the affinity of SUUR for replication forks is substantially diminished in the absence of the SNF2 domain. Our work raises questions about the biological significance of SUUR binding to heterochromatin, since without the SNF2 domain SUUR is still constitutively bound to heterochromatin, yet unable to induce underreplication. Additionally, SUUR dynamically associates with heterochromatin in mitotic cells although heterochromatin is fully replicated (Swenson et al., 2016).

Rif1 controls underreplication

While trying to uncover the molecular mechanism through which SUUR is able to inhibit replication fork progression, we have uncovered an interaction between SUUR and Rif1. Through subsequent analysis, we demonstrated that Rif1 has a direct role in copy number control and that Rif1 acts downstream of SUUR in the underreplication process. Although underreplication is largely dependent on SUUR, there are several sites that display a modest degree of underreplication in the absence of SUUR (Demakova et al., 2007; Sher et al., 2012). In a *Rif1* mutant, however, these sites are fully replicated and there is no longer any detectable levels of underreplication within any regions of the genome. It is possible that Rif1 is capable of promoting underreplication through a mechanism independent of SUUR. Therefore, we conclude that Rif1 is a critical factor in driving underreplication.

Further emphasizing the critical role Rif1 plays in copy number control, we have shown that Rif1 acts downstream of SUUR in promoting underreplication. SUUR is still able to associate with chromatin in the absence of Rif1 but is unable to promote underreplication. Underreplicated regions of the genome, including heterochromatin, tend to be late replicating, raising the possibility that changes in replication timing in a *Rif1* mutant suppresses underreplication. *Rif1* mutant endo cycling cells of *Drosophila* display a cytological pattern of late replication, where heterochromatin is discretely replicated. While Rif1 controls replication timing in *Drosophila* and is necessary for the onset of late replication at the mid-blastula transition (Seller and O'Farrell, 2018), we argue that the changes in copy number associated with loss of Rif1 function are not solely due to a loss of late replication. This is supported by the clear pattern of late replication of heterochromatin in *Rif1* mutant endo cycling cells, although heterochromatin appears to

be fully replicated in these cells. Previous work in mammalian polyploid cells has shown that underreplication is dependent on Rif1, which was attributed to changes in replication timing (Hannibal and Baker, 2016). It is important to note that Rif1-dependent changes in replication timing were not measured in this system and that many genomic regions transition from early to late replication in a *Rif1* mutant (Foti et al., 2016). Our work raises the possibility that Rif1 has a direct role in mammalian underreplication through a mechanism similar to that of Drosophila and may not simply be due to indirect changes in replication timing. Future work will be necessary to define the role of mammalian Rif1 in underreplication.

Rif1 regulates replication fork progression

Our analysis of amplification loci demonstrates that Rif1 controls replication fork progression independently of initiation control, thus demonstrating that Rif1 has a specific effect on replication fork progression. Therefore, we have uncovered a new role for Rif1 in DNA metabolism as a regulator of replication fork progression and copy number control. Rif1 has been identified as part of the replisome in human cells by nascent chromatin capture, a technique that identifies proteins associated with newly synthesized chromatin (Alabert et al., 2014). Multiple studies have assessed whether loss of Rif1 function affects replication fork progression in yeast, mouse and human cells, but have come to different conclusions (Alver et al., 2017; Cornacchia et al., 2012; Hiraga et al., 2017; Yamazaki et al., 2012). DNA fiber assays have been used to measure fork progression in these studies and nearly all have shown that *Rif1* mutants have a slight increase in replication fork progression, although not always statistically significant. There

could be several reasons for these differing results; Rif1 may control replication fork progression in specific genomic regions that may be underrepresented in some assays, Rif1 function could vary among different cell types, or sample sizes may have been too small to reach significance. Our observations, taken together with these previous studies, leave open the possibility that Rif1-mediated control of replication fork progression could be an evolutionarily conserved function of Rif1. We do not suggest that Rif1 is constitutively associated with replication forks in all cell types. Rather, Rif1 could be recruited to replication forks at a specific time in S phase, or in specific developmental contexts, to modulate the progression of replication forks and provide an additional layer of regulation of the DNA replication program.

How could SUUR and Rif1 function in concert to inhibit replication fork progression? We have shown that Rif1 retention at replication forks is dependent on SUUR. Additionally, underreplication depends on Rif1's PP1-binding motif, raising the possibility that a Rif1/PP1 complex is necessary to inhibit replication fork progression. Rif1/PP1 dephosphorylates DDK-activated helicases to control replication initiation (Davé et al., 2014; Hiraga et al., 2017; Hiraga et al., 2014). More recently, however, DDK-phosphorylated MCM subunits were shown to be necessary to maintain CMG association and stability of the helicase (Alver et al., 2017). This result suggests that continued phosphorylation of the helicase is necessary for replication fork progression (Alver et al., 2017). We propose that SUUR recruits Rif1/PP1 to replication forks where it is able to dephosphorylate MCM subunits, ultimately inhibiting replication fork progression. Although this mechanism needs to be tested biochemically, it provides a framework to address the underlying molecular mechanism responsible for controlling DNA copy

number and could provide new insight into the mechanism(s) Rif1 employs to regulate replication timing.

Materials and Methods

Key Resources Table

Reagent type (species) or resource	Designation	Source or reference	Identifiers	Additional information
Gene (*Drosophila melanogaster*)	*Suppressor of Underreplication* (*SuUR*)	NA	FBgn0025355	
Gene (*D. melanogaster*)	*Rap1 interacting factor 1 (Rif1)*	NA	FBgn0050085	
Strain, strain background (*D. melanogaster*)	WT: *Oregon R*			
Strain, strain background (*D. melanogaster*)	*SuUR*	(Makunin et al., 2002) PMID: 11901119		w^{118}; $SuUR^{ES}$
Strain, strain background (*D. melanogaster*)	$SuUR^{\Delta SNF}$	This paper		$SuUR^{ES}$, *PBac*{w^{+} $SuUR^{\Delta SNF}$}
Strain, strain background (*D. melanogaster*)	*hs > FLAG-SUUR*	This paper		*w118; hs > FLAG-SUUR*
Strain, strain background (*D. melanogaster*)	*hs > FLAG-SNF2*	This paper		w^{118}; *hs > FLAG-SNF2*
Strain, strain background (*D. melanogaster*)	$Rif1^{1}$	This paper		w^{118}; $Rif1^{1}$
Strain, strain background (*D. melanogaster*)	$Rif1^{2}$	This paper		w^{118}; $Rif1^{2}$
Strain, strain background (*D. melanogaster*)	$Rif1^{-}$	This paper		w^{118}; $Rif1^{1}/Rif1^{2}$

Strain, strain background (*D. melanogaster)*	*Rif1^{PP1}*	This paper		*w^{118}*; *Rif1^{PP1}*
Cell line (*D. melanogaster*)	S2-DGRC	Drosophila Genomics Resource Center (DGRC)	embryo derived	isolate of S2 used for RNAi in the DRSC modENCODE line
Antibody	anti-SUUR (Guinea pig, polyclonal)	(Nordman et al., 2011) PMID: 25437540)		
Antibody	anti-Rif1 (Guinea pig, polyclonal)	This paper		(1:200)
Antibody	anti-Rif1 (Rabbit, polyclonal)	This paper		(1:1000)
Antibody	HRP-anti-FLAG (Mouse, monoclonal)	Sigma-Aldrich	A8592	(1:1000)
Antibody	anti-HP1 (Mouse, monoclonal)	The Developmental Studies Hybridoma Bank (DSHB)	C1A9	(1:1000)
Antibody	anti-biotin (Mouse, moncolonal)	Sigma-Aldrich	SAB4200680	(1:20,000)
Antibody	anti-biotin (rabbit, polyclonal)	Bethyl	A150-109A	(1:3,000)
Antibody	HRP-secondaries	Jackson ImmunoResearch		(1:20,000)
Recombinant DNA reagent	pCaSpeR-hs	(Thummel and Pirrotta, V.) Drosophila Genomics Resource Center		
Recombinant DNA reagent	pStinger	(Barolo et al., 2000) PMID: 11056799		
Recombinant DNA reagent	CHORI-322 (CH322-163L18)	BACPAC Resources		
Recombinant DNA reagent	pET17b	Millipore-Sigma	69663	
Recombinant DNA reagent	pET17b-Rif1 (694–1094)	This paper		Progenitors:PCR, pET17b
Peptide, recombinant protein	Rif1(694–1094)	This paper		Ni-NTA purified
Commercial assay or kit	PLA probes	Duolink Sigma		
Commercial assay or kit	PLA probemaker	Duolink Sigma	DUO92010	
Commercial assay or kit	PLA Detection Reagents	Duolink Sigma	DUO92008	

Chemical compound, drug	Alexa Fluor Azide 555	Life Technologies	A20012	
Chemical compound, drug	Biotin-TEG Azide	Berry and Associates	BT 1085	
Chemical compound, drug	EdU (5-ethynyl-2-deoxyuridine)	Life Technologies	A10044	
Software, algorithm	Sequest	Thermo Scientific		
Software, algorithm	Scaffold 4.3.4	Proteome Software		
Software, algorithm	Skyline version 4.1	Schilling et al. (2012) (PMID:22454539)		
Software, algorithm	deepTool 2.5.0	Ramírez et al. (2016) (PMID:27079975)		
Software, algorithm	CNVnator 0.3.3	Abyzov et al., 2011 (PMID:21324876)		

Strain List

JTN110: WT – Oregon R

JTN109*: $SuUR^{-}$ – w^{118}; $SuUR^{ES}$*

JTN038*: $SuUR^{\Delta SNF}$ – $SuUR^{ES}$, PBac{w^{+} $SuUR^{\Delta SNF}$}*

JTN143: *w^{118}; hs > FLAG-SUUR*

JTN146: *w^{118}; hs > FLAG-SNF2*

JTN305: w^{118}; $Rif1^{1}$

JTN307: *w^{118}; $Rif1^{2}Rif1^{-}$ – w^{118}; $Rif1^{1}$/$Rif1^{2}$*

JTN292: *$Rif1^{PP1}$ – w^{118}; $Rif1^{PP1}$*

BAC-mediated recombineering

BAC-mediated recombineering (Sharan et al., 2009) was used to delete the portion of the *SuUR* gene corresponding to the SNF2 domain. An *attB-P[acman]* clone with a 21

kb genomic region containing the *SuUR* and a *galK* insertion in the *SuUR* coding region (described in [Nordman et al., 2014]) was used as a starting vector. Next, a gene block (IDT) was used to replace the gal*K* cassette and generate a precise deletion within the *SuUR* gene. The resulting vector was verified by fingerprinting, PCR and sequencing. The *SuUR*$^{\Delta SNF}$ BAC was injected into a strain harboring the *86* F8 landing site (Best Gene Inc.).

Generation of heat shock-inducible, FLAG-tagged SuUR transgenic lines

The portion of the *SuUR* gene encoding the SNF2 domain (amino acids 1 to 278) was fused to the SV40 NLS (Barolo et al., 2000) and a 3X-FLAG tag sequence was added to the 5' end of *SuUR SNF2* sequence. The resulting construct was cloned into the pCaSpeR-hs vector, which contains a *hsp70* promoter (Thummel and Pirrotta, V.: Drosophila Genomics Resource Center), using the NotI and XbaI restriction sites. A 3X-FLAG tag sequence was added to the 5' end of the *SuUR* coding region and cloned into the pCaSpeR-hs vector also using the NotI and XbaI restriction sites. The resulting constructs were verified by sequencing and injected into a *w*^{1118} strain (Best Gene Inc.).

CRISPR mutagenesis

To generate null alleles of *Rif1*, gRNAs targeting the 5' and 3' ends of the *Rif1* gene were cloned into the pU6-BbsI plasmid as described (Gratz et al., 2015) using the DRSC Find CRISPRs tool (http://www.flyrnai.org/crispr2/index.html). Both gRNAs were co-injected into a *nos-Cas9* expression stock (Best Gene Inc.). Surviving adults were individually crossed to *CyO*/*Tft* balancer stock and *CyO*-balanced progeny

were screened by PCR for a deletion of the *Rif1* locus. Stocks harboring a deletion were further characterized by sequencing. Both $Rif1^1$ and $Rif1^2$ mutants had substantial deletions of the *Rif1* gene and both had frame shift mutations early in the coding region. $Rif1^1$ has a frame shift mutation at amino acid 14, whereas $Rif1^2$ has a frame shift mutation at amino acid 11.

To generate a *Rif1* allele defective for PP1 binding, the pU6-BbsI vector expressing the gRNA targeting the 3' end of *Rif1* was co-injected with a recovery vector that contained the mutagenized SILK and RVSV (SAAK and RASA) sites with 1 kb of homology upstream and downstream of the mutagenized region. Surviving adults were crossed as above and screened by sequencing.

Cytological analysis and microscopy

Ovaries were dissected from females fattened for two days on wet yeast in Ephrussi Beadle Ringers (EBR) medium (Beadle and Ephrussi, 1935). Ovaries were pulsed with 5-ethynyl-2-deoxyuridine (EdU) for 30 min, fixed in 4% formaldehyde and prepared for immunofluorescence (IF) as described (Nordman et al., 2014).

For IF using both anti-Rif1 and anti-SUUR antibodies, ovaries were dissected, pulsed with 50 μM EdU and fixed. Ovaries were then incubated in primary antibody (1:200) overnight at 4°C. Alexa Fluor secondary antibodies (ThermoFisher) were used at a dilution of 1:500 for 2 hr at room temperature. EdU detection was performed after incubation of the secondary antibody using Click-iT Alexa Fluor-555 or −488 (Invitrogen). All images were obtained using a Nikon Ti-E inverted microscope with a Zyla sCMOS

digital camera. Images were deconvolved and processed using NIS-Elements software (Nikon).

For salivary gland IF, third instar larvae were collected prior to the wandering stage. Salivary glands were dissected in EBR, pulsed with 50 μM EdU for 30 min and fixed with 4% formaldehyde. Salivary glands were incubated in anti-HP1 antibody (Developmental Studies Hybridoma Bank; C1A9) overnight at 4°C. Alexa Fluor secondary antibodies staining and Click-iT EdU labeling were performed as described above.

Image quantification

All images were quantified using Nikon NIS- Elements AR v4.40. To determine Rif1 and SUUR signal intensities at sites of gene amplification, Regions Of Interest (ROIs) were identified based on the EdU intensity. SUUR or Rif1 mean signal intensity was then determined within each ROI. Ten randomly selected regions outside of the nucleus were selected and the mean signal intensity for these regions were averaged to determine the background signal for each image. The average background signal was subtracted from the signal at amplified regions to normalize each image for varying amounts of background. To quantify the SUUR signal intensity at heterochromatin, SUUR ROIs were manually defined due to their non-uniform shape. The sum intensity of the fluorescent signal within these regions were extracted. The sum signal intensity was then normalized to ROI area to account for the difference in shape of each ROI. To quantify PLA signals, ROIs were generated based on DAPI signal to mark all nuclei. PLA foci were then identified for each image and the number of foci in each DAPI ROI was determined.

Rif1 antibody production

Rif1 antiserum was produced in guinea pigs and rabbits (Cocalico Biologicals Inc.). Briefly, a Rif1 protein fragment from residues 694 – 1094 (Sreesankar et al., 2012) was C-terminally six-histidine tagged and and expressed in *E. coli* Rossetta DE3 cells and purified using Ni-NTA Agarose beads (Qiagen). The purified protein was used for injection (Cocalico Biologicals Inc.) and serum was affinity purified as described (Moore and Orr-Weaver, 1998). Affinity purified guinea pig anti-Rif1 antibody was used for immunofluorescence.

IP-mass spec

Flies containing heat shock-inducible *SuUR* transgenes were expanded into population cages. 0 – 24 hr embryos were collected, incubated at 37°C for 1 hr, and allowed to recover for one hour following heat shock treatment. Wild-type embryos were used as a negative control. Embryos were dechorionated in bleach and fixed for 20 min in 2% formaldehyde. Approximately 0.5 g of fixed and dechorionated embryos were used for each replicate. Embryos were disrupted by douncing in Buffer 1 (Shao et al., 1999), followed by centrifugation at 3000 x g for 2 min at 4°C and resuspended in lysis buffer 3 (MacAlpine et al., 2010). Chromatin was prepared by sonicating nuclei for a total of 40 cycles of 30’ ON and 30’ OFF at max power using a Bioruptor 300 (Diagenode) with vortexing and pausing after every 10 cycles. Cleared lysates were incubated with anti-FLAG M2 affinity gel (Sigma) for 2 hr at 4°C. After extensive washing in LB3 and LB3 with 1M NaCl, proteins were eluted using 3X FLAG peptide (Sigma). Crosslinks were reversed by boiling purified material in Laemmli buffer with β-mercaptoethanol for 20 min.

Immunoprecipitated samples were separated on a 4 – 12% NuPAGE Bis-Tris gel (Invitrogen), proteins were stained with Novex colloidal Coomassie stain (Invitrogen), and destained in water. Coomassie stained gel regions were cut from the gel and diced into 1 mm^3 cubes. Proteins were reduced and alkylated, destained with 50% MeCN in 25 mM ammonium bicarbonate, and in-gel digested with trypsin (10 ng/μL) in 25 mM ammonium bicarbonate overnight at 37°C. Peptides were extracted by gel dehydration with 60% MeCN, 0.1% TFA, the extracts were dried by speed vac centrifugation, and reconstituted in 0.1% formic acid. Peptides were analyzed by LC-coupled tandem mass spectrometry (LC-MS/MS). An analytical column was packed with 20 cm of C18 reverse phase material (Jupiter, 3 μm beads, 300 Å, Phenomenox) directly into a laser-pulled emitter tip. Peptides were loaded on the capillary reverse phase analytical column (360 μm O.D. x 100 μm I.D.) using a Dionex Ultimate 3000 nanoLC and autosampler. The mobile phase solvents consisted of 0.1% formic acid, 99.9% water (solvent A) and 0.1% formic acid, 99.9% acetonitrile (solvent B). Peptides were gradient-eluted at a flow rate of 350 nL/min, using a 120 min gradient. The gradient consisted of the following: 1 – 3 min, 2% B (sample loading from autosampler); 3 – 98 min, 2 – 45% B; 98 – 105 min, 45 – 90% B; 105 – 107 min, 90% B; 107 – 110 min, 90–2% B; 110 – 120 min (column re-equilibration), 2% B. A Q Exactive HF mass spectrometer (Thermo Scientific), equipped with a nanoelectrospray ionization source, was used to mass analyze the eluting peptides using a data-dependent method. The instrument method consisted of MS1 using an MS AGC target value of 3e6, followed by up to 15 MS/MS scans of the most abundant ions detected in the preceding MS scan. A maximum MS/MS ion time of 40 ms was used with a MS2 AGC target of 1e5. Dynamic exclusion was set to 20 s, HCD collision energy was set to 27 nce, and peptide

match and isotope exclusion were enabled. For identification of peptides, tandem mass spectra were searched with Sequest (Thermo Fisher Scientific) against a *Drosophila melanogaster* database created from the UniprotKB protein database (www.uniprot.org). Search results were assembled using Scaffold 4.3.4 (Proteome Software).

Genome-wide copy number profiling

Embryos were collected immediately after 2 hr of egg laying. Salivary glands were dissected in EBR from 50 wandering 3rd instar larvae per genotype and flash frozen. Ovaries were dissected from females fattened for 2 days on wet yeast in EBR and 50 stage 13 egg chambers were isolated for each genotype and flash frozen. Tissues were thawed on ice, resuspended in LB3 and dounced using a Kontes B-type pestle. Dounced homogenates were sonicated using a Bioruptor 300 (Diagenode) for 10 cycles of 30’ on and 30’’ off at maximal power. Lysates were treated with Rnase and Proteinase K and genomic DNA was isolated by phenol-chloroform extraction. Illumina libraries were prepared using NEB DNA Ultra II (New England Biolabs) following the manufacturers protocol. Barcoded libraries were sequenced using Illumina NextSeq500 platform.

Bioinformatics

Reads were mapped to the Drosophila genome (BDGP Release 6) using BWA-MEM with default parameters (Li and Durbin, 2009). CNVnator 0.3.3 was used for the detection of underreplicated regions using a bin size of 1000 (Abyzov et al., 2011). Regions were identified as underreplicated if they were not identified as underreplicated in 0 – 2 hr embryonic DNA and were greater than 10 kb in length. The number of reads

for underreplicated regions was called by using bedtools multicov tool for the underreplicated and uncalled regions. Average read depth per region was determined by multiplying the number of reads in a region by the read length and dividing by the total region length. Read depth was normalized between samples by scaling the total reads obtained per sample. Statistical comparison between the regions was with a t-test. For read depth in pericentric heterochromatin regions, the chromatin arm was binned into 10 kb windows and the number of reads for each window was called using bedtools multicov using only uniquely mapped reads.

Half maximum analysis of amplicon copy number profiles was performed as described previously (Alexander et al., 2015; Nordman et al., 2014). Briefly, $\log_2$ ratios were generated using bamCompare from deepTools 2.5.0 (Ramírez et al., n.d.) by comparing stage 13 follicle cell profiles to a 0 – 2 hr embryo sample. Smoothed $\log_2$-transformed data was used to determine the point of maximum copy number associated with each amplicon. The chromosome coordinate corresponding to half the maximum value for each arm of the amplicon was then determined.

Copy number analysis by droplet-digital PCR (ddPCR)

Genomic DNA was extracted from salivary glands isolated from wandering third instar larvae as described above. Primer sets annealing to the mid-point of the indicated UR regions were used (previously described in [Nordman et al., 2014; Sher et al., 2012]). ddPCR was performed according to manufacture's recommendations (BioRad). All ddPCR reactions were performed in triplicate from three independent biological replicates. The concentration value for each set of primers in an underreplicated domain

was divided by the concentration value of a fully replicated control to generate the bar graph. Error bars represent the SEM.

Western blotting

Ovaries were dissected from females fattened for 2 days on wet yeast and suspended in Laemmli buffer supplemented with DTT. Ovaries were homogenized and boiled and extracts were loaded on a 4–20% Mini-PROTEAN TGX Stain-Free gel (BioRad). After electrophoresis the gel was activated and imaged according to the manufacturers recommendations. Protein was transferred to a PDVF membrane using a Trans-Blot Turbo Transfer System (BioRad). After blocking and incubation with antibodies, blots were imaged using an Amersham 600 CCD imager.

iPOND mass spectrometry

We obtained *D. melanogaster* S2 cells directly from the Drosophila Genomics Resource Center (DGRC). Cells were checked for mycoplasma contamination by PCR. S2 cells propagated as recommended by the DGRC. *Drosophila* S2 cells were grown in Schneider's Drosophila Medium with 10% heat-inactivated FBS (Gemini Bio Products) and 100 units/mL Penicillin-Streptomycin (Life Technologies). For each biological replicate, 5×10^8 cells were pulsed with 10 μM EdU and immediately fixed in 2% formaldehyde (pulse samples) or pulsed with 10 μM EdU for 10 minutes and chased with 100 μM Thymidine for 30 min prior to fixation (chase samples). iPOND purifications were done according to (Dungrawala and Cortez, 2014) with the exception that LB3 was used

in place of RIPA buffer. Purifications were processed for mass spectrometry as described above.

To quantify protein abundance in by mass spectrometry, raw mass spectrometry data were imported into Skyline version 4.1 (Schilling et al., 2012). Chromatographic traces were manually inspected for proper peak picking and where necessary adjusted manually in the chromatographic window. Only matching isotopic envelopes that had an error <5 ppm, an isotope dot product >0.9, and similar retention times between samples were used. MS1 peak areas from each peptide and observed charge state were summed to get the intensity for a given protein. To account for variation between samples, each sample was normalized to histone H3 summed areas.

Proximity Ligation Assay (PLA) with nascent DNA

S2 cells were grown in Schneider's Drosophila Medium with 10% heat-inactivated FBS (Gemini Bio Products) and 100 units/mL Penicillin Streptomycin (Life Technologies). For nascent DNA PLA, asynchronously growing S2 cells were seeded onto Concanavalin A-coated coverslips. After attaching to coverslips for 1 hr, cells were pulsed with 125 μM EdU for 10 min. Cells were washed with PBS and fixed in 4% paraformaldehyde for 15 min, then permeabilized in PBS + 0.25% Triton X-100 for 60 min. The cells were biotinylated using standard click chemistry conditions for 30 min. After washing 3 times, blocking was performed for 1 hr with Duolink blocking solution. Cells were incubated with their primary antibody overnight at 4°C. The following day, cells were washed in Duolink Wash Buffer A, then incubated at 37°C with the appropriate Plus and Minus PLA probes at a 1:5 dilution. After an hour, the cells were washed in Wash Buffer A twice, ligation

buffer was made at 1:40 dilution and incubated for 30 min at 37°C. Cells were washed 2x in Wash Buffer A, then incubated in amplification buffer at 1:80 for 100 min at 37°C. Slides were washed in Wash Buffer B, then 1:100 dilution of Wash Buffer B before being mounted in Duolink In Situ Mounting Media with DAPI.

Data access

Data sets described in this manuscript can be found under the GEO accession number: GSE114370.

Acknowledgements

We thank Kristie Rose and Hayes McDonald at the Vanderbilt Proteomics core for mass spectrometry and Olivia Koues from the VANTAGE core at Vanderbilt for Illumina sequencing. We would like to thank Terry Orr-Weaver, Stephen Bell, Katherine Friedman, James Dewar, Dave Cortez and members of the Nordman lab for providing critical comments on the manuscript. We thank Brooke Hamilton for assistance in generating the Rif1 mutants. This work was supported by an NIH award P30 AI110527 to SM and an NIH R00 award 5R00GM104151 to JTN.

Author contributions

Alexander Munden, Zhan Rong, Formal analysis, Investigation, Visualization; Amanda Sun, Formal analysis, Investigation, Methodology; Rama Gangula, Formal analysis, Methodology; Simon Mallal, Supervision, Methodology; Jared T Nordman,

Conceptualization, Formal analysis, Supervision, Funding acquisition, Validation, Investigation, Visualization, Writing—original draft.

Supplementary Table 2-1: Underreplicated regions called by CNVnator

chr	start	end	OregonR	*SuUR*$^{-}$	*SuUR*$^{\Delta SNF}$	*Rif1*$^{-}$	*Rif1*^{PP1}	*Rif1*^{PP1}*/+*
chrX	9001	52000	+		+			
chrX	80001	108000	+					
chrX	2976001	3125000	+					+
chrX	12052001	12382000	+					+
chrX	14062001	14101000	+					
chrX	14292001	14563000	+					+
chrX	20686001	20957000	+					+
chrX	20962001	20998000	+					+
chrX	21525001	21544000	+	+		+		+
chrX	21667001	21807000	+	+	+			+
chrX	21814001	21829000	+					+
chrX	21843001	21895000	+	+	+			+
chrX	21904001	21965000	+	+	+			+
chrX	21972001	22433000	+	+	+		+	+
chrX	22611001	22787000	+	+				+
chrX	23053001	23064000	+	+				
chrX	23175001	23205000	+					+
chrX	23285001	23535000	+	+	+			+
chr2L	4538001	4777000	+					
chr2L	8013001	8024000	+					
chr2L	11587001	11777000	+					
chr2L	12781001	12799000	+					
chr2L	14722001	14946000	+					+
chr2L	15306001	15721000	+					+
chr2L	15960001	16154000	+					+
chr2L	16161001	16217000	+					+
chr2L	16948001	17199000	+					+
chr2L	17201001	17312000	+					+
chr2L	17520001	17951000	+		+			+
chr2L	19345001	19358000	+					
chr2L	20128001	20199000	+	+	+			+
chr2L	21833001	22085000	+					+
chr2L	22284001	22522000	+					+
chr2L	22614001	22752000	+					+
chr2L	23198001	23406000	+	+	+	+	+	+
chr2L	23415001	23513712	+		+	+		+

chr2R	1	699000	+	+	+	+	+	+
chr2R	1194001	1206000	+					
chr2R	1379001	1501000	+	+	+			+
chr2R	1557001	1589000	+					
chr2R	1609001	1700000	+					+
chr2R	1707001	1968000	+	+	+			+
chr2R	1975001	2163000	+	+	+	+		+
chr2R	2170001	2409000	+	+	+	+		+
chr2R	2421001	2500000	+	+	+			+
chr2R	2508001	2546000	+	+	+			+
chr2R	2551001	3506000	+	+		+	+	+
chr2R	3513001	3871000	+	+	+	+	+	+
chr2R	4414001	4425000	+	+				
chr2R	4871001	5057000	+					+
chr2R	6283001	6476000	+	+				+
chr2R	10623001	10637000	+			+		
chr2R	23133001	23313000	+					+
chr3L	4850001	5034000	+					+
chr3L	5043001	5075000	+					+
chr3L	13559001	13805000	+					+
chr3L	15196001	15475000	+					+
chr3L	18190001	18431000	+					+
chr3L	22577001	22627000	+					
chr3L	22803001	22820000	+					
chr3L	23157001	23173000	+		+			
chr3L	23355001	23538000	+					+
chr3L	23550001	23679000	+					
chr3L	23775001	24005000	+					+
chr3L	24056001	25075000	+	+	+			+
chr3L	25135001	25838000	+	+	+			+
chr3L	25844001	25965000	+		+			+
chr3L	26085001	26161000	+		+			+
chr3L	26166001	26311000	+	+				+
chr3L	26315001	26705000	+	+	+		+	+
chr3L	27391001	27815000	+			+	+	+
chr3L	28042001	28110227	+					
chr3R	1	1257000	+	+	+	+	+	+
chr3R	1266001	1655000	+	+			+	+
chr3R	1664001	2569000	+	+	+		+	+

chr3R	2572001	2824000	+	+	+	+	+	+
chr3R	2831001	3034000	+	+	+	+	+	+
chr3R	3040001	3129000	+	+		+	+	+
chr3R	3136001	3533000	+	+	+		+	+
chr3R	3674001	3692000	+	+				
chr3R	3827001	3842000	+	+				
chr3R	3890001	4175000	+		+			+
chr3R	6159001	6327000	+					
chr3R	6515001	6624000	+					
chr3R	7572001	7714000	+		+			+
chr3R	10919001	11142000	+		+			+
chr3R	16712001	16948000	+					+
chr3R	19704001	19715000	+					
chr3R	22142001	22303000	+			+		
chr3R	28020001	28252000	+					+

Supplementary Table 2-2: Half-Max called follicle widths

Wild type		**max (log2)**	**left arm (bp)**	**right arm (bp)**	**half max total (bp)**	**fold change relative to wild type**
7F	*chrX*	*3.911*	8439400	8518500	79100	1
22B*	*chr2L*	*1.961*	1888300	1937200	48900	1
30B	*chr2L*	*1.798*	9504800	9587600	82800	1
34B	*chr2L*	*2.33*	13371800	13438500	66700	1
62D	*chr3L*	*1.678*	2231600	2314900	83300	1
66D	*chr3L*	*5.494*	8694700	8765800	71100	1

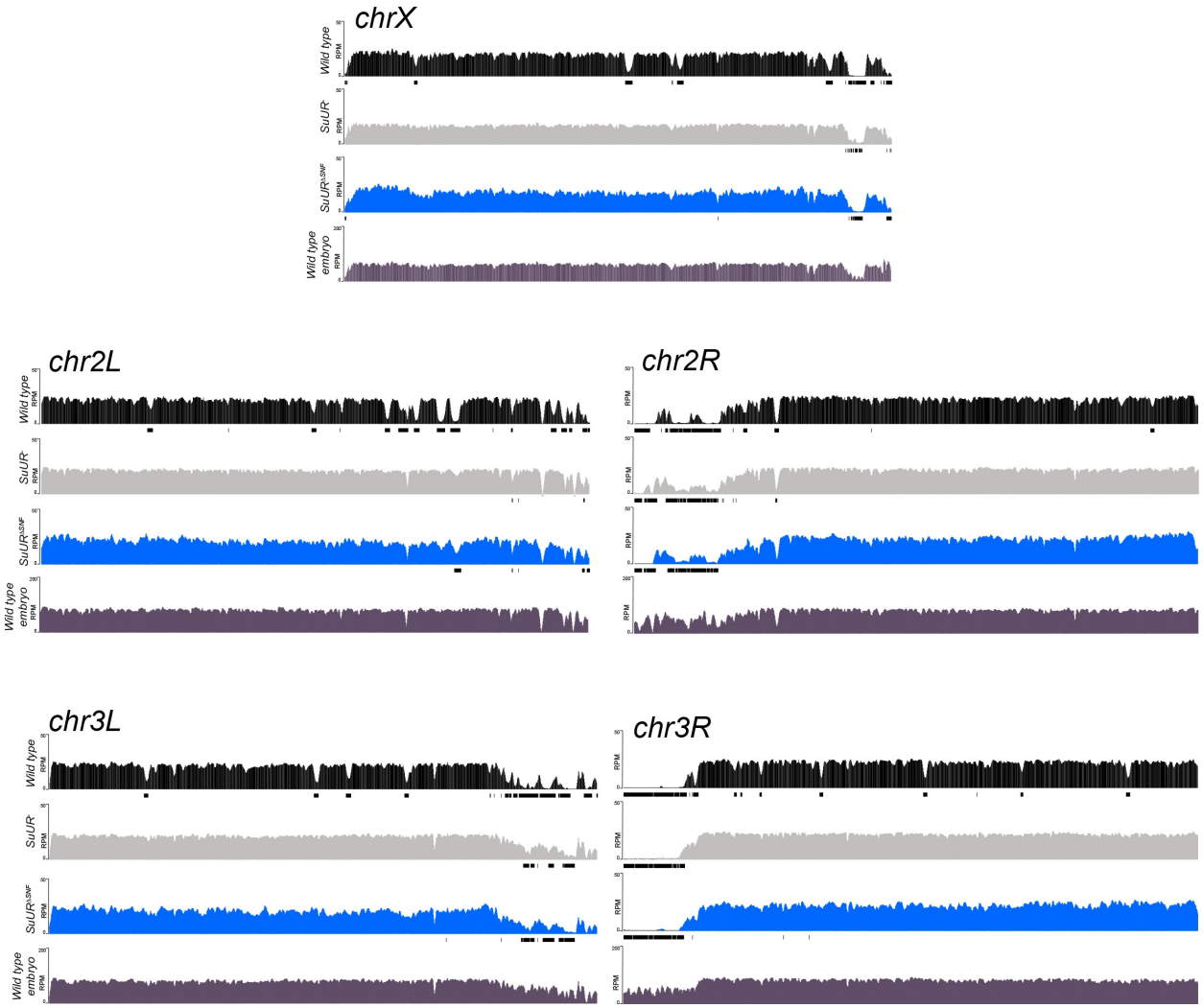
half max position

SuUR-		**max (log2)**	**left arm (bp)**	**right arm (bp)**	**half max total (bp)**	
7F	*chrX*	*3.528*	8425000	8528900	103900	1.313527181
22B*	*chr2L*	*NA*	NA	NA	NA	NA
30B	*chr2L*	*1.682*	9506100	9607700	101600	1.22705314
34B	*chr2L*	*2.355*	13364800	13473500	108700	1.629685157
62D	*chr3L*	*1.745*	2221200	2342400	121200	1.454981993
66D	*chr3L*	*4.88*	8685700	8778600	92900	1.306610408

half max position

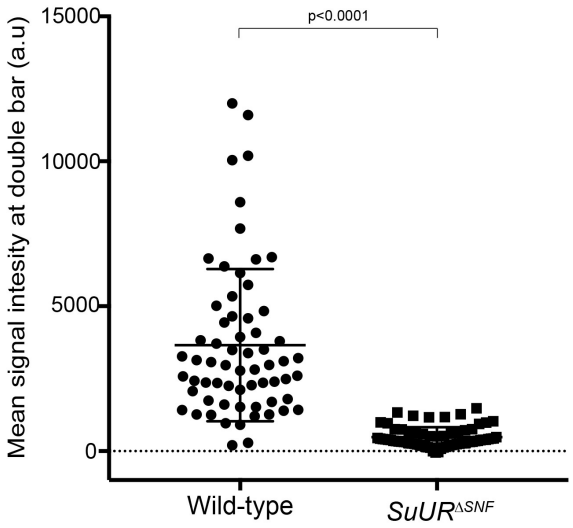
Rif1-		**max (log2)**	**left arm (bp)**	**right arm (bp)**	**half max total (bp)**	
7F	*chrX*	*3.824*	8420700	8540700	120000	1.517067004
22B*	*chr2L*	*NA*	NA	NA	NA	NA
30B	*chr2L*	*1.807*	9496800	9607300	110500	1.334541063
34B	*chr2L*	*2.474*	13361400	13474400	113000	1.694152924
62D	*chr3L*	*1.719*	2217900	2335500	117600	1.411764706
66D	*chr3L*	*5.465*	8679700	8783500	103800	1.459915612

*22B is a strain specific amplicon present in Oregon R and not *SuUR* and *Rif1* mutants

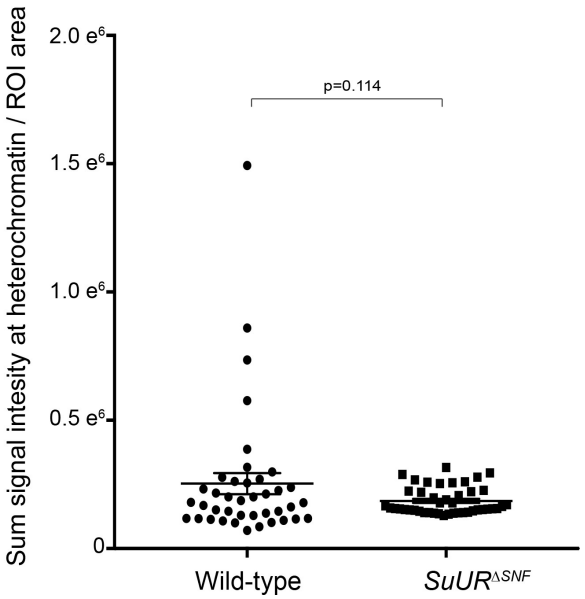


Supplemental Figure 2-1: **Genome-wide copy number profile of the *SuUR$^{\Delta SNF}$* mutant.** Illumina-based copy number profiles of all chromosome arms except the fourth for larval salivary glands of the indicated genotypes and wild type 0 – 2 hr embryos in which DNA is fully replicated. Black bars below each profile represent called underreplicated regions. Contributions: Analysis and visualization.

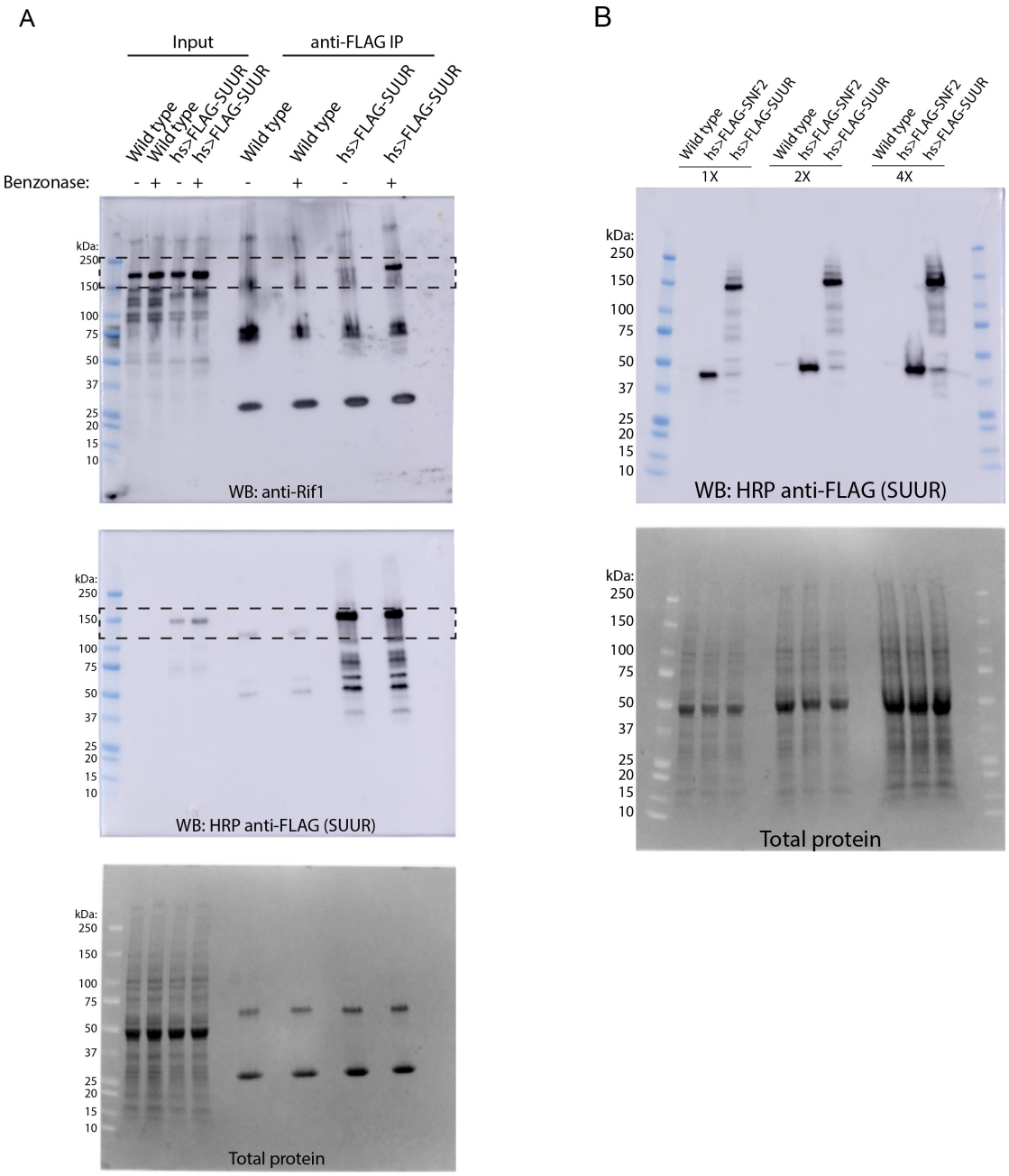
A



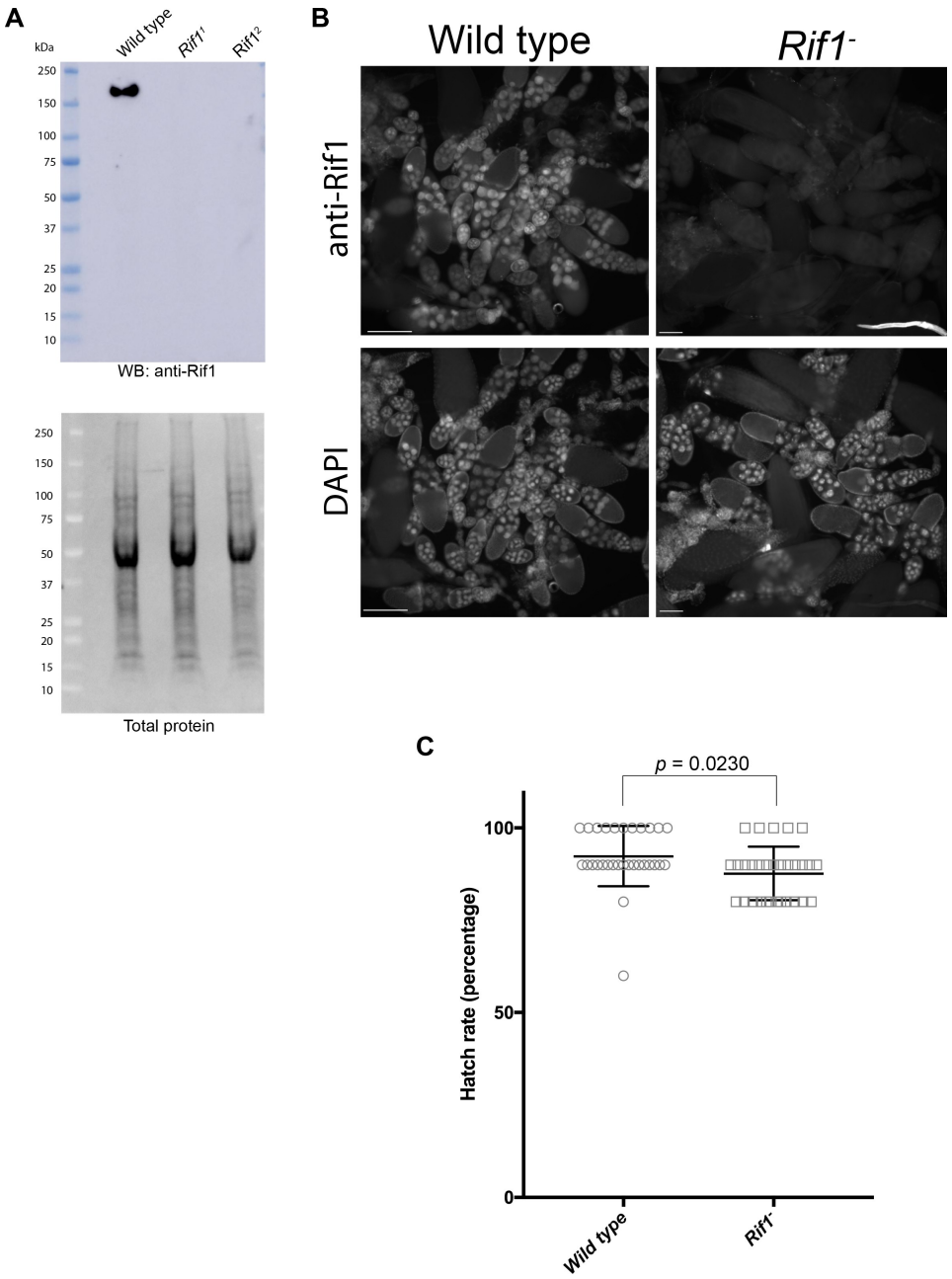
B



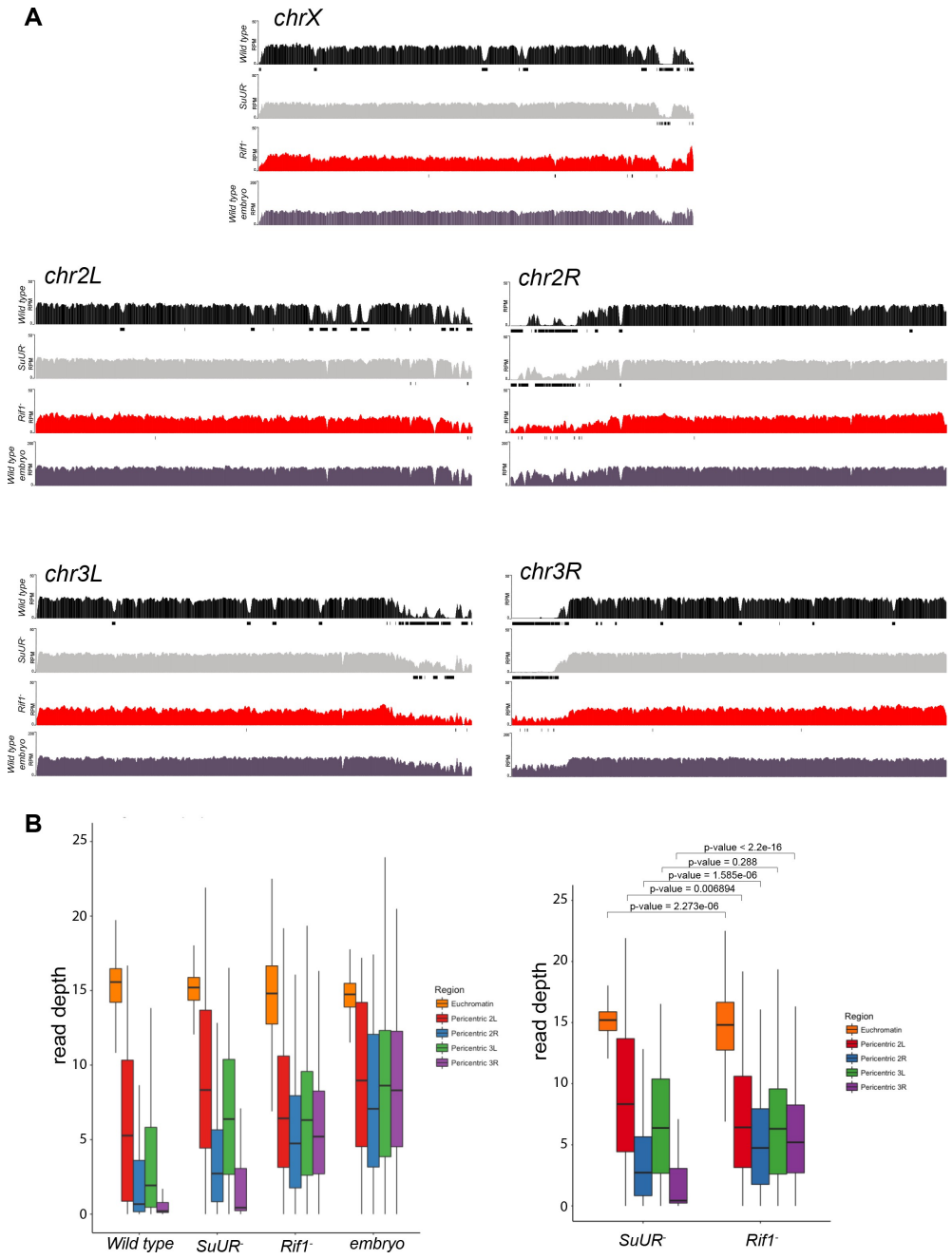
Supplemental Figure 2-2: **Quantification of SUUR and *SUUR$^{\Delta SNF}$* signal intensities at replication forks and heterochromatin. (A)** SUUR and *SUUR$^{\Delta SNF}$* mean signal intensities, normalized for background levels, at double bar structures from stage 12 egg chambers. Results are from two biological replicates. A two-tailed Welch's t test was used to determine significance. n = 64 for wild-type and n = 69 for the *SuUR$^{\Delta SNF}$* mutant. **(B)** SUUR and *SUUR$^{\Delta SNF}$* signal intensity, normalized to area, at heterochromatin in stage 12 egg chambers. Results are from two biological replicates. A two-tailed Welch's t test was used to determine significance. n = 40 for wild-type and n = 44 for the *SuUR$^{\Delta SNF}$* mutant. No outliers were excluded. Contributions: None.



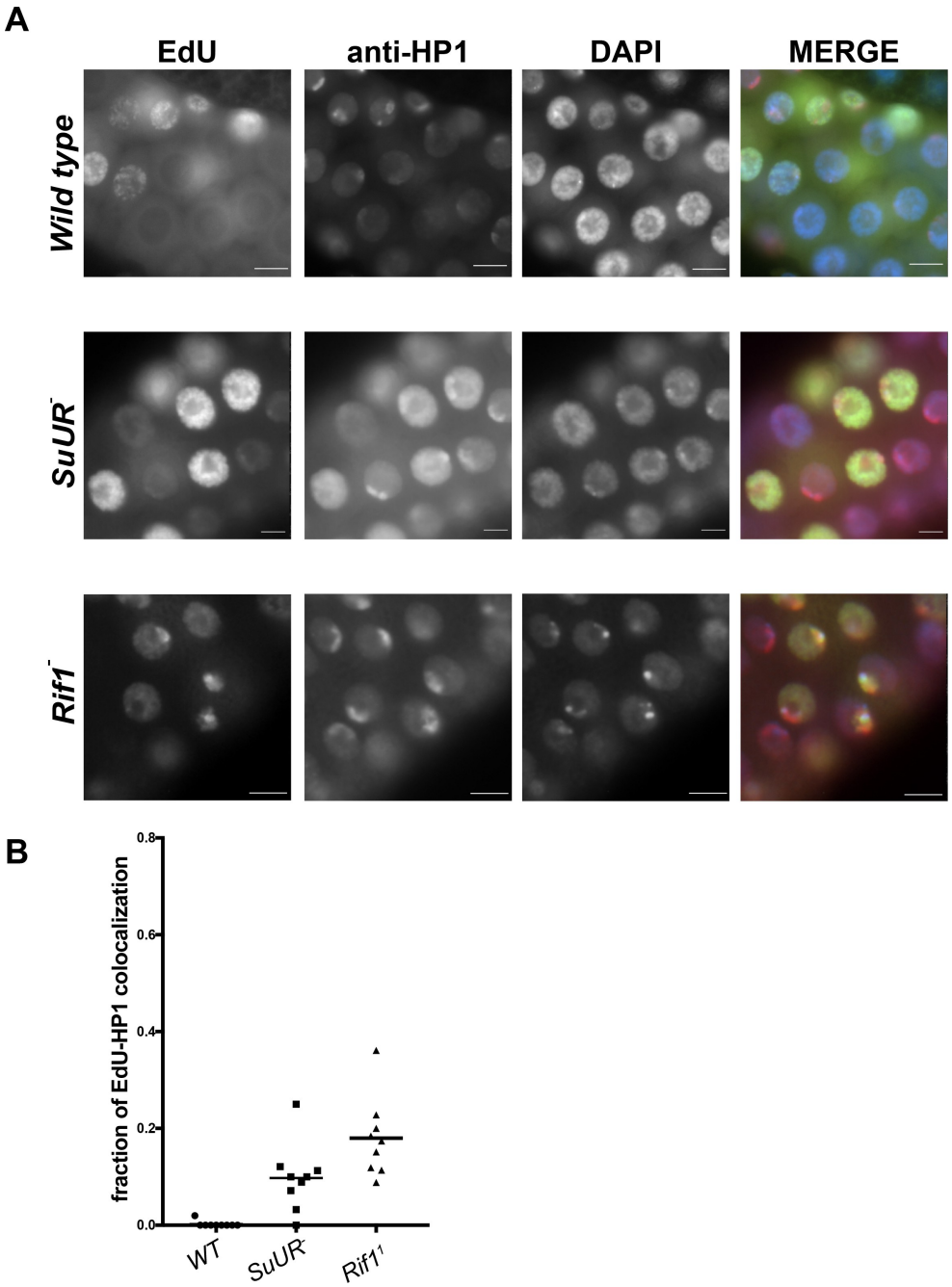
Supplemental Figure 2-3: **Western blot analysis of heat-shock inducible SUUR constructs. (A)** Full Western blots of images used in Figure 2B with total protein loading control. **(B)** Western blot analysis of FLAG-SUUR and FLAG-SNF2 heat-shocked 0 – 24 hr embryos with a total protein loading control. Contributions: None



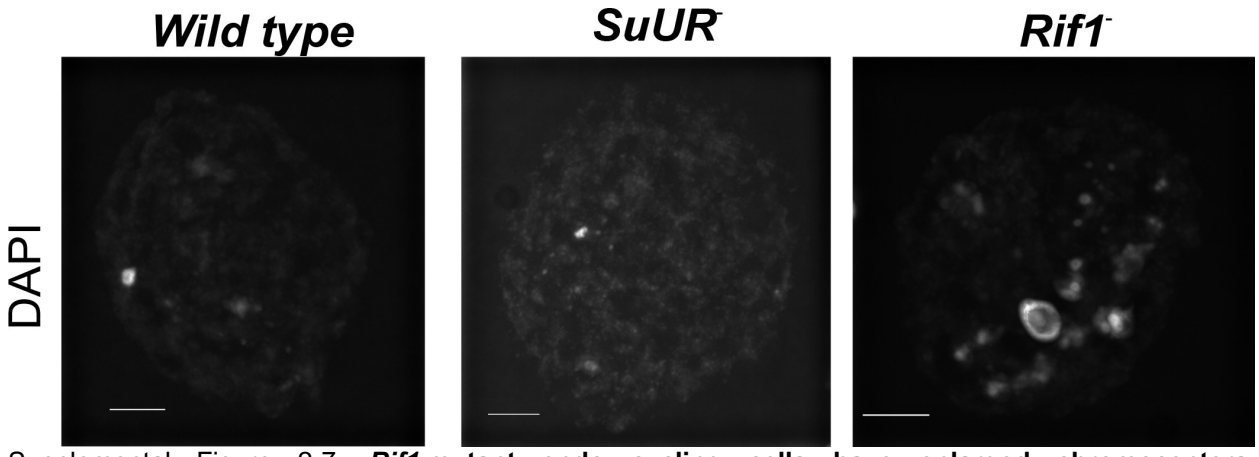
Supplemental Figure 2-4: **Verification of *Rif1* mutants and validation of anti-Rif1 antibody. (A)** Western blot analysis of ovary extracts prepared from the indicated genotypes. Serum produced in guinea pigs was used at 1:1000 dilution. **(B)** Immunofluorescence of ovaries using affinity purified anti-Rif1 antibody produced in guinea pigs. Exposure times were equal between the two genotypes. **(C)** Embryo hatch rate assay comparing embryos laid by wild-type or *Rif1*^{1}*/Rif1*^{2} mutant mothers. n = 300 embryos per genotype. Each data point represents the hatch rate of a group of 10 embryos. An unpaired student t-test was used to generate the p value. Contributions: None.



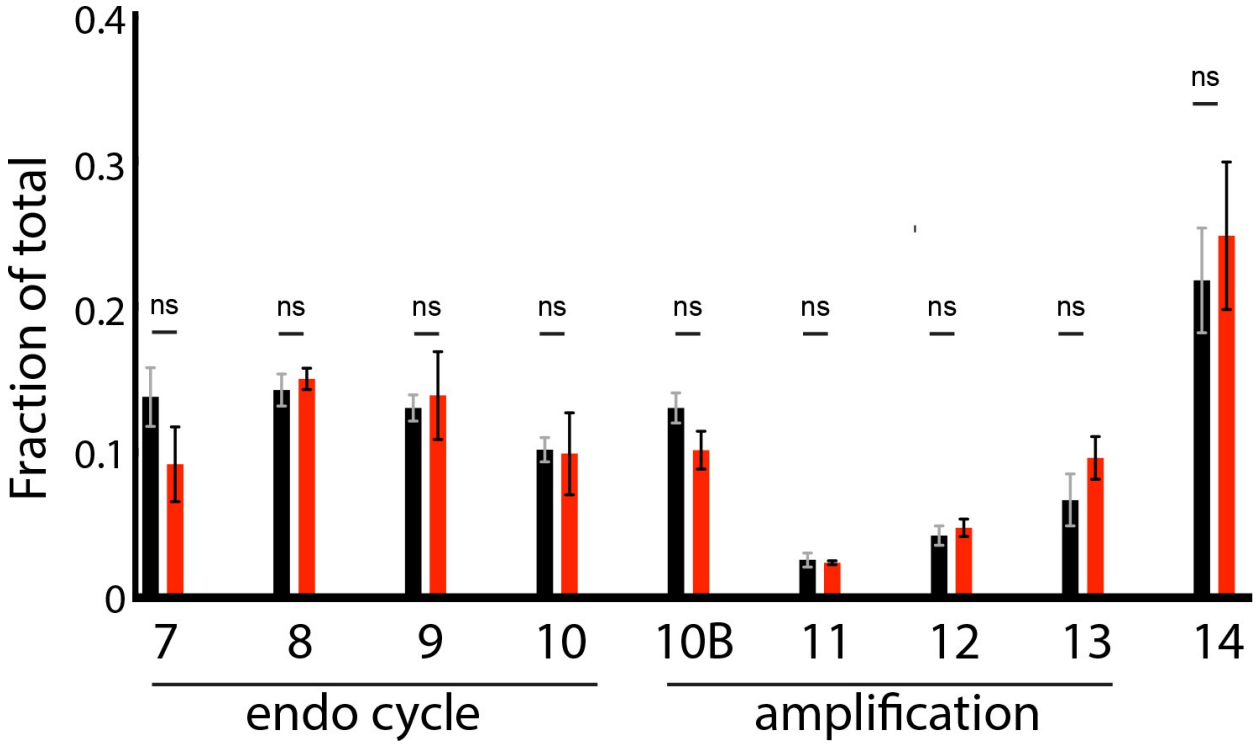
Supplemental Figure 2-5: **Genome-wide copy number profile of the *Rif1* mutant. (A)** Illumina-based copy number profiles of all chromosome arms except the fourth for larval salivary glands of the indicated genotypes. Black bars below each profile represent called underreplicated regions. **(B)** Box plot represents read depth in 10 kb bins in the pericentric chromatin regions for *chr 2L, 2R, 3L* and *3R*. A Welch Two Sample t-test was used to compare the same regions between *SuUR* and *Rif1* mutants. The same wild-type, *SuUR* and 0 – 2 hr embryo plots as in Supplemental 2-1. Contributions: Analysis and visualization.



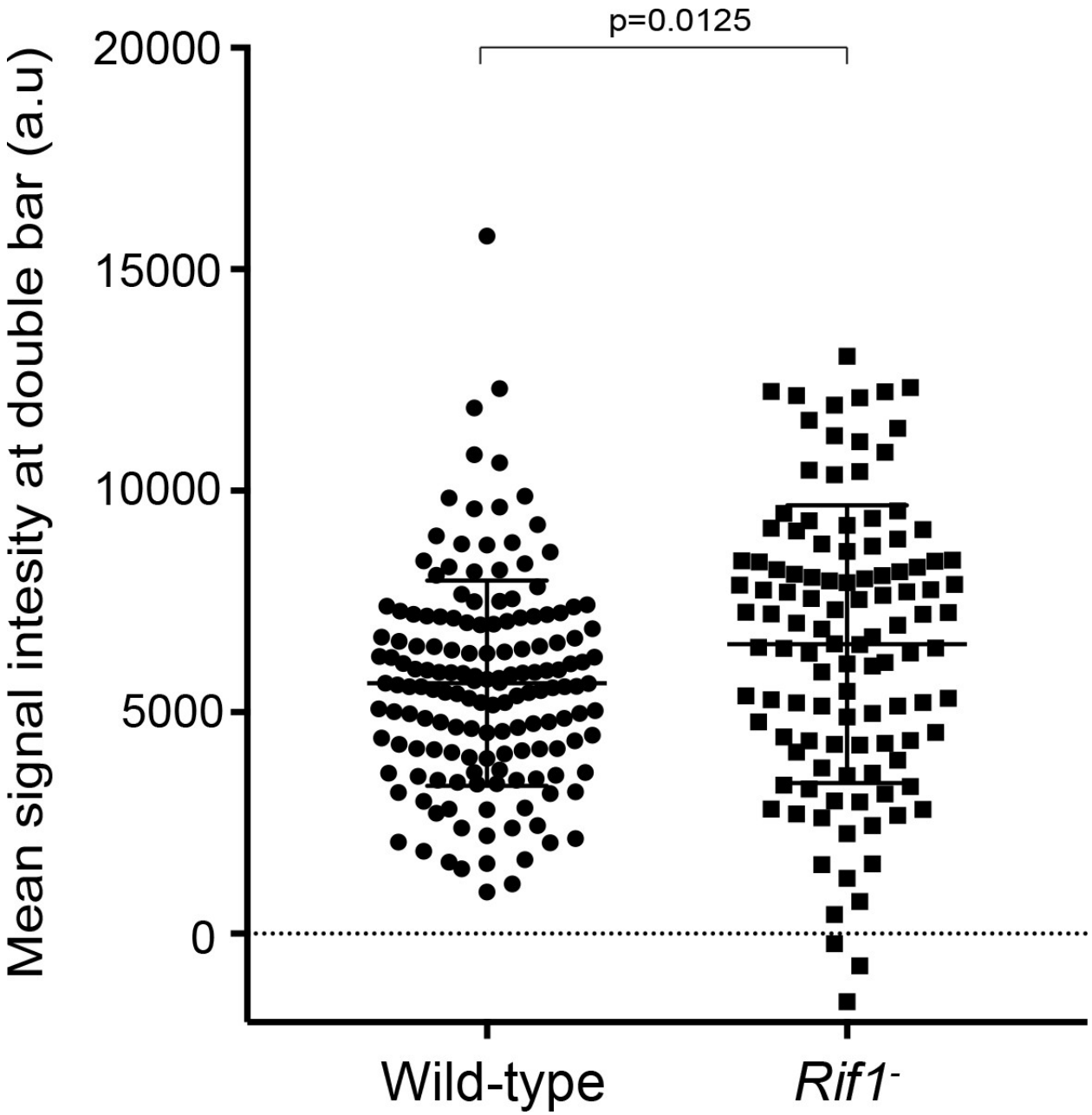
Supplemental Figure 2-6: **Rif1 mutant salivary gland cells display a pattern of late replication.** (**A**) Representative immunofluorescent images of 3rd instar salivary glands pulse labeled with EdU and stained with anti-HP1 to mark heterochromatin. Wild-type cells fail to incorporate EdU into regions of heterochromatin due to underreplication, whereas EdU can be detected in the heterochromatic regions of *SuUR* and *Rif1* mutants. DAPI = blue, EdU = green, HP1 = red (**B**) Quantitation of three biological replicates. Out of the total number of EdU-positive cells, the fraction incorporating EdU predominantly in the heterochromatic (HP1) regions were measured. More than 200 EdU-positive cells were scored for each genotype. Contributions: None.



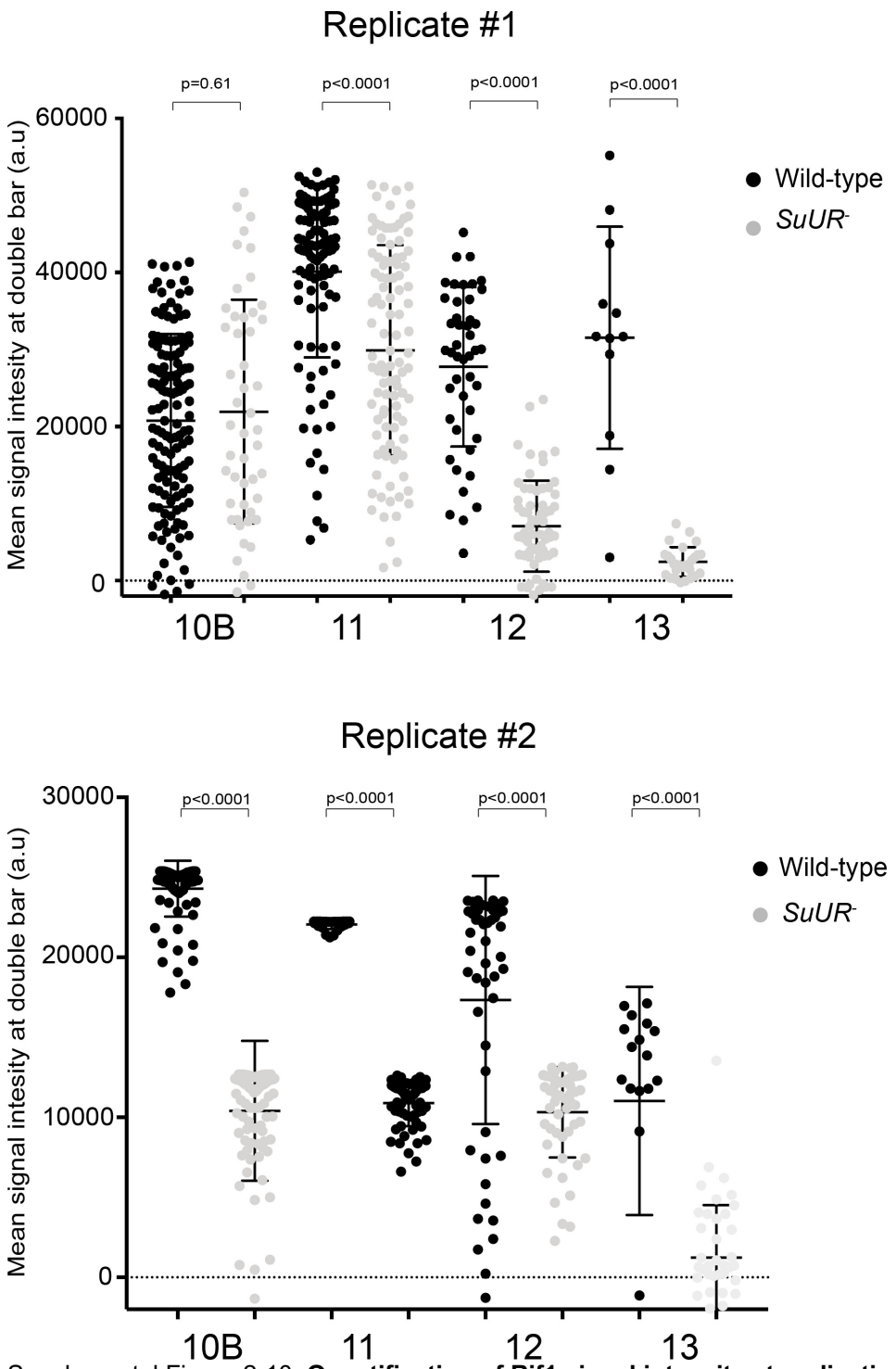
Supplemental Figure 2-7: ***Rif1*** **mutant endo cycling cells have enlarged chromocenters.** Representative images of single nurse cell nuclei from stage 10 egg chambers. Egg chambers were stained with DAPI. Scale bar is 10 μm. Exposure times and scaling are equal in all images. Contributions: None.



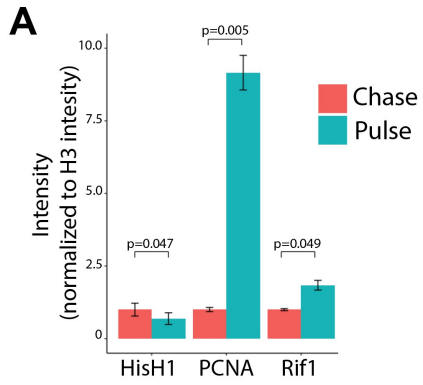
Supplemental Figure 2-8: **The developmental window of gene amplification is not affected by loss of Rif1 function.** Egg chamber distribution from wild-type and *Rif1* mutant ovaries fattened for 2 days on wet yeast. Bars represent the fraction of a given egg chamber stage relative to the total population of counted egg chambers (stages 7 – 17) for five biological replicates. Error bars represent the SEM. A student t test was used to compare the fraction of staged egg chambers for each biological replicate between wild-type and the *Rif1* mutant. There was no significant difference for any stage when comparing wild-type and Rif1 mutant ovaries p=0.12 stage 7; p=0.79 stage 8; p=0.77 stage 9; p=0.92 stage 10; p=0.33 stage 10B; p=0.94 stage 11; p=0.86 stage 12; p=0.33 stage 13 and p=0.30 stage 14). Total number of egg chambers counted: 800 for wild-type and 800 for the *Rif1* mutant. No outliers were excluded. Contributions: None.

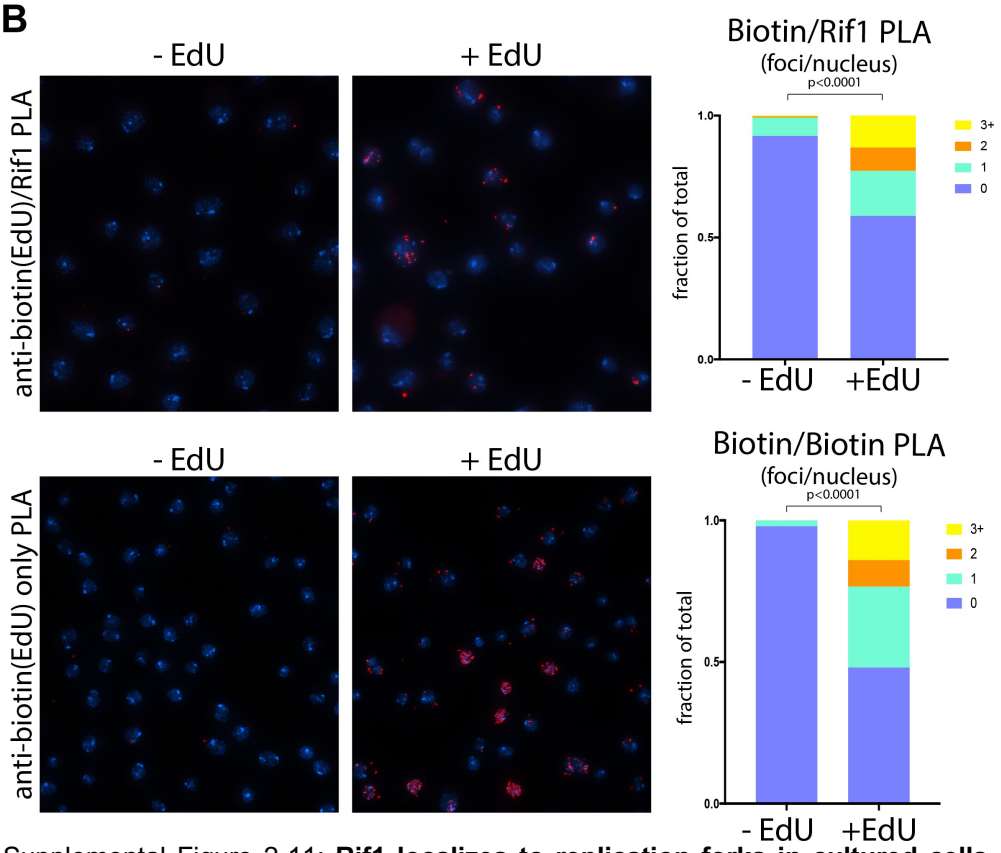


Supplemental Figure 2-9: **Quantification of SUUR signal intensity at replication forks in the presence and absence of Rif1.** SUUR mean signal intensity at double bar structures, normalized for background levels, from stage 12 egg chambers. Results are from two biological replicates. A two-tailed Welch's t test was used to determine significance. n = 156 for wild-type and n = 113 for the *Rif1* mutant. No outliers were excluded. Contributions: None.



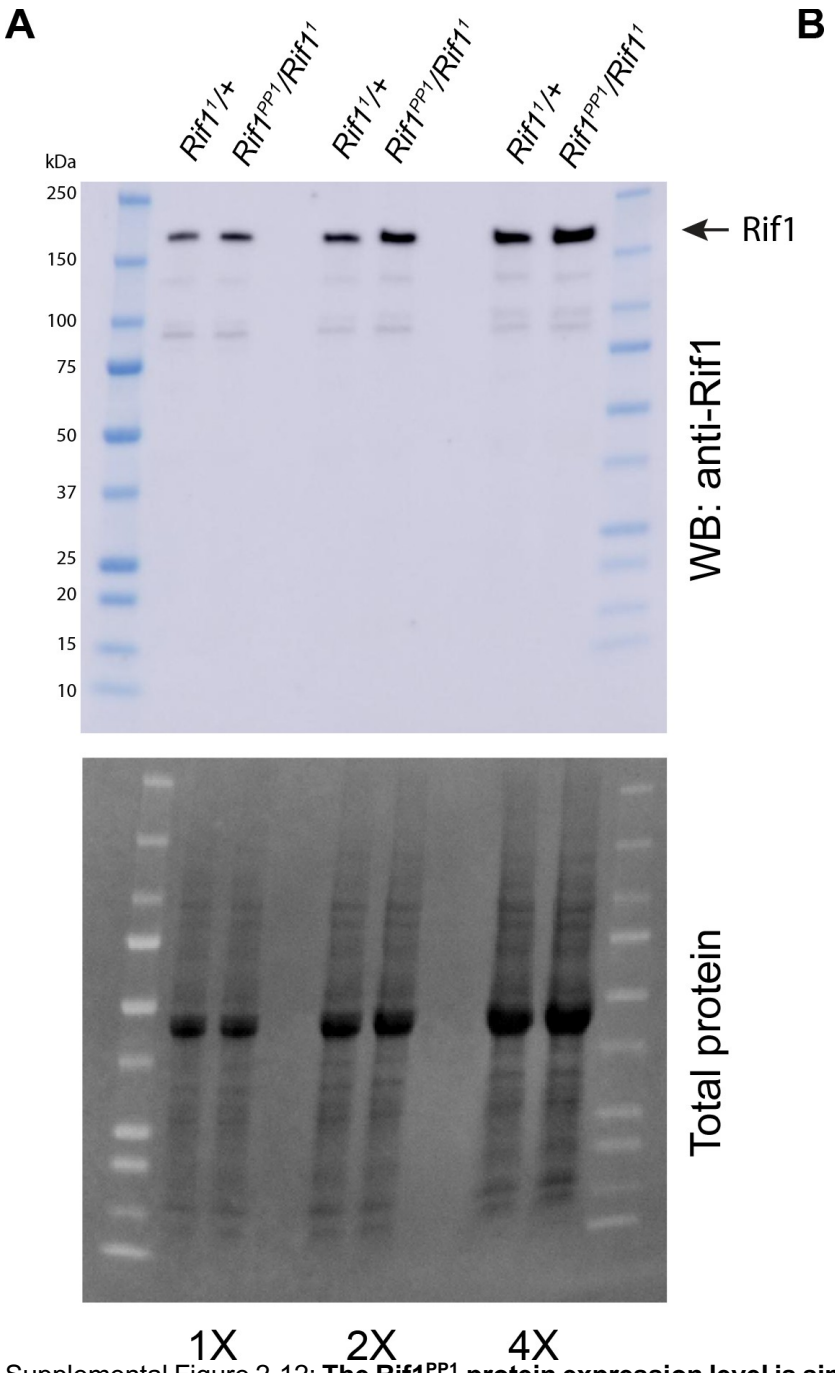
Supplemental Figure 2-10: **Quantification of Rif1 signal intensity at replication forks in the presence and absence of SUUR.** Rif1 mean signal intensity at double bar structures from stage 10B, 11, 12 and 13 egg chambers. Results from two biological replicates are shown independently. A two-tailed Welch's t test was used to determine significance between the same stage of different genotypes. No outliers were excluded. Contributions: None.



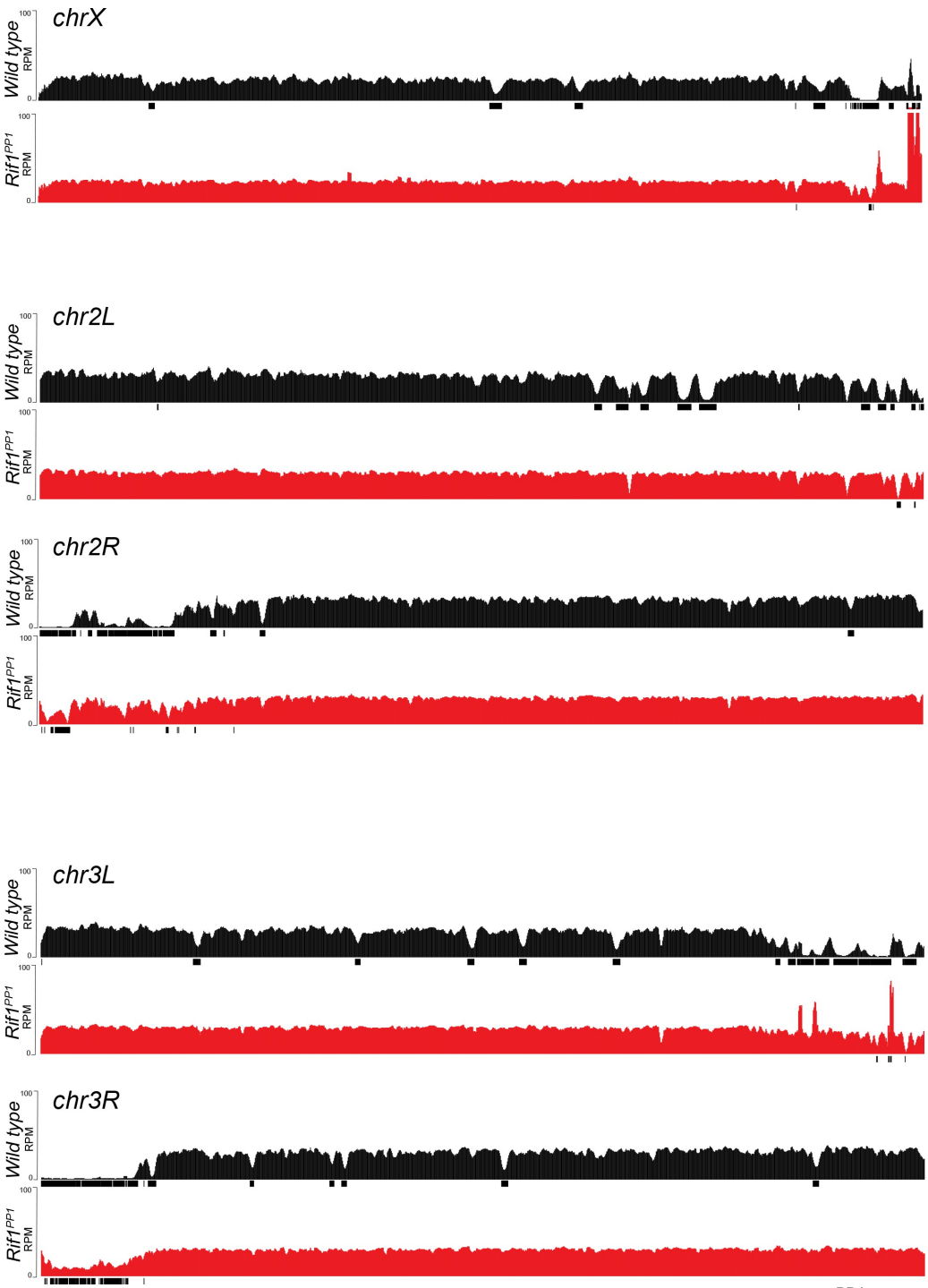


Supplemental Figure 2-11: **Rif1 localizes to replication forks in cultured cells.** (**A**) Quantification of protein intensity from iPOND mass spec data in cultured S2 cells. Intensities represent the summed MS1 spectrum for each peptide identified for Histone H1, PCNA or Rif1. Each sample was normalized to the protein intensity for Histone H3 to account for differences in protein abundance between each sample. Bars represent the average of three biological replicates and the error bars are the S.E.M. A paired t test was used to determine significance. (**B**) Proximity Ligation Assay (PLA) with nascent chromatin in cultured S2 cells reveals a signal between biotinylated EdU (nascent DNA) and Rif1. Representative images from anti-biotin and anti-Rif1 assay in the presence or absence of an EdU pulse. As a positive control, mouse and rabbit anti-biotin antibodies were used together in the presence or absence of an EdU pulse. Number of PLA foci per nucleus in quantified. Quantification of two biological replicates were used per condition. N (total number of nuclei counted)=775 for –EdU and 669 for + EdU (Biotin only). N = 773 for –EdU and 406

for + EdU (Rif1 and Biotin). A two-tailed Welch's t test was used to determine significance. Contributions: Experiment, Analysis, and visualization for A. Trained undergraduate who performed experiment in B.



Supplemental Figure 2-12: **The Rif1^{PP1} protein expression level is similar to wild-type Rif1.** (**A**) Western blot analysis of ovary extracts from *Rif1^{PP1}/Rif1^{1}* and *Rif1^{1}*/+adults. Serum was produced in guinea pigs and used at 1:1000 dilution. Contributions: None.



Supplemental Figure 2-13: **Genome-wide copy number profile of the *Rif1*^{PP1} mutant.** Illumina-based copy number profiles of all chromosome arms except the fourth for larval salivary glands of the indicated genotypes. Black bars below each profile represent called underreplicated regions. Contributions: Analysis and visualization.

Chapter III: Identification of replication fork-associated proteins in Drosophila embryos and cultured cells using iPOND coupled to quantitative mass spectrometry

Abstract

Replication of the eukaryotic genome requires the formation of thousands of replication forks that must work in concert to accurately replicate the genetic and epigenetic information. Defining replication fork-associated proteins is a key step in understanding how genomes are replicated and repaired in the context of chromatin to maintain genome stability. To identify replication fork-associated proteins, we performed iPOND (Isolation of Proteins on Nascent DNA) coupled to quantitative mass spectrometry in Drosophila embryos and cultured cells. We identified 76 and 278 fork-associated proteins in post-MZT embryos and Drosophila cultured S2 cells, respectively. By performing a targeted screen of a subset of these proteins, we demonstrate that BRWD3, a targeting specificity factor for the DDB1/Cul4 ubiquitin ligase complex (CRL4), functions at or in close proximity to replication forks to promote fork progression and maintain genome stability. Altogether, our work provides a valuable resource for those interested in the DNA replication, repair and chromatin assembly during development.

* This chapter has been published as Munden, A., Wright, M. T., Han, D., Tirgar, R., Plate, L. & Nordman, J. T. Identification of replication fork-associated proteins in Drosophila embryos and cultured cells using iPOND coupled to quantitative mass spectrometry. *Scientific Reports* **12**, 6903 (2022).

Introduction

Each and every time a cell divides it must accurately replicate both its genetic and epigenetic information. Core replication factors are known to assemble at replication forks to replicate the genome (e.g. helicase, polymerases). There are, however, likely hundreds of proteins that function at or in close proximity to the replication fork to facilitate replication of difficult-to-replicate sequences, propagate epigenetic information and coordinate replication with other chromatin-related processes such as transcription (Wessel et al. 2019; Dungrawala et al. 2015; Alabert et al. 2014). Replication of the eukaryotic genome requires thousands of replication forks functioning simultaneously to complete replication in a timely manner. Errors generated at a single replication fork during genome duplication can result in mutations or genomic alterations with the potential to cause cell lethality or drive tumor formation (Tomasetti et al. 2017). Further complicating DNA replication is the need to allow regulatory flexibility to accommodate cell-type specific changes in cell division and cell cycle rates that occur during cell differentiation and development (Shermoen et al. 2010; Matson et al. 2017). How replication fork composition and activity is remodeled in response to difficult-to-replicate regions of the genome and in response to changes in developmentally programed changes in S phase regulation has yet to be defined.

Drosophila provides an ideal system to understand how developmentally-programed changes in S phase impact replication fork composition. In contrast to the ~8hr S phases associated with mitotic cell division in differentiated cells, S phases during early embryonic development are extremely rapid. During early embryogenesis and prior to the maternal-to-zygotic transition (MZT) S phases are 3-4 minutes in length. S phase

gradually lengthens as development approaches the MZT and slows to ~75 minutes at the MZT (Yuan et al. 2016; Shermoen et al. 2010). While S phase length can drastically differ during development, the rate of replication fork progression is similar in these different contexts (Blumenthal et al. 1974). The chromatin context that replication forks must navigate also change with development. In pre-MZT embryos, chromatin is devoid of heterochromatin and transcription is largely inactive. Around the time of the MZT, condensed heterochromatin is formed and zygotic transcription is activated (Tadros and Lipshitz 2009; Shermoen et al. 2010). In fact, the extension of S phase at the MZT is largely driven by the onset of late replication and the bulk of S phase is dedicated to replication of heterochromatic sequences (Seller and O'Farrell 2018; Shermoen et al. 2010).

In recent years, several techniques have been established to isolate active replication forks to identify replication fork-associated proteins (Sirbu et al. 2011; Alabert et al. 2014; Gambus et al. 2006). One technique, isolation of proteins on nascent DNA (iPOND), has become widely employed due to its ease of use and the only technical requirement being a short pulse of the nucleotide analog 5-ethynyl-2′-deoxyuridine (EdU) (Sirbu et al. 2011). For iPOND, cells are incubated with a brief pulse of EdU and proteins are crosslinked to nascent DNA. EdU can be biotinylated using click chemistry and newly synthesized DNA and associated proteins are purified using streptavidin beads (Dungrawala and Cortez 2014). A key to identifying proteins at or in close proximity to active replication forks, rather than general chromatin-associated proteins, is a chase sample where a thymidine chase is introduced after the EdU pulse. Proteins enriched in pulse only samples relative to the chase samples are largely replication fork-associated

proteins (Sirbu et al. 2011, 2013; Dungrawala et al. 2015). Another advantage of iPOND is that it can be coupled to quantitative mass spectrometry to identify replication fork-associated proteins in an unbiased manner (Wessel et al. 2019; Dungrawala et al. 2015; Cortez 2017). While iPOND coupled to quantitative mass spectrometry has been used extensively in mammalian cultured cells, it has not been applied in Drosophila or in a developing organism.

To identify proteins at or in close proximity to active replication forks in Drosophila, and to determine if replication fork composition is influenced by development, we have performed iPOND in combination with tandem mass tag (TMT)-based quantitative mass spectrometry in Drosophila post-MZT embryos and cultured cells. Using an iPOND-TMT approach, together with a stringent statistical analysis, we identified 76 and 278 replication fork-associated proteins in post-MZT embryos and Drosophila cultured S2 cells, respectively. While we have confirmed many known replication fork components, we have identified many proteins that do not have known roles at the replication fork. By performing a targeted RNAi-based screen of select factors, we have identified the Cul4 E3 ubiquitin ligase specificity factor, BRWD3, as a replication fork-associated protein that affects replication fork progression.

Results

Establishing iPOND in the developing embryo

To define the landscape of proteins at or in close proximity to active replication forks during development, we turned to Drosophila due to its well-characterized S phase programs that are known to significantly change during development. To identify

replication fork-associated proteins, we chose to use iPOND because it does not require protein tags or extensive multi-step purifications (Sirbu et al. 2011). We chose post-MZT Drosophila embryos (3-5 hours after egg laying -AEL) for our embryonic sample. During this developmental time point, S phase is ~ 75 minutes with the bulk of that time devoted to replication of heterochromatin (Fig. 3-1A) (Shermoen et al. 2010).

Nucleotide analogs and other small molecules are unable to enter embryos without permeabilization or direct injection (Limbourg and Zalokar, 1973). To obtain sufficient EdU-labeled embryos for iPOND, we developed a large-scale permeabilization strategy. Starting with 3–5 h embryos collected from a population cage, embryos were permeabilized and pulse labeled with EdU for 10′ using custom collection baskets (see "Experimental procedures"; Fig. 3-1B). Using this approach, we could routinely isolate 100–200 mg of EdU-labeled embryos from a single collection basket. To determine if EdU-labeled 3–5 h post-MZT embryos could be used for iPOND, we biotinylated embryos using Click chemistry as previously described and the EdU-labeling efficiency was determined by staining embryos with fluorescently labeled streptavidin (Fig. 3-1C) (Dungrawala and Cortez, 2017). Two key controls were also used; following the 10′ pulse of EdU, embryos were immediately transferred into medium containing thymidine for 30′ (chase sample). Second, age-matched embryos were mock treated and biotinylated exactly as the pulse and chase samples (no EdU control). To determine if iPOND could be used to isolate replication-dependent chromatin, we performed a single-step purification of biotinylated EdU-containing chromatin from our pulse, chase and no-EdU samples. We probed lysates for histone H3 as a mark of total chromatin (Fig. 3-1D) (Sirbu et al. 2011). We found that the recovery of chromatin was dependent on EdU

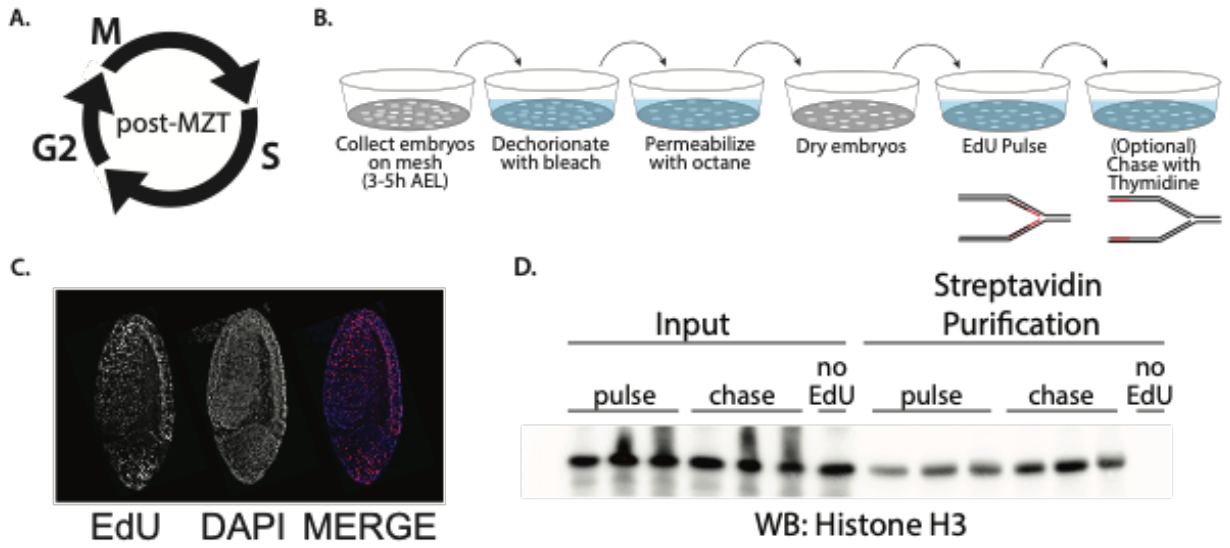


Figure 3-1: Establishing iPOND in the developing embryo. (**A**) A schematic of the rapid cell cycle in post-MZT embryos (3–5 h AEL). (**B**) Experimental design for large-scale EdU labeling of embryos for iPOND. (**C**) Representative image of an EdU-labeled post-MZT embryo used for iPOND purifications. Embryo labeling was deemed successful if > 50% of the embryos were uniformly labeled. (**D**) Western blot of three biological replicates for pulse and chase iPOND samples with a no EdU pulse control. Anti-H3 antibody is used as a marker of total chromatin recovery. Contributions: None.

incorporation. This indicates that iPOND can be applied to Drosophila embryos to isolate native chromatin.

iPOND mass spectrometry identifies proteins at or in close proximity to active replication forks in Drosophila embryos

Now that we established iPOND as a technique to identify proteins at or in close proximity to active replication forks in Drosophila embryos, we wanted to identify the repertoire of proteins associated with replication forks in early embryos in an unbiased manner using quantitative mass spectrometry. Therefore, we coupled our iPOND purifications to tandem mass tag (TMT) labeling, which allows us to multiplex and quantify the relative abundance of peptides across multiple biological replicates in a single mass spectrometry experiment (McAlister et al. 2012). We optimized the amount of labeled

embryos necessary for reproducible purification and mass spectrometry experiments. Ultimately, we found that 0.5g of EdU-labeled embryos routinely provided robust and reproducible mass spectrometry results. We collected EdU-pulsed embryos from four biological replicates of 3-5h embryos. EdU-pulsed embryos were either fixed immediately (pulse) or chased with thymidine for 30 minutes prior to fixation (chase). After EdU purification and verification via Western blot, peptides derived from pulse and chase samples were TMT labeled, separated using multidimensional protein identification technology (MudPIT) and quantified by mass spectrometry (Fig. 3-2A).

To identify proteins at or in close proximity to active replication forks, we focused on proteins that were enriched in the EdU pulse samples relative to the thymidine chase controls. To ensure that the differences were not due to differences in purification and/or labeling efficiencies, we normalized proteins to histone H4 (see Methods). Using this analysis, we identified 76 proteins that were significantly enriched in either the EdU pulse or thymidine chase samples (Supp. Table 3-1). Most of the proteins enriched in our experiments were derived from the EdU pulse samples (Fig. 3-2B; 74 of 76). This is likely due to the relatively short thymidine chase time we adopted to allow us to focus on replication fork-associated proteins. Several lines of evidence indicate that our iPOND strategy is effective in isolating replication fork-associated proteins from Drosophila embryos. First, out of the top 25 enriched proteins in our data set, 18 are known replication factors (Supp. Table 3-2). Second, a Gene Ontology (GO) analysis of the 76 proteins enriched in the EdU pulse samples was highly enriched for DNA replication and DNA replication-associated processes (Fig. 3-2C). Therefore, we conclude that iPOND is an

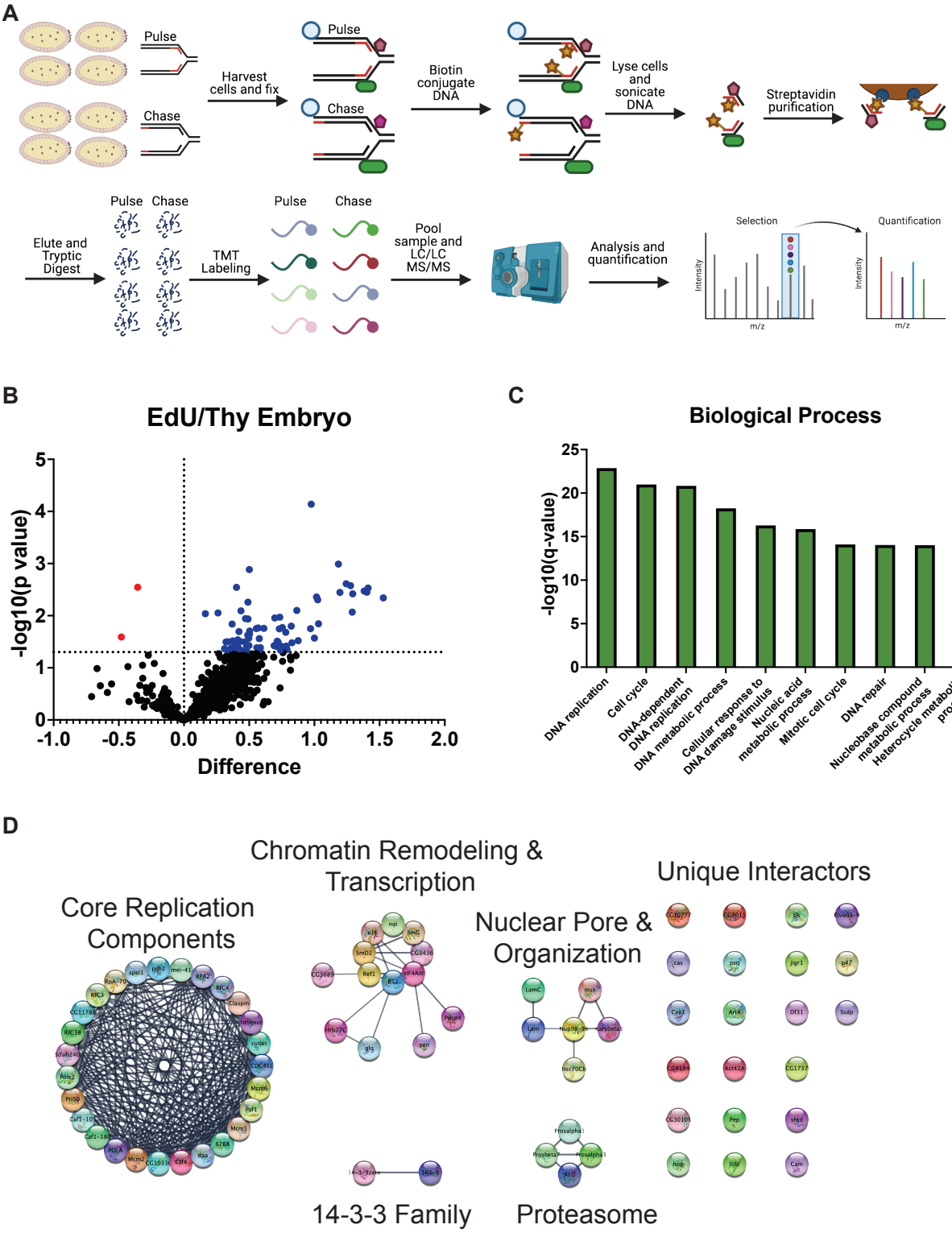


Figure 3-2: **iPOND coupled to quantitative mass spectrometry in the post-MZT embryos.** (**A**) A schematic of the labeling and mass spectrometry process for iPOND-TMT in Drosophila post-MZT

embryos. (**B**) Volcano plot visualizing proteins identified as enriched or depleted in the pulse versus the chase embryo samples. Enrichment on the X-axis (log2[pulse]-$\log_2$[chase]) and $-\log_{10}$(p-value) on the Y-axis. (**C**) The top 10 enriched biological processes of the proteins enriched in the pulse sample as determined by Gene Ontology (GO) analysis. (**D**) Network map of the proteins enriched in the pulse sample, clustered into groups of known interactors using the STRING database with no additional interactors added. Contributions: TMT labeling for the experiment, analysis, visualization.

effective strategy to proteins at or in close proximity to active replication forks during Drosophila embryogenesis.

We wanted to categorize the proteins in our data set in an unbiased manner to identify existing and potentially new protein networks centered around the replication machinery. To this end, we analyzed all enriched proteins using the STRING network in Cytoscape to identify proteins known to interact with one another. This analysis identified a network cluster of 27 known DNA replication and repair proteins (Fig. 3-2D). This cluster contains known helicase subunits, DNA polymerases, clamp loading factors and other factors (Fig. 3-2D). Additionally, it contains proteins involved in replication fork stability and response to DNA damage (Mei-41/ATR, Timeout/Timeless, CG10336/Tipin and Claspin) (Sibon et al. 1999; Benna et al. 2010; Lee et al. 2012; Gotter et al. 2007; Saldivar et al. 2017). Unexpected clusters were also identified. For example, we identified a cluster of proteins involved in RNA processing and a cluster involved in nuclear organization and the nuclear pore. We also identified several unique replication fork-associated proteins that did not readily form interaction networks. Together, we conclude that iPOND can be used in Drosophila embryos to identify existing and potentially new replication fork-associated proteins.

iPOND mass spectrometry identifies proteins at or in close proximity to active replication forks in Drosophila cultured cells

To extend the utility of iPOND in Drosophila, we performed iPOND in Drosophila S2 cultured cells. We previously performed iPOND in S2 cells, but did not couple iPOND to quantitative mass spectrometry (Munden et al. 2018). First, we validated that iPOND functions in S2 cells (Supp. Fig. 3-1A). Next, we performed iPOND coupled to quantitative mass spectrometry with TMT labeling using ~10^9 cells/ biological replicate (Fig. 3-3A). Similar to our results in embryos, all of the enriched proteins were found in the pulse sample rather than the chase (Fig. 3-3B). This is likely due to the short chase time we used in these experiments. One difference we noted, however, is that we identified 278 proteins at or in close proximity to active replication forks in S2 cells (compared to 76 in embryos) (Supp. Table 3-3). While significantly higher than embryos, this protein number is similar to other iPOND and iPOND-like data sets in mammalian cells.

Similar to our embryo data set, multiple lines of evidence indicate that our purifications successfully captured replication fork-associated proteins. Out of the top 25 enriched proteins in our data set, 22 are known replication factors (Supp. Table 3-4). Next, a Gene Ontology (GO) analysis of proteins enriched in the EdU pulse samples was highly enriched for DNA replication and DNA replication-associated processes (Fig. 3-3C). We attempted to generated an unbiased interaction network map using the STRING network in Cytoscape for the 278 enriched proteins, however, the networks were too dense to effectively visualize any meaningful interaction network hubs (Supp. Fig. 3-1B). For prioritization, we selected the proteins with an adjusted p value of < 0.05 and greater than 1.8-fold enrichment in the pulse relative to the chase. These stringent statistical cutoffs

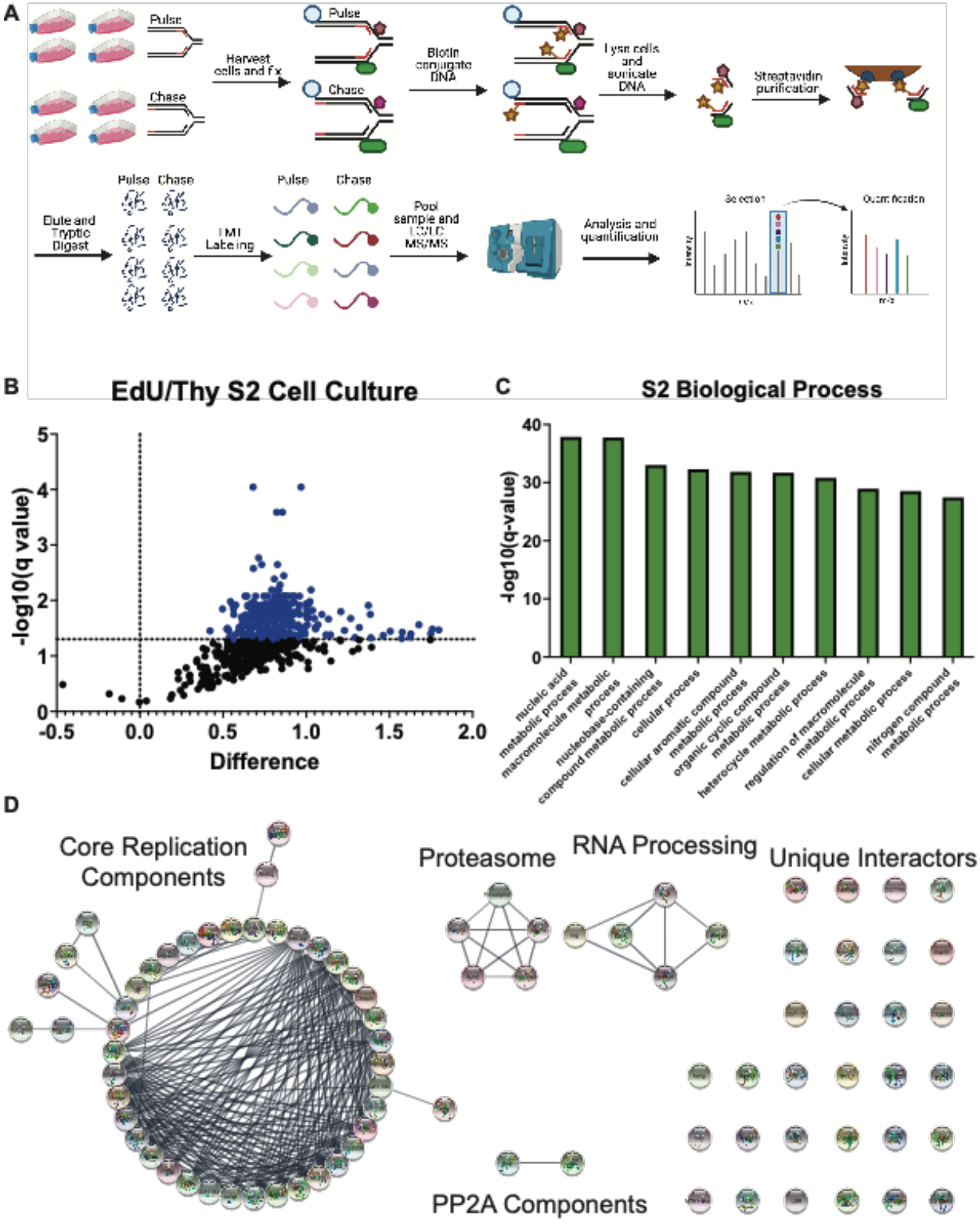


Figure 3-3: **iPOND coupled to quantitative mass spectrometry in S2 cells.** (**A**) A schematic of the labeling and mass spectrometry process for iPOND-TMT in Drosophila S2 cells. (**B**) Volcano plot visualizing

those proteins identified as enriched or depleted in the pulse versus the chase cell culture samples. Enrichment ($log2$[pulse]-log_2[chase]) on the X-axis and $-\log_{10}$(p-value) on the Y-axis. (**C**) The top 10 enriched biological processes of the proteins enriched in the pulse sample as determined by Gene Ontology (GO) analysis. (**D**) Network map of the proteins enriched in the pulse sample, clustered into groups of known interactors using the STRING database with no additional interactors added. For visualization, we included proteins with a corrected p value of < 0.05 and a > 1.8-fold fold enrichment (99 total proteins). The full list of enriched interactors can be found in Supplemental Table 4. Contributions: Experiment, analysis, and visualization.

revealed 99 high-confidence proteins that were ultimately used to generate interaction network clusters, which consisted of known replication fork factors, further validating this data set and statistical analysis (Fig. 3-3D). Also, we identified networks containing proteosome components, RNA processing factors, protein phosphatase 4 complex (PP4) and a number of proteins with no recognized network connections (Fig. 3-3D)

BRWD3 affects genome stability and replication fork progression

To determine if any of the replication fork-associated factors we identified affect genome stability, we used RNAi to deplete select factors and measured the global level of DNA damage. We chose to perform this targeted screen in S2 cells rather than post-MZT embryos due to the rapid and efficient depletion that can be obtained in S2 cells without the need to generate new reagents (Echeverri and Perrimon 2006). To quantify the global levels of DNA damage, we measured the level of phosphorylated H2Av (ɣ-H2Av), the Drosophila equivalent to mammalian ɣ-H2Ax, which is found at double strand breaks and stalled replication forks by immunofluorescence (Madigan et al. 2002; Mah et al. 2010). Of the 15 factors we chose, some but not all have known functions in DNA replication or DNA repair (Jin et al. 2006; Vannier et al. 2013; Townsend et al. 2021; Bell et al. 2011; Bandura et al. 2005; Mansfield et al. 1994; Kappes et al. 2011; Sousa-Nunes et al. 2009; Klymenko et al. 2006; Sibon et al. 1999). We validated knock down efficiency

and the effect on cell proliferation for all factors (Supp. Fig 3-2A and 2B). As our negative control, we used a non-targeting RNA to *GFP* that is not present in S2 cells. As a positive control we targeted DNA polymerase alpha (*DNA polα*), which is necessary for continual priming of the lagging strand (Fig 3-4a) (Muzi-Falconi et al. 2003). Depletion of several factors resulted in increased H2Av phosphorylation (Fig. 3-4a). For example, depletion of *Cul4*, *RTEL*, *ELG1* and *BRWD3* all caused increased DNA damage consistent with mammalian studies (Jin et al. 2006; Vannier et al. 2013; Townsend et al. 2021; Bell et al. 2011). Interestingly, knockdown of *polybromo*, a component of the Brahma chromatin remodeling complex (Thompson 2009), also caused an increase in DNA damage (Fig. 3-4a). Depletion of several factors caused a decrease in ɣ-H2Ax signal intensity, suggesting these factors contribute to DNA damage detection or signaling (Fig. 3-4a). Consistent with this hypothesis, depletion of *mei41* (the Drosophila ATR ortholog) decreased ɣ-H2Av intensity.

BRWD3 is a targeting specificity factor for the DDB1/Cul4 ubiquitin ligase complex (CRL4) (Jackson and Xiong 2009). In mammalian cells, one of the BRWD3 orthologs DCAF14/PHIP associates with replication forks upon DNA replication stress (Townsend et al. 2021). Depletion of DCAF14 results in a modest increase in DNA damage, which is exacerbated upon replication stress (Townsend et al. 2021). Depletion of BRWD3 in Drosophila S2 cells causes an increase in ɣ-H2Ax levels in unstressed cells (Fig. 3-4a). This suggests that BRWD3/DCAF14 has an evolutionarily conserved role at the replication fork to maintain genome stability. Given these observations, we wanted to determine if BRWD3 affects replication fork progression in unchallenged Drosophila cells. To this end, we developed a DNA combing protocol for Drosophila S2 cells. While we

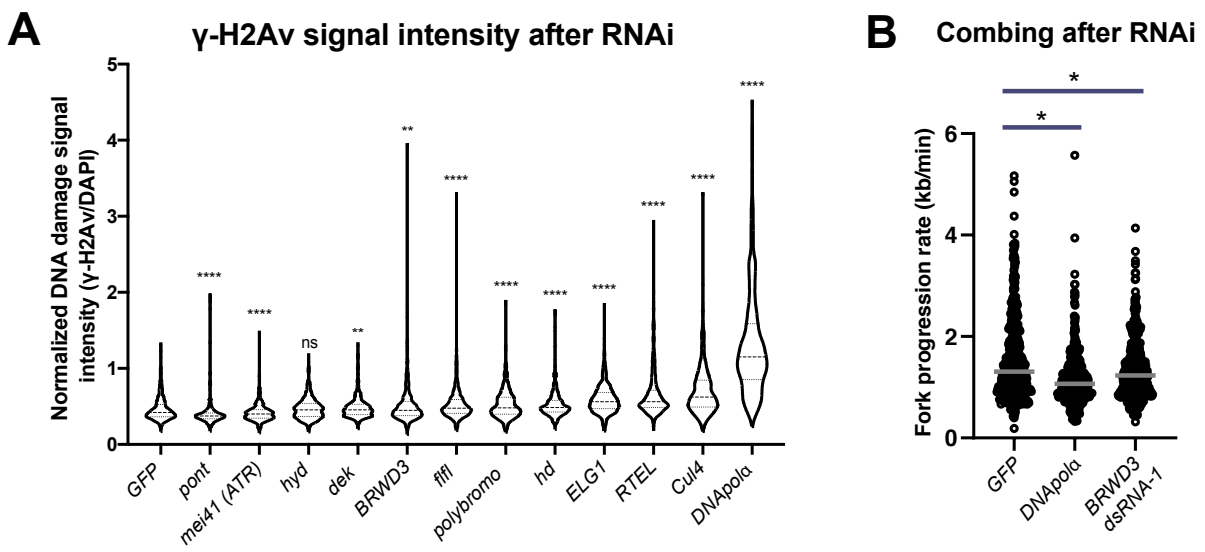


Figure 3-4: **BRWD3 affects genome stability and replication fork progression.** (**A**) RNAi-based depletion screen of candidate replication fork-associated proteins in S2 cells. Violin plots of the γ-H2Av intensity per nucleus normalized to total DNA content. Each distribution represents the signal intensities of 700 randomly selected cells from two biological replicates. ****$p < 0.0001$ and **$p < 0.01$ using a Kruskal–Wallis one-way analysis of variance. (**B**) Rate of fork progression in control and BRWD3 depleted S2 cells. 400 fibers from two biological replicates were pooled. BRWD3 dsRNA-1 was used for this experiment. Bars represent the median fork speed. *$p < 0.05$ using a Kruskal–Wallis one-way analysis of variance followed by a Dunn's multiple comparison post-test. Contributions: None.

initially attempted to perform DNA combing with both IdU and CldU nucleoside analogs, we were unable to successfully perform combing with IdU (data not shown). This would have allowed us to measure fork rate, fork asymmetry and inter-origin distance. To solely measure the rate of fork progression, we performed DNA combing analysis with CldU as the sole nucleotide analog. As positive and negative controls, we used interfering RNAs against *DNA polα* and *GFP*, respectively. Depletion of *BRWD3* caused a decreased rate of fork progression in untreated cells (Fig. 3-4b). To rule out an off-target effect of the RNAi construct, we performed the DNA combing assay with an independent RNAi construct (Supp. Fig. 3-3A). We also validated the knock down efficiency of both RNAi constructs by Western blot (Supp. Fig. 3-3B). Thus, we conclude that BRWD3 functions

at or in close proximity to the replication fork to promote replication fork progression and genome stability in Drosophila.

Discussion

By developing a large-scale EdU labeling protocol in Drosophila embryos, we were able to perform iPOND in a developing organism. By coupling iPOND to quantitative mass spectrometry we identified 76 replication fork-associated proteins in Drosophila post-MZT embryos. Giving confidence to this method of identifying replication fork-associated proteins, 32 proteins we identified have known roles in DNA replication or repair. We note, however, that not all know replication fork-associated proteins were identified in our data set. Multiple reasons likely explain this observation. First, we used a stringent statistical cut off in our analysis to avoid false positives (see Methods). Second, either due to loss in purification or difficulty in mass spectrometry, some replication proteins are simply not detected by mass spectrometry, resulting in false negatives. Therefore, we suspect that 76 proteins are an underestimate of the total number of replication fork-associated proteins in post-MZT embryos.

While iPOND-TMT identified 76 proteins in post-MZT embryos, the same technique uncovered 278 proteins in Drosophila cultured cells. Although this number of proteins is higher than what we observed in embryos, it is similar to recent iPOND and iPOND-like experiments coupled to quantitative mass spectrometry performed in mammalian cells (Wessel et al. 2019; Alabert et al. 2014). The difference in protein number between post-MZT embryos and cultured cells could be due to cell-type-specific factors in S2 cells or technical differences when performing iPOND in embryos vs.

cultured cells. It should be noted, however, that the rate of replication fork progression is similar in Drosophila embryos and cultured cells (Blumenthal et al. 1974). Given that a single pulse of EdU is the only technical limitation with iPOND, it seems unlikely that differences in the amount of EdU labeling are responsible for the differences in protein number between the two developmental states. One complicating factor when trying to compare iPOND data sets for cell-type-specific factors is that lack of a protein in one sample could be due to a limitation in peptide detection in mass spectrometry. Therefore, we cannot use the lack of a protein in one developmental sample as direct evidence that a protein is cell-type specific. Nonetheless, our data reveal numerous replication fork-associated proteins in Drosophila embryos and cultured cells that can serve as a resource for anyone interested in replication fork composition and activity.

One factor that we identified as a replication fork-associated protein is BRWD3. Interestingly, one of the BRWD3 orthologs in mammalian cells also functions at the replication fork to maintain genome stability upon replication stress (Townsend et al. 2021). One key difference, however, is that in Drosophila BRWD3 functions at or in close proximity to active replication forks in the absence of exogenous replication stress. Therefore, while BRWD3 and DCAF14 are both substrate specificity factors for CRL4, they likely function differently in mammalian cells and Drosophila. While it is tempting to speculate that $CRL4^{BRWD3}$ targets a critical factor for ubiquitylation at the replication fork, further work will be necessary to test this hypothesis. For example, BRWD3 could alter the activity of a factor that directly controls fork progression away from a replication fork. Therefore, although BRWD3 can be found at or in close proximity to active replication forks, it's effect on replication fork progression could be indirect.

In summary, we have developed a protocol for the biochemical isolation of replication fork-associated proteins in Drosophila embryos and cultured cells. Our work suggests that replication fork composition can be modulated during development. Importantly, we have provided a resource of replication fork-associated factors in Drosophila for those interested in DNA replication, DNA repair and chromatin dynamics during replication.

Materials and Methods

EdU pulsing of embryos

Oregon R flies were expanded into population cages on grape juice plates supplemented with wet yeast. Cages were kept at 25^{o}C in a humidified room and plates changed daily. Prior to embryo collections, flies were precleared for at least two hours. To acquire post-MZT embryos, flies were allowed to lay for two hours, and the plate was aged for three hours at 25^{o}C to obtain 3-5 hours AEL embryos. Embryos were transferred to a container with a wire mesh bottom, washed in water and embryos were dechorionated in 50% bleach for two minutes. After washing, embryos were arranged in a monolayer on the mesh and bucket were dried with paper towels. Embryos were allowed to air dry 4-10 minutes, then submerged in octane for precisely 3.5 minutes with gentle shaking. Embryos were then air dried for one minute while shaking. Permeabilized embryos were pulsed with 10 M EdU in EBR for 10 minutes. For chase samples, EdU-pulsed embryos were transferred to a new solution containing 20M of thymidine for an additional 30 minutes. After pulse/chasing, embryos were transferred to a scintillating flask in 10mL of heptane. 10mL of 4% PFA was added (2% final) and embryos were

shaken vigorously at room temperature for 20 minutes. After fixation, the bottom layer of PFA was removed and an equal volume of methanol was added. Embryos were shaken by hand for one minute, settled and heptane was removed. Embryos were washed in methanol twice and transferred to PBS + 0.1% Triton X-100 and permeabilized overnight at 4°C. For each batch of embryos, a small fraction was taken and biotinylated and incubated with 568-Streptavidin to ensure that at least 50% of embryos were labeled. Successful collections were pooled to obtain 500 L of embryos per biological replicate.

EdU pulsing of S2 cells

S2 cells were obtained directly from the DGRC. Cells were confirmed negative for mycoplasma contamination via PCR. Cells were grown in Schneider's Drosophila Medium with 10% heat-inactivated FBS (Gemini Bio Products) and 100 U/mL of Penicillin/Streptomycin (Fisher Scientific) and kept at 25°C. Cells were pulsed as described in (Dungrawala and Cortez 2014). Briefly, three T225 flasks of 70% confluent cells were pulsed with 10 M of EdU for 9 minutes. Cells were scraped and spun down for three minutes at 300xg. 10mL of 2% paraformaldehyde (PFA) was added to each flask and samples were fixed at room temperature on a nutator for 20 minutes. Paraformaldehyde was neutralized with glycine and cells were centrifuged for five minutes at 900xg at 4°C and resuspended in PBS with 0.1% Triton X-100 at 4°C until processing. For the chase sample, after centrifuging the cells were resuspended in cell media with 20 M thymidine and incubated for 30 minutes in the cell culture incubator before fixation. Three T225 flasks were pooled for each replicate (~$7.5e^8$ cells per replicate).

iPOND

Embryos and S2 cells were biotinylated as described in (Dungrawala and Cortez 2014). Briefly, PBS, $CuSO_4$, Biotin-Azide, and sodium ascorbate were mixed and added to labeled cells and embryos for 30 minutes. After biotinylation, cells or embryos were washed with PBS + 0.1% Triton X-100. A crude nuclear extract was generated by douncing embryos in Buffer 1 (15 mM HEPES pH 7.6, 10 mM KCl, 5 mM $MgCl_2$, 0.1 mM EDTA, 0.5 mM EGTA, 350 mM sucrose) (Shao et al. 1999)twelve times using a B-type homogenizer and centrifuged for 15 minutes at 8000xg. This pellet was resuspended in 1.2mL of LB3 (1 mM EDTA, 0.5 mM EGTA, 10 mM Tris pH 7.5, 100 mM NaCl, 0.1% Na-Deoxycholate, 0.5% N-Lauroyl sarcosine) (MacAlpine et al. 2010) with 2X protease inhibitors. Cells were resuspended in 1.2 mL LB3 lysis buffer with 2x protease inhibitors. Samples were sonicated in a Bioruptor Plus (Diagenode) at high power, 10 cycles at 30" seconds on/30" seconds off. After a short break, samples were vortexed and this was repeated until 40 total cycles were achieved. 100 L of Streptavidin C1 Dynabeads were extensively washed with LB3 and added to each sample. Samples were incubated at 4^{o}C for two hours on a nutator. The unbound material was reserved to verify chromatin fragmentation. Beads were washed five times in LB3, with the 4th wash containing 500 mM NaCl. To elute, samples were incubated at 65^{o}C overnight on thermoblock in 1:1 combination of LB3:SB (20% glycerol, 20% SDS, 120 mM Tris pH 6.8). The next day, the eluate was removed from the beads and added to 2x Laemmli buffer with DTT and boiled for 10 minutes. This lysate was used for western blot and mass spectrometry experiments.

Western blotting

Lysates from iPOND samples were loaded onto a 4-15% Mini-Protean Stain-free protein gel (BioRad). After running the gel, samples were transferred onto 0.2 M PVDF using the Transblot Turbo system (BioRad). Membranes were blocked in 5% milk, and incubated with the appropriate antibody for 1 hour at room temperature. Histone H3 (abcam 21054, 1:3000) was used to verify the success of iPOND. After washing in TBS + 0.1% Tween-20 (TBST), secondary antibodies (Jackson Labs) conjugated with HRP were added at 1:10,000 (mouse) or 1:20,000 (rabbit). After 30 minutes at room temperature, membranes were washed with TBST, incubated with Clarity ECL for 5 minutes (Bio-Rad) and visualized using a Bio-Rad ChemiDoc MP Imaging System.

TMT Labeling

After verifying iPOND was successful by Western blot (5% of total material), the remaining purified material was precipitated using methanol and chloroform and washed with methanol to remove excess detergent. Protein was resuspended in 5 L fresh 1% Rapigest. 32.5 L of mass spectrometry grade water with HEPES (pH 8.0 at a final concentration of 100mM). Disulfide bonds were reduced with freshly made 5mM TCEP and incubated for 30 minutes at room temperature. Fresh Iodoacetamide was added at a final concentration of 10mM to acetylate free sulfhydryl bonds. Protein was digested overnight with 0.5 g trypsin at 37^{o}C with shaking and covered from light. The next day, samples were labeled using a TMT10plex kit (Thermo Scientific catalog #90110). TMT labels were resuspended in acetonitrile and each sample was incubated with the appropriate amount of TMT reagent for 1 hour at room temperature. Excess label was

neutralized with 0.4% final concentration of ammonium bicarbonate for 1 hour. Samples were mixed and acidified with formic acid to a pH 2. The mixed sample was reduced to 1/6 of the original volume using a SpeedVac, and brought back up to original volume with Buffer A (5% acetonitrile, 0.1% formic acid). Rapigest was cleaved by incubating for one hour at 42^{o}C. The samples were centrifuged at 14,000 rpm for 30 minutes and the supernatant was transferred to a fresh tube and stored at -80^{o}C until mass spectrometry analysis.

Liquid Chromatography – Tandem Mass Spectrometry

MudPIT microcolumns were prepared as previously described (Fonslow et al. 2012). Peptide samples were directly loaded onto the columns using a high-pressure chamber. Samples were then desalted for 30 minutes with buffer A (97% water, 2.9% acetonitrile, 0.1% formic acid v/v/v). LC-MS/MS analysis was performed using a Q-Exactive HF (Thermo Fisher) or Exploris480 (Thermo Fisher) mass spectrometer equipped with an Ultimate3000 RSLCnano system (Thermo Fisher). Embryo samples were analyzed on the Exploris480 while the S2 cell culture were analyzed on the Q-Exactive HF. MudPIT experiments were performed with 10μL sequential injections of 0, 10, 30, 60, and 100% buffer C (500mM ammonium acetate in buffer A), followed by a final injection of 90% buffer C with 10% buffer B (99.9% acetonitrile, 0.1% formic acid v/v) and each step followed by a 130 minute gradient from 5% to 80% B with a flow rate of 300nL/minute when using the Q-Exactive HF and 500nL/minute when using the Exploris480 on a 20cm fused silica microcapillary column (ID 100 um) ending with a laser-pulled tip filled with Aqua C18, 3μm, 100 Å resin (Phenomenex). Electrospray ionization

(ESI) was performed directly from the analytical column by applying a voltage of 2.0kV when using the Q-Exactive HF and 2.2kV when using the Exploris480 with an inlet capillary temperature of 275°C. Using the Q-Exactive HF, data-dependent acquisition of mass spectra was carried out by performing a full scan from 300-1800 m/z with a resolution of 60,000. The top 15 peaks for each full scan were fragmented by HCD using normalized collision energy of 38, 0.7 m/z isolation window, 120 ms maximum injection time, at a resolution of 45,000 scanned from 100 to 1800 m/z and dynamic exclusion set to 60s. Using the Exploris480, data-dependent acquisition of mass spectra was carried out by performing a full scan from 400-1600m/z at a resolution of 120,000. Top-speed data acquisition was used for acquiring MS/MS spectra using a cycle time of 3 seconds, with a normalized collision energy of 36, 0.4m/z isolation window, 120ms maximum injection time, at a resolution of 45,000 with the first m/z starting at 110. Peptide identification and TMT-based protein quantification was carried out using Proteome Discoverer 2.4. MS/MS spectra were extracted from Thermo Xcalibur .raw file format and searched using SEQUEST against a Uniprot *Drosophila melanogaster* proteome database (downloaded February 6th, 2019 and containing 21114 entries). The database was curated to remove redundant protein and splice-isoforms, and supplemented with common biological MS contaminants. Searches were carried out using a decoy database of reversed peptide sequences and the following parameters: 10ppm peptide precursor tolerance, 0.02 Da fragment mass tolerance, minimum peptide length of 6 amino acids, trypsin cleavage with a maximum of two missed cleavages, dynamic methionine modification of 15.995 Da (oxidation), static cysteine modification of 57.0215 Da (carbamidomethylation), and static N-terminal and lysine modifications of 229.1629 Da.

iPOND-TMT data analysis

To determine enrichment or depletion of the proteins, the TMT intensities for each protein was $\log_2$ transformed and samples were normalized based on median TMT intensity per channel. Log2-transformed, median normalized TMT intensities were further normalized to the level of Histone H4, as the resulting incorporation of this histone should be identical between each sample. Enrichment values were calculated based on this normalized data. Cellular localization data was determined for each protein using the Gene Ontology Cellular Compartment (FlyBase v2021_05). Proteins that lacked any nuclear or chromatin compartmental data were removed from the datasets. To determine if a protein was significantly enriched or depleted in the pulse or chase embryo samples, an unpaired t-test was performed for each protein. Our uncorrected p values were validated because our positive controls (known replication proteins) were identified. For S2 cell data, an unpaired t-test was performed for each protein with a Benjamini, Krieger and Yekutieli multiple test correction and false discovery rate of 5%.

For the pathway enrichment analysis of enriched proteins, PANTHER Gene Ontology was used (Ashburner et al. 2000; Carbon et al. 2020; Mi et al. 2019). Enriched proteins were inputted and the default background for *Drosophila melanogaster* was selected. The biological process pathway was used, and the results were exported to Excel and the top 10 pathways were chosen by q-value, and visualized in Graphpad Prism

For network clustering, all of the proteins enriched in the embryo and S2 pulse were loaded as separate networks in Cytoscape v3.9.0 (Shannon et al. 2003). The resulting interactions were visualized using the STRING network with the stringApp, using

the *Drosophila melanogaster* setting with 0 additional interactors and a confidence score cutoff of 0.8 (Szklarczyk et al. 2021; Doncheva et al. 2019).

RNAi and immunofluorescence in S2 cells

RNAi in S2 cells was performed as described (Rogers and Rogers 2008). Briefly, dsRNA against each candidate RNA was designed to be 200-500 bp. Primers used to generate dsRNA are listed in Supplemental Table 3-5. The dsRNAs were synthesized using the Invitrogen MEGAscript T7 Transcription Kit (Ambion). For each sample, 1.5 million S2 cells were seeded in 1 ml non-serum medium in a 6-well plate and 30 µg of dsRNA was added. After 45 minutes incubation at room temperature, 2ml of serum-containing medium was added and cells were incubated for an additional five days. Reverse transcription and quantitative PCR (RT-qPCR) and Western blotting was performed to determine the knock down efficiency using a rabbit anti-BRWD3 antibody at 1:500 (Morgan et al. 2017). For immunofluorescence, RNAi-treated cells were attached to Concanvan A-coated slides for 15 minutes, fixed for 15 minutes in 4% paraformaldehyde and permeabilized for 15 minutes in PBS supplemented with 0.3% Triton-X-100 (PBT). Cells were then blocked for 60 minutes in blocking buffer, containing 1% BSA and 0.2% goat serum in 0.1% PBT. After blocking, cells were incubated with rabbit anti-γ-H2Av (1:500, Rockland, # 600-401-914) antibody overnight at 4°C in blocking buffer. After washing with PBS, cells were incubated with goat anti-rabbit IgG secondary antibody (1:500, Life Technologies, # A11011) in blocking buffer for one hour at room temperature and stained with DAPI (0.1 µg/mL) in PBT for 10 minutes and mounted in Vectasheild (Vector Labs). All images were obtained using Nikon Ti-E inverted

microscope with a Zyla sCMOS digital camera with a 20X oil objective. For each biological replicate, all samples were captured at the same magnification and same exposure time. For quantitative analysis of γ-H2Av levels, regions of interest (ROIs) were defined based on the DAPI signal. The mean signal intensity of ɣ-H2Av was extracted for each ROI. The signal was normalized to the DAPI signal intensity to account for differences in the total amount of DNA. 350 randomly selected cells were used for each biological replicate. Two biological replicates were used for the data analysis. Kruskal-Wallis one-way analysis of variance was performed in GraphPad Prism for statistical significance.

DNA molecular combing

Drosophila S2 cells were pulsed with 20uM of CldU nucleoside (Sigma-Aldrich, C6891) for 20 minutes. Cells were washed with PBS then ~1.5-3.0 million cells were embedded in agarose plugs. The assay was performed as described in Genomic Vision's manufacturer instructions. The stretched and denatured DNA was stained with a CldU-specific antibody (Abcam Cat#ab6326) for 1 hour, washed in PBS, then probed with a secondary antibody (Thermo, A11007) for 30min. Coverslips were washed with PBS then mounted. Stained coverslips were imaged using a Nikon Ti-E inverted microscope with a Zyla sCMOS digital camera with a 40X oil objective. For each sample, 200 DNA fiber lengths were measured manually using Nikon NIS-Elements AR v4.40. Investigator was blinded to sample identity. Two biological replicates were performed per sample. The length of a given fiber is directly proportional to the rate of replication fork progression. Therefore, fiber lengths were converted to fork progression rates given the 20-minute pulse time (Fiber length *20min / 2kb•min^{-1}). Kruskal-Wallis one-way analysis of variance

followed by Dunn's multiple comparisons post-test was performed in GraphPad Prism for statistical significance.

Acknowledgments

We thank Martina Brienza-Ramos for assistance with EdU labeling of embryos used in this study. We thank David Cortez and Kavi Mehta for advice and guidance with DNA combing. We thank A. Shilatifard for providing the Drosophila anti-BRWD3 antibody. We thank Sarah Wessel and members of the Nordman lab for providing critical feedback on the manuscript. This work was supported by National Institutes of Health (NIH) General Medical Sciences awards R35GM133552 to L.P. and R35GM128650 to J.T.N.. M.T.W was supported by the Vanderbilt Chemistry-Biology Interface Training Program (T32GM065086) and the National Science Foundation Graduate Research Fellowship Program.

Author Contributions

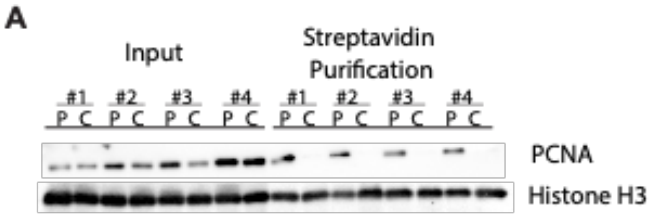
A.M. and J.T.N planned and designed the research; A.M., R.T, D.S performed experiments; A.M., M.W, D.H., and R.T. analyzed data with supervision from L.P and J.T.N; A.M. and J.T.N. wrote the manuscript with input from all of the authors. A.M., M.W., D.H., R.T., L.P. and J.T.N. edited the manuscript.

Data Availability Statement

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD031165 http://www.ebi.ac.uk/pride/archive/projects/PXD031165

Additional Information

Supplementary information. Two supplemental figures and five supplemental tables. Competing interests: The authors declare no competing interests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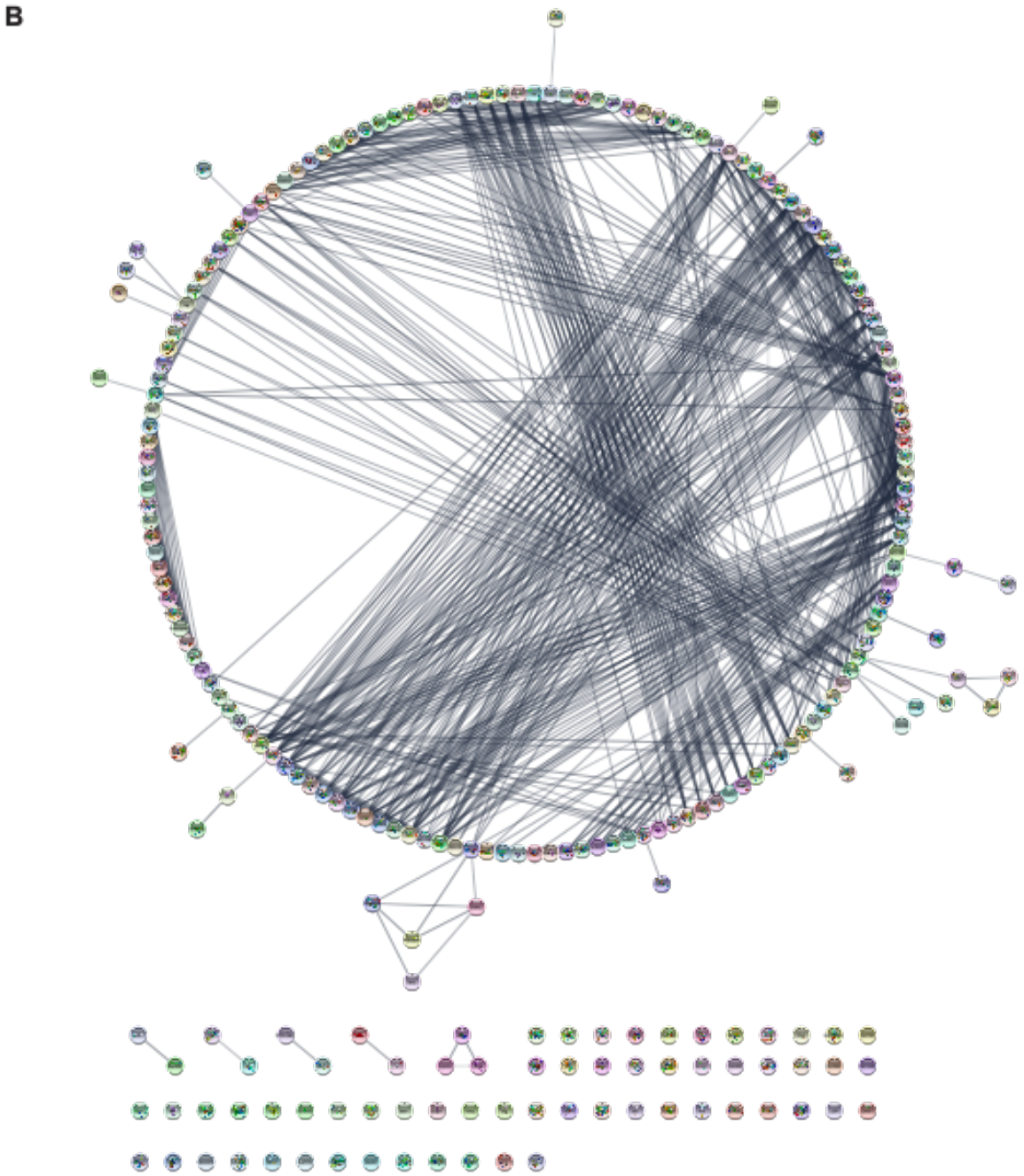
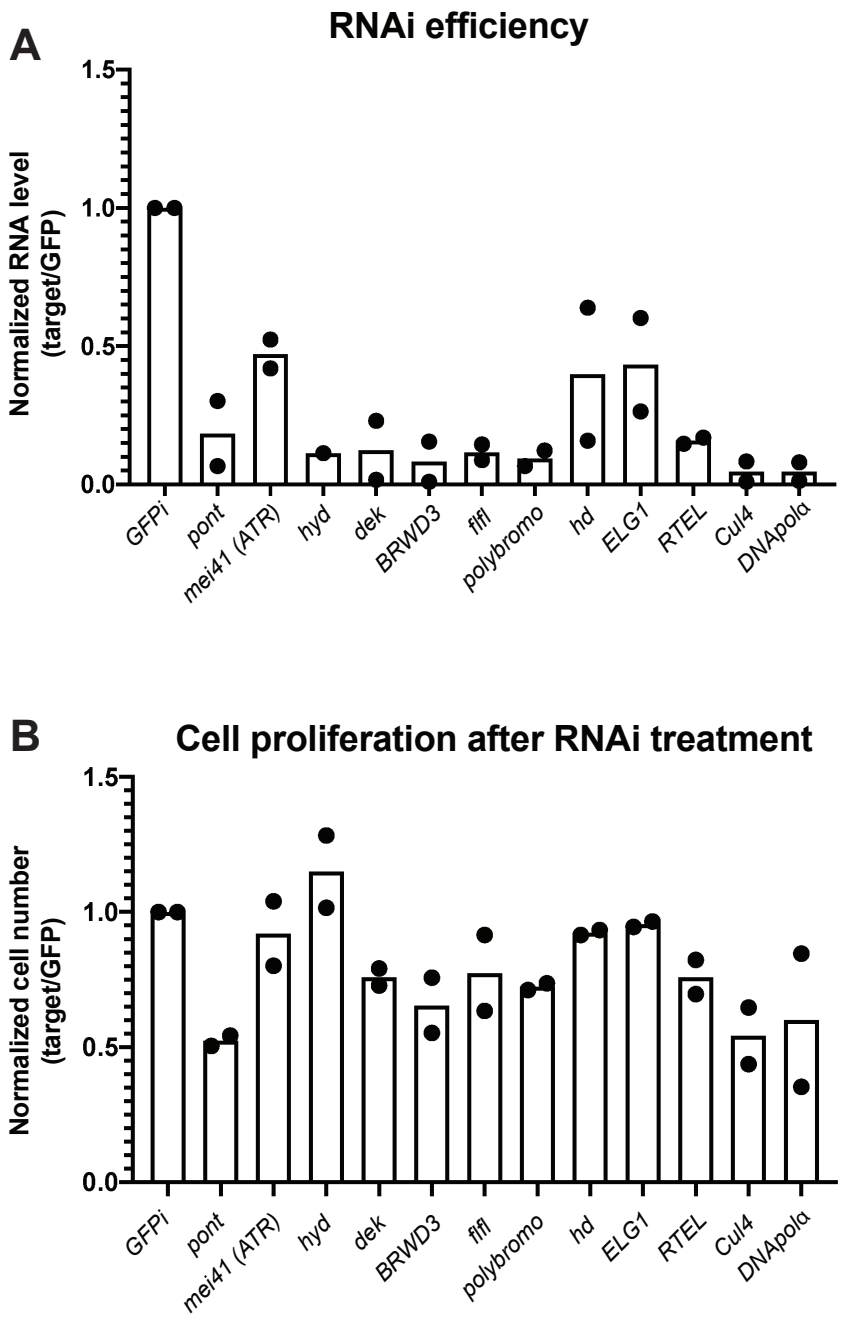
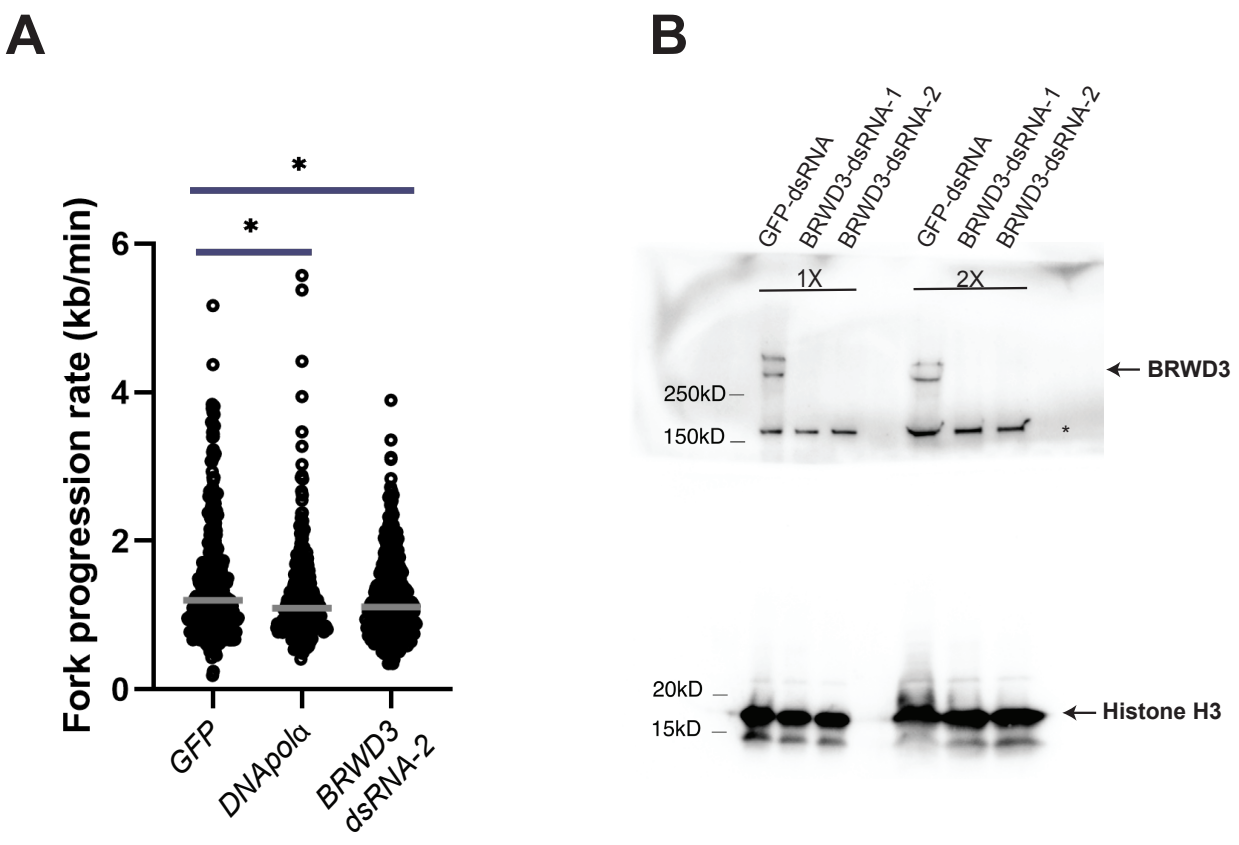

B

Supplemental Figure 3-1. **Analysis of iPOND and iPOND-TMT in S2 cultured cells.** (**A**) Western blot confirmation of iPOND in S2 cells. The first eight lanes are from input and the last eight from the streptavidin purifications. PCNA is a marker for active replication forks and is enriched in the pulse sample purifications. Histone H3 is a general marker of chromatin and enriched in both the pulse and chase samples. P = Pulse, C = Chase, and #1-4 represent the replicate numbers. (**B**) Total network map of the 278 replisome-associated proteins in S2 cells. Contributions: Experiment, analysis, and visualization of A.



Supplemental Figure 3-2: **Validation of RNAi-based depletion of targets. (A)** Normalized depletion efficiency for two biological replicates. The normalized ratio is the target/*Tubulin* in the non-targeting *GFP* control divided by target/*Tubulin* in the RNAi-treated cells **(B)** Cell proliferation after five days of RNAi depletion relative to the *GFP* non-targeting control. Contributions: None.



Supplemental Figure 3-3: **Validation of BRWD3 combing and knockdown. (A)** A second replicate of DNA fiber combing was performed for a second, independent BRWD3 RNAi. **(B)** Validation of the BRWD3 knockdown using western blot. Contributions: None.

Supplemental Table 3-1: Unnormalized TMT Intensities for Embryo iPOND Replicates

Accession	Description	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	# AAs	MW [kDa]	calc. pI	Score Sequest HT	# Peptides	# Razor Peptides	EdU Pulse R1	Edu Pulse R2	EdU Pulse R3	EdU Pulse R4	Thy Chase R1	Thy Chase R2	Thy Chase R3	Thy Chase R4
Q6AWN0	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Drosophila melanogaster OX=	25	4	5	4	186	22.2	5.35	1.61	4	0	20.1	22.6	25.4	17.6	13.2	24.8	30.2	20.1
A1Z992	1,4-Alpha-Glucan branching enzyme OS=Drosophila melanogaster OX=7227 GN=AGBE F	11	7	18	7	685	79.1	6.25	19.43	7	0	353	409.5	386	325.7	256.5	414.4	443.8	332.3
P48375	12 kDa FK506-binding protein OS=Drosophila melanogaster OX=7227 GN=FK506-bp2 PE	24	2	15	2	108	11.7	8.13	32.7	2	0	225.1	206.3	201.6	138	121.4	206.4	216.4	112.7
P92177	14-3-3 protein epsilon OS=Drosophila melanogaster OX=7227 GN=14-3-3epsilon PE=1 S	33	6	99	5	262	29.8	4.78	110.56	6	0	1963.2	2148.3	2132	1578.2	1421.9	1853.4	2301.7	1873.7
P29310	14-3-3 protein zeta OS=Drosophila melanogaster OX=7227 GN=14-3-3zeta PE=1 SV=1	32	6	70	5	248	28.2	4.88	100.3	6	2	1361.5	1569.6	1513.9	1263.7	1112.6	1323.9	1697.7	1346.9
Q9VFE9	2-(3-amino-3-carboxypropyl)histidine synthase subunit 2 OS=Drosophila melanogaster OX	8	2	2	2	469	52.1	5.25	0	2	0								
Q9V3U6	26-29kD-proteinase OS=Drosophila melanogaster OX=7227 GN=26-29-p PE=1 SV=1	3	2	6	2	549	62.1	6.74	7.76	2	0	126.4	160.6	153.5	169	149.3	170.4	272.2	193.8
A0A0B4KI10	26S proteasome non-ATPase regulatory subunit 1 OS=Drosophila melanogaster OX=722	8	8	24	8	1029	114.1	5.19	34.34	8	0	571.5	702.4	759.1	610.8	544.5	701	1103	639.2
Q9V3G7	26S proteasome non-ATPase regulatory subunit 6 OS=Drosophila melanogaster OX=722	22	7	27	7	389	45.4	6.48	50.09	7	0	775.3	846.5	923.3	742.8	658.8	942.6	1112.5	814
Q9VFS8	26S proteasome non-ATPase regulatory subunit 9 OS=Drosophila melanogaster OX=722	10	2	5	2	220	23.9	5.66	2.65	2	0	69.4	72.4	73.7	52.4	56	80.7	103.8	62
Q9V436	26S proteasome regulatory complex subunit p30 OS=Drosophila melanogaster OX=7227	16	4	25	4	264	30.2	6.06	43.78	4	0	290.6	347.7	374.1	330.2	254.2	365.3	500.5	336.1
Q9V405	26S proteasome regulatory complex subunit p48A OS=Drosophila melanogaster OX=722	6	3	6	3	413	47	5.38	12.05	3	0	265.9	260.1	282.2	234.6	168.5	283.3	325.1	207
Q7KMQ0	26S proteasome regulatory complex subunit p48B OS=Drosophila melanogaster OX=722	29	11	45	11	433	48.5	6.04	40.38	11	0	709.3	762.9	784.7	507.8	413.3	851.6	968.2	565
Q9V3V6	26S proteasome regulatory complex subunit p50 OS=Drosophila melanogaster OX=7227	23	6	41	6	428	47.8	5.34	69.08	6	0	485.3	622.5	580.7	361.5	509	592.8	712.7	388.6
P48601	26S proteasome regulatory subunit 4 OS=Drosophila melanogaster OX=7227 GN=Rpt2 P	8	3	38	3	439	49.3	6.58	32.09	3	0	466.1	494.4	423.2	312.7	282.9	561.1	534.5	351.4
O18413	26S proteasome regulatory subunit 8 OS=Drosophila melanogaster OX=7227 GN=Rpt6 P	8	3	14	3	405	45.8	8.41	18.33	3	0	453.5	528.2	552	500.9	371.9	532.9	715.4	557.6
Q0E9B6	40S ribosomal protein S11 OS=Drosophila melanogaster OX=7227 GN=RpS11 PE=1 SV=	12	2	13	2	155	18.1	10.93	18.18	2	0	362.3	440.1	446.4	360.4	588	597.4	713	533.3
Q03334	40S ribosomal protein S13 OS=Drosophila melanogaster OX=7227 GN=RpS13 PE=1 SV=	12	2	11	2	151	17.2	10.55	16.83	2	0	227.4	308.6	297.3	280	460.7	391	439.4	367
C0HKA1	40S ribosomal protein S14b OS=Drosophila melanogaster OX=7227 GN=RpS14b PE=2 S	17	2	16	2	151	16.3	10.35	25.18	2	0	260.9	225.8	227	148.4	180.3	369.6	360.5	191
P39018	40S ribosomal protein S19a OS=Drosophila melanogaster OX=7227 GN=RpS19a PE=1 S	17	3	21	3	156	17.3	10.11	34.94	3	0	240.9	352.8	367.1	246.7	299.6	378.5	494.2	274.3
P31009	40S ribosomal protein S2 OS=Drosophila melanogaster OX=7227 GN=RpS2 PE=1 SV=2	8	2	10	2	267	28.9	10.15	11.44	2	0	121.5	175.2	115.4	105	205.5	212.4	291.6	139.4
P55828	40S ribosomal protein S20 OS=Drosophila melanogaster OX=7227 GN=RpS20 PE=1 SV=	21	2	10	2	120	13.5	10.33	0	2	0	32.8	50.9	45.7	50.5	54.3	44.9	57.4	43.7
Q06559	40S ribosomal protein S3 OS=Drosophila melanogaster OX=7227 GN=RpS3 PE=1 SV=1	9	2	21	2	246	27.5	9.39	47.42	2	0	380.5	538	608.7	488.7	852.1	675.3	872.4	565.1
P55830	40S ribosomal protein S3a OS=Drosophila melanogaster OX=7227 GN=RpS3A PE=1 SV=	19	4	28	4	268	30.3	9.61	50.59	4	0	704	748.4	716.5	544.9	741	1042.6	1015.5	681.9
P41042	40S ribosomal protein S4 OS=Drosophila melanogaster OX=7227 GN=RpS4 PE=1 SV=2	8	2	6	2	261	29.1	10.18	8.19	2	0	164	213.4	209.7	211.1	251.9	299.8	333	218.5
Q9VFE4	40S ribosomal protein S5b OS=Drosophila melanogaster OX=7227 GN=RpS5b PE=2 SV=	7	2	16	2	230	25.7	8.54	34.46	2	0	484.1	652.8	679.5	608.7	851	867.8	1047.1	742.1
P29327	40S ribosomal protein S6 OS=Drosophila melanogaster OX=7227 GN=RpS6 PE=1 SV=1	8	2	21	2	248	28.4	10.74	44.1	2	0	432.4	503	432.3	479.1	730.1	789.7	792.7	628
A0A0B4K6N1	40S ribosomal protein S8 OS=Drosophila melanogaster OX=7227 GN=RpS8 PE=3 SV=1	31	5	91	5	208	23.7	10.48	184.13	5	0	1030.7	1069	838.1	790.1	859.3	2367.4	2403.2	1780.1
P38979	40S ribosomal protein SA OS=Drosophila melanogaster OX=7227 GN=sta PE=1 SV=3	17	2	7	2	270	30.2	4.87	10.21	2	0	173.8	491	258.4	119	174.5	572.3	296	145
M9PEY6	5'-3' exoribonuclease OS=Drosophila melanogaster OX=7227 GN=Rat1 PE=1 SV=1	5	4	9	4	908	103.9	7.05	13.21	4	0	352.1	238.9	273	236.1	160.6	318.7	331.2	268.7
M9PIS3	6-phosphogluconate dehydrogenase, decarboxylating OS=Drosophila melanogaster OX=	12	3	16	3	481	52.5	6.32	18	3	0	44.8	55.5	67	46.5	49	50.3	77.4	42.7
P41126	60S ribosomal protein L13 OS=Drosophila melanogaster OX=7227 GN=RpL13 PE=1 SV=	17	4	26	4	218	24.9	10.99	33.96	4	0	716.3	901.2	893.7	824.5	1133.5	1260.4	1569.1	1159.2
Q9VNE9	60S ribosomal protein L13a OS=Drosophila melanogaster OX=7227 GN=RpL13A PE=1 S	7	2	5	2	205	23.6	11.03	5.21	2	0	97	141.1	127.5	127.4	242.2	182.3	247.9	158.5
P55841	60S ribosomal protein L14 OS=Drosophila melanogaster OX=7227 GN=RpL14 PE=1 SV=	12	2	30	2	166	19.2	11.18	71.17	2	0	403.4	510.8	508	519.5	724	752.8	878	666.3
O17445	60S ribosomal protein L15 OS=Drosophila melanogaster OX=7227 GN=RpL15 PE=1 SV=	12	3	33	3	204	24.3	11.47	57.04	3	0	1481.4	1811.5	1378	1372.3	1183.8	1465.8	1705.3	1525.6
Q9VS34	60S ribosomal protein L18 OS=Drosophila melanogaster OX=7227 GN=RpL18 PE=1 SV=	18	2	43	2	188	21.7	11.53	55.79	2	0	249.7	354.4	331	346.6	498.5	410.1	545.9	397.9
P41093	60S ribosomal protein L18a OS=Drosophila melanogaster OX=7227 GN=RpL18A PE=1 S	11	2	12	2	177	21	10.62	18.93	2	0	246.5	358.5	342.2	326.1	438.8	365.1	518.8	377.7
P36241	60S ribosomal protein L19 OS=Drosophila melanogaster OX=7227 GN=RpL19 PE=1 SV=	20	4	20	4	203	24	11	42.3	4	0	377.9	477.2	433.9	473.4	553.5	695.1	771.1	548
P50887	60S ribosomal protein L22 OS=Drosophila melanogaster OX=7227 GN=RpL22 PE=1 SV=	11	2	9	2	299	30.6	10.11	13.31	2	0	94.5	106.2	74.7	61.1	70.4	221.7	137.7	88.6
O16797	60S ribosomal protein L3 OS=Drosophila melanogaster OX=7227 GN=RpL3 PE=1 SV=3	11	4	15	4	416	46.9	10.24	23.45	4	0	464.1	537.1	482.6	347.7	596.5	894.9	1055.8	587.4
Q9V597	60S ribosomal protein L31 OS=Drosophila melanogaster OX=7227 GN=RpL31 PE=1 SV=	21	3	17	3	124	14.5	10.2	26.93	3	0	578.1	641.4	541.9	738.7	589.5	787.1	907.8	608.6
Q9W5R8	60S ribosomal protein L5 OS=Drosophila melanogaster OX=7227 GN=RpL5 PE=1 SV=2	13	4	11	4	299	34	9.77	11.09	4	0	252.7	232.6	225.9	132.1	219	393.2	424.9	150.3
A1Z7K8	AaRS-interacting multifunctional protein 1 OS=Drosophila melanogaster OX=7227 GN=AI	15	3	10	3	323	34.4	8.91	7.58	3	0	7.9	11.9	8.3	9	10.5	8.8	17.5	12.1
Q9VJ12	Acinus, isoform A OS=Drosophila melanogaster OX=7227 GN=Acn PE=1 SV=1	9	6	16	6	739	83.7	6.7	13.5	6	0	341.9	331.7	253.2	213.8	150.5	377.2	369.8	227.9
Q9VIE8	Aconitate hydratase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mAcon1 F	3	2	3	2	787	85.3	8.24	1.97	2	0	11	9.4	22.4	8.1	23.4	16.6	11.3	5.6
P02572	Actin-42A OS=Drosophila melanogaster OX=7227 GN=Act42A PE=1 SV=3	22	6	98	2	376	41.8	5.48	170.32	6	4	1949.8	2228.7	2426.6	2159.3	3133	2152.1	2746.8	1970.1
P53501	Actin-57B OS=Drosophila melanogaster OX=7227 GN=Act57B PE=1 SV=1	16	5	78	1	376	41.8	5.39	134.97	5	0	13.2	14.6	18.7	16	29.9	14.3	14.8	11.1
Q9VU68	Actin-interacting protein 1 OS=Drosophila melanogaster OX=7227 GN=flr PE=2 SV=1	4	3	9	3	608	66.5	6.73	16.13	3	0	287.6	399	442.9	381.5	322.7	394.9	444.7	377.4
P45889	Actin-related protein 1 OS=Drosophila melanogaster OX=7227 GN=Arp1 PE=2 SV=2	5	2	3	2	376	42.7	7.3	3.37	2	0	28	46.7	44.5	43.4	46.4	43.2	49.1	44.6
Q9VMH2	Actin-related protein 2/3 complex subunit 4 OS=Drosophila melanogaster OX=7227 GN=A	11	2	3	2	168	19.6	8.46	3.6	2	0	31.8	37.4	38.7	32.9	38.9	31.8	47.5	30.4
Q9VX09	Actin-related protein 8 OS=Drosophila melanogaster OX=7227 GN=Arp8 PE=1 SV=1	8	4	4	4	607	67.7	7.69	7.82	4	0	42.6	54.4	62.3	66.8	45.4	68.6	73	66.4
Q7KSM5	Activator of SUMO 1 OS=Drosophila melanogaster OX=7227 GN=Aos1 PE=1 SV=1	26	7	58	7	337	37.7	5.44	98.32	7	0	678.8	695.9	609.5	403.3	293.7	770.2	715.6	419.4
M9NFF9	Ada2a-containing complex component 3, isoform D OS=Drosophila melanogaster OX=722	5	2	5	2	583	64	8.29	8.22	2	0	35.7	33.7	33.8	35.9	22.8	43.9	48.8	37.3
Q9XYM0	Adapter molecule Crk OS=Drosophila melanogaster OX=7227 GN=Crk PE=1 SV=1	16	4	11	4	271	31.2	5.26	6.51	4	0	136.8	135.2	135.6	105.9	89.8	149	150.2	112.2
Q9VHH7	Adenosine deaminase-like protein OS=Drosophila melanogaster OX=7227 GN=Ada PE=2	8	2	3	2	337	37.6	5.48	0	2	0	24.4	29.5	31.4	30.5	28.9	34.3	38.9	29.9
X2JF40	Adenosylhomocysteinase OS=Drosophila melanogaster OX=7227 GN=Ahcy PE=3 SV=1	5	2	8	2	432	47.3	6.2	15.74	2	0	133.7	120.2	109.4	76.1	70	179.2	145.6	83.8
Q9Y0Y2	Adenylosuccinate synthetase OS=Drosophila melanogaster OX=7227 GN=AdSS PE=2 SV	11	4	14	4	447	48.9	6.84	19.64	4	0	62.7	75.5	78.9	61.7	60.9	68.2	87.1	69.3
P25160	ADP-ribosylation factor-like protein 1 OS=Drosophila melanogaster OX=7227 GN=Arl1 PE=	13	2	3	2	180	20.2	6.57	4.96	2	0	19.8	32.7	33.6	23.4	30.3	29.8	34.6	28.6
Q26365	ADP,ATP carrier protein OS=Drosophila melanogaster OX=7227 GN=sesB PE=2 SV=4	12	4	17	4	312	34.2	9.8	33.24	4	0	197.2	292.8	461.7	347.6	1166.9	461.3	366.6	202.6
Q9VLM8	Alanine--tRNA ligase, cytoplasmic OS=Drosophila melanogaster OX=7227 GN=AlaRS PE=	9	7	20	7	966	107.7	6.13	23.08	7	0	281.7	354.6	350.5	302.5	276.4	314.2	383.2	280.5
P00334	Alcohol dehydrogenase OS=Drosophila melanogaster OX=7227 GN=Adh PE=1 SV=2	10	2	25	2	256	27.7	7.96	28.7	2	0	279	291.3	244.1	211	147.9	285.5	321	248.4
Q9VLC5	Aldehyde dehydrogenase OS=Drosophila melanogaster OX=7227 GN=Aldh PE=1 SV=1	7	4	6	4	520	57	6.8	11.49	4	0	31.8	46.9	52.1	42.2	74.6	59.8	45.2	23.3
Q9VB05	ALG-2 interacting protein X OS=Drosophila melanogaster OX=7227 GN=ALiX PE=1 SV=1	5	4	10	4	836	92.5	5.45	14.8	4	0	116.1	180.1	194.6	177.4	140.3	169.9	221	188.1
M9PFB5	Alien, isoform D OS=Drosophila melanogaster OX=7227 GN=alien PE=4 SV=1	11	3	7	3	444	51.5	5.62	0	3	0	22.2	40.8	28.3	20.6	14.6	31.4	43.8	22.3
M9PGV6	Alpha spectrin, isoform B OS=Drosophila melanogaster OX=7227 GN=alpha-Spec PE=4 S	2	4	4	4	2457	282.4	5.2	6.04	4	0	25.2	37.1	33.7	30.3	106.7	44.5	41.6	30.1
A4UZZ4	Alpha-1,4 glucan phosphorylase OS=Drosophila melanogaster OX=7227 GN=GlyP PE=1	8	7	31	7	844	96.9	6.52	52.07	7	0	651.9	803.4	838.9	717.3	649	802.9	994.8	708.6
P18091	Alpha-actinin, sarcomeric OS=Drosophila melanogaster OX=7227 GN=Actn PE=1 SV=2	6	5	10	5	924	107	5.69	7.61	5	0	85.7	101.2	115	94.5	167.2	105.4	124.7	95
A0A0B4K6V8	Alpha-Esterase-5, isoform B OS=Drosophila melanogaster OX=7227 GN=alpha-Est5 PE=	3	2	3	2	543	61.4	6.19	4.09	2	0	40.7	55.4	58.1	56.3	36.1	57.9	68.9	53
Q23983	Alpha-soluble NSF attachment protein OS=Drosophila melanogaster OX=7227 GN=alpha	10	3	4	3	292	33	5.45	1.87	3	0	72.5	60.1	58	37.4	26.7	86.3	73.8	42.4
Q961C5	Alphabet, isoform E OS=Drosophila melanogaster OX=7227 GN=alph PE=1 SV=1	5	2	7	2	374	41.6	5.24	6.2	2	0	147	165.2	174	156.2	129	180.7	205.5	150.1
Q960Y8	Aluminum tubes, isoform G OS=Drosophila melanogaster OX=7227 GN=alt PE=1 SV=1	10	7	11	7	874	98.5	7.34	0	7	0	60.7	73	77.8	60.2	77.2	101.6	120.6	81
Q0KI00	Aminopeptidase OS=Drosophila melanogaster OX=7227 GN=SP1029 PE=1 SV=1	3	2	2	2	932	108	6.6	0	2	0	6.4	11.7	13.8	12.3	8.5	6.9	14	9
X2JEY5	AMP deaminase OS=Drosophila melanogaster OX=7227 GN=AMPdeam PE=1 SV=1	6	4	6	4	798	91.5	6.1	12.67	4	0	135.2	160.9	164.1	106.3	90.9	165.2	211.3	143.3
Q9V4P1	Anillin OS=Drosophila melanogaster OX=7227 GN=scra PE=1 SV=3	4	5	12	5	1239	135.9	6.24	14.94	5	0	148.8	172.8	180.6	157	121.1	219.8	238.8	193.3
P22465	Annexin B10 OS=Drosophila melanogaster OX=7227 GN=AnxB10 PE=2 SV=3	15	4	22	4	321	35.7	4.74	46.28	4	0	203.9	280.4	284.1	237.6	176.4	268.6	333.9	276.6
A0A0B4KH34	Annexin OS=Drosophila melanogaster OX=7227 GN=AnxB9 PE=1 SV=1	10	4	8	4	324	35.9	5.06	12.29	4	0	160.3	205.2	182.9	133.8	176.7	187.9	243.7	184.6
Q24050	Anon-i1 protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2034 PE=1 SV=1	11	3	8	3	262	28.9	4.82	15.94	3	0	123.5	154.5	179.5	155.1	167.5	158.3	217	155.2
O16043	Anon1A4 OS=Drosophila melanogaster OX=7227 GN=Df31 PE=1 SV=1	32	4	9	4	183	18.8	4.27	21.09	4	0	422.2	323.6	286.5	264.6	203.5	181.2	326.7	240.3
Q9VN55	Antimeros, isoform A OS=Drosophila melanogaster OX=7227 GN=atms PE=1 SV=1	12	5	9	5	538	60.8	9.29	13.89	5	0	149.3	134.6	117.5	89.3	89.4	177.2	203.3	120
P54362	AP-3 complex subunit delta OS=Drosophila melanogaster OX=7227 GN=g PE=1 SV=4	7	4	25	4	1034	114.8	7.28	35.52	4	0	129.5	111.6	150.3	102.3	107.5	171.2	433.7	204.2
Q9V496	Apolipophorins OS=Drosophila melanogaster OX=7227 GN=apolpp PE=1 SV=2	1	5	8	5	3351	372.4	7.97	3.31	5	0	120.6	173.5	129.5	103.7	238.3	126.8	179.7	146.5
A0A0B4KGD0	Apontic, isoform F OS=Drosophila melanogaster OX=7227 GN=apt PE=1 SV=1	8	4	14	4	499	56.3	6.54	15.35	4	0	223.6	281	277.9	249.4	168.4	261.4	298.1	251
Q9V431	Apoptosis inhibitor 5 homolog OS=Drosophila melanogaster OX=7227 GN=Aac11 PE=2 S	16	6	24	6	536	59.9	6.76	44.06	6	0	192.9	206.4	210.2	173	141.3	253.7	279.5	200.5

Q7JVG2	Aps, isoform A OS=Drosophila melanogaster OX=7227 GN=Aps PE=1 SV=1	16	2	2	2	177	19.9	6.05	2.47	2	0	15.4	17.6	14.1	16.2	11.6	16.1	15.9	17.5
Q9VGW7	Arginine methyltransferase 1 OS=Drosophila melanogaster OX=7227 GN=Art1 PE=1 SV=	13	4	11	4	376	42.8	5.15	16.01	4	0	195.7	284.4	276.4	256.2	194.6	256.4	360.2	258.2
Q9VFB3	Arginine methyltransferase 3, isoform A OS=Drosophila melanogaster OX=7227 GN=Art3 I	6	2	3	2	516	58.9	4.73	6.93	2	0	16.3	17.3	22.5	14.4	16.8	16.8	25.5	13.8
F0JAI1	Arginine methyltransferase 4, isoform B OS=Drosophila melanogaster OX=7227 GN=Art4 I	9	5	18	5	530	59.7	6.13	28.67	5	0	301.4	378.2	380.8	359.7	239	352.9	419.3	324.7
Q7K486	Armadillo repeat-containing protein 6 homolog OS=Drosophila melanogaster OX=7227 GN	11	4	16	4	464	51.3	5.55	24.25	4	0	202.9	278.9	261.7	223.4	220.3	275.8	323.9	240.8
Q7KTW9	Asparagine synthetase OS=Drosophila melanogaster OX=7227 GN=AsnS PE=2 SV=1	8	4	7	4	558	63.2	6.49	5.17	4	0	54.9	71.4	67.7	63.1	49.6	77.7	78.6	61.2
Q9V434	Asparaginyl-tRNA synthetase, isoform A OS=Drosophila melanogaster OX=7227 GN=AsnI	7	4	9	4	558	63.9	5.96	10.4	4	0	188.5	265.4	294.3	207.3	267	274.5	337.9	231.9
Q8IPY3	Aspartate aminotransferase OS=Drosophila melanogaster OX=7227 GN=Got2 PE=1 SV=	6	2	4	2	431	48.1	8.5	10.38	2	0	30.2	52.7	84.5	79.4	192.3	70	63.8	42.7
Q7K0E6	Aspartyl-tRNA synthetase, isoform A OS=Drosophila melanogaster OX=7227 GN=AspRS I	4	2	6	2	531	59	6.81	4.64	2	0	61.7	85.6	105.7	82.9	118	92.1	117	86.2
Q9VJH2	Aspartyl-tRNA synthetase, mitochondrial, isoform A OS=Drosophila melanogaster OX=722	8	7	18	7	1082	121.4	5.82	16.98	7	0	147.4	160.7	148.3	123.9	114	192.9	193.3	148.7
Q9VV75	AT02348p OS=Drosophila melanogaster OX=7227 GN=UQCR-C2 PE=1 SV=1	6	2	3	2	440	45.4	9.44	1.76	2	0	12.5	16.6	22.6	18.3	59.6	17.9	22	16.3
Q9VDV2	AT06125p OS=Drosophila melanogaster OX=7227 GN=BEST:GH15838 PE=1 SV=1	4	2	3	1	363	40.6	8.57	3.89	2	1	113.9	124.1	186.7	133.4	213.8	252.3	170.1	122.9
Q9VXF9	AT13091p OS=Drosophila melanogaster OX=7227 GN=mgo PE=1 SV=1	13	4	19	4	458	50.5	5.16	22.83	4	0	215.2	226.9	210.4	148.6	151.5	255.8	259.6	145.2
Q8IQF8	AT18092p OS=Drosophila melanogaster OX=7227 GN=ESTS:34F4T PE=1 SV=1	13	3	18	3	350	40.1	7.9	20.19	3	0	385.3	464.3	469.7	416.4	359.3	519.5	521	467.2
Q8T8W3	AT21416p OS=Drosophila melanogaster OX=7227 GN=Past1 PE=1 SV=1	8	5	9	5	540	61.5	6.42	11.49	5	0	127.5	129.4	145.8	100.2	117.9	146.9	159.8	106.9
Q9VM14	AT21758p OS=Drosophila melanogaster OX=7227 GN=muc PE=1 SV=1	3	2	3	2	512	54.2	9.57	7	2	0	23.4	24.1	36.1	26.7	28	33.3	41.3	20
Q7K2L1	AT22044p1 OS=Drosophila melanogaster OX=7227 GN=Orc3 PE=1 SV=1	6	3	16	3	721	82.2	7.37	21.54	3	0	55.2	62.3	57.5	63.8	52.6	163.5	77	86.7
Q9VGH5	AT27789p OS=Drosophila melanogaster OX=7227 GN=glo PE=1 SV=1	10	4	12	4	586	61.4	6.04	28.38	4	0	265.3	293.5	225.7	307.1	208.3	266.3	300.4	289.8
B9A0M7	AT31036p OS=Drosophila melanogaster OX=7227 GN=BcDNA:LD21969 PE=1 SV=1	7	4	8	4	543	62.9	8.47	11.91	4	0	149.6	155.6	115.9	116.3	82	217.5	192.5	131.4
P35381	ATP synthase subunit alpha, mitochondrial OS=Drosophila melanogaster OX=7227 GN=b	15	7	36	7	552	59.4	9.01	75.51	7	0	371.5	474.3	608.6	548.2	1835.7	619	599.4	432.6
L0MQ04	ATP synthase subunit beta OS=Drosophila melanogaster OX=7227 GN=ATPsynbeta PE=	13	5	23	5	511	54.6	5.27	37.42	5	0	64	69.8	84.2	107.9	392.9	81.4	100.3	77.6
O01666	ATP synthase subunit gamma, mitochondrial OS=Drosophila melanogaster OX=7227 GN=	7	2	4	2	297	32.9	9.22	3.97	2	0	39.9	50.6	61.2	39.7	106.1	46	48.7	37.2
Q24439	ATP synthase subunit O, mitochondrial OS=Drosophila melanogaster OX=7227 GN=ATPs	10	2	10	2	209	22.4	9.63	7.86	2	0	57.1	128.9	103.6	146.5	192.2	118.6	129.9	102.5
Q7KN85	ATP-citrate synthase OS=Drosophila melanogaster OX=7227 GN=ATPCL PE=1 SV=1	10	8	39	8	1112	121.3	7.31	61.06	8	0	301.1	325.6	343.3	357.5	312.5	450.7	495.9	364.5
A0A0B4K7L1	ATP-dependent 6-phosphofructokinase OS=Drosophila melanogaster OX=7227 GN=Pfk P	11	8	14	8	950	105.2	8.54	16.03	8	0	91.7	115.5	155.5	122.2	151.1	130.6	155.1	117.7
Q9V9T4	ATP-dependent chromatin assembly factor large subunit OS=Drosophila melanogaster OX	10	12	80	12	1476	170.3	6.87	119.17	12	0	1480.9	1862.1	1719.6	1563.5	1052.4	2225.1	1884.5	1642.9
Q23976	ATP-dependent DNA helicase 2 subunit 1 OS=Drosophila melanogaster OX=7227 GN=Irb	3	3	5	3	631	72.5	6.68	3.45	3	0	44.9	64.7	54.4	59.5	44.7	70.3	84.9	57.4
Q9I7M8	ATP-dependent DNA helicase II subunit 2 OS=Drosophila melanogaster OX=7227 GN=Ku	5	2	3	2	699	79.8	5.38	6.82	2	0	33.9	52.4	41.4	42.8	34.9	59.1	65.3	50.4
Q9VNV3	ATP-dependent RNA helicase Ddx1 OS=Drosophila melanogaster OX=7227 GN=Ddx1 PE	3	2	3	2	727	80.8	6.87	2.01	2	0	51.3	63.5	54.3	51.7	46	60.4	74.2	51.9
A1Z9L3	ATP-dependent RNA helicase DHX8 OS=Drosophila melanogaster OX=7227 GN=pea PE	6	7	9	6	1242	141.8	8.76	12.28	7	1	93.3	124.7	98	103	76.6	144.2	140	115.5
Q8SY39	ATP-dependent RNA helicase OS=Drosophila melanogaster OX=7227 GN=CG6994 PE=1	4	3	3	3	827	93.3	9.72	5.23	3	0	27.3	31.6	30.4	24.2	18.6	44.4	40	37.6
P19109	ATP-dependent RNA helicase p62 OS=Drosophila melanogaster OX=7227 GN=Rm62 PE	20	14	77	14	719	78.5	9.6	156.95	14	0	1431.2	1527.8	1345	1325.2	875.9	1746.3	1763.4	1478.2
Q27268	ATP-dependent RNA helicase WM6 OS=Drosophila melanogaster OX=7227 GN=Hel25E I	15	5	42	5	424	48.6	5.66	55.51	5	0	773.4	874.3	843.6	727.4	527.1	1050.1	1003.7	815.3
Q9VEX6	ATPase family AAA domain-containing protein 3A homolog OS=Drosophila melanogaster (	6	4	5	4	604	68.3	9.17	4.54	4	0	57.6	56.9	62.6	65.7	77.7	87.6	95.8	60.1
M9PER1	Autophagy-related 18a, isoform E OS=Drosophila melanogaster OX=7227 GN=Atg18a PE	4	2	3	2	447	47.9	6.74	1.95	2	0	59.6	72	80.4	55.7	54.7	83.8	97.1	74.4
A4V3G8	Ballchen, isoform B OS=Drosophila melanogaster OX=7227 GN=ball PE=1 SV=1	6	4	24	4	599	66	9.86	39.25	4	0	726.8	829.2	699	738.8	711.8	1248.3	1075.1	926.8
Q7K204	Barricade, isoform A OS=Drosophila melanogaster OX=7227 GN=barc PE=1 SV=1	4	2	4	2	556	63.9	5.05	1.61	2	0	21.3	21.7	17.5	8.4	4.7	25.4	22.7	12.3
Q9Y162	BcDNA.GH02678 OS=Drosophila melanogaster OX=7227 GN=Vps4 PE=1 SV=1	7	4	8	4	442	49.6	6.96	14.29	4	0	240.2	276.8	271.2	246.5	193.9	289.6	362.5	268.1
Q7KMM4	BcDNA.GH04962 OS=Drosophila melanogaster OX=7227 GN=GCS2alpha PE=1 SV=1	3	3	7	3	924	105.7	6.51	12.83	3	0	123.6	195.7	185.2	192.5	211.3	164.4	342.6	167.3
Q9Y112	BcDNA.GH10614 OS=Drosophila melanogaster OX=7227 GN=AKR2E3 PE=1 SV=1	14	4	15	4	316	36.3	7.08	20.18	4	0	309.6	391.6	367.4	317.1	232.9	442.3	480.4	348.4
Q9V397	BcDNA.GH12558 OS=Drosophila melanogaster OX=7227 GN=Mtpalpha PE=1 SV=1	7	5	6	5	783	84	9.17	5.35	5	0	18.7	34.6	44.6	26.6	83.6	43.9	39.3	22.1
Q7KLW9	BcDNA.LD02793 OS=Drosophila melanogaster OX=7227 GN=Prp19 PE=1 SV=1	7	3	9	3	505	55.2	6.9	10.07	3	0	262.2	285.2	264.9	249.1	152.1	328.6	347.6	293.5
Q9V3I1	BcDNA.LD08534 OS=Drosophila melanogaster OX=7227 GN=dUTPase PE=1 SV=1	30	5	53	5	188	19.9	5.47	103.65	5	0	1379.6	1346	1211.4	968.2	726.5	1388.6	1502.9	1020.4
Q8I077	BcDNA.LD22910 OS=Drosophila melanogaster OX=7227 GN=Usp1 PE=1 SV=1	2	2	2	2	1078	116.3	7.23	1.67	2	0	12	14.6	12.7	11.7	9.1	17.5	19	12.5
Q7KMI3	BcDNA.LD23371 OS=Drosophila melanogaster OX=7227 GN=BcDNA.LD23371 PE=2 SV	6	5	13	5	1004	113.7	7.81	14.14	5	0	205.9	218.3	192.5	222	187.5	327	326.4	214.4
Q9V3Y5	BcDNA.LD23634 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4119 PE=1 SV=1	6	6	13	6	998	112.6	6.49	26.58	6	0	298.2	324.5	287.9	276.5	176.3	379.2	381.6	281.7
Q7KMH9	BcDNA.LD26050 OS=Drosophila melanogaster OX=7227 GN=wde PE=1 SV=1	5	7	16	7	1420	156.7	4.73	12.92	7	0	216.8	175.6	150.8	106	65.9	230.4	198.3	113.1
Q9V3H9	BcDNA.LD27873 OS=Drosophila melanogaster OX=7227 GN=Nab2 PE=1 SV=1	2	2	3	2	1004	112.9	9.58	1.85	2	0	15.7	18.5	13.1	17	12.2	18.4	22.2	17
Q9VHH8	Beag OS=Drosophila melanogaster OX=7227 GN=beag PE=1 SV=1	7	3	7	3	557	61.4	6.86	8.73	3	0	33.1	48	37.3	51.7	29.5	50.2	53.7	43.1
A0A0B4KGU4	Belle, isoform B OS=Drosophila melanogaster OX=7227 GN=bel PE=4 SV=1	7	5	7	4	801	85.4	7.77	9.73	5	1	136	181.6	199.3	156.3	211.8	167.7	217.1	148.9
Q9Y118	BG:DS07295.3 OS=Drosophila melanogaster OX=7227 GN=Pol32 PE=1 SV=1	12	3	8	3	431	47	9.28	17.23	3	0	95	138	87.4	65.8	47.7	104.9	109.5	70.7
P28668	Bifunctional glutamate/proline--tRNA ligase OS=Drosophila melanogaster OX=7227 GN=G	4	5	6	5	1714	189.3	8.63	1.63	5	0	35	46	52.7	41.8	67.9	51.6	68.6	44.8
Q7K4H4	Bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66 OS=Drosophila me	6	4	12	4	653	73.1	7.84	18.47	4	0	242.1	253.4	207.9	204.1	134.3	465.8	372.5	272.4
Q9V4D4	Bip2 OS=Drosophila melanogaster OX=7227 GN=bip2 PE=1 SV=1	2	2	3	2	1406	154.4	9.23	0	2	0	32.5	27.9	22	24.8	27.5	47.8	47.4	27.9
Q9VRL8	Blanks OS=Drosophila melanogaster OX=7227 GN=blanks PE=1 SV=1	8	2	2	2	324	35.6	8.27	2.24	2	0	20.2	23.7	16.4	18.1	17.9	25.6	27.6	16.3
Q9VGI8	Bloom syndrome protein homolog OS=Drosophila melanogaster OX=7227 GN=Blm PE=1	2	3	4	3	1487	166	8.5	3.97	3	0	87	116.3	115.1	91.7	54.3	120.4	123.9	83.3
A0A0B4KGE5	Bonus, isoform C OS=Drosophila melanogaster OX=7227 GN=bon PE=1 SV=1	3	3	4	3	1207	130.1	6.55	3.89	3	0	55.5	56	49.4	35.3	24.7	65.1	70.6	36.4
Q94513	Boundary element associated factor OS=Drosophila melanogaster OX=7227 GN=BEAF-3	12	4	5	4	282	31.8	6.54	5.81	4	0	168.1	164	126.3	141.7	118.5	210	215.9	166.9
P52172	Box A-binding factor OS=Drosophila melanogaster OX=7227 GN=srp PE=1 SV=2	2	2	3	2	1264	134.1	7.02	1.94	2	0	19.7	27.6	18.9	20	16.6	23.2	24.4	19
Q9W384	Brahma associated protein 111kD OS=Drosophila melanogaster OX=7227 GN=Bap111 P	3	2	15	2	749	78.6	7.52	9.53	2	0	38.7	40.4	44.8	33.9	15.5	36.8	47.6	37.5
Q9VF03	Brahma associated protein 155 kDa OS=Drosophila melanogaster OX=7227 GN=mor PE=	9	10	25	10	1209	131.3	5.73	27.86	10	0	438.9	459.4	410.2	383.1	274.1	501.1	503.8	355.8
A1Z6M0	Brahma associated protein 170kD OS=Drosophila melanogaster OX=7227 GN=Bap170 P	3	4	9	4	1688	182.9	8.46	12.06	4	0	116.5	127.8	118.5	88.1	63.8	137.4	148.6	87.9
Q7K012	Brahma associated protein 55kD OS=Drosophila melanogaster OX=7227 GN=Bap55 PE=	12	3	3	3	425	47.3	5.49	2.83	3	0	47.7	65.7	55.2	52	30.4	51	69.4	53
Q9VYG2	Brahma-associated protein of 60 kDa OS=Drosophila melanogaster OX=7227 GN=Bap60	17	7	24	7	515	58.1	9.32	29.04	7	0	236	270.9	249.3	223.3	163	262.7	328.7	224
M9PFS6	Brahma, isoform E OS=Drosophila melanogaster OX=7227 GN=brm PE=4 SV=1	9	14	30	14	1658	187	7.56	28.78	14	0	583.5	677.8	696.8	610.4	408.2	752.1	813.7	630.5
Q9VEL2	Brf, isoform A OS=Drosophila melanogaster OX=7227 GN=Brf PE=1 SV=2	3	2	2	2	662	73.6	5.1	0	2	0	18.8	18.2	16.6	36.5	21.1	24.4	24.8	20.2
Q9VDE4	Bride of doubletime OS=Drosophila melanogaster OX=7227 GN=Bdbt PE=1 SV=1	7	2	3	2	286	32.9	8.38	4.63	2	0	64	102.7	91	93.3	70.8	95.8	123.9	79.3
Q9VAM5	Bromodomain containing 8 OS=Drosophila melanogaster OX=7227 GN=Brd8 PE=1 SV=1	9	5	6	5	872	94.1	5.25	6.85	5	0	60.3	52.3	56.9	28.6	18.5	69.2	64.7	33.5
Q7JVP4	Bromodomain-containing protein, 140kD, isoform A OS=Drosophila melanogaster OX=722	3	3	7	3	1430	157	7.14	21.29	3	0	61.8	78.7	65.7	54.3	42	97.5	74.7	48.7
Q9VC96	BRWD3 OS=Drosophila melanogaster OX=7227 GN=BRWD3 PE=1 SV=2	6	11	20	11	2232	248.5	6.61	15.95	11	0	191.1	248.3	213.1	289.7	136.6	253.4	257.7	206.1
contaminant_INT	BSA	10	6	39	6	607	69.2	6.11	64.8	6	0	441.5	834.5	661.2	572.4	368	511.6	428.3	377.6
Q9VAJ2	Bub3, isoform A OS=Drosophila melanogaster OX=7227 GN=Bub3 PE=1 SV=1	10	3	9	3	326	37.4	6.54	14.98	3	0	259.2	296.4	313.3	266.6	198.6	348.6	380.4	278.2
Q9VIE7	Burgundy, isoform B OS=Drosophila melanogaster OX=7227 GN=bur PE=1 SV=3	14	7	38	7	683	76.7	6.8	67.78	7	0	433.3	522.3	609.6	533.6	369.2	588.8	682.4	513.2
M9PGQ6	Bx42, isoform B OS=Drosophila melanogaster OX=7227 GN=Bx42 PE=4 SV=1	7	3	4	3	547	61.1	9.38	4.91	3	0	54	48.4	54.1	45.9	23.4	61.2	61	35.7
P51406	Bystin OS=Drosophila melanogaster OX=7227 GN=bys PE=1 SV=2	6	3	6	3	436	49.9	8.46	6.63	3	0	50	65.4	56.4	52.9	50	74.4	68.5	63.9
A0A0B4KGZ7	C-terminal binding protein, isoform H OS=Drosophila melanogaster OX=7227 GN=CtBP P	3	2	10	2	481	51.2	6.83	14.8	2	0	386	423.8	397	338.9	264.5	415.1	484.2	393.4
P05990	CAD protein OS=Drosophila melanogaster OX=7227 GN=r PE=1 SV=3	3	4	4	4	2224	246.5	6.64	2.42	4	0	21.8	30.8	33.5	23.6	33.9	32.6	43.8	31.3
P22700	Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type OS=Drosophila mel	6	5	12	5	1020	111.6	5.41	15.17	5	0	158.1	207.6	225.5	196.6	343.9	216.2	325.5	218.4
A0A0B4LF57	Calmodulin, isoform C OS=Drosophila melanogaster OX=7227 GN=Cam PE=1 SV=1	26	4	9	4	149	16.8	4.22	11.89	4	0	266.4	271.8	248	275.8	176.9	138.8	196.9	171.8
P29413	Calreticulin OS=Drosophila melanogaster OX=7227 GN=Calr PE=1 SV=2	6	2	4	2	406	46.8	4.58	7.55	2	0	65.1	65.2	66.4	59.1	98.2	51.3	90.5	60
Q9VM49	Caper, isoform A OS=Drosophila melanogaster OX=7227 GN=Caper PE=1 SV=1	14	6	19	6	594	66.4	10.01	41.26	6	0	191.4	209.4	170	168.3	136.5	249.7	259.4	175.7
Q9I7D3	Caprin homolog OS=Drosophila melanogaster OX=7227 GN=Capr PE=1 SV=1	2	2	7	2	961	103.5	6.51	8.45	2	0	141.7	184.8	192.6	120.5	176	208.5	277.2	159.9
Q9I7X6	Carnosine N-methyltransferase OS=Drosophila melanogaster OX=7227 GN=CG11596 PE	7	3	3	3	439	50.5	5.15	4.28	3	0	40.2	37.3	39.5	30	22.1	60.9	51.1	34.3
A4V2B8	Casein kinase IIalpha, isoform C OS=Drosophila melanogaster OX=7227 GN=CkIIalpha P	6	2	6	2	336	39.9	7.24	1.68	2	0	133.8	158.8	156.4	117	77.7	157.5	189.1	142
Q7JUP3	Caspar, isoform A OS=Drosophila melanogaster OX=7227 GN=casp PE=1 SV=1	3	2	3	2	695	78.4	4.89	3.52	2	0	73	87.2	92.1	71.1	46.1	82.6	90	74.5
Q95029	Cathepsin L OS=Drosophila melanogaster OX=7227 GN=Cp1 PE=2 SV=2	5	2	9	2	371	41.6	7.21	11.02	2	0	284.2	392.8	352.2	304.9	302.5	555.1	700.4	477.2

A0A0B4JD46	CCHC-type zinc finger nucleic acid binding protein, isoform B OS=Drosophila melanogaste	18	3	11	3	165	17.6	8.65	22.72	3	0	315.7	436.1	302	384.3	353.9	390.5	450.3	401.8
O96989	CDC45L OS=Drosophila melanogaster OX=7227 GN=CDC45L PE=1 SV=1	5	3	7	3	575	65.8	5.67	6.07	3	0	98	174.8	185.4	125.1	53.1	84.8	83.9	69.1
M9PEA2	CDK2-associated protein 1, isoform B OS=Drosophila melanogaster OX=7227 GN=CDK2A	8	2	5	2	295	30.7	8.44	5.73	2	0	13.3	11.7	11.5	14.3	14.4	17.9	19.7	12.5
Q7KPG8	CDK7/cyclin H assembly factor MAT1 OS=Drosophila melanogaster OX=7227 GN=Mat1 PE	11	2	4	2	320	36.6	5.08	4.11	2	0	46.1	72.6	56.3	110	67.3	42.9	101.5	31.4
Q9VCN6	Cell division cycle 16 OS=Drosophila melanogaster OX=7227 GN=Cdc16 PE=1 SV=1	2	2	4	2	718	81.7	5.52	5.37	2	0	79.5	98.3	111.6	95.8	73	113.5	145	83.1
Q9I7L8	Cell division cycle 23, isoform A OS=Drosophila melanogaster OX=7227 GN=Cdc23 PE=2	4	2	10	2	678	77.5	6.51	12.56	2	0	63.4	96.5	82.6	84.6	323	81.8	140.1	80.3
Q9W0R0	Cell division cycle 5, isoform A OS=Drosophila melanogaster OX=7227 GN=Cdc5 PE=1 SV	9	7	17	7	814	93	8.19	28.94	7	0	376.8	451.4	416.4	424.5	305.3	660	569.6	503.1
Q9VHP9	Centromeric protein-C, isoform A OS=Drosophila melanogaster OX=7227 GN=Cenp-C PE=	1	2	4	2	1411	157.6	8.41	6.72	2	0	30	34.8	36.4	43.5	29.3	59.1	56.9	44
Q24478	Centrosome-associated zinc finger protein CP190 OS=Drosophila melanogaster OX=7227	12	10	32	10	1096	121.6	4.67	54.38	10	0	688.6	779.8	743.6	697.1	553.7	959	1022.6	784.8
Q9VXT3	Cervantes, isoform A OS=Drosophila melanogaster OX=7227 GN=cerv PE=1 SV=2	12	2	4	2	230	26.1	5.53	3.89	2	0	49.2	56	38.6	39.9	26.9	59.4	56.9	40.4
Q9VM69	CG10206-PA OS=Drosophila melanogaster OX=7227 GN=nop5 PE=1 SV=2	7	3	19	3	511	57.1	8.59	32.93	3	0	595.5	570.7	542.9	475.2	467.8	1020.2	852.5	832.1
O76752	CG12117-PA OS=Drosophila melanogaster OX=7227 GN=Sptr PE=1 SV=1	16	4	9	4	261	29.2	7.03	10.78	4	0	125.7	147.5	142.3	143.2	86.6	131.7	186.2	141.1
Q7K0D3	CG12909 protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12909 PE=1 SV=	12	3	4	3	281	32.1	8.95	9.36	3	0	66.8	75.8	57.8	79.9	56	92.4	93.6	77.6
F6J1D0	CG3595 OS=Drosophila melanogaster OX=7227 GN=sqh PE=1 SV=1	12	2	5	2	174	19.9	4.81	4.05	2	0	29.1	44.3	32.3	38.6	58.4	56.3	61	46
Q9W3T2	CG4593-PA OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4593 PE=1 SV=1	7	2	5	2	209	24.8	6.57	8.4	2	0	180.9	201.9	169.2	154.1	171.3	188.8	220.8	159.9
A1ZB29	CG5757-PA OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5757 PE=1 SV=1	11	2	2	2	211	23.8	7.44	2.68	2	0	12.7	18.3	20.5	18.1	18	31.5	24	15.4
Q9VIH1	CG9273 protein OS=Drosophila melanogaster OX=7227 GN=RPA2 PE=1 SV=2	9	2	15	2	246	26.4	5.08	27.41	2	0	390	491.8	570.3	348.3	132.6	258.6	275.3	204.5
A4V391	Chaperonin containing TCP1 subunit 1, isoform B OS=Drosophila melanogaster OX=7227	14	6	24	6	557	59.5	6.39	40.14	6	0	248.4	392	476.8	389.3	519.5	424.1	590.4	408
Q9W392	Chaperonin containing TCP1 subunit 2 OS=Drosophila melanogaster OX=7227 GN=CCT2	27	11	46	11	535	58	5.85	63.75	11	0	349.5	423.8	488.6	336.5	492.3	432.1	590.3	334.8
Q9VXQ5	Chaperonin containing TCP1 subunit 6 OS=Drosophila melanogaster OX=7227 GN=CCT6	4	3	8	3	533	58.2	6.62	12.09	3	0	252.6	283.4	341	197	252.5	340.8	351.4	211.2
Q7K3J0	Chaperonin containing TCP1 subunit 8 OS=Drosophila melanogaster OX=7227 GN=CCT8	21	9	39	9	546	59.4	5.31	54.15	9	0	541.3	774.5	877.1	702.6	868.9	710.8	1012.8	697.9
A0A0B4K7A3	Charlatan, isoform F OS=Drosophila melanogaster OX=7227 GN=chn PE=4 SV=1	3	3	4	3	1286	137.2	9.35	3.91	3	0	15.6	24.1	20.6	15	12.6	21.3	23.4	19.1
Q9VEG6	Chorion peroxidase OS=Drosophila melanogaster OX=7227 GN=Pxt PE=2 SV=3	4	2	4	2	809	90.5	6.9	7.76	2	0	19.9	32.2	25.1	28.7	21.1	19.9	29	22.3
A1Z898	Chromatin assembly factor 1, p105 subunit OS=Drosophila melanogaster OX=7227 GN=C	5	3	9	3	747	83.3	8.22	13.16	3	0	122.3	127.9	163.9	113.7	71	120	115.3	89.7
Q9W3D1	Chromatin assembly factor 1, p180 subunit OS=Drosophila melanogaster OX=7227 GN=C	7	7	25	7	1183	133.4	7.03	31.57	7	0	602.4	734.5	806.5	611.1	266.8	574.2	587.6	495.8
E1JIL4	Chromatin assembly factor 1, p55 subunit, isoform B OS=Drosophila melanogaster OX=72	7	3	10	1	429	48.5	4.89	7.62	3	2	134.5	250.9	226.1	512.7	219	217.7	245.1	246.1
Q9VDY1	Chromatin-remodeling ATPase INO80 OS=Drosophila melanogaster OX=7227 GN=Ino80	1	2	2	2	1638	187	9.04	2.13	2	0	22.3	27.8	25.3	30.3	25.4	34.2	44.5	31.1
Q24368	Chromatin-remodeling complex ATPase chain Iswi OS=Drosophila melanogaster OX=7227	22	19	108	19	1027	118.8	8.29	150.51	19	0	2142.4	2324.4	2085.8	1810.9	1342.2	3164	2694.6	1991
Q86BS3	Chromator, isoform A OS=Drosophila melanogaster OX=7227 GN=Chro PE=1 SV=1	10	5	17	5	926	101	7.17	51.68	5	0	60.1	80	74.6	87.1	82.8	105.3	112.5	117.6
M9ND16	Chromodomain-helicase-DNA-binding protein 1, isoform B OS=Drosophila melanogaster O	1	3	5	3	1900	213.8	6.47	2.06	3	0	70.1	69.1	64.3	80.8	45.9	88.8	102	75.7
O16102	Chromodomain-helicase-DNA-binding protein 3 OS=Drosophila melanogaster OX=7227 GI	5	4	7	4	892	103	8.48	10.12	4	0	109	131.5	115.6	126.1	90.8	195.3	177.9	148.6
Q9V3I5	Chromosomal serine/threonine-protein kinase JIL-1 OS=Drosophila melanogaster OX=722	1	2	5	2	1207	137	6.6	10.46	2	0	102	120.5	113.5	118.9	102.3	145	144.4	115.2
A1Z987	Chromosome associated protein G, isoform F OS=Drosophila melanogaster OX=7227 GN=	5	5	17	5	1351	153.8	7.55	17.57	5	0	122.3	138.2	141.3	139.9	122	212.4	179.7	149.2
Q494K2	Chromosome transmission fidelity 4 OS=Drosophila melanogaster OX=7227 GN=Ctf4 PE=	5	4	11	4	895	96.6	5.34	18.1	4	0	257.8	311.1	379.1	259.6	97.8	233	266	206.9
Q9VN58	Circadian trip, isoform A OS=Drosophila melanogaster OX=7227 GN=ctrip PE=1 SV=4	1	3	3	3	3140	336.4	7.25	1.85	3	0	7.9	7.4	9.4	10.3	10.4	10.5	15.7	13.2
Q8IRB5	Claspin OS=Drosophila melanogaster OX=7227 GN=Claspin PE=1 SV=1	10	11	37	11	1465	165.2	4.79	56.77	11	0	575.5	609	648	445.4	311.6	497.9	570.2	477.6
X2JC31	Clathrin heavy chain OS=Drosophila melanogaster OX=7227 GN=Chc PE=3 SV=1	5	6	8	6	1678	191.1	5.72	15.51	6	0	59.6	78.3	83.4	63.9	144	90.6	122.6	93.1
Q9VE51	Cleavage and polyadenylation specificity factor 73 OS=Drosophila melanogaster OX=7227	4	3	6	3	684	76.8	5.67	6.3	3	0	43	52.9	50.4	46.9	27.8	56	62.8	49.4
Q9V726	Cleavage and polyadenylation specificity factor subunit 1 OS=Drosophila melanogaster O	4	5	8	5	1455	164.6	6.2	17.43	5	0	150.6	180.5	169.5	148.8	124.6	215.9	227.6	184.6
Q9V9V0	Cleavage stimulation factor 50 kD subunit OS=Drosophila melanogaster OX=7227 GN=Cs	4	2	5	2	424	46.9	5.95	8.64	2	0	61.8	77.1	70.5	59.2	43.7	83.4	91.3	79
Q9VE52	Cleavage stimulation factor 64 kD subunit OS=Drosophila melanogaster OX=7227 GN=Cs	7	3	8	3	419	46.2	5.78	7.25	3	0	78.9	87.6	82.3	71.1	43.7	93.4	111.1	79.1
P45437	Coatomer subunit beta OS=Drosophila melanogaster OX=7227 GN=betaCOP PE=2 SV=2	3	3	3	3	964	107.3	6.32	3.81	3	0	6.7	8.9	13	10.6	22	8.8	14.4	11.1
P45594	Cofilin/actin-depolymerizing factor homolog OS=Drosophila melanogaster OX=7227 GN=ts	33	5	62	5	148	17.1	7.17	102.33	5	0	1459.4	1545.7	1380.4	1119.9	900.2	1804.2	1812.2	1275.3
Q9VAJ1	Condensin complex subunit 1 OS=Drosophila melanogaster OX=7227 GN=Cap-D2 PE=1	5	7	15	7	1380	157.4	5.86	30.24	7	0	239.6	292.1	291.5	245.7	231	393.9	380.9	271.4
Q9VIP9	Condensin complex subunit 2 OS=Drosophila melanogaster OX=7227 GN=barr PE=1 SV=	7	4	13	4	735	82.7	5.58	19.29	4	0	99.6	94.5	96.3	93.4	78.9	123.9	121.8	97.7
contaminant_KE	contaminant_KERATIN02	25	11	147	11	622	62	5.24	219.84	11	0	8850.8	3206.7	2719.7	2209.3	3992.8	2742.3	3607.2	3461.4
contaminant_KE	contaminant_KERATIN03	33	17	363	13	593	59.5	5.21	593.8	17	4	8627.2	7738.4	7305.7	4691.2	6675	8399.9	12993.7	9667.1
contaminant_KE	contaminant_KERATIN04	25	14	71	8	458	49.6	4.93	124.71	14	4	1644.5	1418.2	1096.5	449.1	1712.5	1314.8	1671.4	766.3
contaminant_KE	contaminant_KERATIN05	28	13	128	5	471	51.5	5.16	190.6	13	4	2407.8	1061.7	887.1	470.1	778.5	1241.4	2127.8	1029.4
contaminant_KE	contaminant_KERATIN08	23	11	82	5	469	50.5	5	127.18	11	0	1426.9	422.3	501.3	271.1	434.7	868.5	1183.2	524.9
contaminant_KE	contaminant_KERATIN10	16	7	44	1	400	44.1	5.14	86.38	7	0	86.8	35	43.3	17.9	27.6	40.2	62	52.7
contaminant_KE	contaminant_KERATIN12	29	13	53	7	431	47.9	5.02	98.85	13	1	423.5	359.5	398.2	279.6	480.7	628.8	937.7	583.8
contaminant_KE	contaminant_KERATIN13	23	12	672	10	643	65.5	6.62	1011.91	12	1	18646.1	10028.6	8399.5	6783.4	10780.1	9007.7	12966	11915.8
contaminant_KE	contaminant_KERATIN15	4	2	165	1	629	64.5	6.48	260.01	2	0								
contaminant_KE	contaminant_KERATIN16	9	5	456	3	534	57.2	6.61	613.34	5	0	306.2	347.3	217.4	93	290.5	333.2	204.5	63.4
contaminant_KE	contaminant_KERATIN17	16	10	210	7	590	62.4	8.06	353.32	10	0	1392.3	751.2	610	438.7	606.7	651.6	1268.9	718.3
contaminant_KE	contaminant_KERATIN18	19	11	223	7	562	59.8	7.94	392.25	11	1	2151.1	1048.5	1067.2	692.5	790.6	1477.8	2726.7	902.5
contaminant_KE	contaminant_KERATIN22	30	15	326	11	645	65.8	8	590.18	15	4	8746.8	5993.6	5958.1	4982.8	6331	6501.8	11523.1	7969.4
Q8SYG2	COP9 signalosome complex subunit 3 OS=Drosophila melanogaster OX=7227 GN=CSN3	12	5	20	5	445	50.7	6.25	50.79	5	0	377.8	453.1	475.5	434.3	327.7	496.9	589.3	428.7
Q9V345	COP9 signalosome complex subunit 4 OS=Drosophila melanogaster OX=7227 GN=CSN4	16	6	27	6	407	46.4	6.32	44.23	6	0	493.6	567.1	617.2	497.6	370.9	581.7	710.2	513.6
Q9XZ58	COP9 signalosome complex subunit 5 OS=Drosophila melanogaster OX=7227 GN=CSN5	9	2	5	2	327	37.1	5.58	12.42	2	0	62.1	85.7	82.6	68.8	52.1	83.3	93.3	66.3
Q9V4S8	COP9 signalosome complex subunit 7 OS=Drosophila melanogaster OX=7227 GN=CSN7	14	3	11	3	278	31	6.7	24.08	3	0	163.9	201.6	184.2	148.3	103.5	179.2	233.9	155.3
Q7KTH8	COP9 signalosome complex subunit 8 OS=Drosophila melanogaster OX=7227 GN=CSN8	14	3	7	3	182	21.4	4.87	9.95	3	0	169.9	193.4	194.3	173.2	138	183.6	225.7	183.1
C7LAG1	CoRest, isoform G OS=Drosophila melanogaster OX=7227 GN=CoRest PE=1 SV=1	3	3	4	3	824	87.3	6.47	0	3	0	48.5	62.5	48.1	33	23.1	57.3	62.1	47.4
A0A0B4KEJ7	Coronin OS=Drosophila melanogaster OX=7227 GN=coro PE=1 SV=1	3	2	4	2	535	58	6.38	4.13	2	0	113	158.2	146.7	141.5	252.9	473.4	151.3	176.4
D6W4T8	Coronin OS=Drosophila melanogaster OX=7227 GN=pod1 PE=1 SV=1	2	3	5	3	1266	140.1	6.6	8	3	0	83.9	97.1	91.7	72.9	80.1	111.6	117.7	80.8
Q9V9R2	Cullin 2, isoform A OS=Drosophila melanogaster OX=7227 GN=Cul2 PE=1 SV=3	13	9	22	9	753	87.3	6.92	27.95	9	0	184.9	246.5	256.8	237.9	168.8	283.7	321.1	230.8
Q8IP45	Cullin 3, isoform F OS=Drosophila melanogaster OX=7227 GN=Cul3 PE=1 SV=2	5	4	7	4	934	106.8	9.09	8.52	4	0	54.9	63.3	72.6	61.3	50.1	67.5	87.5	61.5
Q5BI50	Cullin 4, isoform A OS=Drosophila melanogaster OX=7227 GN=Cul4 PE=1 SV=1	13	10	31	10	821	94.3	8.66	40.61	10	0	532	1559.2	636.8	568.6	366.8	637.4	734	564.5
Q9VAQ0	Cullin 5 OS=Drosophila melanogaster OX=7227 GN=Cul5 PE=1 SV=1	3	3	6	3	852	96.9	8.34	5.49	3	0	54.1	61.6	55.6	53.7	42.1	64.4	75.8	49.9
Q24311	Cullin homolog 1 OS=Drosophila melanogaster OX=7227 GN=Cul1 PE=1 SV=2	5	4	14	4	774	89.5	7.9	16.18	4	0	234.4	262.1	275.3	217.7	155.4	298.8	321.6	226.2
M9PB90	Cullin-associated and neddylation-dissociated 1, isoform B OS=Drosophila melanogaster O	4	5	20	5	1248	139.3	5.87	14.92	5	0	339.7	355	385.5	315	223.2	444.2	461.9	328.1
Q8IQ05	Cutlet OS=Drosophila melanogaster OX=7227 GN=cutlet PE=1 SV=2	5	5	10	5	993	111.7	8.51	25.33	5	0	255.7	317.1	374.1	228.7	108.2	212.4	229.2	189.9
A1Z8J0	CWF19-like protein 1 homolog OS=Drosophila melanogaster OX=7227 GN=CG7741 PE=2	3	2	6	2	545	62.1	6.62	8.22	2	0	162.3	191.7	188.7	148.6	121.5	256.2	274.7	175.5
A0A0B4KHT9	Cyclin B3, isoform B OS=Drosophila melanogaster OX=7227 GN=CycB3 PE=3 SV=1	4	2	7	2	575	64.7	8.79	9.75	2	0	131.5	149.7	146.5	140.8	87	232.6	231.8	169.1
P23572	Cyclin-dependent kinase 1 OS=Drosophila melanogaster OX=7227 GN=Cdk1 PE=1 SV=1	7	2	10	2	297	34.4	6.87	19.78	2	0	221.9	241.6	234	191.4	159.5	281.2	280	210.9
Q9VP22	Cyclin-dependent kinase 12 OS=Drosophila melanogaster OX=7227 GN=Cdk12 PE=1 SV	2	3	6	2	1157	128.3	9.63	9.39	3	1	149.3	187	156	155.5	143.9	203.8	216.6	152.9
E1JIR3	Cyclin-dependent kinase 2, isoform C OS=Drosophila melanogaster OX=7227 GN=Cdk2 P	11	3	8	2	314	35.9	8.24	11.14	3	0	50.3	52.7	68.1	52.1	37.9	65.1	64.9	55
O96433	Cyclin-T OS=Drosophila melanogaster OX=7227 GN=CycT PE=1 SV=2	3	3	5	3	1097	118.2	9.52	1.68	3	0	76.4	87.6	92.1	84.2	73.4	108.3	136.7	89.2
Q9VRD9	Cystathionine beta-synthase OS=Drosophila melanogaster OX=7227 GN=Cbs PE=1 SV=	7	2	13	2	522	56.8	7.06	27.67	2	0	43.2	43.9	55.2	38.5	37.6	48.3	55.7	37.3
Q7KN90	Cysteine–tRNA ligase, cytoplasmic OS=Drosophila melanogaster OX=7227 GN=CysRS PE	3	2	4	2	741	84.2	6.3	1.72	2	0	6.5	9.6	11.9	12.4	18.4	7.9	11.2	8.7
Q9V4N3	Cytochrome b5 OS=Drosophila melanogaster OX=7227 GN=Cyt-b5 PE=2 SV=1	19	2	3	2	134	15.2	5.05	4.74	2	0	67.4	59.8	72.9	60	84.9	65.1	82.5	59.5
Q9VWD1	Cytochrome c oxidase subunit OS=Drosophila melanogaster OX=7227 GN=COX6B PE=1	18	2	7	2	96	11.4	8.7	5.18	2	0	83.1	93.9	80.6	85.6	109.1	82.5	90.5	94.9
Q9VSD6	D-Importin 7/RanBP7 OS=Drosophila melanogaster OX=7227 GN=msk PE=1 SV=1	7	7	31	7	1049	119.2	4.86	49.74	7	0	689.6	804.6	790	774.9	554.1	774.4	1013.4	737.4
A4V3J9	Darkener of apricot, isoform N OS=Drosophila melanogaster OX=7227 GN=Doa PE=1 SV=	3	2	2	2	580	67.9	9.67	4.31	2	0	37.2	39.5	26.7	30.8	22.5	31.2	49.8	35.9
Q9VAT2	DDB1- and CUL4-associated factor 10 homolog OS=Drosophila melanogaster OX=7227 G	4	2	2	2	621	69.5	7.72	0	2	0	18	22.1	23.1	11.8	11.6	21.9	24.9	20.6

L7EEU0	Dead box protein 80, isoform E OS=Drosophila melanogaster OX=7227 GN=Ddp80 PE=1	7	3	6	3	481	53.5	6.76	6.16	3	0	88.1	108.5	107.9	71	61.2	101.4	115.8	81.8
Q7K3M5	DEAH-box helicase 15, isoform A OS=Drosophila melanogaster OX=7227 GN=Dhx15 PE=	10	7	14	6	729	82.6	7.06	21.26	7	0	319.2	344.8	347.4	354.2	302.5	448.6	524.4	395.4
M9NDR9	Defective in cullin neddylation protein OS=Drosophila melanogaster OX=7227 GN=SCCRC	11	2	7	2	297	34.7	5.57	4.08	2	0	7.2	8.4	10.7	9.3	5.3	13.5	16.2	12.2
Q8T0D3	Dek, isoform B OS=Drosophila melanogaster OX=7227 GN=Dek PE=1 SV=1	11	6	24	6	669	72.5	4.88	37.82	6	0	640.3	712.3	684	619.2	389.3	701.7	771.1	631.2
Q9VX98	Density-regulated protein homolog OS=Drosophila melanogaster OX=7227 GN=DENR PE	15	2	7	2	189	21.3	5.14	11.83	2	0	96.8	123.4	143.7	106	76.7	117.9	137.6	110
Q9V9U4	Deoxyhypusine hydroxylase OS=Drosophila melanogaster OX=7227 GN=nero PE=2 SV=	7	2	6	2	302	33.5	4.73	5.73	2	0	72.4	81.8	83.2	57.6	48.1	81.3	123.3	68.3
Q9VSU6	Dihydropteridine reductase OS=Drosophila melanogaster OX=7227 GN=Dhpr PE=1 SV=1	18	3	9	3	235	24.5	6.34	9.48	3	0	155.3	181	161.5	127.5	91.4	170.7	204.5	139.7
M9PEI6	Dikar, isoform F OS=Drosophila melanogaster OX=7227 GN=dikar PE=1 SV=1	1	2	8	2	3261	357.5	8.69	14.91	2	0	196	160.8	126.2	95	117.8	217.5	252.2	171.6
Q9VFQ9	Dipeptidase B, isoform A OS=Drosophila melanogaster OX=7227 GN=Dip-B PE=1 SV=2	17	7	34	7	508	55.5	6.76	47.65	7	0	329.5	492.9	500.9	587.9	711.8	482.2	663.5	669.9
Q9VHR8	Dipeptidyl peptidase 3 OS=Drosophila melanogaster OX=7227 GN=DppIII PE=2 SV=2	12	9	28	9	786	89.1	6.43	34.83	9	0	685.2	809.9	753	706.1	548.6	836	1022.1	729.7
Q9VC93	Dis3, isoform A OS=Drosophila melanogaster OX=7227 GN=Dis3 PE=1 SV=1	13	9	24	9	982	112.1	6.68	21.73	9	0	257.8	271.6	263.8	277.9	212	326.9	332.5	282.3
Q9XYZ5	DNA damage-binding protein 1 OS=Drosophila melanogaster OX=7227 GN=pic PE=1 SV=	12	10	61	10	1140	126	5.36	91.73	10	0	711.1	770.5	786.7	659.7	469.6	876.9	946.6	671.8
A0A0B4LEV2	DNA helicase OS=Drosophila melanogaster OX=7227 GN=dpa PE=1 SV=1	15	13	86	13	866	96.6	7.52	128.51	13	0	1506.2	1753.8	1920.5	1483.1	818.2	1797	1693	1287.9
Q9V433	DNA helicase RECQE OS=Drosophila melanogaster OX=7227 GN=RecQ5 PE=2 SV=1	2	2	2	2	1058	121.1	8.97	0	2	0	5.1	12.5	8.6	9.3	5.4	13.6	9.7	11.9
Q9W1H4	DNA ligase 1 OS=Drosophila melanogaster OX=7227 GN=DNAlig1 PE=1 SV=2	11	7	39	7	747	84.7	6.62	63.02	7	0	484.6	655.3	650.9	498.7	335.2	662	709.8	488.6
P26019	DNA polymerase alpha catalytic subunit OS=Drosophila melanogaster OX=7227 GN=DNA	11	13	38	13	1488	169.8	8.02	35.04	13	0	593.5	732.5	871.6	541.3	199.4	444.7	485.5	376.2
P54358	DNA polymerase delta catalytic subunit OS=Drosophila melanogaster OX=7227 GN=DNAp	10	10	32	10	1092	124.8	6.92	32.26	10	0	569	696.4	750.5	541.2	373.9	719.5	728.6	503
Q9W088	DNA polymerase delta small subunit OS=Drosophila melanogaster OX=7227 GN=CG1201	18	6	22	6	431	48	6.52	49.33	6	0	588.8	661.5	693.2	452.2	279	715.6	679	491.9
Q9VCN1	DNA polymerase epsilon catalytic subunit OS=Drosophila melanogaster OX=7227 GN=DN	8	17	64	17	2236	256.5	6.47	79.52	17	0	986.7	1384.3	1612.8	1032.8	434.7	795.7	900.8	643.5
Q9VRQ7	DNA polymerase epsilon subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-eps	18	7	14	7	525	58.7	6.48	24.56	7	0	94.6	126.9	125.9	84.2	44.6	66.7	86.3	61.5
Q9VPH2	DNA primase large subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-alpha60 I	12	7	23	7	533	61.4	6.96	46.25	7	0	663	913.3	1014.4	664	243.3	465.5	545.1	411
Q24317	DNA primase small subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-alpha50 I	18	7	26	7	438	50.2	7.5	29.05	7	0	325.5	469.6	502.4	389	136.9	263.2	283.7	216.6
Q9V3W9	DNA repair protein Rad23 OS=Drosophila melanogaster OX=7227 GN=Rad23 PE=1 SV=	14	4	14	4	414	45.8	4.67	23.9	4	0	134.1	168.3	144.5	134.1	101.3	147	256.5	135.5
P49735	DNA replication licensing factor Mcm2 OS=Drosophila melanogaster OX=7227 GN=Mcm2 I	18	12	98	12	887	100.4	5.11	129.3	12	0	1799.3	2083.6	2236.3	1711.6	865.2	1938.7	1953	1471.7
Q9XYU1	DNA replication licensing factor Mcm3 OS=Drosophila melanogaster OX=7227 GN=Mcm3 I	24	15	69	15	819	90.9	6.4	142.14	15	0	2062.2	2237	2256.5	1607.4	851.7	2316.3	2052.9	1469.6
Q9VGW6	DNA replication licensing factor Mcm5 OS=Drosophila melanogaster OX=7227 GN=Mcm5 I	16	8	60	8	733	82.2	7.84	114.52	8	0	629.7	824	839.7	760	387.2	796.6	828.1	621.4
Q9V461	DNA replication licensing factor Mcm6 OS=Drosophila melanogaster OX=7227 GN=Mcm6 I	21	14	87	14	817	92.3	5.38	134.76	14	0	1653.9	1978.7	2121.8	1624.3	934.4	1926.9	1945.7	1596
Q9XYU0	DNA replication licensing factor Mcm7 OS=Drosophila melanogaster OX=7227 GN=Mcm7 I	19	11	54	11	720	81.2	6.99	103.24	11	0	936.6	1038	776.8	551.9	390.2	877.9	832.8	497.5
Q94883	DNA replication-related element factor, isoform A OS=Drosophila melanogaster OX=7227 (	10	7	31	7	709	80.7	5.86	44.03	7	0	702.4	704.8	674.3	583.6	507.3	946.6	846.8	651.7
P15348	DNA topoisomerase 2 OS=Drosophila melanogaster OX=7227 GN=Top2 PE=1 SV=1	16	20	260	20	1447	164.3	8.22	453.21	20	0	5533.2	5798	4743.8	5903.8	3797.4	9080.4	6208.6	4890.3
B7YZZ9	DNA-(apurinic or apyrimidinic site) lyase OS=Drosophila melanogaster OX=7227 GN=Rrp1	13	8	61	8	706	77.3	8.91	87.75	8	0	1633.3	1724.5	1250.5	1237.3	1327.2	2938.9	2266.6	1811.7
P13469	DNA-binding protein modulo OS=Drosophila melanogaster OX=7227 GN=mod PE=1 SV=2	6	2	32	2	542	60.3	5.43	68.44	2	0	306.8	326	297.7	268.1	237.8	527.3	425.2	416.6
P91875	DNA-directed RNA polymerase I subunit RPA1 OS=Drosophila melanogaster OX=7227 GN	4	7	15	7	1642	185.3	7.64	11.56	7	0	208.2	230.2	213.3	256.4	220.3	366.2	356.1	283.1
P20028	DNA-directed RNA polymerase I subunit RPA2 OS=Drosophila melanogaster OX=7227 GN	4	3	5	3	1129	128.4	8.41	10.5	3	0	12.4	12.8	18.6	18.3	14.2	22.9	18.6	16.1
P04052	DNA-directed RNA polymerase II subunit RPB1 OS=Drosophila melanogaster OX=7227 G	6	9	22	9	1887	209	7.81	38.62	9	0	300.5	357.1	367.1	311.4	262.8	488.7	491	347
P08266	DNA-directed RNA polymerase II subunit RPB2 OS=Drosophila melanogaster OX=7227 G	6	8	16	8	1176	134	7.05	19.51	8	0	250.1	338.8	319.1	316.7	260.2	415.9	471.5	351.5
Q9VEA5	DNA-directed RNA polymerase II subunit Rpb4 OS=Drosophila melanogaster OX=7227 GI	12	2	3	2	139	16.2	4.82	5.63	2	0	69.1	48.3	46.9	29.2	28.4	65.9	51.8	38.9
Q53ZT0	DNAJ-1 OS=Drosophila melanogaster OX=7227 GN=DnaJ-1 PE=1 SV=1	13	3	15	3	334	37	8.85	22.22	3	0	296.3	320.9	250.1	189.7	148	311.1	369.8	271.7
Q9VFV9	DnaJ-like-2, isoform A OS=Drosophila melanogaster OX=7227 GN=Droj2 PE=1 SV=1	15	6	21	6	403	45.2	6.48	34.38	6	0	490.1	509.9	509.5	423.7	334.5	532.3	617.7	426.9
Q7KN75	Dodeca-satellite-binding protein 1, isoform A OS=Drosophila melanogaster OX=7227 GN=	9	12	26	12	1301	144.2	6.2	26.12	12	0	302.2	396.5	452	386.2	558.3	412.1	516.7	417
Q24319	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Drosop	6	2	6	2	449	50	5.59	8.05	2	0	60.2	85.4	92.4	71.8	140.6	78.6	135.4	89.5
A0A0B4LFX8	Domino, isoform G OS=Drosophila melanogaster OX=7227 GN=dom PE=1 SV=1	1	4	8	4	3233	353.5	8.98	8.85	4	0	172.3	185.8	193.7	144.4	130.8	269.7	358.2	166.4
P24785	Dosage compensation regulator OS=Drosophila melanogaster OX=7227 GN=mle PE=1 S	4	4	14	4	1293	143.6	7.23	15.61	4	0	126.4	131.6	135.8	113.9	87.9	176.4	184.3	138.9
Q9XYZ4	Double-strand break repair protein OS=Drosophila melanogaster OX=7227 GN=mre11 PE	5	4	6	4	620	69.2	5.95	9.61	4	0	165.8	166.7	159.5	123	88.2	172.2	189.2	130.4
O18335	Drab11 OS=Drosophila melanogaster OX=7227 GN=Rab11 PE=1 SV=1	9	2	3	2	214	24.2	5.73	0	2	0	35	16.4	18.2	12.3	22.5	26.3	26.6	13.4
Q9V3I2	Drab5 OS=Drosophila melanogaster OX=7227 GN=Rab5 PE=1 SV=1	14	2	6	2	219	23.9	8.41	1.73	2	0	37.4	57	59.4	65.6	76	69.7	112.3	62.9
Q7KNF1	Drosha OS=Drosophila melanogaster OX=7227 GN=drosha PE=2 SV=1	2	2	3	2	1327	152.7	7.34	3.77	2	0	29.3	25.6	19.8	12.1	10.9	40.7	27.1	11.2
Q9V3V0	DXl6 protein OS=Drosophila melanogaster OX=7227 GN=x16 PE=1 SV=1	14	3	9	3	258	27.9	11.56	13.26	3	0	203.6	210.6	142.9	188.6	112.3	181.7	196.1	155.7
P13496	Dynactin subunit 1 OS=Drosophila melanogaster OX=7227 GN=DCTN1-p150 PE=1 SV=2	3	3	3	3	1265	141.1	5.62	3.97	3	0	12	16.1	17.6	19.6	15.9	20.7	22.3	15
M9PBQ3	Dynein heavy chain 64C, isoform I OS=Drosophila melanogaster OX=7227 GN=Dhc64C P	1	3	3	3	4661	532.3	6.35	3.57	3	0	16.8	21.4	25.7	20.3	40.3	27.6	50.3	22.7
A0A0B4K7J2	E3 SUMO-protein ligase RanBP2 OS=Drosophila melanogaster OX=7227 GN=Nup358 PE	2	5	8	5	2718	298.7	6.11	9.51	5	0	78.4	96.5	95.8	91.3	120.4	107.9	180.7	100.9
X2JGB3	E3 ubiquitin protein ligase OS=Drosophila melanogaster OX=7227 GN=Bre1 PE=3 SV=1	10	11	29	11	1044	119	6.21	45.34	11	0	578.2	564.1	545.3	503.8	397.3	811.5	770	538.7
Q9VB08	E3 ubiquitin-protein ligase RING1 OS=Drosophila melanogaster OX=7227 GN=Sce PE=1	5	2	2	2	435	47.2	7.12	1.73	2	0	22.8	28.8	24.8	18.1	16.2	28.5	34.8	23.4
Q7JZD3	Eb1, isoform A OS=Drosophila melanogaster OX=7227 GN=Eb1 PE=1 SV=1	18	4	4	4	291	32.6	5.34	3.79	4	0	77.2	49.2	34.4	20.6	18.4	55.6	33.7	20.5
O76876	EG:132E8.1 protein OS=Drosophila melanogaster OX=7227 GN=ssx PE=1 SV=1	8	4	8	4	485	53.4	7.01	15.8	4	0	143.9	155.1	128.8	128	95.6	149.8	172.3	160
O46048	EG:133E12.4 protein OS=Drosophila melanogaster OX=7227 GN=east PE=1 SV=1	1	3	6	3	2342	250	6.23	5.88	3	0	86	106.2	94.1	97.1	60.5	110.9	114.6	96
O18399	EG:152A3.5 protein (Fbgn0003116;pn protein) OS=Drosophila melanogaster OX=7227 G	7	3	5	3	405	45.2	6.37	3.38	3	0	64.7	70.3	69.1	64.4	48.3	71.3	96.2	71.8
O46067	EG:25E8.1 protein OS=Drosophila melanogaster OX=7227 GN=EG:25E8.1 PE=1 SV=1	7	5	10	5	923	103.4	5.12	18.54	5	0	62.4	80	87.9	77.5	96.4	71.5	132.2	82.5
O46307	EG:8D8.4 protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11417 PE=4 SV=	6	4	5	4	771	88.5	4.98	5.99	4	0	69.4	72	72.6	63	43.7	122	84.1	67.4
Q9XZ29	EG:BACR25B3.9 protein OS=Drosophila melanogaster OX=7227 GN=Klp3A PE=1 SV=1	8	9	29	9	1212	135.7	7.01	30.53	9	0	291.5	361.1	356.2	357.4	273	544	463.2	414.9
Q9NJH0	Elongation factor 1-gamma OS=Drosophila melanogaster OX=7227 GN=eEF1gamma PE=	20	6	30	6	431	48.9	7.05	46.15	6	0	391.6	511.4	570.5	454.1	507.4	551.4	688.8	472.1
P13060	Elongation factor 2 OS=Drosophila melanogaster OX=7227 GN=EF2 PE=1 SV=4	12	7	77	7	844	94.4	6.6	147.65	7	0	882.3	1045.9	1160.1	706.2	950.9	1165.9	1268.4	701.7
Q9V3V9	Endonuclease G inhibitor, isoform A OS=Drosophila melanogaster OX=7227 GN=EndoGI	25	7	32	7	359	40.6	4.6	39.19	7	0	525.9	621.4	644.2	523	391.7	640.3	793.9	618.1
P29844	Endoplasmic reticulum chaperone BiP OS=Drosophila melanogaster OX=7227 GN=Hsc70	11	6	50	5	656	72.2	5.36	67.1	6	0	337.7	406.1	389.1	355.4	421	353.8	677.3	395.5
Q86BP6	Enhanced level of genomic instability 1, isoform C OS=Drosophila melanogaster OX=7227	4	5	11	5	1162	129.3	9.39	3.89	5	0	84.7	102.4	109.9	73.3	42.4	100	79.8	65.6
M9PDH1	Enhancer of bithorax, isoform H OS=Drosophila melanogaster OX=7227 GN=E(bx) PE=1 S	3	9	27	9	2761	311.2	8.27	46.41	9	0	675.2	662.7	554.9	487.3	382.1	935.5	923	513.2
Q9VKK1	Enhancer of mRNA-decapping protein 4 homolog OS=Drosophila melanogaster OX=7227	1	2	2	2	1354	149.2	5.9	3.48	2	0	17.3	25	31.2	23.4	65.2	22.9	45.2	26.8
Q9VHJ3	Enhancer of variegation 3-9 OS=Drosophila melanogaster OX=7227 GN=E(var)3-9 PE=1 S	9	4	6	4	588	66.1	5.22	8.95	4	0	104.6	121.8	113.4	107.4	68.7	105.6	132.3	100
M9PI16	Enhancer of yellow 3, isoform C OS=Drosophila melanogaster OX=7227 GN=e(y)3 PE=4 S	3	7	13	7	2012	213.2	7.52	18.81	7	0	242.1	276.1	262.7	271.9	169.2	317.4	326.5	257.7
M9PHZ5	Enhancer of zeste, isoform C OS=Drosophila melanogaster OX=7227 GN=E(z) PE=4 SV=	3	2	8	2	765	87.4	6.42	6.08	2	0	73	67.7	72.5	53.6	38.8	98.5	80.3	57.4
Q9VF92	ENL/AF9-related, isoform A OS=Drosophila melanogaster OX=7227 GN=ear PE=1 SV=1	3	2	6	2	931	100.2	9.6	12.52	2	0	38.2	31.9	25.2	20	22.5	67.9	101.3	53.5
P15007	Enolase OS=Drosophila melanogaster OX=7227 GN=Eno PE=1 SV=2	5	2	119	2	500	54.3	8.53	241.61	2	0	1033.8	1153	1101.4	978.2	785.7	1102.4	1375.4	978.9
Q9VHY6	ER membrane protein complex 1, isoform A OS=Drosophila melanogaster OX=7227 GN=E	3	3	3	1	915	100.9	8.13	5.85	3	2	21.3	32.1	36.2	34.2	59.1	35.9	58.6	38.4
A0A0B4LGV1	ER membrane protein complex 1, isoform C OS=Drosophila melanogaster OX=7227 GN=E	3	3	3	1	908	100	8.25	3.98	3	0	5.5	5.3	5.8	4.7	6.5	12.2	19.1	2.4
Q9VDL1	Esterase CG5412 OS=Drosophila melanogaster OX=7227 GN=CG5412 PE=2 SV=1	8	2	5	2	279	30.6	5.29	5.99	2	0	27	30.5	30.4	22.4	14.4	30.7	37.6	27.3
Q9VHS8	Eukaryotic initiation factor 4A-III OS=Drosophila melanogaster OX=7227 GN=CG7483 PE=	7	3	13	3	399	45.6	6.02	20.99	3	0	320.1	410.8	416.7	414.1	286.7	414.7	558.7	357.5
Q7PLL3	Eukaryotic initiation factor 4B OS=Drosophila melanogaster OX=7227 GN=eIF4B PE=1 SV	8	4	9	4	459	52.2	6.96	16.82	4	0	285.4	314.2	328.2	225.2	233.9	318.3	345.5	270.8
A0A0B4LFL3	Eukaryotic translation elongation factor 1 beta, isoform C OS=Drosophila melanogaster OX	8	2	8	2	222	24.2	4.58	15.61	2	0	186.1	222.1	253	173.3	191.2	198.7	306.3	192
P41374	Eukaryotic translation initiation factor 2 subunit 1 OS=Drosophila melanogaster OX=7227 (	9	3	13	3	341	38.6	4.94	34.9	3	0	251.9	339.3	389.4	321	488.1	414.8	463.2	363.3
P41375	Eukaryotic translation initiation factor 2 subunit 2 OS=Drosophila melanogaster OX=7227 (	10	3	12	3	312	35.2	5.77	5.31	3	0	213.5	255.2	309.3	204.8	339.7	432.8	473.3	348.7
A0A0B4KGP8	Eukaryotic translation initiation factor 2 subunit gamma, isoform D OS=Drosophila melanog	5	3	8	2	475	51.5	8.73	17.33	3	0	44.2	54.6	68.4	40.1	70.9	76.9	68.7	47.4
Q9VN25	Eukaryotic translation initiation factor 3 subunit A OS=Drosophila melanogaster OX=7227	7	9	18	9	1140	133.8	9.01	24.52	9	0	324.6	442.6	534.2	400.3	626.5	471.3	699.8	451.2
E2QCG7	Eukaryotic translation initiation factor 3 subunit B OS=Drosophila melanogaster OX=7227	3	2	4	2	690	80.4	6.28	5.82	2	0	49.7	71.4	79.2	65.3	89.8	69.9	98.9	63.7
A0A0B4LFL2	Eukaryotic translation initiation factor 3 subunit C OS=Drosophila melanogaster OX=7227	8	7	16	7	910	105.6	6.06	14.77	7	0	193.3	235.5	290.3	219.9	358.7	283.4	382.3	257.3
Q9VCK0	Eukaryotic translation initiation factor 3 subunit D-1 OS=Drosophila melanogaster OX=722	13	6	9	6	560	63.8	7.02	14.03	6	0	208.6	314.3	314.6	244.1	285.3	293.8	455.1	241.9
Q9U9Q4	Eukaryotic translation initiation factor 3 subunit H OS=Drosophila melanogaster OX=7227	5	2	5	2	338	38.4	6.1	11.05	2	0	121.3	137.4	145.7	107.2	141.7	181.2	179	114.2

O02195	Eukaryotic translation initiation factor 3 subunit I OS=Drosophila melanogaster OX=7227 G	8	2	4	2	326	36.1	5.34	0	2	0	18.3	18.3	27.4	16.8	18.3	25.9	23.8	18.9
C9QP42	Eukaryotic translation initiation factor 4A, isoform E OS=Drosophila melanogaster OX=722	23	8	105	8	403	45.8	5.66	142.05	8	0	1608.2	2046	2035.4	1921.8	1584.3	2055.7	2581.1	1925.6
A8DZ29	Eukaryotic translation initiation factor 4G1, isoform B OS=Drosophila melanogaster OX=72	3	5	8	5	1919	211	8.35	8.62	5	0	87.1	113.6	145.1	105.1	163	137.7	193.6	137.9
X2JC79	Eukaryotic translation initiation factor 4H1, isoform D OS=Drosophila melanogaster OX=72	17	6	20	6	388	41.7	9.79	29.97	6	0	408.2	336.9	320.2	209.5	178.5	389	359.2	227.9
Q9VXK6	Eukaryotic translation initiation factor 5 OS=Drosophila melanogaster OX=7227 GN=eIF5 I	6	3	6	3	464	51.7	5.26	7.44	3	0	92.1	101	111.3	95.2	114.6	108.6	125.3	89.6
Q9GU68	Eukaryotic translation initiation factor 5A OS=Drosophila melanogaster OX=7227 GN=eEF	22	2	31	2	159	17.6	5.15	36.92	2	0	196.2	195.8	205.3	140.5	107.5	212	238	174.3
Q9VZP5	Eukaryotic translation initiation factor 5B, isoform B OS=Drosophila melanogaster OX=722	6	6	25	6	1144	127.1	5.52	29.15	6	0	719.1	693.2	620	572.7	454.7	695.5	685	633
P56538	Eukaryotic translation initiation factor 6 OS=Drosophila melanogaster OX=7227 GN=eIF6 I	13	2	2	2	245	26.5	4.73	2.16	2	0	17.3	18.9	17.1	15.5	17.7	14.9	26.4	18.1
M9PFR9	Eukaryotic translation release factor 1, isoform I OS=Drosophila melanogaster OX=7227 G	12	4	13	4	447	49.7	7.46	15.2	4	0	83.9	97.8	97.5	73.5	63.9	99.6	113.5	75.2
Q9VK85	Eukaryotic translation release factor 3, isoform A OS=Drosophila melanogaster OX=7227 (	4	2	2	2	619	66.4	5.35	0	2	0	17.4	21.4	22.3	15.3	23.6	18.6	30.9	19.4
Q9TVM2	Exportin-1 OS=Drosophila melanogaster OX=7227 GN=emb PE=1 SV=1	8	6	48	6	1063	122.7	5.87	69.41	6	0	442.7	517.2	502.9	395.9	434.3	648.1	769.1	445.4
Q9XZU1	Exportin-2 OS=Drosophila melanogaster OX=7227 GN=Cse1 PE=2 SV=2	7	5	20	5	975	110.1	5.82	33.75	5	0	309.4	424.4	425.3	398	303.9	405.4	517.2	338.2
P48603	F-actin-capping protein subunit beta OS=Drosophila melanogaster OX=7227 GN=cpb PE=	12	4	7	4	276	31.3	5.44	10.68	4	0	119	140.4	129.4	81.3	86.3	149.8	181.7	83.4
Q8IRG6	FACT complex subunit spt16 OS=Drosophila melanogaster OX=7227 GN=dre4 PE=1 SV=	12	13	69	13	1083	123.5	6.29	129.64	13	0	1243.1	1476.5	1346.9	1059	658.5	1899.1	1565.9	1130.4
Q05344	FACT complex subunit Ssrp1 OS=Drosophila melanogaster OX=7227 GN=Ssrp PE=1 SV=	7	5	61	5	723	81.5	5.63	95.32	5	0	649.6	819.9	808	632.7	389	962	902.4	737.3
Q95RI5	Failed axon connections OS=Drosophila melanogaster OX=7227 GN=fax PE=1 SV=1	7	3	4	3	418	47.1	5.25	4.99	3	0	32.8	37.8	44.4	46.5	125.9	43	60.5	38.7
Q8MYL1	Fancd2 OS=Drosophila melanogaster OX=7227 GN=Fancd2 PE=2 SV=1	2	3	4	3	1478	167.4	6.89	3.3	3	0	33	40	39.2	41.2	25.5	58	49.7	35.8
A1Z7L1	Fanconi anemia complementation group I OS=Drosophila melanogaster OX=7227 GN=FA	3	4	4	4	1481	169.9	6.89	0	4	0	47.9	46.2	45.8	46.9	35.6	51.8	59.9	45
Q9VR31	Farnesyl transferase alpha, isoform A OS=Drosophila melanogaster OX=7227 GN=Fnta PI	8	3	6	3	331	38.9	5.17	6.02	3	0	138.6	133.9	126.3	102.4	72	126	170.6	98.1
Q9VZ62	Fascetto OS=Drosophila melanogaster OX=7227 GN=feo PE=1 SV=1	4	3	11	3	671	78.1	8.98	15.59	3	0	198	263.2	245.8	229.7	219.6	336.2	358.9	281.1
Q8INK3	Fatty acid binding protein, isoform C OS=Drosophila melanogaster OX=7227 GN=fabp PE	20	3	23	3	157	17.1	6.01	32.01	3	0	757.5	959	860.3	607.6	491.8	791.6	1130.1	665.7
M9PJC7	Female sterile (1) homeotic, isoform G OS=Drosophila melanogaster OX=7227 GN=fs(1)h I	1	3	8	3	2046	205.9	9.23	9.86	3	0	110.6	123.9	98	113.2	68.5	134.7	155	128.1
A0A0B4KI27	Ferritin OS=Drosophila melanogaster OX=7227 GN=Fer1HCH PE=1 SV=1	11	2	5	2	245	27.9	6.05	4.49	2	0	62.8	63	63.2	91.3	92.8	70.6	111.3	82.5
A0A0B4KHF0	Ferritin OS=Drosophila melanogaster OX=7227 GN=Fer2LCH PE=1 SV=1	7	2	11	2	236	26.2	6.52	24.25	2	0	484	587.9	526.6	621.7	550	554	758.1	560
Q9VUS0	FI01202p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7372 PE=1 SV=2	3	3	6	3	971	109.3	7.15	6.69	3	0	106.6	130	119.9	93.5	67.5	140.5	139	123.1
Q9VW53	FI01414p OS=Drosophila melanogaster OX=7227 GN=Mtr3 PE=1 SV=1	9	3	5	3	326	36.6	5.21	3.77	3	0	76.6	95.6	95.9	78.4	63.2	96.4	106.7	89.2
Q9W2I4	FI01566p OS=Drosophila melanogaster OX=7227 GN=Sgf29 PE=1 SV=2	8	2	3	2	289	32.1	8.63	0	2	0	9.8	9.6	12.2	9.8	5.8	11.2	15.8	9.8
Q9VVM8	FI02004p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5290 PE=1 SV=1	4	3	4	3	798	92.1	6.06	3.92	3	0	44.4	41.7	56.3	43.4	44.1	62.2	103.4	41.7
Q9VDE8	FI02071p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7044 PE=1 SV=1	2	2	2	2	974	112.9	6.14	1.67	2	0	25	23.5	26.3	29.2	23.3	27.5	38.1	22
Q9VWC7	FI02109p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12702 PE=1 SV=1	4	3	6	3	870	97.1	6.71	3.11	3	0	5.7	10.7	13.5	6.7	9.9	10.8	11.3	8
Q9W3R9	FI03239p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1677 PE=1 SV=2	2	2	8	2	1000	109	5.76	12.89	2	0	164.1	194.5	165.9	170.1	104	224.4	230.9	181.9
Q9W247	FI03324p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4752 PE=1 SV=2	2	2	2	2	1294	139.5	6.47	4.33	2	0	21.2	22.2	32.4	26.6	19.8	25.3	37.2	22
A4V1N8	FI03688p OS=Drosophila melanogaster OX=7227 GN=Prm PE=1 SV=1	2	2	2	2	879	102.3	5.58	1.65	2	0	19.5	52.5	35.5	46.8	84.9	40.2	38.2	28.6
Q9W0G4	FI03834p OS=Drosophila melanogaster OX=7227 GN=l(3)02640 PE=1 SV=1	3	2	4	2	652	68.9	6.89	3.41	2	0	63.9	82	71.4	68.5	62.7	72.2	96.9	71.8
Q9Y095	FI04011p OS=Drosophila melanogaster OX=7227 GN=XRCC1 PE=1 SV=1	6	3	4	3	614	68.7	9.22	4.8	3	0	73.1	86.8	82.4	77.1	58.3	112.8	109.4	84.2
Q95WY3	FI04781p OS=Drosophila melanogaster OX=7227 GN=Nop56 PE=1 SV=1	8	3	12	3	496	54.8	9.28	21.48	3	0	291.4	265.5	235.1	190.4	180	527.4	378.4	335.8
Q9VKB0	FI05224p OS=Drosophila melanogaster OX=7227 GN=ThrRS PE=1 SV=2	8	6	6	6	747	85.9	7.78	8.28	6	0	98.7	117.6	122.6	64.7	88.1	122.3	143.2	88.3
Q9VYE9	FI05227p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1622 PE=1 SV=1	10	2	4	2	398	45.4	9.39	0	2	0	5.9	7.5	10.2	10.4	5.6	13.1	16.9	9.4
Q9VGZ2	FI06805p OS=Drosophila melanogaster OX=7227 GN=Rrp46 PE=1 SV=3	9	2	3	2	233	25.7	5.33	1.6	2	0	42.6	51.7	43.6	33.5	29.6	46.5	57.9	46.8
Q8IRL9	FI06813p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2990 PE=1 SV=1	12	13	32	13	1100	124.5	6.74	45.97	13	0	469.9	617.1	673.1	475.8	282.7	609	625.1	487.8
Q9W396	FI06908p OS=Drosophila melanogaster OX=7227 GN=HP1b PE=1 SV=1	10	2	5	2	240	26	4.77	3.71	2	0	59.5	49.1	45	42.8	22.3	63.6	77.5	48.4
Q9VN44	FI07923p OS=Drosophila melanogaster OX=7227 GN=Karybeta3 PE=1 SV=1	7	7	26	7	1105	123.5	4.73	29.92	7	0	366.6	476	498.9	458.5	387.5	457.9	550.6	378.8
Q9VKI2	FI09336p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4788 PE=1 SV=1	10	3	15	3	252	26.6	9.29	26.46	3	0	333.6	370.6	345.1	344.8	185.2	334	389.3	302.9
Q7KND8	FI09619p OS=Drosophila melanogaster OX=7227 GN=Mad1 PE=1 SV=1	2	2	4	2	730	85	6.49	5.64	2	0	96.7	100.9	109.7	79.1	64.6	106.2	109.4	64.8
Q9VIG1	FI12406p OS=Drosophila melanogaster OX=7227 GN=l(2)05287 PE=1 SV=2	3	2	3	2	1071	119.9	8.72	3.33	2	0	20.4	11.3	10.3	9.5	17.1	30.8	17.1	19
Q9VPU4	FI17537p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4291 PE=1 SV=1	6	2	3	2	338	38.8	8.15	3.53	2	0	63.5	71.3	60.6	60.9	42.1	76.5	89.8	58.2
H0RNI8	FI17821p1 OS=Drosophila melanogaster OX=7227 GN=CG3760-RB PE=1 SV=1	15	3	4	3	265	29	5.31	10.62	3	0	99.9	95.9	100.5	91.1	83.5	87.2	115	95.8
A1Z9G2	FI18620p1 OS=Drosophila melanogaster OX=7227 GN=fand PE=1 SV=1	5	4	12	4	883	103.3	5.64	3.95	4	0	77.4	82.5	84.8	86.2	53.9	103.2	118.4	76.7
Q9VUK8	FI18749p1 OS=Drosophila melanogaster OX=7227 GN=GlyRS PE=1 SV=1	3	2	5	2	765	85.1	7.74	11.98	2	0	116.7	139.5	131.5	69.9	97.8	144.7	148.6	108.5
B7Z0E2	FI18812p1 OS=Drosophila melanogaster OX=7227 GN=Unr PE=1 SV=1	3	2	2	2	1057	118.4	6.55	0	2	0								
Q8IPT2	FI18910p1 OS=Drosophila melanogaster OX=7227 GN=SMC5 PE=1 SV=3	4	4	9	4	1034	117.8	8.07	13.42	4	0	102.2	121.3	102.3	112.9	84.1	161.3	150.8	130.3
Q8IQZ7	FI19014p1 OS=Drosophila melanogaster OX=7227 GN=Fim PE=1 SV=1	5	3	4	3	641	72	5.55	1.62	3	0	20.1	27.3	30.3	22.5	21.1	31.8	34.4	24.8
Q8IRH1	FI19310p1 OS=Drosophila melanogaster OX=7227 GN=Psa PE=1 SV=1	9	9	27	9	1075	122.7	6.34	24.32	9	0	244	321.7	332.9	387.5	241.4	313.3	450.9	283.2
Q9VZ00	FI19420p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1737 PE=1 SV=1	7	6	23	6	943	102.1	9.95	29.55	6	0	356.9	405.4	402.5	425.7	345.9	442.2	527.2	404.3
A1Z8D5	FI20187p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG18004 PE=2 SV=1	6	2	3	2	297	32.3	6.65	3.64	2	0	43.5	50.4	46.9	39.9	29.3	65.4	51.5	44.8
Q24113	FI21126p1 OS=Drosophila melanogaster OX=7227 GN=nonA-I PE=1 SV=2	6	4	11	1	630	69.6	8.62	21.53	4	0	9	14.7	10.7	11.7	11.1	12.9	14.5	10.2
Q9VHC7	FI21236p1 OS=Drosophila melanogaster OX=7227 GN=rump PE=1 SV=1	5	4	34	4	632	66.7	7.85	76.17	4	0	621.1	594.9	414.3	496.2	337	752	749.7	441.4
T2FFI3	FI21265p1 OS=Drosophila melanogaster OX=7227 GN=mei-9 PE=2 SV=1	7	5	9	5	961	109.5	6.95	4.88	5	0	31.9	40.6	40.2	38.5	22.9	48.9	55.9	46
A1Z6L9	FI21274p1 OS=Drosophila melanogaster OX=7227 GN=Trap1 PE=1 SV=1	7	4	18	3	691	77.9	7.59	35.28	4	0	3.9	5.3	7.4	11.7	20.6	8.2	7.8	4.9
Q9VJZ1	FI21342p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9302 PE=1 SV=1	4	2	2	2	510	57.9	8.78	0	2	0	31.4	31.7	29.4	21.1	15.5	48.6	48.8	28.9
Q9W0D6	FI22004p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7879 PE=1 SV=1	6	5	6	5	985	109.5	9.2	1.94	5	0	55.3	63.7	51.9	60.1	47.8	73	96.2	69.9
Q9VYT3	FI23714p1 OS=Drosophila melanogaster OX=7227 GN=Nrd1 PE=1 SV=2	3	4	8	4	1147	132.7	5.15	10.33	4	0	65.4	71.4	85.1	71.1	50.5	83.5	80.7	62
Q9VPB0	FI23914p1 OS=Drosophila melanogaster OX=7227 GN=HIPP1 PE=1 SV=2	2	2	3	2	926	99.9	6.89	0	2	0	16.7	14.6	16.6	17	17.3	24.9	19.4	16
Q9VSE6	FI24603p1 OS=Drosophila melanogaster OX=7227 GN=RecQ4 PE=1 SV=1	8	10	28	10	1579	175.8	7.24	44.75	10	0	293.3	359.3	331.8	335.1	197	415.8	406.3	334.2
Q9VL78	FK506-binding protein 59 OS=Drosophila melanogaster OX=7227 GN=FKBP59 PE=1 SV	12	5	22	5	439	48.8	5.41	37.54	5	0	663.5	723.6	787.7	548	434.7	784.2	834.1	557
Q9VWN4	Fl(2)d-associated complex component OS=Drosophila melanogaster OX=7227 GN=Flacc I	4	4	4	4	1150	128.9	9.25	5.1	4	0	43.2	54.1	50.7	39.3	34.1	61.6	66	52.6
Q7K7A9	Flap endonuclease 1 OS=Drosophila melanogaster OX=7227 GN=Fen1 PE=2 SV=1	14	4	35	4	385	42.9	8.53	37.34	4	0	823.4	871.8	873.2	788.8	593	1646.6	1129.2	930.5
A0A0B4K618	Fmr1, isoform G OS=Drosophila melanogaster OX=7227 GN=Fmr1 PE=1 SV=1	7	4	10	4	729	81	8.7	10.85	4	0	76	90.1	110.4	99.3	89.1	99.7	122.3	98.6
Q8IQE9	Forkhead box K, isoform G OS=Drosophila melanogaster OX=7227 GN=FoxK PE=1 SV=2	2	2	5	2	746	80.5	7.88	1.68	2	0	48.8	49.6	40.4	48.5	28.9	54.4	52.3	35.6
Q7KSD3	Frayed, isoform A OS=Drosophila melanogaster OX=7227 GN=fray PE=1 SV=1	5	2	3	2	552	60.3	6	0	2	0								
A4V3G1	Fructose-bisphosphate aldolase OS=Drosophila melanogaster OX=7227 GN=Ald1 PE=1 S	24	7	44	7	363	39.5	7.08	73.64	7	0	526	651.1	571.5	516.5	526.9	551.7	693.2	524.1
Q9NHN2	Fumble OS=Drosophila melanogaster OX=7227 GN=fbl PE=1 SV=1	4	2	2	2	512	56.7	7.69	0	2	0	21.6	22.9	21.4	18.2	23.6	26.7	20.5	23.8
Q9W1J3	Gastrulation defective protein 1 homolog OS=Drosophila melanogaster OX=7227 GN=CG	5	3	5	3	655	73.6	7.01	8.38	3	0	105.6	125.4	133.7	111.9	103.5	223.6	237.5	121.4
Q7K0S5	GDI interacting protein 3, isoform B OS=Drosophila melanogaster OX=7227 GN=Gint3 PE	7	3	6	3	441	50	7.11	3.81	3	0	40.6	36.5	48.1	32.9	30.5	41.8	44.3	32.6
Q7JX41	Geminin OS=Drosophila melanogaster OX=7227 GN=geminin PE=1 SV=1	15	3	6	3	192	21.4	4.63	12.89	3	0	141.9	154.9	147.2	152.6	95.4	161.1	186.7	149.1
Q05913	General transcription factor IIF subunit 1 OS=Drosophila melanogaster OX=7227 GN=TfIIF	10	5	11	5	577	64.4	7.88	21.26	5	0	282.9	315	264.6	268.5	163.1	308	339.2	253.5
P41900	General transcription factor IIF subunit 2 OS=Drosophila melanogaster OX=7227 GN=TfIIF	8	2	4	2	277	32.1	8.94	6.74	2	0	90.3	77	78.7	50.7	28.5	107.4	102.5	43.4
Q9VUR1	General transcription factor IIH subunit 4 OS=Drosophila melanogaster OX=7227 GN=mm	4	2	3	2	499	56.6	8.32	0	2	0	29.1	35.3	42.1	32.7	25	44.5	44.2	33
O77430	GEO01111p1 OS=Drosophila melanogaster OX=7227 GN=SkpA PE=1 SV=1	30	4	19	4	162	18.6	4.65	19.87	4	0	371.1	392.8	372.1	332.7	260.8	425.3	440.4	401.4
Q7KLX3	GEO05407p1 OS=Drosophila melanogaster OX=7227 GN=Tapdelta PE=1 SV=1	13	2	5	2	166	17.6	8.54	4.61	2	0	49.8	46.7	48.8	33	65.5	145.5	62.3	55.9
Q9VRL1	GEO06356p1 OS=Drosophila melanogaster OX=7227 GN=Uev1A PE=1 SV=1	12	2	5	2	145	16.7	6.14	9.15	2	0	189.8	270.8	223.5	175.1	131.3	207.1	280.3	178
X2JEM4	GEO07185p1 OS=Drosophila melanogaster OX=7227 GN=RpS28b PE=2 SV=1	32	2	14	2	65	7.5	10.37	37.94	2	0	863	658.4	576.7	255.6	251.5	835.8	693.7	320.7
Q9VVU2	GEO07453p1 OS=Drosophila melanogaster OX=7227 GN=RpL26 PE=1 SV=1	12	3	16	3	149	17.3	10.95	24.7	3	0	368.1	319.6	297.6	220.2	246	561.8	446	237.4
Q9VMH8	GEO07746p1 OS=Drosophila melanogaster OX=7227 GN=Pfdn1 PE=1 SV=2	13	2	4	2	126	14.7	8.91	8.06	2	0	92.1	113.6	113.1	90.3	88.4	92.9	113.2	99.1
A0A0B4LG52	GEO08239p1 OS=Drosophila melanogaster OX=7227 GN=RpS16 PE=2 SV=1	16	3	20	3	148	16.8	10.17	26.06	3	0	410.6	515.5	603.4	472.5	650.8	699.6	863.8	600.1
M9PCI2	GEO11453p1 OS=Drosophila melanogaster OX=7227 GN=NHP2 PE=2 SV=1	11	2	8	2	160	17.7	8.1	9.07	2	0	142.7	144.9	147.5	107.7	102.1	221	204.8	151.7

Q9VE98	GH01043p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8064 PE=1 SV=1	4	3	6	3	922	103.1	6.4	3.68	3	0	22	22.8	21.7	20.2	18.2	42.7	32.5	28.5
Q9VFF0	GH01077p OS=Drosophila melanogaster OX=7227 GN=UQCR-C1 PE=1 SV=2	5	3	3	3	470	51.8	6	6.95	3	0	74.5	83	108.5	89.1	191.7	102	122.8	60.2
Q7KRS9	GH01331p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1815 PE=1 SV=1	3	6	11	6	1664	181.8	8.35	11.7	6	0	145.3	160.4	144.1	158.9	104.7	192.4	220.8	154.5
Q7K3Z3	GH01724p OS=Drosophila melanogaster OX=7227 GN=p47 PE=1 SV=1	19	6	26	6	407	43.4	5.62	27.1	6	0	211.6	251.2	220.9	214.8	147	195	313	205.4
Q9VCW6	GH03051p OS=Drosophila melanogaster OX=7227 GN=Gclm PE=1 SV=1	6	2	2	2	285	31.5	5.74	1.72	2	0	33	33.3	34.7	32.7	24.4	32.7	42.9	35.5
Q9VKI8	GH03305p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6287 PE=1 SV=1	5	2	5	2	332	35.2	7.36	3.79	2	0	111.2	104.9	90.8	62.6	52.1	97	115.3	67.3
Q9VEP9	GH03554p OS=Drosophila melanogaster OX=7227 GN=Sf3a1 PE=1 SV=1	3	3	8	3	784	88	6.37	8.63	3	0	276.8	279.6	236.9	245.6	157	309.3	316.7	230.5
Q9VT38	GH03795p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG18178 PE=1 SV=1	8	2	2	2	374	42.5	9.16	3.02	2	0	53.8	33.8	24.4	17.9	20.1	91.2	49.5	23.9
Q9VNH5	GH04919p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2091 PE=1 SV=1	12	5	20	5	374	43	5.3	30.59	5	0	473.7	526.1	507.3	415.7	281.9	541.8	600.5	449.8
Q9W255	GH05812p OS=Drosophila melanogaster OX=7227 GN=qkr58E-1 PE=1 SV=1	10	4	8	4	396	45.4	9.07	5.83	4	0	150.1	165.7	153.8	162.3	95.7	198.6	208.4	127.1
Q7K5M2	GH05836p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10139 PE=2 SV=1	18	4	19	4	224	25.5	7.33	27.4	4	0	406.9	444.3	366.4	432	324.9	474.2	511.7	440
Q95U54	GH06271p OS=Drosophila melanogaster OX=7227 GN=Mms19 PE=1 SV=1	4	2	2	2	959	107	5.91	5.72	2	0	27.8	32.5	37.9	30.7	34.9	30.4	34	39.7
Q9VTB3	GH06691p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11811 PE=1 SV=1	11	2	2	2	233	25.9	7.44	2.27	2	0	9.6	10.5	8.7	9.5	14.9	12.1	16.5	12.8
Q9VKU0	GH06740p OS=Drosophila melanogaster OX=7227 GN=Lrr47 PE=2 SV=1	4	2	2	2	428	47.9	9.42	0	2	0	4.4	12.2	7.2	6	14.2	12.5	16.7	6.1
O97183	GH07456p OS=Drosophila melanogaster OX=7227 GN=RpII33 PE=1 SV=1	13	2	12	2	275	31.2	4.82	25.6	2	0	153.4	179.6	168.6	164.3	127.9	212	211.6	178.8
Q9VEK8	GH07711p OS=Drosophila melanogaster OX=7227 GN=sds22 PE=1 SV=1	29	5	19	5	326	37.8	5.03	29.08	5	0	143.4	170.9	154.8	102.7	79.7	158.6	199.7	126.8
Q9VHX2	GH08043p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3223 PE=1 SV=1	8	3	7	3	415	45.1	5.25	9.22	3	0	100.5	100.9	109	99.2	73.7	120.7	140.5	106
Q24090	GH08712p OS=Drosophila melanogaster OX=7227 GN=Snr1 PE=1 SV=2	8	3	10	3	370	41.9	5.27	14.8	3	0	223.2	278.5	272.5	260	173.5	298.1	300.2	266.9
Q7K1H0	GH09096p OS=Drosophila melanogaster OX=7227 GN=CG6491 PE=1 SV=1	6	2	3	2	324	36.5	6.65	2.16	2	0	73.3	96.7	75.5	88	106	111.2	122.5	89.4
Q8MZI3	GH10652p OS=Drosophila melanogaster OX=7227 GN=p90 PE=1 SV=1	4	2	7	2	818	88.2	9.36	9.73	2	0	86.8	115.3	112.1	114.4	118.8	166.2	191	139
O96880	GH11150p OS=Drosophila melanogaster OX=7227 GN=TfIIEalpha PE=1 SV=1	13	4	8	4	429	48.3	5	9.33	4	0	43	30.6	27.8	13	5.9	51.7	33.8	14.6
Q9V3Z4	GH11341p OS=Drosophila melanogaster OX=7227 GN=Rpn5 PE=1 SV=1	9	5	14	5	502	57.7	5.8	16.74	5	0	306.4	386.4	445.9	301.5	265.3	415.4	496.5	349.6
Q7KK90	GH14654p OS=Drosophila melanogaster OX=7227 GN=GstE1 PE=1 SV=1	10	2	11	2	224	24.9	5.91	8.16	2	0	89.1	134.5	130.4	141	97.9	110	209.8	88.2
Q9VA53	GH23275p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2246 PE=1 SV=2	8	3	8	3	406	44.8	8.21	10.48	3	0	91.5	110.4	123.8	88	91.5	111.3	134.9	95.4
Q8T0L3	GH24511p OS=Drosophila melanogaster OX=7227 GN=Uba1 PE=1 SV=1	16	12	84	12	1191	130.7	5.29	147.91	12	0	1091.1	1178.6	1165	829.8	642.1	1367	1386.7	888.7
Q9VSK9	GH24787p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6745 PE=1 SV=1	13	9	24	9	734	82.7	5.64	34.82	9	0	554.9	586.2	554.8	389.2	306.5	651.6	761	437.8
Q9VK60	GH25425p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6180 PE=1 SV=2	12	3	14	3	257	28.7	8.82	16.06	3	0	271.4	302.9	300.4	285.3	264.5	317.9	415.6	290.9
Q9VVA4	GH26789p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9674 PE=1 SV=2	3	8	20	8	2114	231.9	6.42	19.31	8	0	252.7	334.7	383	322.9	274.2	333.5	423.4	345.7
Q6NL44	GH28815p OS=Drosophila melanogaster OX=7227 GN=CG18238 PE=1 SV=1	4	2	3	2	478	53.6	7.05	3.72	2	0	33.5	41.4	44.7	38.4	30.9	51	53.9	41.4
Q9VJD1	Glucosidase 2 beta subunit, isoform A OS=Drosophila melanogaster OX=7227 GN=GCS2	4	2	4	2	548	61.5	4.46	4.73	2	0	58.4	75	66.3	75	88.7	71.5	106	70.6
Q7JVI6	Glutathione S transferase E13, isoform A OS=Drosophila melanogaster OX=7227 GN=Gst	10	2	4	2	226	25.8	6.61	4.37	2	0	22.5	29.9	31.5	30	23.1	24.1	32.1	28
A1ZB72	Glutathione S transferase E7 OS=Drosophila melanogaster OX=7227 GN=GstE7 PE=1 S	11	2	3	2	223	25.5	6.57	0	2	0	22.9	29.4	29.8	28.8	20.2	31.7	36.9	25
Q9VSL6	Glutathione S transferase O1 OS=Drosophila melanogaster OX=7227 GN=GstO1 PE=1 S	6	2	3	2	254	30	7.44	3.78	2	0	105.2	125.6	118.5	117.2	90.5	103.5	145.5	98.2
Q9VSL4	Glutathione S transferase O2, isoform B OS=Drosophila melanogaster OX=7227 GN=GstO	8	2	8	2	250	28.7	7.05	0	2	0	187.5	186.7	182.8	159.5	124.9	181.6	237.4	186.9
A0A0B4KFT5	Glutathione S transferase S1, isoform D OS=Drosophila melanogaster OX=7227 GN=GstS	12	3	8	3	250	27.8	4.59	3.89	3	0	97	109.9	110.5	109.6	84.2	98	138.3	94.1
M9PJN8	Glyceraldehyde-3-phosphate dehydrogenase OS=Drosophila melanogaster OX=7227 GN	6	2	39	2	332	35.3	8.44	71.2	2	0	549.8	882.7	932.3	890.7	649.8	780.2	1096	771.6
Q9VFC8	Glycogen [starch] synthase OS=Drosophila melanogaster OX=7227 GN=GlyS PE=1 SV=2	3	3	4	3	709	81.7	6.65	1.7	3	0	53.4	63.6	67.1	64.5	60.6	77.6	83	58.9
A1Z6H7	Glycoprotein 210 kDa, isoform A OS=Drosophila melanogaster OX=7227 GN=Gp210 PE=	3	4	7	4	1876	209.7	6.47	9.92	4	0	17.2	29.3	25.2	42.4	36.4	23.8	35.5	30.1
Q9VAY2	Glycoprotein 93 OS=Drosophila melanogaster OX=7227 GN=Gp93 PE=1 SV=1	12	8	17	8	787	90.2	5.02	17.56	8	0	173.8	230.5	204.9	217.6	297	170.3	339.1	216.9
Q9VGQ1	GM01350p OS=Drosophila melanogaster OX=7227 GN=alpha-KGDHC PE=1 SV=1	9	3	5	3	468	49.9	9.47	6.86	3	0	30.2	34.9	38.9	34.2	118	40.5	38.3	29.2
Q9VNH2	GM13341p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2100 PE=1 SV=1	4	2	4	2	477	55.3	9.01	3.65	2	0	70.4	94.4	92	84	58.9	104.4	106.7	80.5
Q9VPL0	GM13767p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3436 PE=1 SV=1	5	2	7	2	347	38.8	6.92	11.21	2	0	205.5	232.3	224	203.6	167.3	227.7	259.7	205.7
Q9V9T5	GM14617p OS=Drosophila melanogaster OX=7227 GN=Mccc1 PE=1 SV=2	9	6	10	6	698	76.5	6.2	21.64	6	0	99.9	131.6	186.7	156.3	192	260.1	176.5	124
Q7JVK6	GM27569p OS=Drosophila melanogaster OX=7227 GN=trsn PE=1 SV=1	9	2	4	2	235	27	5.5	5.62	2	0	42.8	42.3	39	28	34.4	45.4	46.9	33.3
Q9VN19	Golgi to ER traffic protein 4 homolog OS=Drosophila melanogaster OX=7227 GN=CG9853	5	2	7	2	339	38.5	6.54	7.83	2	0	118.2	137	129.8	142.3	125	155.8	168.6	155.9
M9PHT1	Grunge, isoform J OS=Drosophila melanogaster OX=7227 GN=Gug PE=1 SV=1	2	3	4	3	2007	213	7.46	4.69	3	0	75.4	75.3	72.6	63.5	42.5	77.7	110.7	76.2
Q6NP69	GST-containing FLYWCH zinc-finger protein OS=Drosophila melanogaster OX=7227 GN=g	3	2	9	2	1045	119.2	5.99	12.02	2	0	7	6.5	9	5.1	4.6	9.6	14	3.4
P32234	GTP-binding protein 128up OS=Drosophila melanogaster OX=7227 GN=128up PE=2 SV=	6	2	3	1	368	41.1	8.6	1.65	2	0								
O18640	Guanine nucleotide-binding protein subunit beta-like protein OS=Drosophila melanogaster	10	3	25	3	318	35.6	7.47	43.87	3	0	468.9	590.9	648.3	555.5	790.4	751.5	865.8	581
Q8MT06	Guanine nucleotide-binding protein-like 3 homolog OS=Drosophila melanogaster OX=722	8	4	15	4	581	65.9	9.36	21.47	4	0	190.6	219	175.6	178.3	146.7	294.4	276	261.5
O44081	H/ACA ribonucleoprotein complex subunit 4 OS=Drosophila melanogaster OX=7227 GN=N	9	4	22	4	508	56.8	9.28	29.95	4	0	681.7	568.8	506	320.3	331.3	1077.3	1175.4	555.2
B7Z0Z1	Hangover, isoform C OS=Drosophila melanogaster OX=7227 GN=hang PE=1 SV=1	2	3	11	3	2223	242.2	5.82	22.51	3	0	117.8	116.4	103.5	89.3	55.4	139.7	131.2	96.5
Q9VM75	HEAT repeat-containing protein 1 homolog OS=Drosophila melanogaster OX=7227 GN=I(	2	3	4	3	2096	237.1	6.87	9.52	3	0	52.1	49.3	37.3	55.2	52.5	78.4	68.4	74.3
P11147	Heat shock 70 kDa protein cognate 4 OS=Drosophila melanogaster OX=7227 GN=Hsc70-	20	8	307	7	651	71.1	5.52	571.9	8	1	2538.7	2998.7	2901	2309	1832.7	3226.6	3666.5	2768.3
P29845	Heat shock 70 kDa protein cognate 5 OS=Drosophila melanogaster OX=7227 GN=Hsc70-	8	5	9	5	686	74	6.35	19.76	5	0	56.6	69.7	86.6	75.9	101.8	88	78.4	71.7
Q4H2F7	Heat shock factor, isoform D OS=Drosophila melanogaster OX=7227 GN=Hsf PE=1 SV=1	4	3	5	3	733	81.6	5.06	2.03	3	0	57.7	60.9	69.3	53.7	32.3	75.9	84.2	53.5
O02649	Heat shock protein 60A OS=Drosophila melanogaster OX=7227 GN=Hsp60A PE=1 SV=3	9	4	8	4	573	60.8	5.49	11.39	4	0	102.9	131.1	199.4	204.7	446.9	175	164.5	122.4
M9PBL3	Heat shock protein 83, isoform B OS=Drosophila melanogaster OX=7227 GN=Hsp83 PE=	26	14	97	13	717	81.8	5.02	136.26	14	1	2420.9	2754.5	2870.7	2056.6	2030.5	3061.7	3549.6	2151.6
E8NHA2	HECT and RLD domain containing E3 ubiquitin ligase 4, isoform C OS=Drosophila melano	2	2	2	2	1062	119.4	6.27	2.25	2	0	30.6	32.8	34.9	27.3	24.3	43.3	49.5	44.4
Q9VF02	Helicase 89B, isoform B OS=Drosophila melanogaster OX=7227 GN=Hel89B PE=1 SV=3	2	2	5	2	1923	212.9	7.01	7.69	2	0	18.4	24.4	17.9	17	16.1	27.4	32.1	27.1
P05205	Heterochromatin protein 1 OS=Drosophila melanogaster OX=7227 GN=Su(var)205 PE=1	44	6	32	6	206	23.2	5.08	70.57	6	0	538.1	376.6	342.5	297.4	192.2	574.1	461.7	295.9
Q9VYY7	Heterochromatin protein 5, isoform B OS=Drosophila melanogaster OX=7227 GN=HP5 PE	11	5	21	5	837	92.6	5.97	49.05	5	0	266.2	298.3	241.5	251.5	209.6	355.3	381.9	293.4
P48809	Heterogeneous nuclear ribonucleoprotein 27C OS=Drosophila melanogaster OX=7227 GN	18	4	14	4	421	44.7	6.8	21.14	4	0	125.2	166.6	164.5	155.3	128.1	157.8	191.6	144.2
A1ZBW0	Heterogeneous nuclear ribonucleoprotein K, isoform C OS=Drosophila melanogaster OX=	8	4	16	4	502	51	9.2	27.4	4	0	332.4	378.8	309	356.9	248.7	372.5	486.4	402.2
A0A0B4KG96	Hiiragi, isoform D OS=Drosophila melanogaster OX=7227 GN=hrg PE=1 SV=1	10	7	21	7	827	92.3	7.75	26.22	7	0	262.3	321.1	313.2	306.6	227.9	420.2	424.5	333.8
Q8IQX8	Histidyl-tRNA synthetase, isoform D OS=Drosophila melanogaster OX=7227 GN=HisRS PE	10	6	16	6	564	62.3	7.47	32.85	6	0	421.4	513.5	551.4	394.8	359.4	584.5	560.8	386.3
Q9W1A9	Histone acetyltransferase OS=Drosophila melanogaster OX=7227 GN=enok PE=1 SV=2	2	3	5	3	2291	254.5	8.43	4.03	3	0	25.3	23.4	23.3	29.5	23.4	35.4	40	27.5
Q0KIB3	Histone acetyltransferase type B catalytic subunit OS=Drosophila melanogaster OX=7227	6	2	12	2	405	47.9	6.73	17.74	2	0	225.1	272.6	251.2	148.1	114.8	334.9	332.4	171.7
Q94517	Histone deacetylase Rpd3 OS=Drosophila melanogaster OX=7227 GN=Rpd3 PE=1 SV=2	10	3	8	3	521	58.3	5.76	8.05	3	0	121	129.5	131.6	110.1	98.5	143.6	154	115.8
A0A0B4KH25	Histone H2A OS=Drosophila melanogaster OX=7227 GN=His2Av PE=3 SV=1	20	3	53	3	141	15	10.24	50.14	3	0	1774.3	1910.6	1542.7	1381.3	2113.3	2923.7	3431	2134.8
P02283	Histone H2B OS=Drosophila melanogaster OX=7227 GN=His2B PE=1 SV=2	24	3	48	3	123	13.7	10.35	78.2	3	0	1506.9	1659.4	1485.4	1547.2	1918.3	2497.9	2858.2	2008.2
Q9V6Q2	Histone H3-like centromeric protein cid OS=Drosophila melanogaster OX=7227 GN=cid PE	8	2	2	2	225	26	10.2	1.89	2	0	23.4	18.5	17.6	24.6	17	33.5	28.7	22.8
P84040	Histone H4 OS=Drosophila melanogaster OX=7227 GN=His4 PE=1 SV=2	17	2	248	2	103	11.4	11.36	277.5	2	0	4142.2	5783.1	4680.4	5830.6	8188.4	6861.1	10487.4	6164.4
Q9VNI3	Histone PARylation factor 1-like OS=Drosophila melanogaster OX=7227 GN=CG1218 PE=	8	3	12	3	449	51.1	7.03	23.01	3	0	196.2	226.2	212.6	197.4	122.7	273.3	290.4	209.3
Q9VW15	Histone-lysine N-methyltransferase ash1 OS=Drosophila melanogaster OX=7227 GN=ash	1	2	2	2	2226	246.1	9.57	1.99	2	0	40	44.5	43.3	42.7	38.2	55.4	63.1	45.2
Q32KD2	Histone-lysine N-methyltransferase eggless OS=Drosophila melanogaster OX=7227 GN=e	4	4	8	4	1262	141.9	5.49	7.14	4	0	58	59.5	53.6	51.9	72.6	63.2	58.7	38.2
Q9VFK6	Histone-lysine N-methyltransferase PR-Set7 OS=Drosophila melanogaster OX=7227 GN=P	4	2	3	2	691	76.4	7.37	1.99	2	0	6.9	10.6	10.1	10.1	5.3	11.3	14.3	13.5
P45975	Histone-lysine N-methyltransferase Su(var)3-9 OS=Drosophila melanogaster OX=7227 GN	8	5	20	4	635	71.9	8.35	33.48	5	1	379.8	482.1	438.4	450.3	443	688.5	623.2	508.1
Q86CW5	Hmr OS=Drosophila melanogaster OX=7227 GN=Hmr PE=4 SV=1	2	3	4	3	1413	158.5	9.55	1.65	3	0	60.5	70.8	72.3	59.7	56.2	98.3	96.2	77.5
Q9V4C8	Host cell factor OS=Drosophila melanogaster OX=7227 GN=Hcf PE=1 SV=2	4	5	12	5	1500	160.1	7.68	26.99	5	0	208	230.5	228.4	181.3	161.4	271.5	541.5	224.1
Q9VNI8	Hpr1 OS=Drosophila melanogaster OX=7227 GN=Hpr1 PE=1 SV=1	5	4	11	4	701	80.7	5.05	8.86	4	0	169	199.7	218	244.8	109.8	217.4	250	159
E2QD63	Hsc/Hsp70-interacting protein related, isoform B OS=Drosophila melanogaster OX=7227 G	11	3	14	3	377	41	5.35	23.63	3	0	460.9	453.9	432	174.3	157.1	502.9	483.8	211.8
M9MSL3	Hsc70Cb, isoform G OS=Drosophila melanogaster OX=7227 GN=Hsc70Cb PE=1 SV=1	16	10	53	10	836	91.8	5.36	96.36	10	0	976.1	1194.2	1186.7	1048.8	780.7	1154.3	1470.3	1014.4
Q24276	Hsp90 co-chaperone Cdc37 OS=Drosophila melanogaster OX=7227 GN=Cdc37 PE=1 SV	5	2	4	2	389	45.1	5.06	8.39	2	0	131.7	128.7	141.5	98.3	90.7	129.4	161.7	106.3
A0A126GUQ3	Humpty dumpty, isoform B OS=Drosophila melanogaster OX=7227 GN=hd PE=4 SV=1	9	4	9	4	568	63.4	6.62	14.14	4	0	78	88.9	105.2	90.1	41.3	89.8	97.5	77.4
A0A0B4LGZ6	Hyperplastic discs, isoform B OS=Drosophila melanogaster OX=7227 GN=hyd PE=1 SV=1	3	10	22	10	2887	318.9	5.96	29.46	10	0	286.2	345.8	347.4	317.4	238.6	410	486	329.1

Q9VHI1	Hyrax OS=Drosophila melanogaster OX=7227 GN=hyx PE=2 SV=1	8	5	10	5	538	61.3	9.63	7.95	5	0	146.5	197.7	193.3	166.6	134.6	227	260.6	209.4
M9NF14	IGF-II mRNA-binding protein, isoform L OS=Drosophila melanogaster OX=7227 GN=Imp P	2	2	3	2	638	69.9	8.15	1.73	2	0	59.5	73.5	63.3	64.5	89.2	62.9	106	68.1
X2JEB6	Imaginal disc growth factor 4, isoform C OS=Drosophila melanogaster OX=7227 GN=Idgf4	9	3	4	3	442	48.6	7.83	1.73	3	0	17.7	26.2	22.2	12	22.6	19.9	28	21.3
O76521	Importin subunit alpha OS=Drosophila melanogaster OX=7227 GN=Kap-alpha1 PE=2 SV	5	2	4	2	543	60	5.34	3.8	2	0	20	19.2	27.5	20.7	14.1	20.1	26	18.9
Q9V455	Importin subunit alpha OS=Drosophila melanogaster OX=7227 GN=Kap-alpha3 PE=1 SV	9	4	11	4	514	57	5.26	13.03	4	0	326.9	366.8	338.1	330.5	222.1	441.4	384	339.1
P52295	Importin subunit alpha OS=Drosophila melanogaster OX=7227 GN=Pen PE=1 SV=2	16	6	78	6	522	57.8	5.35	91.69	6	0	569.9	714.3	658.3	645	350.6	570.7	671.8	525.7
O18388	Importin subunit beta OS=Drosophila melanogaster OX=7227 GN=Fs(2)Ket PE=1 SV=2	12	7	18	7	884	98.6	5.03	19.79	7	0	271	328.9	312	293.4	224.4	347.8	433	270.3
Q7JRJ9	Inner centromere protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Incenp P	6	4	7	4	755	83.5	9.28	12.76	4	0	252	241.5	229.2	195.8	157.9	357.9	351.1	247.5
O77460	Inorganic pyrophosphatase OS=Drosophila melanogaster OX=7227 GN=Nurf-38 PE=1 SV	12	3	23	3	338	37.9	7.01	41.99	3	0	443	432.7	438.5	259.3	296.5	407	449.1	278.3
O97477	Inositol-3-phosphate synthase OS=Drosophila melanogaster OX=7227 GN=Inos PE=1 SV	6	3	8	3	565	62.2	6.23	11.64	3	0	75.9	90	96.3	87.8	82.4	96.5	117.5	97
Q9VHG5	Insulator binding factor 1, isoform A OS=Drosophila melanogaster OX=7227 GN=Ibf1 PE=	23	5	10	5	242	27.7	6.44	13.83	5	0	302.8	322.1	266.8	235.4	204	365.9	373.1	332.3
Q9VHG6	Insulator binding factor 2 OS=Drosophila melanogaster OX=7227 GN=Ibf2 PE=1 SV=1	18	2	6	2	195	21.9	8.03	15.82	2	0	153	156.2	131.4	83.8	68.8	226.6	188.8	115.1
Q9W1C5	Integrator complex subunit 1 OS=Drosophila melanogaster OX=7227 GN=IntS1 PE=1 SV	3	5	9	5	2053	234.9	6.61	5.72	5	0	31.5	36.4	35.7	31.9	26.8	37.6	48.8	35.4
Q9VZM7	Integrator complex subunit 10 OS=Drosophila melanogaster OX=7227 GN=IntS10 PE=1 S	6	4	7	4	631	72.2	5.88	3.79	4	0	66.6	70.2	81.1	72.8	56.4	96.7	108.4	71.3
Q9VPY0	Integrator complex subunit 14 OS=Drosophila melanogaster OX=7227 GN=IntS14 PE=1 S	3	2	5	2	587	65	7.31	2.14	2	0	42.9	56.4	61.4	67.6	59.9	58.4	74.8	72.1
Q7PLS8	Integrator complex subunit 3 OS=Drosophila melanogaster OX=7227 GN=IntS3 PE=1 SV	7	6	22	6	1068	123.9	7.11	40.4	6	0	169	231	232.1	210.7	151.6	278.3	297.8	262.6
Q9VT41	Integrator complex subunit 7 OS=Drosophila melanogaster OX=7227 GN=defl PE=1 SV=	3	3	4	3	1001	112.2	8.18	3.51	3	0	40.4	52.2	42.1	36.4	25	69.9	66.8	32.5
A1ZAK1	Integrator complex subunit 8 OS=Drosophila melanogaster OX=7227 GN=IntS8 PE=1 SV	2	3	3	3	1007	113.4	6.49	5.89	3	0	68.4	78.7	67	77.8	49.9	90.7	100.1	81.1
Q9V400	Integrin linked kinase, isoform A OS=Drosophila melanogaster OX=7227 GN=Ilk PE=1 SV	3	2	2	2	448	50.7	7.44	4.36	2	0	28.2	41	44.9	37.4	37.5	35.2	37.2	32.7
Q9W0I7	IP07275p OS=Drosophila melanogaster OX=7227 GN=Psf1 PE=1 SV=2	24	4	10	2	202	23.3	7.77	13.82	4	2	288.7	370.1	429	272.2	93.3	180	213.6	170.8
Q9VEB1	IP09655p OS=Drosophila melanogaster OX=7227 GN=Mdh2 PE=1 SV=1	5	2	4	2	336	35.3	9.11	1.67	2	0	17.4	37.7	37.2	45.4	43.4	41.9	51	36
Q4V3Z5	IP10727p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11788 PE=2 SV=1	24	8	20	8	425	48.8	5.11	37.47	8	0	269.1	358.5	367.1	246.5	136.1	210.7	222.8	202.2
Q9VPM7	IP13529p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG17078 PE=1 SV=2	5	3	9	3	610	67.5	7.49	18.32	3	0	254.5	297.9	291.9	242.9	207	383.4	405.4	287.9
Q9VTE6	IP14658p OS=Drosophila melanogaster OX=7227 GN=anon-EST:fe2H6 PE=1 SV=3	5	4	5	4	1174	131.9	6.19	4.24	4	0	43.2	48.4	35	52.2	40.2	71.4	57.3	53.5
Q9VKC1	IP16805p OS=Drosophila melanogaster OX=7227 GN=RpL7-like PE=1 SV=2	9	3	6	3	257	29.1	10.1	10.1	3	0	126.1	153.7	115.1	160.9	100	182.2	178.8	161.1
Q9VCV4	Iron regulatory protein 1A OS=Drosophila melanogaster OX=7227 GN=Irp-1A PE=1 SV=1	7	6	11	2	902	98.7	5.78	16.34	6	4	295	324.7	330.9	285	212.4	302.4	406.5	253.7
Q9VGZ3	Iron regulatory protein 1B OS=Drosophila melanogaster OX=7227 GN=Irp-1B PE=1 SV=1	7	6	13	2	899	98.5	5.95	15.42	6	0	11.9	10.2	10.3	12.9	8.6	8.7	13	10.4
B7Z0E0	Isocitrate dehydrogenase [NADP] OS=Drosophila melanogaster OX=7227 GN=Idh PE=1 S	10	4	27	4	479	53.6	7.3	25.85	4	0	528.6	634.3	744.3	580.8	517.5	684.3	860.8	607.6
Q8MSW0	Isoleucyl-tRNA synthetase, isoform A OS=Drosophila melanogaster OX=7227 GN=IleRS P	3	4	8	4	1229	141	7.52	10.63	4	0	100.5	169.2	188	145.8	270.2	172.8	264.2	191.9
Q9VGR7	J domain-containing protein CG6693 OS=Drosophila melanogaster OX=7227 GN=CG669	18	4	16	4	299	34.9	8.59	26.64	4	0	598.2	625.9	485.8	427.8	357.6	762.8	713.3	488.6
B7YZK5	Jabba, isoform C OS=Drosophila melanogaster OX=7227 GN=Jabba PE=1 SV=1	5	2	4	2	560	62.6	5	8.8	2	0	101.3	192.4	185.7	202.3	204.8	148.2	265.7	155.5
A0A0B4KGX1	Jaguar, isoform L OS=Drosophila melanogaster OX=7227 GN=jar PE=1 SV=1	3	4	4	4	1268	144.8	8.68	1.82	4	0	22.4	29.6	29.3	30.1	35	33.2	43.2	31.5
Q9VBP5	Jing interacting gene regulatory 1, isoform A OS=Drosophila melanogaster OX=7227 GN=	10	3	18	3	336	38.8	6.18	35.56	3	0	405.4	513.6	542	442.1	282.8	437	471.4	368.7
Q9VT00	Jumonji, AT rich interactive domain 2 OS=Drosophila melanogaster OX=7227 GN=Jarid2 P	3	6	10	6	2351	252.4	9.11	10.86	6	0	114.6	323.2	131.7	122.7	142	169.1	202	158.5
Q9VPR6	Kinase OS=Drosophila melanogaster OX=7227 GN=Ipk2 PE=3 SV=2	10	2	3	2	309	35.3	7.94	6.71	2	0								
P17210	Kinesin heavy chain OS=Drosophila melanogaster OX=7227 GN=Khc PE=1 SV=2	4	4	6	4	975	110.3	5.77	8.27	4	0	80.6	105.5	121.8	99.2	112.8	123.5	150.2	98.8
M9PF24	Kinesin light chain, isoform B OS=Drosophila melanogaster OX=7227 GN=Klc PE=4 SV=1	6	3	5	3	508	58	6.25	5.42	3	0	60.3	65.4	74.4	60.1	74	78.2	102	65.8
Q9VSW5	Kinesin-like protein at 67A, isoform A OS=Drosophila melanogaster OX=7227 GN=Klp67A	10	9	15	9	814	92.3	9.19	20.81	9	0	224.8	256.4	231.9	259.8	158.3	321.5	314.9	259.6
A4V4A1	Kinesin-like protein OS=Drosophila melanogaster OX=7227 GN=Klp10A PE=1 SV=1	4	3	6	3	805	88.6	7.21	7.53	3	0	64	82.6	68.1	56.7	43.7	98	102.9	74
A0A0B4LI25	Kinesin-like protein OS=Drosophila melanogaster OX=7227 GN=ncd PE=1 SV=1	8	6	20	6	700	77.4	9.17	29.76	6	0	426.1	397.3	367.3	296.6	208.7	590.8	550.4	363.4
Q9VZF5	Kinesin-like protein OS=Drosophila melanogaster OX=7227 GN=pav PE=1 SV=1	4	3	6	3	887	100.6	9.23	8.41	3	0	37.2	43.1	37	33.6	29.3	71.4	59.8	35.1
A0A0B4LGW1	Kinesin-like protein OS=Drosophila melanogaster OX=7227 GN=sub PE=3 SV=1	15	9	26	9	628	71.3	5.48	43.75	9	0	391.3	445.1	391.9	416.8	271.3	585.9	607.3	473.8
B7Z002	Kismet, isoform C OS=Drosophila melanogaster OX=7227 GN=kis PE=1 SV=1	2	9	14	9	5517	593.1	5.63	12.54	9	0	188.4	248.2	261.4	254.1	187.9	269.4	296	245.9
Q8SX89	Kugelkern, isoform A OS=Drosophila melanogaster OX=7227 GN=kuk PE=1 SV=1	5	2	4	2	570	60.1	5.48	6.52	2	0	81.6	82.2	94.3	92.8	65.2	91.9	140.4	76.5
Q9Y134	L.2.35Df OS=Drosophila melanogaster OX=7227 GN=Mtr4 PE=1 SV=1	8	8	15	8	1055	118.9	6.77	19.63	8	0	233	257.7	246.8	212.9	153.4	304.5	331.4	219.7
Q9VZ22	L(3)mbt interacting protein 1, isoform A OS=Drosophila melanogaster OX=7227 GN=Lint-1	5	2	2	2	602	67.9	8.68	1.83	2	0	9.3	16.7	17.5	17.9	9.3	19.1	21.4	10.4
P40796	La protein homolog OS=Drosophila melanogaster OX=7227 GN=La PE=1 SV=2	13	4	27	4	390	44.9	7.58	37.3	4	0	610.2	680.3	638.8	568.7	381.7	695.8	864.1	673.4
A0A0B4KFY9	Lamin C, isoform B OS=Drosophila melanogaster OX=7227 GN=LamC PE=3 SV=1	11	6	8	6	640	72.1	6.67	12.25	6	0	86.4	100.5	94.9	89.3	99.5	88.5	121	79.6
Q8MLV1	Lamin-B receptor OS=Drosophila melanogaster OX=7227 GN=LBR PE=1 SV=1	3	2	5	2	741	83.1	9.79	6.42	2	0	27.2	46.4	39.8	47.9	56.1	53.5	81.5	42.7
M9NE89	Lamin, isoform B OS=Drosophila melanogaster OX=7227 GN=Lam PE=3 SV=1	33	20	93	20	622	71.3	6.47	151.13	20	0	2049.9	2394.1	2082.3	2408.4	2027.6	2028.9	3194.5	1989.3
Q95RY2	LD01461p OS=Drosophila melanogaster OX=7227 GN=CG17014 PE=1 SV=1	10	3	14	3	262	29.3	5.62	15.72	3	0	222.7	254.4	260.8	217.8	201	275	347.2	260.6
Q9VL07	LD02225p OS=Drosophila melanogaster OX=7227 GN=Utx PE=2 SV=3	5	4	7	4	1136	129.3	7.81	8.4	4	0	88.8	108.4	116	117	83	143.2	164.1	141.6
Q7K180	LD02709p OS=Drosophila melanogaster OX=7227 GN=Map60 PE=1 SV=1	9	4	38	4	440	47.6	6.77	20.26	4	0	353.9	575.6	352.4	431	308.9	461.6	533	423.5
Q9VXR5	LD02975p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9281 PE=1 SV=1	9	4	12	4	611	69.5	7.53	18.47	4	0	128.1	175.7	181.7	170.7	204.7	171.5	232.1	174.9
Q9VPN5	LD03220p OS=Drosophila melanogaster OX=7227 GN=Stip1 PE=1 SV=1	13	4	16	4	490	55.7	6.81	16.75	4	0	166.6	207.1	203	173.7	146.1	190	246.1	161.4
Q9VYW4	LD04461p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1703 PE=1 SV=1	11	8	32	8	901	101.5	5.82	51.32	8	0	499.3	469.7	583.2	421	411.3	784.5	691.7	519.5
Q9VVU6	LD04472p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6841 PE=1 SV=2	11	9	26	9	931	105.2	7.44	40.54	9	0	411.8	482.6	513	415.5	290.8	589.1	616.5	473.5
Q9VB52	LD05287p OS=Drosophila melanogaster OX=7227 GN=l(3)mbt PE=1 SV=1	2	3	7	3	1477	162.9	8.7	8.91	3	0	74.3	91.7	88	97.5	55.6	102.3	105.3	99.3
Q9VYT5	LD06533p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10347 PE=1 SV=1	7	5	8	5	580	65.3	5.78	10.81	5	0	131.2	141.7	141.4	125.5	123.5	174.1	189.3	142
Q9VQB4	LD06553p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3609 PE=1 SV=1	10	3	15	3	335	37.3	7.52	30.24	3	0	217.3	292.3	272.3	248.1	212.3	275.8	336.5	247.7
Q9W542	LD07342p OS=Drosophila melanogaster OX=7227 GN=mip130 PE=1 SV=3	4	4	7	4	986	110.4	5.27	8.1	4	0	84.9	91.9	93.4	93.4	80.6	115	137.6	106.9
Q9VSL0	LD07728p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6683 PE=1 SV=1	13	2	4	2	197	22.1	6.86	7.14	2	0	33.4	32.2	29.7	27.4	19.4	32.2	35.8	39.1
Q9VCH9	LD07883p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10375 PE=1 SV=1	18	5	12	5	254	30.3	9.03	12.13	5	0	207.6	215.7	193.2	203.2	133.2	248.4	258.2	230.7
Q9VDQ3	LD08906p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4936 PE=1 SV=1	6	2	6	2	521	58.7	5.85	12.64	2	0	68.7	76.5	69.6	73.9	52.6	96.9	93.1	76.5
Q9W362	LD09531p OS=Drosophila melanogaster OX=7227 GN=Larp7 PE=1 SV=1	4	2	2	2	595	67.3	7.36	0	2	0	10	11.6	9.8	3.1	6.6	9.8	10	7.1
Q95RV3	LD09786p OS=Drosophila melanogaster OX=7227 GN=Lhr PE=2 SV=1	7	2	5	2	334	38.6	9.36	7.75	2	0	48.2	57.2	54.6	57.9	38.1	57.3	76.1	62.5
Q9W3C3	LD10016p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2004 PE=1 SV=1	18	6	21	6	425	48.3	5.21	42.97	6	0	421.7	491.8	445.4	357.5	289.2	535.7	595.9	456.2
Q8T0D1	LD10183p OS=Drosophila melanogaster OX=7227 GN=CG4639 PE=1 SV=1	9	3	14	3	337	38.1	6.2	26.73	3	0	214.5	260	225.9	220.7	165	294.1	315.2	254.5
Q9VIJ9	LD10773p OS=Drosophila melanogaster OX=7227 GN=Ns4 PE=1 SV=1	5	2	2	2	575	66.6	6.51	0	2	0	7.2	6.5	5.4		3.9	10.5	5.1	4.2
Q5U0X8	LD10780p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12325 PE=1 SV=1	3	3	4	3	949	105.9	5.34	7.94	3	0	81.2	83.9	74.2	81.3	75.1	123.7	113.2	105.3
A1Z909	LD11307p OS=Drosophila melanogaster OX=7227 GN=Nol1Nt PE=1 SV=1	9	7	19	7	891	99.8	5.5	22.01	7	0	372.1	408.7	319.5	340.2	238.7	542.4	495.4	426.5
A1Z9W4	LD11480p OS=Drosophila melanogaster OX=7227 GN=Pcf11 PE=1 SV=2	2	3	5	3	1953	212.6	6.23	5.53	3	0	63.9	69.5	63.2	53.4	45.2	82.8	85.8	65.9
Q6NQY9	LD11580p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9143 PE=1 SV=1	3	2	3	2	813	91.5	8.78	0	2	0								
Q9VCX7	LD12377p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG31156 PE=2 SV=3	9	9	15	9	948	106.4	8.87	17.86	9	0	322.6	359.1	305	304.2	267.3	567.8	440.4	373.5
Q9W4R9	LD13611p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10802 PE=1 SV=2	9	3	5	3	436	49.1	6.23	6.95	3	0	21.9	25	23.1	22.2	27.1	29.1	36.2	24.1
C6SUW3	LD13662p OS=Drosophila melanogaster OX=7227 GN=RpS9 PE=1 SV=1	12	3	17	3	195	22.6	10.61	32.78	3	0	580.6	712.6	673.3	698.8	963.3	1005.2	1138.9	695.8
Q9VRY4	LD13895p OS=Drosophila melanogaster OX=7227 GN=velo PE=1 SV=3	2	3	4	3	1833	202.5	7.14	3.68	3	0	71.3	83	88.8	77	51.2	85.2	95	78.9
Q7JQN4	LD15481p OS=Drosophila melanogaster OX=7227 GN=Rs1 PE=1 SV=1	8	4	14	4	782	87.8	9.47	29.02	4	0	197.8	204.6	138.9	158.9	98.8	239.6	212.5	241.7
Q95RQ8	LD15650p OS=Drosophila melanogaster OX=7227 GN=pita PE=1 SV=1	11	5	21	5	683	78.3	7.28	30.44	5	0	212.4	222.8	203.4	234.4	170.4	273.3	279.5	260
Q9VP57	LD15904p OS=Drosophila melanogaster OX=7227 GN=pzg PE=1 SV=1	11	7	34	7	996	105	4.89	86.17	7	0	787.1	729.8	690.7	587.7	431.4	1014.1	984	640.4
Q9VR53	LD15927p OS=Drosophila melanogaster OX=7227 GN=wap PE=1 SV=2	7	2	2	2	343	38.5	5.64	2.47	2	0	21.7	21.6	23.8	14.4	22.5	36.8	38.2	25.8
Q9VW59	LD16419p OS=Drosophila melanogaster OX=7227 GN=RhoGDI PE=1 SV=1	37	6	22	6	201	23.2	5.64	20.06	6	0	387.5	481	439	314.4	284.8	449.4	943.2	340.4
Q8MSW9	LD17611p OS=Drosophila melanogaster OX=7227 GN=U3-55K PE=1 SV=1	6	3	7	3	484	53.3	8.73	12.61	3	0	59.2	70.5	56.3	61	62.2	121.7	108.2	94.7
Q9VUE5	LD17962p OS=Drosophila melanogaster OX=7227 GN=stwl PE=1 SV=1	8	6	24	6	1037	112.8	9.39	35.93	6	0	392.9	431.1	407.2	419.3	281.5	497.2	488.4	384
Q7K110	LD18774p OS=Drosophila melanogaster OX=7227 GN=OstDelta PE=1 SV=1	7	3	3	3	634	69.2	9.17	3.02	3	0	19.8	44.2	38.2	29.1	53.6	29.3	49.1	31.6
Q9VT75	LD19812p OS=Drosophila melanogaster OX=7227 GN=vnc PE=1 SV=1	16	3	6	3	196	22.3	6.95	4.39	3	0	101.3	132.2	139.2	116.7	128.8	143.5	169.9	130

Q9VTT2	LD20590p OS=Drosophila melanogaster OX=7227 GN=vers PE=1 SV=1	7	2	6	2	391	44.8	5.81	11.02	2	0	34.2	45	39.1	45.7	22.7	51.6	55.3	34
Q7K231	LD20635p OS=Drosophila melanogaster OX=7227 GN=CYC4 PE=1 SV=1	10	4	9	4	517	58.9	8.13	11.87	4	0	78.9	97.2	94.9	91.1	64.8	112.2	111.9	102.3
Q9VY91	LD21074p OS=Drosophila melanogaster OX=7227 GN=Pdcd4 PE=1 SV=2	10	4	14	4	509	56.3	5.97	30.72	4	0	278.4	390.5	359.1	332.7	284.3	317.9	432.5	351
Q59E33	LD21442p OS=Drosophila melanogaster OX=7227 GN=scaf6 PE=1 SV=1	2	2	4	2	960	107.5	9.22	7.32	2	0	90.9	99.1	110.3	97.8	61.9	130.6	124.8	106.4
Q9VXW5	LD21606p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9114 PE=2 SV=1	3	2	3	2	619	71.3	5.25	2.11	2	0	41.9	39.2	36.3	36.6	38.6	49.2	118.6	34.8
Q9VW10	LD21924p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9300 PE=1 SV=1	4	2	3	2	673	76.3	5.63	1.77	2	0	10.6	10.3	9	9.6	6.5	20.9	14.5	14.3
Q9VD52	LD21931p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6015 PE=1 SV=1	3	2	4	2	576	65.4	7.34	3.78	2	0	62.4	85.1	75.5	71.8	55.5	101.4	100.9	86
Q9I7Z8	LD21943p OS=Drosophila melanogaster OX=7227 GN=CG13372 PE=1 SV=3	3	4	5	4	1377	157.6	7.68	1.92	4	0	36.6	41.2	29.8	43.3	40.8	70.3	52.4	57.7
Q7KUA4	LD22577p OS=Drosophila melanogaster OX=7227 GN=Uba2 PE=1 SV=1	14	7	43	7	700	77.6	5.02	47.51	7	0	652.5	746	607.9	298.5	209.5	821.7	811.1	256.3
Q9VLX2	LD22651p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7154 PE=1 SV=1	3	2	4	2	861	95.9	6.1	9.19	2	0	44.2	47.8	47.1	53.6	36.9	58.7	85.5	41.5
Q9V9V7	LD23072p OS=Drosophila melanogaster OX=7227 GN=pasha PE=2 SV=1	5	3	3	3	642	72	5.81	2.18	3	0	47.6	35	36	29.1	20.7	48.9	47.1	30.5
Q9VL91	LD23102p OS=Drosophila melanogaster OX=7227 GN=zf30C PE=1 SV=2	5	2	8	2	777	88.3	8.13	15.29	2	0	51.3	48.5	47.7	51.5	35.4	69.8	68	55.1
Q95TU2	LD23187p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6686 PE=1 SV=1	8	5	15	5	970	112.5	7.21	30.21	5	0	164.9	169.6	156.6	151.3	107.1	212.5	223.6	155.6
Q9VCF8	LD23561p OS=Drosophila melanogaster OX=7227 GN=anon-WO0118547.306 PE=1 SV=	8	2	4	2	371	41.8	5.62	8.45	2	0	21.1	24.9	27.8	26.4	25.2	30.2	35.7	30.1
Q9VK59	LD23647p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5787 PE=1 SV=2	14	13	50	13	950	100.2	9.74	68.81	13	0	1486	1457.9	1144.8	1281.1	985.6	1600	1666.2	1269.2
Q9VAA9	LD23804p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7946 PE=1 SV=1	18	8	50	8	475	52.8	8.18	35.36	8	0	571.7	550.8	500	479.2	386.5	812.8	701.1	562.4
Q9VNG2	LD24014p OS=Drosophila melanogaster OX=7227 GN=Wdr33 PE=1 SV=2	2	2	4	2	807	90.5	8.79	7.62	2	0	56.5	68.9	74.8	52.9	46.7	74.5	85.8	62.5
Q9W1C8	LD24355p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3163 PE=1 SV=2	6	2	2	2	368	41.5	8.34	1.85	2	0	22.3	32.2	34.1	15	16.5	36.6	30.1	22.4
Q8SX76	LD24646p OS=Drosophila melanogaster OX=7227 GN=pch2 PE=1 SV=1	12	5	10	5	421	46.5	5.69	13.42	5	0	150.8	190.3	187.3	175.2	146.7	181.4	207.6	159.8
Q7JVH6	LD24696p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9436 PE=1 SV=1	10	3	7	3	311	35.4	6.76	11.39	3	0	205.4	187.9	185.9	143.5	96.9	221.6	203.2	128.5
Q9VQK5	LD24714p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3542 PE=1 SV=1	4	3	5	3	806	91.3	8.84	4.12	3	0	32.2	44.5	30.9	40.7	58.4	54.7	59.1	33
Q9VY54	LD24737p OS=Drosophila melanogaster OX=7227 GN=l(1)G0007 PE=1 SV=2	5	5	5	5	1222	139.5	7.4	6.38	5	0	80.6	93.5	85.3	79.1	64.2	103.6	105.5	96.7
Q9V3E7	LD24793p OS=Drosophila melanogaster OX=7227 GN=Ref1 PE=1 SV=1	8	2	10	2	266	27.8	10.55	19.66	2	0	252.4	271.1	232	237.3	161.4	232.3	296.3	245.4
Q9VK44	LD24832p OS=Drosophila melanogaster OX=7227 GN=ufd2 PE=1 SV=1	5	7	15	7	1217	138.5	5.87	10.67	7	0	229.7	284.9	273.5	235.2	220.4	320.8	371.3	280.5
Q9VJE3	LD24839p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG15141 PE=1 SV=1	14	5	11	5	404	45.9	4.93	18.03	5	0	323.1	331.3	319.6	271	180	356.7	378.3	326.8
Q9VG60	LD24919p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12267 PE=2 SV=2	3	2	3	2	522	59.8	6.61	2.4	2	0	63.3	68.5	73.4	68.5	59.1	90	100	83
Q9W403	LD24968p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3847 PE=2 SV=1	6	3	7	3	380	43.6	4.83	1.82	3	0	176.1	179	146.9	135.6	105.9	216.1	227.1	137.4
Q8MSW4	LD25448p2 OS=Drosophila melanogaster OX=7227 GN=CG42374-RA PE=2 SV=1	7	2	2	2	213	24	6.43	4.12	2	0	46.6	67	69.3	49.1	43.1	67.4	78.3	64.3
Q9VIZ3	LD25692p OS=Drosophila melanogaster OX=7227 GN=l(2)37Cb PE=1 SV=1	6	3	8	3	894	102.8	6.52	11.66	3	0	94.7	107.1	95.4	83.9	68.2	112.9	113.7	92.5
Q7K4R2	LD26477p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11504 PE=2 SV=1	6	2	9	2	410	46.4	6.6	7.62	2	0	123.7	133.8	122.5	118.9	96.1	204.3	158.2	159.2
Q9VT61	LD27033p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8108 PE=1 SV=1	6	5	15	5	919	102.9	6.21	19.52	5	0	524.8	509.1	342.8	240.1	202.7	608.1	559.4	275.1
Q95RI7	LD28068p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG17454 PE=1 SV=1	17	3	8	3	243	28.2	8.54	4.12	3	0	54.7	65.3	52.4	56	35.2	78.2	74.3	57.3
Q8T051	LD28458p OS=Drosophila melanogaster OX=7227 GN=CG4639 PE=2 SV=1	3	2	3	2	639	73.2	6.42	4.69	2	0	81.1	94.9	90.5	88.1	75	118.5	127.2	99.9
Q9VAX8	LD28793p OS=Drosophila melanogaster OX=7227 GN=Snu114 PE=1 SV=1	12	9	28	9	975	110.6	5.03	23.99	9	0	107.1	133.9	139.5	118.1	96.5	168.9	178	125.6
Q9VRX7	LD29573p OS=Drosophila melanogaster OX=7227 GN=Rexo5 PE=1 SV=1	20	9	25	9	681	76.7	6.21	27.16	9	0	166.4	142.7	130.5	123.7	81	196.3	156.4	174.8
Q9VL71	LD29830p OS=Drosophila melanogaster OX=7227 GN=Srp54 PE=1 SV=1	4	2	4	2	513	58.3	11.33	1.77	2	0	126.1	131.4	75.6	124.2	63	136.4	136.7	129.5
Q9VN21	LD30155p OS=Drosophila melanogaster OX=7227 GN=lost PE=1 SV=1	11	5	9	5	545	59.7	9.06	15.62	5	0	190.7	192.2	195.1	135.3	222.5	187.1	240.3	160.2
Q9VHM3	LD30467p OS=Drosophila melanogaster OX=7227 GN=M1BP PE=1 SV=1	10	3	16	3	418	48.1	5.52	26.73	3	0	220.8	239.3	213.4	220.6	158	316.4	292.6	243.9
Q9VI64	LD30995p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10098 PE=1 SV=1	5	2	2	2	353	37.5	4.79	2.19	2	0	26.7	36.3	32.9	28.8	30.4	34.8	46.9	27.3
Q9VUR2	LD31322p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12301 PE=1 SV=2	9	6	10	6	771	88.7	9.48	14.63	6	0	113.2	114.2	93.2	109.7	75.7	135.9	147.8	117.7
Q7JVH0	LD32459p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8435 PE=1 SV=1	6	2	5	2	333	37.7	6.86	13.64	2	0	95.9	115.2	104.8	120.2	90.7	116.6	126.8	125.8
Q9V3T8	LD32469p OS=Drosophila melanogaster OX=7227 GN=SC35 PE=1 SV=1	10	2	7	2	195	21.4	11.75	10.81	2	0	263.8	248	202.4	158.1	146.3	244.5	271.4	176.6
Q9VTC1	LD32732p OS=Drosophila melanogaster OX=7227 GN=DmRH27 PE=1 SV=1	12	8	25	8	791	87.2	6.99	36.89	8	0	397.5	468.5	442.2	405.3	289.1	554.5	585.4	458
Q9W3M7	LD32873p OS=Drosophila melanogaster OX=7227 GN=mahe PE=1 SV=1	6	4	8	4	945	100.4	9.14	10.43	4	0	15.9	16.9	17.1	18.6	19	16.4	18.4	16.2
Q9VP85	LD32951p OS=Drosophila melanogaster OX=7227 GN=Sin PE=2 SV=1	4	2	2	2	486	54.9	6.6	2.15	2	0	41.9	48.7	41.1	36.5	28.4	45.4	51.4	43.8
Q9VF83	LD33178p OS=Drosophila melanogaster OX=7227 GN=CG12258 PE=1 SV=2	9	4	11	4	439	50	8.82	14.76	4	0	273.4	287.9	265.3	223.6	169.6	336.6	344.7	275.5
Q7K4L8	LD33749p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7878 PE=1 SV=1	5	2	3	2	703	78.5	6.7	0	2	0								
Q9VM62	LD34181p OS=Drosophila melanogaster OX=7227 GN=SA PE=1 SV=2	5	6	10	6	1127	130	5.4	13.16	6	0	130.3	149.9	154.5	146.1	110.6	197.3	184.4	145.8
Q9VX15	LD35209p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8142 PE=1 SV=2	27	9	40	9	353	39.5	7.87	70.73	9	0	1013.8	1093	1088.7	666.6	364.6	1242.8	925	667.4
Q9VWQ3	LD35981p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6961 PE=2 SV=2	13	5	11	5	474	53	9.74	19.14	5	0	260	260.2	247.8	218.4	154.5	281.5	285.4	225.6
Q9VBX4	LD36051p OS=Drosophila melanogaster OX=7227 GN=CG10057 PE=1 SV=2	2	3	7	3	1150	129.2	9.57	3.95	3	0	27.6	37.8	31.5	42.7	26.1	45.3	42.5	44.1
Q9VEJ1	LD36095p OS=Drosophila melanogaster OX=7227 GN=SF1 PE=1 SV=3	2	2	2	2	787	87.3	9.61	4.85	2	0	148.8	117.6	92.9	70.8	56.2	158.1	143.1	90.9
Q9VX35	LD36501p OS=Drosophila melanogaster OX=7227 GN=CC4 PE=1 SV=1	13	5	13	5	336	37.4	9.73	2.14	5	0	169.9	118	103	80.7	101.1	267.1	145	87.8
Q9VK18	LD36945p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG16812 PE=2 SV=1	7	3	5	3	455	49.8	9.99	3.91	3	0	56.4	69.8	60.5	65.3	50	77.8	76.1	69.5
Q9W379	LD37736p OS=Drosophila melanogaster OX=7227 GN=Zpr1 PE=1 SV=1	7	3	4	3	457	51.3	4.74	2.88	3	0	33.1	51.9	39.6	40.7	34.9	38.2	53.3	29.8
Q9VXL4	LD38104p OS=Drosophila melanogaster OX=7227 GN=Rrp47 PE=1 SV=1	11	2	3	2	159	18.1	6.2	3.63	2	0	77.1	84.2	83.1	65.1	43	81	93	73.3
Q9VWD9	LD38919p OS=Drosophila melanogaster OX=7227 GN=Ubqn PE=1 SV=1	5	2	7	2	547	58.8	5.11	17.8	2	0	40.9	43.4	43	53.1	44.8	40.5	60.4	44.9
Q960Q8	LD39850p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3511 PE=1 SV=1	8	4	8	4	637	71.7	7.14	8.31	4	0	115.9	130.3	141.1	125.2	91.3	173.2	196.7	133.8
Q9VJZ6	LD40224p OS=Drosophila melanogaster OX=7227 GN=Gnx4 PE=1 SV=1	20	2	8	2	216	23.6	4.86	21.35	2	0								
Q7JQY8	LD40262p OS=Drosophila melanogaster OX=7227 GN=p190 PE=2 SV=1	3	4	12	4	1309	145.9	6.19	12.32	4	0	320.7	303.5	240.2	254.1	181.8	409.8	381.7	282.5
Q9V3W7	LD40489p OS=Drosophila melanogaster OX=7227 GN=SF2 PE=1 SV=1	12	3	11	3	255	28.3	9.91	18.94	3	0	536.5	534.8	447.4	463.1	307.4	491.7	585.2	493.6
Q7K4H1	LD40680p OS=Drosophila melanogaster OX=7227 GN=CG8185 PE=2 SV=1	4	2	4	2	521	57.9	4.42	6.34	2	0	51.5	49.4	53.3	33.3	33.4	58.1	77.8	47.1
Q9VKU8	LD40728p OS=Drosophila melanogaster OX=7227 GN=RluA-2 PE=1 SV=2	4	2	3	2	547	62	6.42	1.79	2	0	37.6	20.4	18.7	16.8	7.9	38.2	29.3	14.2
Q9VUM1	LD41209p OS=Drosophila melanogaster OX=7227 GN=Prp31 PE=1 SV=1	3	2	3	2	501	55.5	7.09	4.02	2	0	127.8	144.8	143.8	131.8	90.4	159.1	170.3	148.9
Q9VXW2	LD41277p OS=Drosophila melanogaster OX=7227 GN=Prp5 PE=1 SV=1	6	6	11	6	1224	136.2	8.07	16.01	6	0	177.3	226.8	217.9	216.4	147	323.5	283	232.2
Q95TL8	LD41494p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9911 PE=1 SV=1	4	2	2	2	412	47	5.97	2.08	2	0	35.7	36	39.5	34.9	73.8	41.4	64.8	42.6
Q9V3P2	LD41558p OS=Drosophila melanogaster OX=7227 GN=l(2)34Fd PE=1 SV=1	3	2	2	2	721	83.3	7.39	0	2	0	8.3	10.4	14.8	18.1	9.6	12.7	18.7	20.2
Q9W3K3	LD41718p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2260 PE=1 SV=1	9	4	8	4	609	68.8	9.73	11.8	4	0	63.4	75.6	61.4	68.4	62.5	117.4	102	106.5
Q9VC94	LD41803p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5728 PE=1 SV=2	3	5	16	5	1430	159.7	8.56	31.57	5	0	431.7	419.2	366	369.8	491.3	678.5	606.3	539.6
Q9VHJ7	LD41978p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11964 PE=1 SV=1	11	4	10	4	581	66	5.11	12.56	4	0	31.6	33	38	24.7	26.5	34.4	49.5	36.7
Q9VPY7	LD42035p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5126 PE=1 SV=1	10	5	11	5	455	52.7	6.05	15.6	5	0	156.8	225.3	240.7	212.5	166.7	198.7	286.7	194.4
Q9VGL0	LD43047p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG14712 PE=1 SV=3	1	2	3	2	1266	129.8	10.14	0	2	0	7.5	12.4	6.1	6.7	4.4	7.4	10.7	8.7
Q9W4Z9	LD43561p OS=Drosophila melanogaster OX=7227 GN=EG:25E8.3 PE=1 SV=1	3	2	2	2	535	60.3	9.32	2.35	2	0	36.6	40	42.6	45.5	37.9	81.2	67.6	66.8
Q9V9Q4	LD43819p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1416 PE=1 SV=2	12	4	7	4	354	40.1	6.57	12.07	4	0	236.4	315.7	278.6	287	221.5	330.4	387.9	297.9
Q95RC8	LD44171p OS=Drosophila melanogaster OX=7227 GN=mu2 PE=1 SV=1	2	2	5	2	1280	140.5	6.6	0	2	0	17	15.3	17.6	16.6	9.8	20.9	25.1	21.4
Q8SX57	LD44221p OS=Drosophila melanogaster OX=7227 GN=CG11005 PE=1 SV=1	14	2	10	2	257	26.9	7.09	16.07	2	0	30	36.1	40.2	30.3	17.7	26.2	40.5	24
Q9VT74	LD44422p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6674 PE=2 SV=1	10	2	2	2	233	26.2	9.22	0	2	0	15.3	20.8	18	17.7	14.1	21.8	25.3	21.4
Q9VQK7	LD45152p OS=Drosophila melanogaster OX=7227 GN=Sf3b2 PE=1 SV=2	8	4	7	4	749	84.7	5.34	14.63	4	0	66.7	87.1	69	68.1	52.8	77.9	92.6	73.9
Q9V3P3	LD45860p OS=Drosophila melanogaster OX=7227 GN=REG PE=1 SV=1	18	2	19	2	245	28.1	6.05	40.6	2	0	533.2	624.5	538.9	629.6	356.9	529.4	619.8	553.4
Q95RB1	LD46870p OS=Drosophila melanogaster OX=7227 GN=cg14641 PE=1 SV=1	9	3	8	3	418	47.1	8.57	10.4	3	0	145.9	190	154.8	163.7	115.8	200.6	239.9	196.3
Q7K4B2	LD47540p OS=Drosophila melanogaster OX=7227 GN=l(2)k09848 PE=1 SV=1	10	3	7	3	419	46.6	6.55	9.26	3	0	94.1	133.7	112.1	110.3	98.3	168	166.4	141.6
Q7JQT9	LD47550p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1671 PE=1 SV=1	5	4	4	4	787	88.5	7.44	3.49	4	0	35.5	28.1	27.7	39.4	30.2	44.1	42.5	38.2
Q709R6	LEM domain-containing protein Bocksbeutel OS=Drosophila melanogaster OX=7227 GN=	7	2	2	2	399	44.2	9.23	0	2	0								
Q8IPL4	Lethal (2) 05714, isoform B OS=Drosophila melanogaster OX=7227 GN=l(2)05714 PE=4 S	7	2	6	2	271	31.9	5.11	6.17	2	0	79.7	88.1	69	79	78.4	103.4	95.7	84.2
A0A023GQA5	Lethal (2) 37Cc, isoform D OS=Drosophila melanogaster OX=7227 GN=l(2)37Cc PE=1 SV	20	5	9	5	276	30.4	5.73	19.33	5	0	62.9	85.9	104	111.7	355.2	120.5	141.7	71.2
M9PFG1	Lethal (3) 72Dn, isoform B OS=Drosophila melanogaster OX=7227 GN=l(3)72Dn PE=1 SV	3	2	2	2	699	79	8.84	2.7	2	0	25.8	26.1	22.3	24.7	21.9	50.8	35.3	29.9

Q9VQR8	Leucyl-tRNA synthetase, isoform A OS=Drosophila melanogaster OX=7227 GN=LeuRS PI	2	2	6	2	1182	134.8	7.64	1.75	2	0	7.6	13.9	13.4	15.5	20.7	10	20.5	8.7
Q9VJ39	Leukotriene A(4) hydrolase OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10602 P	7	4	10	4	684	76.8	6.55	7.11	4	0	61.2	35.8	28.9	13.7	7.6	42.4	43.8	12.6
O62602	Licorne OS=Drosophila melanogaster OX=7227 GN=lic PE=1 SV=1	24	8	30	8	334	38.2	6.39	27.17	8	0	505.6	557.6	490.9	405.2	322.2	580.7	628	402.9
Q7KNS3	Lissencephaly-1 homolog OS=Drosophila melanogaster OX=7227 GN=Lis-1 PE=1 SV=2	8	2	2	2	411	46.4	7.56	2.46	2	0	8	6.4	3.8	1.7		6.3	5.3	
M9NEV0	Little imaginal discs, isoform C OS=Drosophila melanogaster OX=7227 GN=lid PE=4 SV=1	4	5	12	5	1838	203.9	6.62	14.51	5	0	140.7	182.3	158.1	144.5	112.6	218.1	243.9	161
P42283	Longitudinals lacking protein, isoform G OS=Drosophila melanogaster OX=7227 GN=lola F	10	8	22	8	891	96.2	6.46	35.01	8	0	367.5	769.8	422.4	403.1	270.4	451.9	461.7	339.3
Q9VMX3	LP03982p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3756 PE=1 SV=1	9	2	2	2	333	38.1	6.74	0	2	0	10.9	12.5	12.7	12.5	9.5	13	13.1	10
Q9VQI5	LP04564p OS=Drosophila melanogaster OX=7227 GN=CG3098 PE=1 SV=2	5	2	2	2	425	47.3	6.28	1.8	2	0	21.3	24.4	24.8	27.5	20.2	23.9	30.9	22.1
Q9VEV3	LP07287p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG14894 PE=1 SV=2	8	2	2	2	263	29.4	4.64	0	2	0								
Q9VKW5	LP07359p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5355 PE=1 SV=2	13	9	22	9	756	86.3	6.19	20.98	9	0	596.8	669.3	680.2	633	502.5	701.9	793.9	653.3
Q9VHN7	LP07963p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8036 PE=1 SV=3	6	3	24	3	626	68	7.11	52.23	3	0	325.7	257.8	265.4	158.7	155.2	447.9	330.5	187
Q9VGP4	LP08082p OS=Drosophila melanogaster OX=7227 GN=Ranbp9 PE=1 SV=1	10	7	28	7	1018	114.3	4.87	34.82	7	0	352.4	416.6	444	283.6	238.3	485.4	496.1	280
Q9VKZ8	LP08774p OS=Drosophila melanogaster OX=7227 GN=Usp14 PE=1 SV=1	10	3	10	3	475	53.7	6.25	11.3	3	0	61.6	44.3	43.5	41	29.3	64.9	58.6	38
Q9W0M4	LP10861p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG13887 PE=1 SV=1	9	2	5	2	228	26.1	9.32	6.72	2	0	72	93.3	101.8	94.4	112.2	93.9	116.2	91.9
Q9W2U7	LP18708p OS=Drosophila melanogaster OX=7227 GN=nocte PE=1 SV=4	1	2	4	2	2309	235.4	9.22	1.64	2	0	48.7	76	69.9	63.8	57.4	64.3	86	68.8
Q9VQL1	LP20978p OS=Drosophila melanogaster OX=7227 GN=SerRS PE=1 SV=1	4	2	3	2	501	56.4	6.49	3.45	2	0	70	66.1	79.7	46.2	56	54.7	79	60.5
Q9W327	Lysine--tRNA ligase OS=Drosophila melanogaster OX=7227 GN=LysRS PE=1 SV=2	8	5	8	5	607	68.5	7.08	5.39	5	0	106.2	177.2	197.1	175.1	227.7	185.4	253	170.1
A0A0B4K8A5	Mahjong, isoform B OS=Drosophila melanogaster OX=7227 GN=mahj PE=4 SV=1	7	11	23	11	1544	172	5	29.4	11	0	424	490.2	499.1	480.5	333.5	566.9	713.9	512.8
Q9VKX2	Malate dehydrogenase OS=Drosophila melanogaster OX=7227 GN=Mdh1 PE=1 SV=2	11	4	29	4	337	36	7.39	49.21	4	0	863.2	987.2	900.5	847.8	569.1	843.7	1090.5	866.7
E1JGK5	Mapmodulin, isoform D OS=Drosophila melanogaster OX=7227 GN=Mapmodulin PE=1 SV	9	2	33	2	363	40.7	4.26	49.33	2	0	237.2	246.4	218.1	185.5	152.3	329.9	329.7	258.8
E1JH57	Mars, isoform B OS=Drosophila melanogaster OX=7227 GN=mars PE=1 SV=1	11	8	19	8	921	101.9	9.98	21.47	8	0	154.1	185.9	141.5	178.4	93.1	239.8	228.3	215.4
Q9VGA4	MBD-R2 OS=Drosophila melanogaster OX=7227 GN=MBD-R2 PE=1 SV=2	4	4	7	4	1169	130.1	8.03	10.4	4	0	39.2	45.7	48.1	50.7	33.5	68.4	57.1	48.9
Q9VW47	Mediator of RNA polymerase II transcription subunit 12 OS=Drosophila melanogaster OX=	1	2	3	2	2531	279.3	7.58	3.97	2	0	58.9	46.6	61.8	43.2	46.1	71.8	63.3	53.7
A8JNW4	Mediator of RNA polymerase II transcription subunit 13 OS=Drosophila melanogaster OX=	1	3	6	3	2768	295.5	6.83	7.6	3	0	66.9	71.1	82.4	70	65.1	83.9	94.3	75.6
Q9VEC1	Mediator of RNA polymerase II transcription subunit 17 OS=Drosophila melanogaster OX=	7	4	7	4	642	71.5	7.37	7.28	4	0	54.7	72.5	65.1	57.1	54.7	77.7	116.9	46.4
Q9W1X7	Mediator of RNA polymerase II transcription subunit 23 OS=Drosophila melanogaster OX=	2	2	7	2	1439	167	7.69	7.03	2	0	24.2	33.6	29.8	20.7	38.8	33.5	41.5	25.8
Q9W0P3	Mediator of RNA polymerase II transcription subunit 30 OS=Drosophila melanogaster OX=	7	2	5	2	318	35.3	8.76	3.51	2	0	37.3	45.4	42.5	48.9	28.9	49.5	65.7	50.9
A0A0B4KFE9	Megator, isoform B OS=Drosophila melanogaster OX=7227 GN=Mtor PE=1 SV=1	9	19	42	19	2346	262.2	5.1	44.18	19	0	593.8	673.9	665	685.8	527.6	813.8	863.7	728
Q0E8J0	MEP-1, isoform A OS=Drosophila melanogaster OX=7227 GN=MEP-1 PE=1 SV=1	3	4	15	4	1152	124	5.03	16.2	4	0	208.2	257.9	239.4	205.4	116.2	270.3	303.3	207.6
A0A0B4KG70	Metastasis associated 1-like, isoform D OS=Drosophila melanogaster OX=7227 GN=MTA1	12	8	24	8	922	100.9	9.29	33.17	8	0	264.8	314.2	330.5	259.3	183	346.7	426.6	304.7
Q9VL89	Methionine aminopeptidase 2 OS=Drosophila melanogaster OX=7227 GN=und PE=1 SV=	11	5	21	5	448	49.8	6.68	32.45	5	0	473.9	505	507.7	464	478.4	711.8	683.3	544.5
Q9VC48	Methionine aminopeptidase OS=Drosophila melanogaster OX=7227 GN=MAP1A PE=1 SV	6	2	5	2	374	41.7	6.93	9	2	0	76.5	80.9	75.8	70.2	54.9	89.8	86	77.9
Q9V9X4	Methylthioribose-1-phosphate isomerase OS=Drosophila melanogaster OX=7227 GN=CG	6	2	5	2	364	39.1	7.01	9.05	2	0	80.1	88	87.6	69	54.7	82.6	107.2	73.8
Q59E34	Mi-2, isoform B OS=Drosophila melanogaster OX=7227 GN=Mi-2 PE=1 SV=1	9	16	84	16	1983	224.2	5.64	161.67	16	0	1628.8	1980.2	1637.5	1449.7	985	2076.7	2195.8	1543.6
E1JH39	Microcephalin, isoform D OS=Drosophila melanogaster OX=7227 GN=MCPH1 PE=1 SV=1	2	2	2	2	1028	115	9.7	3.63	2	0	11.9	13.3	11.3	7.6	5.9	15.7	16	12.1
A0A0B4K700	Mini spindles, isoform D OS=Drosophila melanogaster OX=7227 GN=msps PE=1 SV=1	1	3	6	3	2082	230.3	8.21	3.68	3	0	59.2	65	76.8	57.8	67.2	80	97.7	77.7
Q9VM60	Mini-chromosome maintenance complex-binding protein OS=Drosophila melanogaster OX=	6	2	3	2	605	68	5.78	2.98	2	0	8.5	12.1	14.8	8.8	9.9	14.3	11.7	4.9
Q0E8E8	MIP08013p1 OS=Drosophila melanogaster OX=7227 GN=Mpcp2 PE=1 SV=1	6	2	5	2	356	38.8	8.88	8.16	2	0	53.7	62.7	95.8	71.7	199.2	77.2	85.7	48.1
A4V0N4	MIP16230p OS=Drosophila melanogaster OX=7227 GN=Vha68-2 PE=1 SV=1	12	6	22	6	614	68.3	5.34	36.12	6	0	256.6	325.6	381.9	313.6	421.5	313.8	417.4	321
H5V8B8	MIP33436p1 OS=Drosophila melanogaster OX=7227 GN=Pp2A-29B PE=1 SV=1	14	9	34	9	650	71.8	4.91	68.87	9	0	580.8	768.7	757.2	585.6	569.2	751.6	872.3	663.8
X2JG23	Misato, isoform B OS=Drosophila melanogaster OX=7227 GN=mst PE=4 SV=1	4	2	3	2	574	64.7	5.03	6.75	2	0	33.1	44.4	48.9	52.4	48.4	43.9	43.1	39.1
Q86BR8	Mitochondrial transcription factor A, isoform B OS=Drosophila melanogaster OX=7227 GN=	8	2	4	2	284	33	9.96	4.24	2	0	26.5	28.8	20.2	27.8	33.9	26.9	33.3	30.3
P40417	Mitogen-activated protein kinase ERK-A OS=Drosophila melanogaster OX=7227 GN=rl PE	10	3	5	3	376	43.1	6.07	13.14	3	0	71	75.5	78.6	76.6	66.2	87.3	95.5	82.9
A1Z7C1	Mlh1, isoform A OS=Drosophila melanogaster OX=7227 GN=Mlh1 PE=4 SV=1	3	2	3	2	664	75.7	7.88	1.89	2	0	28.1	25.9	29.5	18.1	16.1	32.1	31	22.6
Q9VAW1	Moca-cyp, isoform A OS=Drosophila melanogaster OX=7227 GN=Moca-cyp PE=1 SV=1	2	2	5	2	970	112.7	10.56	7.79	2	0	116.6	158.1	102.3	132.1	187	136.4	184.9	129.9
Q86B87	Modifier of mdg4 OS=Drosophila melanogaster OX=7227 GN=mod(mdg4) PE=1 SV=1	4	2	8	2	610	67.1	5.07	9.14	2	0	267	265.9	267.4	145	133.2	309.1	324.8	241.8
C7LAH9	Moesin, isoform K OS=Drosophila melanogaster OX=7227 GN=Moe PE=1 SV=1	14	7	46	7	646	75.8	6.16	74.73	7	0	328.9	357.8	327.6	268.3	273.6	395.4	510.1	306.7
A0A0B4K7S6	Molting defective, isoform D OS=Drosophila melanogaster OX=7227 GN=mld PE=4 SV=1	1	2	3	2	1965	218.6	6.24	4.74	2	0	6.8	5.2	2.8	5.1	3	6.3	6.7	4.3
P39205	Molybdenum cofactor synthesis protein cinnamon OS=Drosophila melanogaster OX=7227	3	2	2	2	601	65.7	6.24	4.17	2	0	37.6	57.2	62.5	56.8	60.2	62	76.3	60
A0A0B4KHJ7	MORF-related gene 15, isoform B OS=Drosophila melanogaster OX=7227 GN=MRG15 PE	7	2	5	2	429	47.7	8.13	0	2	0	20.9	26.8	27.1	30.1	21.1	28.5	33.4	28.6
Q9VY44	mRNA-capping enzyme OS=Drosophila melanogaster OX=7227 GN=mRNA-cap PE=2 SV	10	8	23	8	649	74.7	6.95	28.83	8	0	459	636.4	484.8	494.5	457.8	769.4	752	558.8
Q9I7S8	Multifunctional protein ADE2 OS=Drosophila melanogaster OX=7227 GN=ade5 PE=2 SV=	10	4	10	4	429	47.3	8.07	16.11	4	0	154.6	209.3	213.2	193.2	197.5	183	229.7	205.6
M9PFR6	Multiprotein bridging factor 1, isoform E OS=Drosophila melanogaster OX=7227 GN=mbf1	11	2	7	2	188	20.4	10.23	13.94	2	0	215	210.2	152	160	136.9	205.7	221	211.2
Q9VY97	Mutagen-sensitive 101 OS=Drosophila melanogaster OX=7227 GN=mus101 PE=1 SV=1	9	10	24	10	1425	158.3	6.51	23.46	10	0	151.3	156.8	151.3	136.2	91.5	210.9	242.6	170.6
Q9W5E4	Myb-binding protein 1A OS=Drosophila melanogaster OX=7227 GN=Mybbp1A PE=1 SV=	1	2	6	2	1133	127.8	7.55	9.74	2	0	191.5	200.2	157.3	149.3	122.7	282.6	246.2	238.1
M9ND95	Myosin heavy chain, isoform U OS=Drosophila melanogaster OX=7227 GN=Mhc PE=1 SV	13	24	52	1	1949	222.8	6.25	87.99	24	0	9.5	14.1	17	7.6	37.9	17.5	9.7	6.9
A0A0S0WIH4	Myosin heavy chain, isoform V OS=Drosophila melanogaster OX=7227 GN=Mhc PE=1 SV	13	24	51	1	1962	224.4	6.32	83.64	24	22	836.2	1184.1	1319.7	816.5	2987.1	1167.2	857.1	565.6
Q99323	Myosin heavy chain, non-muscle OS=Drosophila melanogaster OX=7227 GN=zip PE=1 SV	12	19	50	19	2057	236.5	5.68	92.95	19	0	507.9	634.3	635.1	521.5	863.4	717.1	787.7	741.5
Q9VWI2	N(Alpha)-acetyltransferase 15/16, isoform A OS=Drosophila melanogaster OX=7227 GN=N	5	4	11	4	890	103	7.27	10.85	4	0	77.9	105.1	130.6	91.1	143.9	107.6	139.9	97.6
Q9VCE6	N6-adenosine-methyltransferase MT-A70-like protein OS=Drosophila melanogaster OX=72	3	2	2	2	608	68.1	5.55	1.76	2	0	41.1	42	45.9	43.2	35.3	52.4	54.3	40.4
Q9VLP7	N6-adenosine-methyltransferase non-catalytic subunit OS=Drosophila melanogaster OX=7	7	2	3	2	397	44.8	8.68	2.45	2	0	24.4	30.2	30.1	32.6	30.3	28.2	39	30.7
Q9VK34	NAD-dependent histone deacetylase sirtuin-1 OS=Drosophila melanogaster OX=7227 GN	3	2	2	2	823	91.8	4.86	1.99	2	0	19.8	18.4	15.3	16.1	10.2	19.2	24.4	13.3
A0A0B4LEY6	Nascent polypeptide associated complex protein alpha subunit, isoform D OS=Drosophila	23	2	4	2	217	23	4.74	9.97	2	0	21.6	19.9	22.3	21	21.5	20.9	30.5	20.9
A1Z968	NAT1, isoform D OS=Drosophila melanogaster OX=7227 GN=NAT1 PE=1 SV=1	2	3	4	3	1488	162.8	8.53	0	3	0	86.2	51.5	85.3	51	48.2	57.4	71.3	61
M9PEU5	NEDD8-activating enzyme E1 regulatory subunit OS=Drosophila melanogaster OX=7227 (	9	4	9	4	524	58.7	5.33	8.11	4	0	160.4	183.4	162.8	125.7	107.7	200.4	227.4	155.8
Q9Y113	Negative elongation factor B OS=Drosophila melanogaster OX=7227 GN=NELF-B PE=1 S	5	2	3	2	594	67.9	6.68	3.66	2	0	33.8	44.1	48.2	35.7	31.3	51.7	56.1	46.9
M9MS40	Nejire, isoform C OS=Drosophila melanogaster OX=7227 GN=nej PE=1 SV=1	1	4	10	4	3282	341.2	8.7	9.53	4	0	129.4	169.5	178.3	172.7	132.5	206.7	408.5	172.6
Q9U9Q2	Neosin, isoform A OS=Drosophila melanogaster OX=7227 GN=Neos PE=2 SV=1	10	3	5	3	371	41.2	6.65	4.68	3	0								
Q9VT40	Nibrin OS=Drosophila melanogaster OX=7227 GN=nbs PE=1 SV=4	4	3	8	3	818	91.4	7.99	8.37	3	0	48.1	50.1	58.2	45.5	41.2	68.3	69	57.8
Q7PLI2	Nipped-B protein OS=Drosophila melanogaster OX=7227 GN=Nipped-B PE=1 SV=3	5	9	27	9	2077	236.6	6.57	29.79	9	0	349.2	360.2	365.5	305.7	222	477.7	468.8	360.2
Q9VWV8	Nitric oxide synthase-interacting protein homolog OS=Drosophila melanogaster OX=7227 (	7	2	4	2	307	34.1	9.22	4.11	2	0	51.6	69.7	56	65.1	47.6	71.5	77.9	59.5
Q8IR16	No on or off transient A, isoform B OS=Drosophila melanogaster OX=7227 GN=nonA PE=	12	9	30	6	742	81.9	9.11	59.71	9	3	807.1	938.6	743	936.5	641.9	929.6	1123.1	925.2
Q7JNE1	Non-histone chromosomal protein Prod OS=Drosophila melanogaster OX=7227 GN=prod	13	4	18	4	346	39.4	5.3	28.79	4	0	347.6	313.8	243.3	236.2	176.4	382.6	360.8	240.8
E2QD16	Non-specific lethal 1, isoform M OS=Drosophila melanogaster OX=7227 GN=nsl1 PE=1 SV	3	3	3	3	1570	169.7	6.81	7.48	3	0	61.1	60.8	58.3	78.8	65.7	84.1	80.8	68.9
Q9VKV4	Non-structural maintenance of chromosomes element 4 OS=Drosophila melanogaster OX=	11	2	5	2	290	33.1	5.15	10.25	2	0	40.1	33.6	33.8	20.3	19.2	56.8	50.3	20.7
Q9W224	Novel spermatogenesis regulator, isoform A OS=Drosophila melanogaster OX=7227 GN=r	5	2	3	2	340	39.6	8.4	6.05	2	0	34.2	46.9	46.1	63.1	32.4	43.8	66.2	52.9
Q7K4N3	Nuclear cap-binding protein subunit 1 OS=Drosophila melanogaster OX=7227 GN=Cbp80	5	3	13	3	800	93.2	6.55	23.79	3	0	116.9	149.9	161.5	117	83.6	150.1	185	110.1
Q9V3L6	Nuclear cap-binding protein subunit 2 OS=Drosophila melanogaster OX=7227 GN=Cbp20	18	3	15	3	154	17.7	7.78	21.03	3	0	395.1	381.9	391.9	291.2	192.6	517.3	461.5	337
Q9VVA6	Nuclear migration protein NudC OS=Drosophila melanogaster OX=7227 GN=nudC PE=1 S	11	3	6	3	332	37.8	5.64	4.1	3	0	84.4	83.5	91.2	103.5	87.7	65	108.3	113
Q9VCW3	Nuclear pore complex protein Nup133 OS=Drosophila melanogaster OX=7227 GN=Nup13	5	4	7	4	1200	135.1	5.63	9.65	4	0	12.1	71.8	16.7	13.9	24.7	14.2	28.2	14.8
Q9V463	Nuclear pore complex protein Nup154 OS=Drosophila melanogaster OX=7227 GN=Nup15	3	3	3	3	1365	153.8	6.58	3.09	3	0	18.2	24.1	21	21	25.5	27.8	39.6	25.2
Q7K0D8	Nuclear pore complex protein Nup50 OS=Drosophila melanogaster OX=7227 GN=Nup50 I	10	5	13	5	564	59.4	8.43	13.47	5	0	227.3	255	247.5	226.9	178.1	286.1	326.6	274.3
Q9GYU8	Nuclear pore complex protein Nup88 OS=Drosophila melanogaster OX=7227 GN=mbo PE	3	2	3	2	702	78.6	5.91	4.33	2	0	7	7.6	8.5	8.9	14.8	10.3	8.5	5.2
Q9VCH5	Nuclear pore complex protein Nup98-Nup96 OS=Drosophila melanogaster OX=7227 GN=I	1	2	3	2	1960	210	6.52	0	2	0	31.9	35.4	43.3	33.5	26.7	32.1	43.8	26.4
Q9VFE7	Nuclear pore protein OS=Drosophila melanogaster OX=7227 GN=Nup93-2 PE=1 SV=1	2	2	2	2	796	90.5	7.15	1.89	2	0	13.2	15.8	15	10.9	10.5	14.9	16.4	10.7
Q9VBP9	Nuclear protein localization protein 4 homolog OS=Drosophila melanogaster OX=7227 GN	10	5	9	5	652	73.3	7.24	10.43	5	0	110.7	147.6	153.1	116.2	104.1	144.8	166.4	120.7

Q9U1H9	Nuclear RNA export factor 1 OS=Drosophila melanogaster OX=7227 GN=sbr PE=1 SV=2	3	2	2	2	672	76.2	9	2.02	2	0	14.2	16.1	20.4	11.3	16	22.9	26.5	13.4
Q9VV73	Nuclear RNA export factor 2 OS=Drosophila melanogaster OX=7227 GN=nxf2 PE=2 SV=1	3	2	5	2	841	96.6	7.4	4.8	2	0	7.1	12	10.4	8.9	7.8	13.9	15.5	11.9
Q9VIF0	Nucleolar complex protein 2 homolog OS=Drosophila melanogaster OX=7227 GN=CG924	3	2	4	2	766	86.6	7.3	7.4	2	0	55	60.8	46.1	42	49.6	95.4	76.2	49.5
Q9VI82	Nucleolar complex protein 3 homolog OS=Drosophila melanogaster OX=7227 GN=CG123	6	3	5	3	822	94.4	8.97	2.67	3	0	11	13.6	10	14	5.4	18.1	13.9	18
A0A0B4LEY9	Nucleolar GTP-binding protein 1 OS=Drosophila melanogaster OX=7227 GN=Non1 PE=1	8	4	8	4	652	75.3	9.54	7.22	4	0	93.8	106	84.1	58.8	43.1	112.8	112.7	77.1
Q7JXU4	Nucleolar GTP-binding protein 2 OS=Drosophila melanogaster OX=7227 GN=Ns2 PE=1 S	4	2	7	2	674	76.6	9.58	10.37	2	0	3.7	6.8	7.6	3.4	6.1	11.3	11.2	8.5
Q8IH00	Nucleolar protein 6 OS=Drosophila melanogaster OX=7227 GN=Mat89Ba PE=1 SV=1	2	2	3	2	1193	136.3	9	1.65	2	0	12.2	19.7	12.9	10.8	13.1	19.3	16.1	6.7
Q9VE85	Nucleoporin 43kD OS=Drosophila melanogaster OX=7227 GN=Nup43 PE=1 SV=1	8	2	3	2	358	40.1	5.22	0	2	0	18.9	20.3	15.3	21.1	22.8	27.5	32.2	25
Q7K2X8	Nucleoporin at 44A, isoform A OS=Drosophila melanogaster OX=7227 GN=Nup44A PE=1	7	3	4	3	354	39.5	6.71	1.72	3	0	37.3	47.8	46.2	52.1	52.3	54.6	65.9	56.7
Q9VDC9	O-GlcNAcase OS=Drosophila melanogaster OX=7227 GN=Oga PE=1 SV=1	4	3	6	3	1019	113.8	4.88	11.52	3	0	58.7	77.5	78.4	65.9	60.6	94.4	115	82.8
E6PBV6	Obg-like ATPase 1 OS=Drosophila melanogaster OX=7227 GN=CG1354-RA PE=1 SV=1	7	2	9	2	397	44.9	6.71	12.94	2	0	171.8	205.9	205.7	188.6	165.6	210.2	227	176.9
O16810	Origin recognition complex subunit 1 OS=Drosophila melanogaster OX=7227 GN=Orc1 PE	9	7	25	7	924	103.2	9.35	34.25	7	0	313.5	355.7	312.1	273	197.3	421.2	414.7	356.6
Q24168	Origin recognition complex subunit 2 OS=Drosophila melanogaster OX=7227 GN=Orc2 PE	4	2	3	2	618	69	6.32	7.53	2	0	53.4	58.8	56.4	52.6	36.1	73.3	76.4	51.7
Q9W102	Origin recognition complex subunit 4 OS=Drosophila melanogaster OX=7227 GN=Orc4 PE	8	3	7	3	459	51.9	8.22	7.44	3	0	80.7	80.9	84	81.7	47.8	118.9	110.7	80.4
Q24169	Origin recognition complex subunit 5 OS=Drosophila melanogaster OX=7227 GN=Orc5 PE	10	4	10	4	460	52.1	6.55	14.73	4	0	146.7	165.8	154.4	116.2	93	224.7	199.9	147.9
E1JIN6	Osa, isoform D OS=Drosophila melanogaster OX=7227 GN=osa PE=1 SV=1	2	5	8	5	2716	283.9	7.44	8.25	5	0	97.2	133.4	125.5	128.6	83.5	137.5	169.8	119.9
P20240	Otefin OS=Drosophila melanogaster OX=7227 GN=Ote PE=1 SV=2	14	3	6	3	424	46.6	9.55	8.34	3	0								
X2J7U0	P-element induced wimpy testis, isoform B OS=Drosophila melanogaster OX=7227 GN=piw	16	13	57	13	843	97.1	9.57	69.05	13	0	926	1112.5	1005.6	865.6	711.9	1358	1454.4	1067.2
A1ZAK8	P-element somatic inhibitor, isoform C OS=Drosophila melanogaster OX=7227 GN=Psi PE	10	8	29	8	797	81.7	8.13	37.7	8	0	547.3	569.8	516.2	447	321.1	685	772.6	561.7
P25007	Peptidyl-prolyl cis-trans isomerase OS=Drosophila melanogaster OX=7227 GN=Cyp1 PE=	13	3	83	3	227	24.7	9.22	84.15	3	0	1086.3	1264.8	1265.5	1295.9	1050.5	1186.8	1481.7	1175.9
Q9W0Q2	Peptidyl-prolyl cis-trans isomerase OS=Drosophila melanogaster OX=7227 GN=Cypl PE=1	19	2	3	2	176	19.5	7.12	4.26	2	0	4.8	8.7	10.5	9.4	5.8	9.7	17	6.3
Q9W227	Peptidyl-prolyl cis-trans isomerase OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2	9	2	7	2	205	22.2	8.75	10.11	2	0	233.9	274.5	229.9	245.1	223.9	217.7	299.4	230.3
Q7K3D4	Peptidylprolyl isomerase OS=Drosophila melanogaster OX=7227 GN=zda PE=1 SV=1	6	3	5	3	397	44.8	5.33	6.05	3	0	70.1	98.7	95.1	85.5	106.7	111.4	158.1	80.3
Q9VEJ0	Peroxiredoxin 3 OS=Drosophila melanogaster OX=7227 GN=Prx3 PE=1 SV=2	8	2	3	2	234	26.4	7.49	3.37	2	0	4.5	10.9	15.5	9.7	26.6	13.5	9.7	10.6
Q9VQI7	Peroxiredoxin 6005 OS=Drosophila melanogaster OX=7227 GN=Prx6005 PE=1 SV=1	12	2	6	2	222	24.8	5.36	5.82	2	0	29.9	19.5	16.6	15	14.5	24.6	14.6	14.3
Q9VCA5	Phenylalanine--tRNA ligase beta subunit OS=Drosophila melanogaster OX=7227 GN=bet	7	3	6	3	589	65.7	6.04	5.9	3	0	61.3	87.9	107	81.8	91.7	90.3	95.4	82.9
A0A0B4KHW1	Phosphatidylserine receptor, isoform B OS=Drosophila melanogaster OX=7227 GN=PSR I	6	2	5	2	441	51	9.58	6.05	2	0	30.9	46.5	41.4	37.4	20.9	51.4	50.7	39.1
Q9VTZ4	Phosphoacetylglucosamine mutase OS=Drosophila melanogaster OX=7227 GN=nst PE=1	6	3	6	3	549	60.5	6.29	6.04	3	0	99.4	121.8	105.4	94.6	82.8	123.5	153	102.8
Q9VUY9	Phosphoglucomutase OS=Drosophila melanogaster OX=7227 GN=Pgm PE=1 SV=1	7	4	11	4	560	60.7	6.7	19.1	4	0	353.4	430.5	425.4	398.7	338.2	391.1	489.3	380.3
Q9VPY2	Phospholipase A2 activator protein, isoform A OS=Drosophila melanogaster OX=7227 GN	6	5	11	5	787	85.7	5.83	19.69	5	0	222.1	240.6	252.5	211.7	140.4	251	296.8	211
A1Z7P1	Phosphomannomutase 45A OS=Drosophila melanogaster OX=7227 GN=Pgm2a PE=1 SV	3	2	5	2	623	69.9	5.45	8.26	2	0	103.4	141.5	144.7	151	127.4	123.5	175.6	150.4
Q9VK58	Pih1D1, isoform D OS=Drosophila melanogaster OX=7227 GN=Pih1D1 PE=1 SV=5	2	2	2	2	1094	127.5	9.74	0	2	0	32.2	31.8	20.9	23.7	20.6	34.4	40.7	23.5
A1Z8A6	Pipsqueak, isoform M OS=Drosophila melanogaster OX=7227 GN=psq PE=1 SV=2	3	3	9	3	1123	119.8	6.87	16.67	3	0	118.7	128.2	150.1	100	54.4	112.1	131	64.8
P35875	Poly [ADP-ribose] polymerase OS=Drosophila melanogaster OX=7227 GN=Parp PE=1 SV	2	2	7	2	994	113.7	8.56	16.01	2	0	109.9	112.3	116.1	108.4	73.3	160.7	147.4	129.4
O46043	Poly(ADP-ribose) glycohydrolase OS=Drosophila melanogaster OX=7227 GN=Parg PE=1	4	2	3	2	723	81.1	5.81	0	2	0	19.7	24.4	25.8	22.3	12.5	24.1	28.5	23.3
Q8T6B9	Poly(U)-binding-splicing factor half pint OS=Drosophila melanogaster OX=7227 GN=hfp PE	7	3	6	3	637	67.9	5.96	0	3	0	60.1	44	49.7	38	47.6	60.5	77.2	62.4
Q7KNF2	Polyadenylate-binding protein 2 OS=Drosophila melanogaster OX=7227 GN=Pabp2 PE=1	10	2	12	2	224	25	5.2	24.61	2	0	88.5	90.5	79.2	66.1	63.1	280.5	671.3	74.3
P21187	Polyadenylate-binding protein OS=Drosophila melanogaster OX=7227 GN=pAbp PE=1 SV	4	2	3	2	634	69.9	9.31	1.9	2	0	20.3	19.6	17	12.2	14.4	27	24.3	11
Q9VC36	Polybromo OS=Drosophila melanogaster OX=7227 GN=polybromo PE=1 SV=1	9	12	28	12	1654	189.6	6.71	40.08	12	0	497.9	645.3	640.8	577.1	369.9	703.2	781.4	551.4
Q9NJG9	Polycomb protein Su(z)12 OS=Drosophila melanogaster OX=7227 GN=Su(z)12 PE=1 SV=	7	3	4	3	900	100	8.91	2.43	3	0								
Q9VK71	POU domain protein 2, isoform B OS=Drosophila melanogaster OX=7227 GN=pdm2 PE=2	4	2	2	2	893	98.4	6.9	0	2	0	10.4	10.8	13.6	9.7	5.6	15.2	18.3	11.6
A1Z8U0	Pre-mRNA processing factor 8 OS=Drosophila melanogaster OX=7227 GN=Prp8 PE=1 SV	5	11	30	11	2396	279.4	8.88	54.46	11	0	623.4	754	731.8	615.8	474	922	956.9	665.2
Q7KRW8	Pre-mRNA-processing factor 39 OS=Drosophila melanogaster OX=7227 GN=CG1646 PE=	8	7	13	7	1066	120.5	5.24	20.69	7	0	235.3	263.3	257.3	247.7	170.2	280.5	336.3	248.1
Q7JVL3	Pre-mRNA-splicing factor 38 OS=Drosophila melanogaster OX=7227 GN=Prp38 PE=1 SV	8	2	4	2	330	40.1	8.98	3.51	2	0	18.4	21	21.3	20.5	22.3	27	36.8	18.6
Q9VJ87	Pre-mRNA-splicing factor CWC22 homolog OS=Drosophila melanogaster OX=7227 GN=nc	4	4	8	4	1330	151.5	9.38	9.41	4	0	81.9	87.2	75.5	64.9	50	102.2	105.6	74.8
Q9VAQ7	Pre-mRNA-splicing factor Slu7 OS=Drosophila melanogaster OX=7227 GN=Slu7 PE=1 SV	8	4	15	4	574	65.9	7.06	19.79	4	0	114.3	127.2	113.8	109.2	93.6	150.5	171.1	131
Q9V5Q4	Pre-mRNA-splicing factor Syf2 OS=Drosophila melanogaster OX=7227 GN=Syf2 PE=2 SV	16	3	3	3	226	26.5	9.57	4.85	3	0	44.8	58.9	50.6	47.1	37.5	56	51.9	44.2
Q9VP47	Pre-rRNA-processing protein TSR1 homolog OS=Drosophila melanogaster OX=7227 GN=I	4	3	5	3	814	93.7	6.87	5.9	3	0	45.9	58.8	55.3	48.4	47.6	60.6	62.7	59.2
A1Z8S6	Precocious dissociation of sisters 5, isoform A OS=Drosophila melanogaster OX=7227 GN	6	6	20	6	1218	138.8	7.64	29.71	6	0	156.8	192.6	186	182.4	132.1	262.2	244.8	198.2
Q9VW52	Precursor RNA processing 3, isoform A OS=Drosophila melanogaster OX=7227 GN=Prp3	7	4	6	4	598	67.3	9.73	10.16	4	0	114.9	136.7	121.3	94.6	71.9	139.3	149.7	114.3
Q9VGP6	Prefoldin subunit 3 OS=Drosophila melanogaster OX=7227 GN=mgr PE=1 SV=3	9	2	4	2	194	22.3	5.11	4.92	2	0	97.4	118.1	129.5	116	109	97.2	146.5	110.2
Q9VZ64	Probable 6-phosphogluconolactonase OS=Drosophila melanogaster OX=7227 GN=CG17	12	2	4	2	243	26.7	8.21	3.84	2	0	67.1	64.1	54.9	19.8	31.4	101.8	70.5	28.5
Q9VXN4	Probable arginine--tRNA ligase, cytoplasmic OS=Drosophila melanogaster OX=7227 GN=A	3	2	3	2	665	75.5	7.44	4.38	2	0	27.8	49.6	47	37.5	59.2	43.1	60.2	44.8
Q86B47	Probable ATP-dependent RNA helicase CG8611 OS=Drosophila melanogaster OX=7227	2	2	7	2	975	107.9	9.5	5.36	2	0	53.5	55.7	44.8	59	35.3	86.5	80.5	66.7
P26802	Probable ATP-dependent RNA helicase Dbp73D OS=Drosophila melanogaster OX=7227	7	4	8	3	687	77.5	8.19	9.48	4	0	71.1	60.4	52.5	50.9	50.5	86.9	72.6	68.5
Q9VD51	Probable ATP-dependent RNA helicase pitchoune OS=Drosophila melanogaster OX=722	6	3	6	3	680	76.9	7.97	8.27	3	0	133.8	133	118.4	129.4	102	192.9	177.8	154.3
Q9W401	Probable citrate synthase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=kdn	8	3	4	3	464	51.5	8.81	3.72	3	0	13.6	17.3	25.9	20.7	38.2	26.1	14.6	15.9
Q9V3D6	Probable cleavage and polyadenylation specificity factor subunit 2 OS=Drosophila melano	9	7	15	7	756	85.4	5.47	17.99	7	0	159.7	234.3	192.5	158.4	114.3	222.1	261.7	178.3
Q9VUM0	Probable DNA mismatch repair protein Msh6 OS=Drosophila melanogaster OX=7227 GN=	6	8	19	8	1190	133.1	7.28	29.21	8	0	422.5	501.9	534.7	354.4	206.9	466.5	469.1	316
Q7KVQ0	Probable H/ACA ribonucleoprotein complex subunit 1 OS=Drosophila melanogaster OX=7	8	2	12	2	237	22.7	11.19	14.95	2	0	376.8	206.2	179.5	103.6	88.2	403.9	290.3	139.4
Q24572	Probable histone-binding protein Caf1 OS=Drosophila melanogaster OX=7227 GN=Caf1 P	7	3	17	1	430	48.6	4.89	19.09	3	0	206.3	110.2	92.8	29.2	31.5	212.5	110.7	35.1
Q8MT36	Probable histone-lysine N-methyltransferase Mes-4 OS=Drosophila melanogaster OX=722	5	7	9	7	1427	158.9	7.65	1.67	7	0	136.5	198.1	135.6	159.8	117.2	180.8	197.7	152.3
Q9V333	Probable lysine-specific demethylase 4A OS=Drosophila melanogaster OX=7227 GN=Kdm	3	2	6	2	495	57	7.24	0	2	0	92	116.3	90.1	104	66.7	132	119.5	101.7
Q9VSA3	Probable medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Drosophila m	10	4	6	4	419	45.8	7.94	7.72	4	0	76.3	94.3	118.1	92.8	168.8	104	93.8	70.2
Q9NHD5	Probable N-acetyltransferase san OS=Drosophila melanogaster OX=7227 GN=san PE=1	15	2	3	2	184	21	8.78	5.92	2	0	49.4	33.2	29.1	21.6	18.4	59.9	45.8	25
Q9VTZ6	Probable phosphomannomutase OS=Drosophila melanogaster OX=7227 GN=CG10688 P	17	4	5	4	254	29.6	5.71	6.36	4	0	73.7	78.4	75.9	63.9	59.5	64.7	103.5	69.1
Q9VTE5	Probable prefoldin subunit 2 OS=Drosophila melanogaster OX=7227 GN=Pfdn2 PE=2 SV	19	2	5	2	143	16.2	5.64	1.73	2	0	28.4	31.1	28.1	20.9	22	23.3	32.3	22.5
Q7K4Q5	Probable protein phosphatase CG10417 OS=Drosophila melanogaster OX=7227 GN=CG	11	5	18	5	662	72.3	4.58	27.07	5	0	179.4	196.7	179.4	138.4	105.5	205.2	201.9	153.2
Q9VWD4	Probable RNA-binding protein CG14230 OS=Drosophila melanogaster OX=7227 GN=CG1	7	3	8	3	580	66.2	8.56	8.59	3	0	15.1	13.3	10	9.5	8.6	24.4	19.1	20.3
Q9V9Z9	Probable rRNA-processing protein EBP2 homolog OS=Drosophila melanogaster OX=7227	7	2	4	2	307	35.1	10.1	2.65	2	0	67.3	52.1	32.9	50.3	42.1	77.4	73.9	58.2
Q9VXE0	Probable small nuclear ribonucleoprotein G OS=Drosophila melanogaster OX=7227 GN=S	17	2	4	2	76	8.5	8.79	6.45	2	0	55.2	69	60.7	63.2	34.4	45.4	78.4	49.2
Q9VI10	Probable small nuclear ribonucleoprotein Sm D2 OS=Drosophila melanogaster OX=7227 G	23	3	19	3	119	13.5	9.95	31.51	3	0	387.4	559.8	433.9	498.8	295.4	405.4	600.2	410.4
Q9W1G0	Probable transaldolase OS=Drosophila melanogaster OX=7227 GN=Taldo PE=2 SV=2	8	2	8	2	331	36.7	7.71	22.48	2	0	310.2	353.6	355.1	360.2	293.9	418.5	452.3	376.8
Q9VK89	Probable tRNA (guanine(26)-N(2))-dimethyltransferase OS=Drosophila melanogaster OX=7	10	5	9	5	578	64.9	7.21	10.37	5	0	40.7	46.9	37.7	36.3	30.7	54.6	61.3	46.6
Q9VQM4	Probable tyrosyl-DNA phosphodiesterase OS=Drosophila melanogaster OX=7227 GN=gkt	6	3	12	3	580	64.2	7.8	14.9	3	0	154.1	179.5	180.5	174.9	130.8	219.5	237.5	202.8
Q9V4Q8	Probable U2 small nuclear ribonucleoprotein A' OS=Drosophila melanogaster OX=7227 G	16	3	17	3	265	29.7	8.51	28.33	3	0	419.7	452.8	410.2	375.1	240.7	434.1	479.3	383.2
P25843	Profilin OS=Drosophila melanogaster OX=7227 GN=chic PE=1 SV=1	33	3	18	3	126	13.7	5.41	29.36	3	0	313.6	388.4	385.3	339.6	301.6	481.4	464.2	346.9
A0A0B4K630	Prospero, isoform I OS=Drosophila melanogaster OX=7227 GN=pros PE=4 SV=1	2	2	2	2	1835	198.3	6.65	2.38	2	0								
Q7K2G1	Proteasomal ubiquitin receptor ADRM1 homolog OS=Drosophila melanogaster OX=7227 (	23	5	31	5	389	42	5.64	33.83	5	0	212.6	141.1	132.3	74.8	56.1	197.7	193	82.8
Q9VEC2	Proteasome assembly chaperone 2 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG	12	2	4	2	247	27.8	6.23	1.72	2	0	18.3	18.3	19.2	21.1	14.8	22.2	19.4	12.7
A0A0B4KEK7	Proteasome inhibitor 31 kDa, isoform D OS=Drosophila melanogaster OX=7227 GN=PI31	9	2	3	2	270	30.1	5.53	0	2	0	35.6	50.6	50.1	37.6	23.9	38	52.9	36
I0DHK3	Proteasome subunit alpha type OS=Drosophila melanogaster OX=7227 GN=Prosalpha6 P	16	4	21	4	279	31	6.55	36.68	4	0	300.9	338.1	345.2	264.3	189.4	343.8	417.4	277.4
P40301	Proteasome subunit alpha type-2 OS=Drosophila melanogaster OX=7227 GN=Prosalpha2	11	2	21	2	234	25.9	6.68	2.93	2	0	144.6	379.9	255.6	425.6	354.5	226.9	645.9	189.4
Q9V5C6	Proteasome subunit alpha type-3 OS=Drosophila melanogaster OX=7227 GN=Prosalpha7	15	4	32	4	253	27.7	5.69	49.18	4	0	1005.6	1062.9	1024.9	771.1	775.4	1001.6	1331.1	836.3
P18053	Proteasome subunit alpha type-4 OS=Drosophila melanogaster OX=7227 GN=Prosalpha3	16	3	21	3	264	29.4	7.15	41.22	3	0	576.5	680.8	688.7	628.2	454.2	625.6	829.2	664.8
Q9XZJ4	Proteasome subunit alpha type-6 OS=Drosophila melanogaster OX=7227 GN=Prosalpha1	15	4	18	4	244	27.1	7.66	40.4	4	0	566.1	761.5	682.6	583	504.5	667.1	911.1	585.7

P22769	Proteasome subunit alpha type-7-1 OS=Drosophila melanogaster OX=7227 GN=Prosalph	12	3	18	3	249	28	8.12	31.87	3	0	550.2	708.5	698.4	485.3	374.2	618.5	847.2	580.4
A0AQH0	Proteasome subunit beta OS=Drosophila melanogaster OX=7227 GN=Prosbeta1 PE=1 S	35	5	70	5	224	24.2	5.25	135.23	5	0	679.2	1030.1	919.6	777.6	605.5	817.1	1157.1	851
Q9VUJ1	Proteasome subunit beta OS=Drosophila melanogaster OX=7227 GN=Prosbeta2 PE=1 S	21	5	33	5	272	29.8	8.66	52.58	5	0	636.4	849.4	838.9	663.1	491.5	679.6	1011.4	770.9
Q9VJJ0	Proteasome subunit beta OS=Drosophila melanogaster OX=7227 GN=Prosbeta4 PE=1 S	9	2	23	2	201	22.5	6.39	29.51	2	0	425.5	464.5	383.7	314.3	211.5	339.7	515.4	399.2
Q7K148	Proteasome subunit beta OS=Drosophila melanogaster OX=7227 GN=Prosbeta5 PE=1 S	14	4	29	4	282	31.1	6.93	50.63	4	0	906.2	1196.7	1270.6	946.8	803.5	1168.9	1506.4	1084.5
Q9VNA5	Proteasome subunit beta type-4 OS=Drosophila melanogaster OX=7227 GN=Prosbeta7 P	18	4	24	4	268	30	6.58	58.35	4	0	214.8	236	212	217.2	194.5	207.4	260.7	198.2
Q9V677	Proteasome-associated protein ECM29 homolog OS=Drosophila melanogaster OX=7227 (	2	3	4	3	1890	212	6.86	3.39	3	0	30.8	31.1	34.4	29.5	27.9	38.9	46.2	31.7
Q9VEX5	Protein asunder OS=Drosophila melanogaster OX=7227 GN=Asun PE=1 SV=1	6	2	4	2	689	75.7	8.46	9.59	2	0	82.3	88.7	83	84.9	53.6	113.1	122	103.4
O76922	Protein aubergine OS=Drosophila melanogaster OX=7227 GN=aub PE=1 SV=1	4	3	3	3	866	98.5	9.28	3.86	3	0	26.8	41.1	39.8	40.4	39	32.9	50.5	33.6
Q9VFR0	Protein BCCIP homolog OS=Drosophila melanogaster OX=7227 GN=CG9286 PE=2 SV=2	7	2	4	2	297	33.4	4.65	9.67	2	0	135.5	153.9	137	131.9	93.5	160.4	174.2	142.5
Q9NK54	Protein chiffon OS=Drosophila melanogaster OX=7227 GN=chif PE=1 SV=2	1	2	3	2	1711	189.1	8.53	1.87	2	0	17.1	20.3	15.1	19.2	14.2	19.6	20.8	20.8
Q7K284	Protein CLP1 homolog OS=Drosophila melanogaster OX=7227 GN=cbc PE=2 SV=1	4	2	6	2	423	46.8	6.89	8.61	2	0	97.1	124.6	117.3	96.1	92.9	130	152.3	109.5
A1ZAB5	Protein clueless OS=Drosophila melanogaster OX=7227 GN=clu PE=1 SV=1	1	2	3	2	1448	160.8	6.6	1.95	2	0	8.4	11.3	12.4	6.4	13.8	13.1	17.5	14.9
P17886	Protein crooked neck OS=Drosophila melanogaster OX=7227 GN=cm PE=2 SV=2	16	8	26	8	702	84.2	5.94	31.02	8	0	261.8	322.2	300.6	276.4	194.5	349.6	374.9	276
Q9VH89	Protein dalmatian OS=Drosophila melanogaster OX=7227 GN=dmt PE=1 SV=1	4	3	5	3	857	96.5	9.39	6.64	3	0	92.5	98.5	94.9	74.7	67.5	130.1	148.8	102.9
Q24573	Protein dead ringer OS=Drosophila melanogaster OX=7227 GN=retn PE=1 SV=2	5	3	16	3	911	97.3	6.23	23.92	3	0	70.3	127.1	111.4	141.1	89.9	110.6	127.1	89
Q3YMU0	Protein disulfide-isomerase (Fragment) OS=Drosophila melanogaster OX=7227 GN=ERp6	11	4	16	4	489	55.3	5.87	9.39	4	0	242.3	296.2	297.1	145.9	206.5	283.8	478.9	230.4
Q9V438	Protein disulfide-isomerase A6 homolog OS=Drosophila melanogaster OX=7227 GN=CaB	6	3	9	3	433	46.7	5.69	4.21	3	0	130.7	137.4	144.1	132.1	177.7	161	231.9	135.6
P54399	Protein disulfide-isomerase OS=Drosophila melanogaster OX=7227 GN=Pdi PE=2 SV=1	8	4	8	4	496	55.7	4.82	19.13	4	0	201.7	241.9	215.9	192.4	268.5	221.7	359.1	213
Q9W032	Protein ecdysoneless OS=Drosophila melanogaster OX=7227 GN=ecd PE=1 SV=1	3	2	2	2	684	77.9	4.87	2.12	2	0	23.3	26.6	31.3	27.8	23.5	27.9	36.1	26
Q9VWE6	Protein ELYS homolog OS=Drosophila melanogaster OX=7227 GN=CG14215 PE=1 SV=	1	2	3	2	2111	235	5.33	0	2	0								
Q9VAY7	Protein FAM50 homolog OS=Drosophila melanogaster OX=7227 GN=CG12259 PE=2 SV	6	2	3	2	359	42.8	6.83	4.34	2	0	16.9	14.9	15.4	13.6	11.9	16.8	19.9	17
P16371	Protein groucho OS=Drosophila melanogaster OX=7227 GN=gro PE=1 SV=3	6	5	28	5	730	80.2	7.17	23.47	5	0	411.7	559.3	524.7	546.4	312.8	560.5	671.2	454.5
O01367	Protein held out wings OS=Drosophila melanogaster OX=7227 GN=how PE=1 SV=1	4	2	6	2	405	44.3	7.93	9.62	2	0	167.6	153.2	131.8	74.2	64.9	187.2	151.2	69.4
Q9VBG6	Protein HGH1 homolog OS=Drosophila melanogaster OX=7227 GN=CG6073 PE=2 SV=2	8	2	3	2	369	41.8	4.97	0	2	0	17.3	28.5	24.1	20.3	28.3	19.3	22.5	23.1
O17468	Protein HIRA homolog OS=Drosophila melanogaster OX=7227 GN=Hira PE=1 SV=2	5	4	8	4	1047	113.3	6.65	8.85	4	0	66.5	79.2	83.2	61.6	47	102.1	90.4	73.3
Q8SYK5	Protein insensitive OS=Drosophila melanogaster OX=7227 GN=insv PE=1 SV=2	11	3	6	3	376	42.2	8.57	8.69	3	0	61.1	59.4	67.6	60.2	42.4	96.9	89.7	68
Q9VNE2	Protein krasavietz OS=Drosophila melanogaster OX=7227 GN=kra PE=1 SV=1	9	4	13	4	422	49.2	5.74	25.09	4	0	454.1	543.7	540.1	403	359.2	587.8	623.6	449.5
Q24371	Protein lethal(2)denticleless OS=Drosophila melanogaster OX=7227 GN=l(2)dtl PE=1 SV=	7	5	7	5	769	84.1	8.76	2.27	5	0	47	45.6	53.2	44	33.4	58.9	56.7	41.7
P91891	Protein Mo25 OS=Drosophila melanogaster OX=7227 GN=Mo25 PE=2 SV=2	12	4	12	4	339	39.4	7.25	9.75	4	0	424	228.7	229.7	186.8	256.2	256.1	281.9	288.6
Q9I7K6	Protein NASP homolog OS=Drosophila melanogaster OX=7227 GN=CG8223 PE=1 SV=1	15	4	28	4	492	51.9	4.39	43.71	4	0	523.5	598.9	540.3	495.3	292.6	535.4	642.1	495.7
Q9W2H9	Protein panoramix OS=Drosophila melanogaster OX=7227 GN=Panx PE=1 SV=1	3	2	3	2	541	61.1	6.46	2.31	2	0	53	64.3	66.2	63.7	34.9	64.9	295.1	54.6
A0A0B4K6G3	Protein partner of snf, isoform B OS=Drosophila melanogaster OX=7227 GN=pps PE=1 S	3	6	12	6	2018	222.1	8.79	4.03	6	0	109	112	109.2	104.3	78.6	128.5	131.8	109.4
P36872	Protein phosphatase PP2A 55 kDa regulatory subunit OS=Drosophila melanogaster OX=	17	7	20	7	499	56.9	7.09	26.1	7	0	388.4	481.8	468.2	445.2	337	505.4	552.4	435
Q9V3J4	Protein SEC13 homolog OS=Drosophila melanogaster OX=7227 GN=Sec13 PE=1 SV=1	5	2	5	2	356	39.5	6.25	3.63	2	0	68.2	83.5	84.5	80.9	97.1	86	102.4	89.2
Q8INM3	Protein slender lobes OS=Drosophila melanogaster OX=7227 GN=sle PE=1 SV=1	8	9	30	9	1420	158.6	5.24	44.2	9	0	627.2	660.9	527	619.5	320.7	746	796	642.7
Q8SX83	Protein split ends OS=Drosophila melanogaster OX=7227 GN=spen PE=1 SV=2	0	2	5	2	5560	599.6	8.63	3.25	2	0	25.5	53	24.9	40.3	21.7	33.9	45.2	32
A8JUV0	Protein strawberry notch OS=Drosophila melanogaster OX=7227 GN=sno PE=1 SV=2	6	7	8	7	1653	180.3	8.41	4.15	7	0	62.1	66.3	65.8	46.9	55.7	106.6	94.8	57.6
P25991	Protein suppressor of forked OS=Drosophila melanogaster OX=7227 GN=su(f) PE=1 SV=	8	6	11	6	765	88.2	8.25	10.86	6	0	279.8	245.9	244.9	191.8	165.9	339	306.3	219.7
Q9VTE2	Protein suppressor of underreplication OS=Drosophila melanogaster OX=7227 GN=SuUR	6	4	13	4	962	107.6	9.77	19.47	4	0	63.6	75	68.5	65.7	68.6	81.7	98.1	87
P20193	Protein suppressor of variegation 3-7 OS=Drosophila melanogaster OX=7227 GN=Su(var)	7	8	27	8	1250	139.9	6.43	57.59	8	0	578	630.5	590.3	654	394.7	712.8	790.9	630.8
Q8INX3	Protein TIPIN homolog OS=Drosophila melanogaster OX=7227 GN=CG10336 PE=2 SV=	11	3	4	3	307	34.1	5.11	4.89	3	0	77.3	103.9	61.5	81.4	39	49.8	52.1	28.2
P42282	Protein tramtrack, alpha isoform OS=Drosophila melanogaster OX=7227 GN=ttk PE=1 SV	2	2	4	2	813	88.3	6.25	0	2	0	36.1	47.6	29.4	29.9	51.2	40.5	38.6	31.4
A0A0B4K5Z8	Protein transport protein SEC23 OS=Drosophila melanogaster OX=7227 GN=Sec23 PE=	4	2	8	2	781	87.5	6.79	7.3	2	0	51.5	56.7	73.2	65.4	67.1	53.8	71.5	42.1
Q9W517	Protein wings apart-like OS=Drosophila melanogaster OX=7227 GN=wapl PE=1 SV=1	5	5	7	5	1741	185	6.54	9.93	5	0	37.9	38.6	40.3	40.6	35.6	57.1	52.6	36.6
A0A0B4KI06	Puffyeye, isoform H OS=Drosophila melanogaster OX=7227 GN=puf PE=1 SV=1	1	3	4	3	3930	442.1	6.2	0	3	0	9.6	9.3	9.5	5.1	7	16.3	15.1	11.4
P23128	Putative ATP-dependent RNA helicase me31b OS=Drosophila melanogaster OX=7227 GI	4	2	6	2	459	51.9	7.64	5.41	2	0	95.2	74.9	63	37.8	50.2	101.6	86.4	49.5
Q9VMQ7	Putative elongator complex protein 4 OS=Drosophila melanogaster OX=7227 GN=CG690	8	2	6	2	437	48.7	5.88	12.07	2	0								
P36951	Putative hydroxypyruvate isomerase OS=Drosophila melanogaster OX=7227 GN=Gip PE=	7	2	6	2	264	29.1	6.54	10.18	2	0	227.3	262.6	253.1	244.1	225.6	229.5	319.8	240.1
P54353	Putative peptidyl-prolyl cis-trans isomerase dodo OS=Drosophila melanogaster OX=7227 (	14	2	7	2	166	18.4	7.44	20.64	2	0	183.2	201	175.8	140.5	104.8	194.2	224.3	168.4
Q9VXK5	Putative rRNA methyltransferase OS=Drosophila melanogaster OX=7227 GN=Dmel\CG89	8	5	12	5	817	93.3	9.04	15.3	5	0	173	199.2	113.9	168.1	113.9	257.4	207.1	211.7
Q9VPK7	Putative tRNA pseudouridine synthase Pus10 OS=Drosophila melanogaster OX=7227 GN	3	2	2	2	500	56.7	8.35	1.84	2	0	30.4	33.4	40.7	27.6	25.3	49.5	48.3	34.7
Q9VUV9	Putative U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Drosophila melanogast	9	15	60	15	2142	244.4	6.04	90.07	15	0	603	812.1	766.9	777.4	521.6	906.1	1019.8	777.3
Q0E9E2	Pyruvate carboxylase OS=Drosophila melanogaster OX=7227 GN=PCB PE=1 SV=1	10	9	45	9	1197	132.6	6.64	66.75	9	0	319.9	418.5	540.7	517.2	654.2	551.1	825	292.5
Q7K5K3	Pyruvate dehydrogenase E1 component subunit beta OS=Drosophila melanogaster OX=	9	3	6	3	365	39.3	7.8	10.89	3	0	39.6	51.1	58.8	66.3	87.2	58.1	67.4	52
O62619	Pyruvate kinase OS=Drosophila melanogaster OX=7227 GN=PyK PE=2 SV=2	14	5	47	5	533	57.4	7.44	82.69	5	0	589.8	812	874.1	746.5	620	756	1047.9	792.9
Q9W2I2	Queuosine salvage protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9752 PE	8	3	6	3	343	39.5	5.73	5.55	3	0	125.3	146.4	159.8	137.1	109	158.2	161.9	142.2
Q9VLB7	Rab GDP dissociation inhibitor OS=Drosophila melanogaster OX=7227 GN=Gdi PE=1 SV=	11	4	23	4	443	49.9	5.72	49.6	4	0	384.7	435.1	454.2	314.9	269.1	439.6	517.8	353.7
A0A0B4K7L0	Rad50, isoform E OS=Drosophila melanogaster OX=7227 GN=rad50 PE=1 SV=1	8	10	20	10	1318	152	7.65	18.33	10	0	193.3	184.3	192.1	147.2	139.4	281.2	312.1	176
A0A126GUM4	Ran-binding protein M, isoform G OS=Drosophila melanogaster OX=7227 GN=RanBPM P	3	3	5	3	1127	123.7	5.19	6.78	3	0	36.4	41.5	44	46	42.6	43.6	69.4	47.8
M9MSD3	Ranbp16, isoform F OS=Drosophila melanogaster OX=7227 GN=Ranbp16 PE=4 SV=1	2	2	2	2	1110	126.9	6.35	1.68	2	0	27.8	26.5	31.1	35.7	31.4	45.9	43.6	39.2
M9MRT6	Rap1 GTPase, isoform B OS=Drosophila melanogaster OX=7227 GN=Rap1 PE=4 SV=1	12	2	5	2	184	20.9	6.68	7.94	2	0	68.7	109	112.1	98.7	133.1	119.6	164	110.2
P48148	Ras-like GTP-binding protein Rho1 OS=Drosophila melanogaster OX=7227 GN=Rho1 PE=	13	2	9	2	192	21.7	7.01	16.49	2	0	201.4	298.5	278.6	272.9	311.9	305.7	365.1	279.8
Q9VNF3	RE01652p OS=Drosophila melanogaster OX=7227 GN=anon-WO0118547.83 PE=1 SV=	16	3	14	3	257	26.9	7.5	16.36	3	0	213.7	223.9	214.4	181.2	147.6	213.8	267	165
Q9VTN7	RE08109p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10907 PE=2 SV=1	6	2	6	2	502	56.6	6.67	7.11	2	0	21.6	23.4	26.3	20.1	17.9	26.9	25.3	27.3
Q8MT58	RE11562p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG17337 PE=1 SV=1	15	5	27	5	478	53.1	5.66	52.19	5	0	226.7	273.3	252	180.2	182.7	297.1	306.1	217.9
Q8IQW5	RE23625p OS=Drosophila melanogaster OX=7227 GN=Dmel21.3 PE=1 SV=1	12	2	4	2	192	21.8	6.57	8.33	2	0	50.8	50.6	52.2	46.7	81.1	47.3	56.3	44.4
Q9VJ19	RE25263p OS=Drosophila melanogaster OX=7227 GN=RpL30 PE=1 SV=1	22	2	14	2	111	12.2	9.58	33.01	2	0	360.7	469.4	465.1	371.9	509	682.1	708.9	539.6
Q9VC18	RE29555p OS=Drosophila melanogaster OX=7227 GN=BEST:GH11240 PE=1 SV=1	13	6	12	6	590	63.3	7.87	16.55	6	0	140.3	117.1	136.4	95.7	86.4	150.9	143.1	107.6
Q9VF04	RE32990p OS=Drosophila melanogaster OX=7227 GN=Rbf2 PE=2 SV=1	3	2	3	1	783	89.8	8	3.95	2	0								
Q7JZF5	RE34924p OS=Drosophila melanogaster OX=7227 GN=Rpb5 PE=1 SV=1	8	2	7	2	210	24.5	6.15	11.15	2	0	224.6	246.9	237.3	218.3	159.3	264.9	280.3	254.5
Q6NR30	RE38958p OS=Drosophila melanogaster OX=7227 GN=BEST:LD13441 PE=1 SV=1	4	2	3	2	512	56	8.73	2.81	2	0	32	34.6	38.8	32.5	25.2	43.8	44.3	28.7
Q8SYR3	RE39606p OS=Drosophila melanogaster OX=7227 GN=Rsf1 PE=1 SV=1	9	2	3	2	200	21.4	10.56	2.34	2	0	95	80.3	62.5	67.5	50.6	92.7	104.9	72.6
Q8IPX7	RE44908p OS=Drosophila melanogaster OX=7227 GN=Rrp40 PE=1 SV=1	14	3	10	3	232	25	8.31	18.51	3	0	92.8	119.5	114.4	96.7	69.5	110.4	130.8	107.1
Q9VL25	RE48269p OS=Drosophila melanogaster OX=7227 GN=cg4901 PE=1 SV=2	4	2	2	2	694	78.3	8.84	2.33	2	0	5	6.6	13.3	10.1	8.7	8.8	15	9.4
Q9VND7	RE50009p OS=Drosophila melanogaster OX=7227 GN=cg2931 PE=1 SV=1	19	5	7	5	302	33.6	10.2	1.89	5	0	154.6	150.7	144.4	141.7	97	162.9	156.9	132.6
Q8INP9	RE51612p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11980 PE=1 SV=1	16	4	11	4	359	40.9	6.95	13.91	4	0	75.1	95.1	93.4	89.1	61.1	100.2	113.9	84.6
Q494M1	RE58921p OS=Drosophila melanogaster OX=7227 GN=Top1 PE=1 SV=1	7	6	22	6	974	111.8	9.01	21.42	6	0	674.5	592.3	445.5	425.5	348	1118.2	1047.4	643.9
Q7JWH6	RE61424p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1888 PE=1 SV=1	14	4	9	4	372	42.2	6.05	6.25	4	0	106.6	118.6	100.7	103	79.7	164.6	146.6	106.2
Q7JZ37	RE62785p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12134 PE=1 SV=1	7	2	2	2	411	45.7	5.06	0	2	0	21.3	26.4	29.5	22	24.4	29.6	27.7	19.5
Q8SYG3	RE63412p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG40045 PE=1 SV=1	15	2	12	2	168	19.4	5.29	36.04	2	0	193.1	204.9	207.1	164.4	133.7	214.1	246.2	226.7
Q9W397	RE67794p OS=Drosophila melanogaster OX=7227 GN=dUTP6 PE=2 SV=1	12	7	14	7	602	70.1	6.6	9.73	7	0	118.9	129.1	122.8	125.6	105	172	163.3	129.3
Q9W4W7	RE68603p OS=Drosophila melanogaster OX=7227 GN=EG:100G10.6 PE=1 SV=1	5	2	3	2	446	49.2	8.7	0	2	0								
Q9VZE4	RE70333p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1316 PE=1 SV=2	7	4	10	4	470	52.4	6.71	20.07	4	0	267.4	309.8	317.1	305.5	217.3	355.5	406.3	341.6
Q8SXG7	RE72132p OS=Drosophila melanogaster OX=7227 GN=Secp43 PE=1 SV=1	8	2	4	2	336	37.4	5.22	4.71	2	0	23.8	23.1	21.1	21.4	10.4	23.9	29.5	18.6
Q9VN39	RE74585p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9775 PE=1 SV=1	5	2	4	2	421	46.1	12.48	6.91	2	0	125.7	120.2	97.5	99.4	72.5	125.8	148.6	103.8

A1Z7S0	Receptor mediated endocytosis 8, isoform A OS=Drosophila melanogaster OX=7227 GN=	1	2	3	2	2408	272.4	7.05	4.05	2	0									
Q76NR6	Regucalcin, isoform D OS=Drosophila melanogaster OX=7227 GN=regucalcin PE=1 SV=1	8	2	7	2	319	35.3	6.39	7.45	2	0	42.2	60	51.8	49.8	53.4	63.1	69.4	51.4	
P25171	Regulator of chromosome condensation OS=Drosophila melanogaster OX=7227 GN=Rcc	12	3	16	3	547	58.8	7.94	22.32	3	0	73.7	44.9	34.3	19.2	13.5	142.6	52.1	29.1	
M9PGH6	Regulator of telomere elongation helicase 1 homolog OS=Drosophila melanogaster OX=7	2	2	3	2	985	109.6	8.69	5.98	2	0	112	143.9	167.9	124.4	65	113.1	107.3	86.4	
M9PIG8	Regulatory particle non-ATPase 10, isoform B OS=Drosophila melanogaster OX=7227 GN	13	4	14	4	396	42.6	4.83	27.73	4	0	313.7	312.3	291.5	250.3	165.5	294	383.3	273.5	
M9PG62	Regulatory particle non-ATPase 3, isoform B OS=Drosophila melanogaster OX=7227 GN=	19	9	39	9	494	56	9	52.46	9	0	885.4	1083.2	1048.7	1009.6	728.7	1077.6	1401.3	1013.9	
A0A0B4K7Z5	Regulatory particle non-ATPase 6, isoform C OS=Drosophila melanogaster OX=7227 GN=	6	3	18	3	422	47.2	5.88	26.62	3	0	659.1	773.3	811.3	676.6	462.4	831.6	1028	735.7	
Q9W414	Regulatory particle triple-A ATPase 4 OS=Drosophila melanogaster OX=7227 GN=Rpt4 PI	14	4	14	4	397	44.9	8.07	22.28	4	0	413.1	468.2	426.6	281.8	241.4	469.5	587.4	321.1	
A0A0B4KER0	Relative of woc, isoform C OS=Drosophila melanogaster OX=7227 GN=row PE=1 SV=1	3	3	9	3	1301	146.1	8.06	13.8	3	0	83.9	104.1	106.2	96.2	73.1	128.5	143.9	111.4	
Q9U9Q1	Replication factor C 38kD subunit, isoform A OS=Drosophila melanogaster OX=7227 GN=	17	6	29	6	356	40.8	8.4	45.61	6	0	550.5	743.4	802	610.9	340.9	678.3	712.5	538.4	
P35600	Replication factor C subunit 1 OS=Drosophila melanogaster OX=7227 GN=Gnf1 PE=1 SV	10	8	85	8	986	108.5	9.31	141.76	8	0	1698.9	1886.2	2010	1540.4	818.5	2203.7	1798.1	1435	
P53034	Replication factor C subunit 2 OS=Drosophila melanogaster OX=7227 GN=RfC4 PE=1 SV	27	7	59	7	331	37.2	7.72	110.43	7	0	769.6	992.4	1021	744.4	402.5	937.9	835.8	676	
Q9VKW3	Replication factor C subunit 3 OS=Drosophila melanogaster OX=7227 GN=RfC3 PE=1 SV	14	4	32	4	332	37.4	7.2	69.87	4	0	437.5	540	572.2	436	257.6	487.8	482.1	400	
Q24492	Replication protein A 70 kDa DNA-binding subunit OS=Drosophila melanogaster OX=7227	15	8	100	8	603	66.6	6.76	186.55	8	0	1868.4	2409.6	2841.2	1700.4	571.2	1255.3	1458.9	1023.9	
Q24472	Retinoblastoma family protein OS=Drosophila melanogaster OX=7227 GN=Rbf PE=1 SV=	9	6	17	5	845	96.8	6.57	13.24	6	1	100.7	113.8	125.4	95.2	78.3	131.5	165.5	105.6	
Q7JX95	RH42110p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11123 PE=1 SV=1	6	3	12	3	665	75.7	7.11	16.43	3	0	59.8	54.7	51	45.8	41	91.9	64.7	65.2	
Q9W3X8	RH42690p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3198 PE=1 SV=2	5	2	3	2	438	49.8	7.34	6.44	2	0	52.3	56.4	53.6	46.3	41	70.2	68.2	58.6	
Q9VJ74	RH55640p OS=Drosophila melanogaster OX=7227 GN=DmRH19 PE=1 SV=2	7	6	19	6	822	94.5	9.47	30.29	6	0	357	358.7	294.7	223.9	156.2	464.4	424.3	250.3	
A0A0B4KFC4	Ribbon, isoform C OS=Drosophila melanogaster OX=7227 GN=rib PE=1 SV=1	3	2	4	2	680	73.1	6.48	6.98	2	0	98.6	91.7	119.5	99	64.7	115.1	97.2	82.2	
Q9VPP5	Ribonuclease H2 subunit A OS=Drosophila melanogaster OX=7227 GN=CG13690 PE=2	7	2	4	2	347	38.7	5.12	3.22	2	0	53.5	60.6	54.3	37.6	28	69.7	64.7	35.5	
P48591	Ribonucleoside-diphosphate reductase large subunit OS=Drosophila melanogaster OX=7	8	5	10	5	812	91.9	7.46	14.93	5	0	142.4	191.7	190.2	182.9	192.2	198.8	241.2	192.9	
P48592	Ribonucleoside-diphosphate reductase subunit M2 OS=Drosophila melanogaster OX=722	13	5	11	5	393	45.1	5.63	14.47	5	0	268.7	295.7	307.1	233.3	193.4	324.5	354.8	237.6	
Q8MLS2	Ribose-5-phosphate isomerase, isoform B OS=Drosophila melanogaster OX=7227 GN=Rp	15	3	6	3	241	26.5	5.88	4.36	3	0	56.2	110.4	41.2	48.5	29.8	55.3	67.4	35.7	
Q9VLK2	Ribosomal L1 domain-containing protein CG13096 OS=Drosophila melanogaster OX=722	9	6	45	6	681	74.3	8.51	57.3	6	0	1003.4	866.6	635.7	630	666.9	1465.8	1236	908.6	
M9PIM0	Ribosomal protein L10, isoform E OS=Drosophila melanogaster OX=7227 GN=RpL10 PE=	21	3	17	3	218	25.5	9.85	28.29	3	0	271.5	384.9	384.9	339.2	517	424.4	648	415.7	
X2JDU0	Ribosomal protein L9, isoform C OS=Drosophila melanogaster OX=7227 GN=RpL9 PE=4	18	2	11	2	190	21.4	9.69	19.81	2	0	233	318.7	365.5	265.1	499.1	425.3	457	341	
Q7K0Y1	Ribosome biogenesis protein BOP1 homolog OS=Drosophila melanogaster OX=7227 GN=	4	4	8	4	784	90.4	5.88	11.17	4	0	149.4	148.5	112	137.7	104.9	197	190.3	177.3	
Q9W3C2	Ribosome biogenesis protein NOP53 OS=Drosophila melanogaster OX=7227 GN=CG178	4	2	3	2	478	55.8	9.76	3.72	2	0	55.7	61.8	49.3	56.7	32.2	82.3	84.4	68.4	
Q9VKQ3	Ribosome biogenesis protein WDR12 homolog OS=Drosophila melanogaster OX=7227 GI	13	4	8	4	420	47.2	5.38	3.39	4	0	43.3	63.8	35.7	37.8	33.9	49.2	52.7	26.4	
Q8I937	Ribosome biogenesis regulatory protein OS=Drosophila melanogaster OX=7227 GN=Dme	8	2	7	2	349	39.4	9.92	9.5	2	0	82.6	95	86.7	83.9	60.4	103	89	73.3	
Q9VEB3	Ribosome production factor 2 homolog OS=Drosophila melanogaster OX=7227 GN=Non3	13	4	9	4	320	36.5	10.26	9.39	4	0	222.5	248.8	265.6	248.2	171.8	334.1	293.1	261.4	
Q9VL31	RIP-like protein OS=Drosophila melanogaster OX=7227 GN=Ripalpha PE=2 SV=1	11	2	6	2	197	23.2	5.49	9.83	2	0	93.7	121.3	131.3	135.6	79.5	114.9	145.1	116.9	
Q9W3C1	RNA cytidine acetyltransferase OS=Drosophila melanogaster OX=7227 GN=l(1)G0020 PE	4	3	10	3	1008	112.8	8.53	13.64	3	0	70.4	77.5	61.1	53.9	49.4	155.8	98.9	99.9	
Q9VX34	RNA helicase OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5800 PE=1 SV=2	2	2	5	2	826	92.8	6.83	8.07	2	0	47.2	51	47.5	54.1	46.5	86.7	66.8	72.8	
Q9VLR5	RNA polymerase II transcriptional coactivator OS=Drosophila melanogaster OX=7227 GN=	33	3	17	3	110	12.2	9.17	34.89	3	0	439.4	481.2	452.8	407.2	400.2	544.1	682	501	
Q9W261	RNA polymerase-associated protein Rtf1 OS=Drosophila melanogaster OX=7227 GN=Rtf1	4	3	10	3	775	87.5	8.53	24.23	3	0	273.2	345.2	359.3	341.3	213.9	385.4	423.6	351.9	
Q9W4D2	RNA-binding protein 4F OS=Drosophila melanogaster OX=7227 GN=Rnp4F PE=1 SV=1	6	5	9	5	941	106.7	5.11	9.72	5	0	149.4	171.2	121.5	103.9	73.3	173.5	172.9	141.5	
Q9V535	RNA-binding protein 8A OS=Drosophila melanogaster OX=7227 GN=tsu PE=1 SV=1	15	3	9	3	165	19	5.27	11.1	3	0	189.6	202.6	173.8	218.5	151.3	197.8	224.5	209	
Q94901	RNA-binding protein lark OS=Drosophila melanogaster OX=7227 GN=lark PE=1 SV=1	14	6	15	6	352	39.9	9.07	29.74	6	0	435.7	472.3	399.6	395.2	312	549.5	558.9	466.4	
Q7KMJ6	RNA-binding protein spenito OS=Drosophila melanogaster OX=7227 GN=nito PE=1 SV=1	6	3	22	3	793	89	9.38	47.33	3	0	314.5	341.1	308.5	304.8	238	405.4	437.7	361.6	
Q9V9W7	Rough deal OS=Drosophila melanogaster OX=7227 GN=rod PE=1 SV=2	1	2	2	2	2089	239.5	6.15	0	2	0									
Q9W1V3	rRNA 2'-O-methyltransferase fibrillarin OS=Drosophila melanogaster OX=7227 GN=Fib PE=	5	2	20	2	344	34.6	10.29	33.06	2	0	525.5	412.8	332.2	166.5	187.1	696.2	491.6	270.3	
Q9VYA7	RRP12-like protein OS=Drosophila melanogaster OX=7227 GN=CG2691 PE=1 SV=2	2	2	2	2	1384	153.5	8.78	3.49	2	0	29.6	34.1	29.2	14.8	16.1	57	38.6	33.9	
Q9W1M9	Rrp4, isoform A OS=Drosophila melanogaster OX=7227 GN=Rrp4 PE=1 SV=1	11	3	9	3	298	33.6	6.19	14.87	3	0	102.8	120.8	118.7	122.3	71.8	106.2	141.3	121.1	
Q9VFF3	Rrp6, isoform B OS=Drosophila melanogaster OX=7227 GN=Rrp6 PE=1 SV=3	2	2	4	2	900	102.9	9.25	3.61	2	0	101.9	141.2	122.5	111.8	82.9	134.9	141.3	121.6	
Q7KVC2	RT07324p OS=Drosophila melanogaster OX=7227 GN=CG32318-PA PE=2 SV=1	16	3	8	1	164	18.7	8.69	11.85	3	0									
Q9VH07	RuvB-like helicase 1 OS=Drosophila melanogaster OX=7227 GN=pont PE=1 SV=1	13	4	12	4	456	50.2	7.34	23.07	4	0	176.6	218.8	205.1	189.9	125.2	204.6	240.1	193.1	
M9PFN1	RuvB-like helicase OS=Drosophila melanogaster OX=7227 GN=rept PE=3 SV=1	18	8	39	8	481	53.5	5.85	78.77	8	0	1029.8	1209.2	1184	1088.1	747	1223.3	1361.7	1122	
A4UZW2	S-adenosylmethionine synthase OS=Drosophila melanogaster OX=7227 GN=Sam-S PE=	3	2	5	2	408	44.8	6.54	8.58	2	0	165.6	197.8	184.8	173	155.2	176.4	233.3	170.2	
A0A0B4KG54	S-methyl-5'-thioadenosine phosphorylase OS=Drosophila melanogaster OX=7227 GN=Mt	11	3	13	3	360	40.3	7.94	11.24	3	0	47.9	33.3	28.6	14.9	12.9	56	37.9	8.6	
Q9VZL3	Sc2 OS=Drosophila melanogaster OX=7227 GN=Sc2 PE=1 SV=1	6	2	4	2	302	34.2	9.61	4.03	2	0	46.3	37.6	37.9	25.9	64.9	79.3	66.6	23.2	
Q8IMV6	Scaffold attachment factor B, isoform B OS=Drosophila melanogaster OX=7227 GN=Saf-B	3	3	7	3	928	102	7.47	12.88	3	0	278.7	256.2	204.5	192.7	125.7	330.1	322.7	191.4	
A0A0B4KEU2	Scribbler, isoform J OS=Drosophila melanogaster OX=7227 GN=sbb PE=1 SV=1	1	2	2	2	2330	233.1	9.19	2.06	2	0	22.3	19.4	18.6	13.8	9.7	29.3	20.5	23.8	
Q960E4	SD04973p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8929 PE=1 SV=1	3	2	3	2	607	68	10.77	0	2	0	63.5	62	54.2	54.8	48.6	68.4	68.3	62.9	
Q960D4	SD06560p OS=Drosophila melanogaster OX=7227 GN=EG:22E5.5 PE=1 SV=1	13	7	12	7	593	65	6.21	9.93	7	0	138.3	153.3	169.9	133.8	119.5	178.7	198.8	133.6	
Q9VVI0	SD09427p OS=Drosophila melanogaster OX=7227 GN=U4-U6-60K PE=1 SV=1	7	3	9	3	553	61.5	6.21	8.17	3	0	193.5	233.6	219.3	196.3	128.6	260	259	215.8	
Q9VPF9	SD10847p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5274 PE=2 SV=1	6	2	2	2	373	41.3	8.51	2.04	2	0	24	29.4	30.2	24.6	22.9	37.6	37.2	25.1	
Q8MRT7	SD26038p OS=Drosophila melanogaster OX=7227 GN=BcDNA:SD26038 PE=1 SV=1	9	2	4	2	174	20.2	5.34	2.06	2	0	40.5	64.8	56.5	56.8	52	62.6	75.3	50.6	
M9PDF2	Second mitotic wave missing, isoform C OS=Drosophila melanogaster OX=7227 GN=swm	8	7	19	7	1063	115.8	9.26	33	7	0	182.8	236.8	218.6	207.9	140.3	239.5	283.5	240.1	
Q9VYB0	Selenoprotein BthD OS=Drosophila melanogaster OX=7227 GN=BthD PE=1 SV=5	27	6	8	6	249	27.8	9.74	7.13	6	0	91.1	113.2	106.4	102.2	93.8	153.9	140.2	126.3	
P42207	Septin-1 OS=Drosophila melanogaster OX=7227 GN=Sep1 PE=1 SV=1	16	3	3	3	361	41.1	6.55	1.8	3	0	8.4	10.7	13.3	6.1	14.9	13	17.3	15.4	
X2J8R0	Septin-interacting protein 1 OS=Drosophila melanogaster OX=7227 GN=sip1 PE=3 SV=1	2	2	2	2	839	94.8	6.19	1.69	2	0	17.5	24	19.3	27.8	19.3	31	33.5	22.5	
A0A0B4KGW6	Sequence-specific single-stranded DNA-binding protein, isoform D OS=Drosophila melano	4	2	10	2	509	51.2	6.39	13.95	2	0	173.5	215.6	203.6	216.2	135.6	175.2	229.3	202.9	
Q9W457	Serine hydroxymethyltransferase OS=Drosophila melanogaster OX=7227 GN=Shmt PE=1	6	4	16	4	537	58.8	9.04	31.78	4	0	426.9	578.8	589.9	582.5	491.6	583.7	693.8	548.8	
P26686	Serine-arginine protein 55 OS=Drosophila melanogaster OX=7227 GN=B52 PE=1 SV=4	13	5	25	5	376	42.8	11.37	40.36	5	0	1257.2	1060.7	812.4	1040.6	585.5	859	1016.9	868.5	
Q5EAK6	Serine/threonine-protein kinase ATM OS=Drosophila melanogaster OX=7227 GN=tefu PE	2	4	7	4	2767	317.8	7.36	8.37	4	0	39.7	55.7	48	42.6	32.1	73.2	68.2	35.8	
Q9VXG8	Serine/threonine-protein kinase ATR OS=Drosophila melanogaster OX=7227 GN=mei-41	1	4	5	4	2517	289.1	7.56	4.12	4	0	69.6	85.9	105.8	84.4	69.3	76.1	88.7	68.6	
Q9VPC0	Serine/threonine-protein kinase PITSLRE OS=Drosophila melanogaster OX=7227 GN=Pit	2	2	4	2	952	108.8	8.05	7.27	2	0	71.4	85.7	73.9	79.7	51.9	99.2	100.7	86.4	
P52304	Serine/threonine-protein kinase polo OS=Drosophila melanogaster OX=7227 GN=polo PE	11	6	17	6	576	66.9	8.88	23.09	6	0	297.6	338.8	316.2	232.6	200.1	430.4	355.7	265.2	
Q9VXF1	Serine/threonine-protein phosphatase 2B catalytic subunit 3 OS=Drosophila melanogaste	6	4	8	1	584	64.2	6.07	13.99	4	3	312	380.6	403.7	311.3	230.6	296.4	405	269.2	
Q9W2U4	Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Drosophila melanogaste	9	5	13	5	609	66.8	4.41	17.97	5	0	348.7	364.4	325.6	311.2	179.1	388.4	430.7	342	
Q9VFS5	Serine/threonine-protein phosphatase 4 regulatory subunit 3 OS=Drosophila melanogaste	5	5	11	5	980	109.2	4.81	15.94	5	0	251.9	272.6	288	246	147.4	316.9	330.5	242.1	
P48461	Serine/threonine-protein phosphatase alpha-1 isoform OS=Drosophila melanogaster OX=	10	2	7	2	327	37.3	6.67	3.97	2	0	27.5	26.6	24.1	19.8	20.3	27.1	37.4	28.9	
Q05547	Serine/threonine-protein phosphatase alpha-3 isoform OS=Drosophila melanogaster OX=	14	3	11	3	302	34.5	5.76	14.74	3	0	184.9	227.8	173.8	159.7	135.4	208.6	241	178	
X2JDI1	Serine/threonine-protein phosphatase OS=Drosophila melanogaster OX=7227 GN=mts PI	24	4	14	3	309	35.4	5.34	15.38	4	0	25.3	45	52.3	41.8	34.7	36.3	51.8	35.2	
M9NE01	Serine/threonine-protein phosphatase OS=Drosophila melanogaster OX=7227 GN=Pp2B-	6	4	14	1	570	63.1	5.88	13.85	4	0	152.3	185.6	188.3	142.7	148.2	150.4	216.6	151.1	
X2JG90	Serine/threonine-protein phosphatase OS=Drosophila melanogaster OX=7227 GN=Pp4-1	19	5	24	4	307	35.3	5.26	41.4	5	1	327.6	430.4	395.3	352	277.4	404.6	455.9	373.3	
Q7K8Y5	Serpin 4 OS=Drosophila melanogaster OX=7227 GN=Spn42Da PE=1 SV=1	6	2	3	2	424	47.6	6.01	1.8	2	0	20.7	23.3	23.5	22.6	19.2	22.9	23.5	22.4	
Q9V9K7	Serrate RNA effector molecule homolog OS=Drosophila melanogaster OX=7227 GN=Ars2	16	15	58	15	943	107.2	5.55	64.97	15	0	1445.4	1459.4	1390.1	1156.6	818.1	1823.6	1740.4	1248.1	
E1JJN9	SET domain containing 2, isoform B OS=Drosophila melanogaster OX=7227 GN=Set2 PE	1	2	2	2	2313	256.6	6.32	4.91	2	0	35.4	35.1	27.2	24.6	21.2	44.2	40	32	
Q9VXV3	Shattered OS=Drosophila melanogaster OX=7227 GN=shtd PE=1 SV=1	1	2	2	2	2030	227.1	6.51	0	2	0	16.4	17.8	21.7	20.6	14.3	19	20.4	15.9	
M9PHQ0	Shibire, isoform N OS=Drosophila melanogaster OX=7227 GN=shi PE=1 SV=1	3	3	5	3	896	99.8	8.57	5.69	3	0	70.4	81.4	85.4	59.4	68.5	81.2	108.1	63.3	
Q9U5L1	Signal recognition particle receptor subunit alpha homolog OS=Drosophila melanogaster O	3	2	2	2	614	67.8	6.83	1.77	2	0	13	23.5	27.8	19.4	31.4	25.9	32	28.9	
Q9VSS2	Signal recognition particle subunit SRP68 OS=Drosophila melanogaster OX=7227 GN=Srp	3	2	3	2	604	69	8.47	1.98	2	0	37.4	36.7	39.3	29	43.7	54.9	53.6	25.3	
A0A0B4K765	Sin3A, isoform G OS=Drosophila melanogaster OX=7227 GN=Sin3A PE=1 SV=1	4	8	20	8	2066	220.9	8.15	35.6	8	0	247	294.7	304	395.8	233.8	362.2	416.3	290.3	
A4V441	Singed, isoform B OS=Drosophila melanogaster OX=7227 GN=sn PE=1 SV=1	18	6	23	6	512	57.2	7.01	36.94	6	0	197.3	264.3	275.7	226.4	219.3	316.1	323.6	246.5	

P54622	Single-stranded DNA-binding protein, mitochondrial OS=Drosophila melanogaster OX=722	22	3	13	3	146	16.4	9.85	29.86	3	0	223.6	353.2	330	402.1	187.9	307.1	292.5	226
M9PC89	Small ribonucleoprotein particle U1 subunit 70K, isoform C OS=Drosophila melanogaster C	5	3	6	3	448	52.9	10.04	9.49	3	0	264.6	287.7	219.7	221.7	151.5	290.7	319.5	261.2
Q9VS62	Smallminded, isoform A OS=Drosophila melanogaster OX=7227 GN=smid PE=1 SV=1	14	9	36	9	944	104.3	5.44	54.89	9	0	249.2	306.9	326.7	254.8	156.5	340.1	366.4	249.4
M9PGZ8	Smrter, isoform G OS=Drosophila melanogaster OX=7227 GN=Smr PE=1 SV=1	1	3	4	3	3607	379.6	9.44	3.46	3	0	44.8	61.8	56.8	59.4	40.6	60.1	80.8	65.5
Q9XZ21	Something that sticks like glue, isoform A OS=Drosophila melanogaster OX=7227 GN=sna	3	3	5	3	1231	139	9.73	3.78	3	0	62.8	65.7	49.9	64	44.1	86.7	86.5	73.4
M9ND86	Spellchecker1, isoform D OS=Drosophila melanogaster OX=7227 GN=spel1 PE=1 SV=1	11	10	46	10	917	103.2	5.92	73.13	10	0	1026.5	1248.6	1329.6	1086.6	642.4	1094.2	1227.7	934.4
Q9VHA1	Spermidine synthase, isoform A OS=Drosophila melanogaster OX=7227 GN=SpdS PE=1	13	3	15	3	287	32.3	5.78	17.85	3	0	228.5	261.2	280.2	262	179.3	288.5	305.9	254.3
O46106	Splicing factor 3A subunit 3 OS=Drosophila melanogaster OX=7227 GN=noi PE=1 SV=1	12	5	11	5	503	58.4	5.62	16.23	5	0	187.9	255.3	221.2	211.3	173.9	229.1	282	168.2
Q9VPR5	Splicing factor 3b subunit 1, isoform A OS=Drosophila melanogaster OX=7227 GN=Sf3b1	3	5	11	5	1340	149.5	6.67	20.57	5	0	287.7	365.3	340.3	314.2	227.1	404.2	442.3	359
Q9W0M7	Splicing factor 3B subunit 3 OS=Drosophila melanogaster OX=7227 GN=Sf3b3 PE=1 SV=	11	12	42	12	1227	136.5	5.47	39.46	12	0	724.7	945.6	892.3	821.3	666.7	1118.6	1200.6	956.5
Q9W0S7	Staphylococcal nuclease domain-containing protein 1 OS=Drosophila melanogaster OX=7	15	12	54	12	926	103	8.05	109.57	12	0	993.9	1318.8	1501.5	1236.3	1539.7	1367.1	1759.6	1204.7
Q9VCB8	Structural maintenance of chromosomes protein 6 OS=Drosophila melanogaster OX=7227	4	5	6	5	1122	129.3	8.32	2.31	5	0	82	93.5	93.9	109.1	84.6	137.1	124.9	119
Q9V3A7	Structural maintenance of chromosomes protein OS=Drosophila melanogaster OX=7227 G	14	13	27	13	1409	159.8	6.15	30.06	13	0	261.6	274.9	287.5	278.9	240.5	406	363.7	304
Q9VCD8	Structural maintenance of chromosomes protein OS=Drosophila melanogaster OX=7227 G	9	11	16	11	1238	142.8	6.73	18.47	11	0	296.8	370.4	338.8	346	288.4	463.2	435.5	492.7
Q7KK96	Structural maintenance of chromosomes protein OS=Drosophila melanogaster OX=7227 G	5	6	18	6	1179	134.3	8.18	18.84	6	0	298.2	308	326	276.2	241.2	452	427	310.4
Q9VXE9	Structural maintenance of chromosomes protein OS=Drosophila melanogaster OX=7227 G	13	13	18	13	1200	139.9	8.1	11.68	13	0	217.5	200.5	209.9	160.4	123.7	252	238.9	150.2
A1Z9S6	Su(Var)2-HP2, isoform A OS=Drosophila melanogaster OX=7227 GN=Su(var)2-HP2 PE=1	6	14	27	14	3257	355.8	6.14	45.32	14	0	732.6	784.8	718.2	681.8	427	803.3	873.7	723
A0A0B4K6W1	Suppressor of hairy wing, isoform C OS=Drosophila melanogaster OX=7227 GN=su(Hw) P	2	2	3	2	941	105.7	6.71	2.29	2	0	43.7	42	42.3	35.4	33.6	61.8	52.4	40.9
Q9VDS6	Surfeit locus protein 6 homolog OS=Drosophila melanogaster OX=7227 GN=Surf6 PE=1 S	6	2	5	2	324	38.1	9.85	4.11	2	0	111.5	103.2	61.3	79.3	55.6	256.2	190.6	175.2
Q9VL72	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A cor	5	4	9	4	844	95.4	8.16	16.37	4	0	167.6	160.3	159.2	105.3	74.6	275.3	194.9	128.1
Q8MSU4	Symplekin OS=Drosophila melanogaster OX=7227 GN=Sym PE=1 SV=1	4	5	11	5	1165	132	6.49	14.4	5	0	165.9	251.4	278.8	267.3	189.3	282.2	357.5	217.7
Q9VK69	T-complex protein 1 subunit delta OS=Drosophila melanogaster OX=7227 GN=CCT4 PE=	11	5	19	5	533	57.1	7.56	27.28	5	0	286.6	387.1	454.3	312.7	519.6	419.2	532.4	357
Q7KKI0	T-complex protein 1 subunit epsilon OS=Drosophila melanogaster OX=7227 GN=CCT5 PE	4	2	8	2	542	59.2	6.25	19.46	2	0	171.5	205.6	234.7	91	134	252.8	253.5	106.1
Q9VHL2	T-complex protein 1 subunit eta OS=Drosophila melanogaster OX=7227 GN=CCT7 PE=1	9	5	17	5	544	59.3	6.34	30.81	5	0	356.3	486.4	580.6	435	602.6	437	635.8	438
A4V303	T-complex protein 1 subunit gamma OS=Drosophila melanogaster OX=7227 GN=CCT3 PE	15	9	33	9	544	59.4	6.8	62.35	9	0	602.2	803.1	934.9	748.4	1019.5	786.3	1077.8	729.9
Q9VH72	TA01656p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9471 PE=1 SV=1	21	4	20	4	204	22.7	7.49	45.32	4	0	208.2	241.3	240.6	186.7	159	247.5	280.5	224
Q07DP5	TATA box binding protein-related factor 2, isoform E OS=Drosophila melanogaster OX=72	3	5	9	5	1715	194.6	5.02	14.01	5	0	197.8	215.7	200.4	177	115.9	238.7	262.4	180.3
A0A0B4KH26	TATA box-binding protein-associated factor RNA polymerase I subunit B, isoform C OS=Dr	2	2	2	2	872	101.7	7.3	1.98	2	0	24.8	29.1	26.8	26.4	19.5	37	24.9	30.4
A0A0B4K602	TBP-associated factor 1, isoform E OS=Drosophila melanogaster OX=7227 GN=Taf1 PE=	2	5	7	5	2172	244	5.31	11.52	5	0	111.3	143.2	143.6	135.7	114.1	178.8	194.8	153.8
B7Z060	TBP-associated factor 4, isoform E OS=Drosophila melanogaster OX=7227 GN=Taf4 PE=	3	3	5	3	1088	117.1	10.14	1.61	3	0	45.1	65.9	58.4	73.3	53.9	73.4	81.2	76.5
Q9XZ34	Telomere-associated protein RIF1 OS=Drosophila melanogaster OX=7227 GN=Rif1 PE=1	13	17	46	17	1416	156.7	6.65	58.48	17	0	904.4	1018.3	1025.7	763.9	518.1	1211.6	1158.1	818.3
Q8IPU3	Tenzing norgay, isoform C OS=Drosophila melanogaster OX=7227 GN=tzn PE=1 SV=1	7	2	4	2	348	38.8	7.58	8.28	2	0	53.9	72.9	61	37.8	51.8	80.9	93.8	46.2
A0A0B4LFZ4	TER94, isoform E OS=Drosophila melanogaster OX=7227 GN=TER94 PE=1 SV=1	17	13	66	13	825	91.9	5.38	120.97	13	0	1646	1884.5	1997.4	1462.4	1039.7	1879.2	2203.6	1517.9
Q9VGU5	Tetratricopeptide repeat protein 14 homolog OS=Drosophila melanogaster OX=7227 GN=	2	2	2	2	872	99.8	10.39	0	2	0	32.2	26.7	24.8	26.3	22	32.1	29.5	22.2
Q9V3W1	Tetratricopeptide repeat protein 2 OS=Drosophila melanogaster OX=7227 GN=Tpr2 PE=1	9	4	7	4	508	58	6.49	6.46	4	0	120.4	112	119.6	98	70.2	135	145.8	103
Q9W147	TFIIF-interacting CTD phosphatase, isoform A OS=Drosophila melanogaster OX=7227 GN	3	2	3	2	880	97.3	4.87	4.65	2	0	81.1	86.3	89.6	84.8	55.4	88.9	94.6	81.6
X2JF59	Thioredoxin peroxidase 1, isoform C OS=Drosophila melanogaster OX=7227 GN=Jafrac1	16	3	33	3	194	21.7	5.71	78.22	3	0	692.1	817.1	850.4	697.3	740.4	837.2	1013.2	742.3
P91938	Thioredoxin reductase 1, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Trxr-1	10	5	34	5	596	64.3	7.91	72.93	5	0	726.1	908.6	916.7	820.3	696.9	803.6	1055.2	795.1
Q9W1F4	THO complex subunit 5 OS=Drosophila melanogaster OX=7227 GN=thoc5 PE=1 SV=2	2	2	2	2	616	70.8	8.44	2.02	2	0	30.3	42.1	37.9	44.9	29	40.4	49.5	32.2
E2QCS8	Tho2, isoform B OS=Drosophila melanogaster OX=7227 GN=tho2 PE=1 SV=1	6	9	21	9	1642	188.5	8.82	35.08	9	0	321.7	375.9	343.7	301.7	188.2	452.5	463.5	301.4
Q8INH7	Timeout OS=Drosophila melanogaster OX=7227 GN=timeout PE=1 SV=2	11	13	44	13	1384	159.3	5.16	80.81	13	0	850.7	1137.1	1289.9	881.8	407.2	728.1	745.4	566
O77277	Torsin-like protein OS=Drosophila melanogaster OX=7227 GN=Torsin PE=2 SV=2	9	3	4	3	340	38.1	8.62	3.49	3	0	18.9	13.6	14	18.1	13.8	22.9	26.9	13.7
B7Z126	Tousled-like kinase, isoform G OS=Drosophila melanogaster OX=7227 GN=Tlk PE=1 SV=	3	5	10	5	1489	162.1	9.17	17.61	5	0	212.6	314.4	356.5	240.7	135.2	270.5	278.2	190.1
M9PF20	Trailer hitch, isoform H OS=Drosophila melanogaster OX=7227 GN=tral PE=1 SV=1	5	3	4	3	657	69.8	9.48	1.95	3	0	85.3	79.1	65.2	62.4	66.2	77.9	104.6	61.5
Q9V460	Transcription elongation factor SPT5 OS=Drosophila melanogaster OX=7227 GN=Spt5 PE	7	7	14	7	1078	119.4	6.25	24.78	7	0	289.4	315.1	318.3	291.6	208.4	384.2	369.2	311.9
N0D8I3	Transcription elongation factor spt6 OS=Drosophila melanogaster OX=7227 GN=Spt6 PE=	8	12	33	12	1831	208.5	5.31	48.95	12	0	394.4	424.4	432.6	372.9	285.8	564.2	592.2	424.1
Q24318	Transcription factor Dp OS=Drosophila melanogaster OX=7227 GN=Dp PE=1 SV=2	7	2	2	2	445	49.7	6.76	2.36	2	0	24.5	23.6	24.6	26.1	23.3	31.2	36.7	27.7
O77051	Transcription factor E2F2 OS=Drosophila melanogaster OX=7227 GN=E2f2 PE=1 SV=1	5	2	2	2	370	41.4	5.21	3.96	2	0	50.5	66.8	64	51.4	35.7	60.5	76.9	60.6
P29052	Transcription initiation factor IIB OS=Drosophila melanogaster OX=7227 GN=TfIIB PE=2 S	15	4	8	4	315	34.3	8.29	19.61	4	0	242.1	258.8	211.2	208.2	160.6	275.7	301.4	199.5
Q24325	Transcription initiation factor TFIID subunit 2 OS=Drosophila melanogaster OX=7227 GN=	7	7	13	7	1221	139.4	7.23	11.44	7	0	111.1	141.2	127.3	151.2	105.1	183.7	193.7	160.6
P49846	Transcription initiation factor TFIID subunit 5 OS=Drosophila melanogaster OX=7227 GN=	4	3	6	3	704	79.3	6.38	6.04	3	0	81.4	79.6	90.6	70	53.4	112.8	117.4	85.8
P49847	Transcription initiation factor TFIID subunit 6 OS=Drosophila melanogaster OX=7227 GN=	3	2	2	2	606	65.6	8.94	1.61	2	0	31.8	37.1	43.2	33.8	20.6	43.8	56.8	33.8
Q9VHY5	Transcription initiation factor TFIID subunit 7 OS=Drosophila melanogaster OX=7227 GN=	8	4	6	4	479	55	5.1	3.16	4	0	121.4	134	112.4	93	78.7	184.2	146.9	98.9
Q27272	Transcription initiation factor TFIID subunit 9 OS=Drosophila melanogaster OX=7227 GN=	11	3	7	3	278	29.3	9.32	6.27	3	0	171.4	151.7	137.2	92	78.2	194.9	162.5	91.6
Q8I8U7	Transcription-associated protein 1 OS=Drosophila melanogaster OX=7227 GN=Nipped-A	1	4	5	4	3790	435.1	7.75	5.63	4	0	108	134.7	147.1	139.2	141.5	156.6	170.4	137.1
Q9GQN5	Transcriptional regulator ATRX homolog OS=Drosophila melanogaster OX=7227 GN=XNP	2	3	9	3	1311	148.1	8.44	6.2	3	0	135.1	143.7	141	104.3	79.5	211.4	168.5	133
Q9VWV6	Transferrin OS=Drosophila melanogaster OX=7227 GN=Tsf1 PE=1 SV=1	2	2	2	2	641	71.8	7.06	3.72	2	0	73.5	61.7	52.5	49.5	42.4	62.7	72.4	48.9
A0A0B4JD97	Transforming acidic coiled-coil protein, isoform K OS=Drosophila melanogaster OX=7227 G	2	2	2	2	1322	147.1	4.98	0	2	0	5.6	8.1	6	7.9	8.3	11.7	11.9	11.3
Q9VZI1	Transgelin OS=Drosophila melanogaster OX=7227 GN=Chd64 PE=1 SV=2	16	3	5	3	188	20.6	8.43	7.72	3	0	47.5	62.4	49.3	44.9	36.4	59.3	77	50.2
Q9VGS2	Translationally-controlled tumor protein homolog OS=Drosophila melanogaster OX=7227 G	26	2	31	2	172	19.6	4.81	28.66	2	0	530.2	582.5	568.6	474.8	455.5	536.5	696.5	557.2
P00967	Trifunctional purine biosynthetic protein adenosine-3 OS=Drosophila melanogaster OX=72	4	5	8	5	1353	144.4	7.37	4.11	5	0	88.3	125.2	120.1	103	74.2	144.3	145.9	110.3
P29613	Triosephosphate isomerase OS=Drosophila melanogaster OX=7227 GN=Tpi PE=1 SV=3	11	2	14	2	247	26.6	6	30.71	2	0	205.6	351.2	277.5	423.5	348.7	318.8	428.8	332.3
Q9V6K1	Tripeptidyl-peptidase 2 OS=Drosophila melanogaster OX=7227 GN=TppII PE=1 SV=2	5	6	11	6	1441	158.6	7.59	15.84	6	0	83.3	118.9	160.7	107	149.5	136.4	189.9	126.7
Q8MS69	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 OS=Drosophila mel	7	3	4	3	444	49.9	6.64	0	3	0	62.9	67.6	74.1	56.1	48.4	83.9	86.7	54.5
Q9W4M9	tRNA (cytosine(34)-C(5))-methyltransferase OS=Drosophila melanogaster OX=7227 GN=Nsu	10	7	18	7	746	84.1	6.83	23.08	7	0	306.9	354.7	351.4	269	239.7	369	429.1	304.3
Q8IRE4	tRNA (guanine(37)-N1)-methyltransferase OS=Drosophila melanogaster OX=7227 GN=CG	9	4	7	4	457	53	8.43	7.57	4	0	49.6	52.5	45.8	57.2	39.3	73.3	74.8	60.4
Q9VIS4	tRNA-dihydrouridine(47) synthase [NAD(P)(+)] OS=Drosophila melanogaster OX=7227 GN	5	3	6	3	604	68	7.24	7.73	3	0	78.6	86.4	75.6	79.5	61	107.4	114.9	86.8
A0A0B4K661	Tropomyosin 1, isoform Q OS=Drosophila melanogaster OX=7227 GN=Tm1 PE=1 SV=1	16	4	21	4	250	29.2	4.87	37.17	4	0	611.8	434.1	433.6	336.1	521.9	340.7	619.7	402.2
A8DYI2	TRPL translocation defect 14, isoform C OS=Drosophila melanogaster OX=7227 GN=Ttd1	4	3	3	3	515	58.1	8.65	5.27	3	0	57.7	74.7	85.5	61	59.2	68.1	85.5	68.7
P06603	Tubulin alpha-1 chain OS=Drosophila melanogaster OX=7227 GN=alphaTub84B PE=1 SV	7	3	41	2	450	49.9	5.14	86.92	3	0	481.1	660.5	798.5	665.3	920	532.8	881.4	538.3
P06606	Tubulin alpha-4 chain OS=Drosophila melanogaster OX=7227 GN=alphaTub67C PE=3 SV	7	3	30	2	462	51.1	5.26	64.59	3	1	573.8	709.2	730.5	515.6	493.3	720.9	792.1	497.3
A1ZBL0	Tubulin beta chain OS=Drosophila melanogaster OX=7227 GN=betaTub56D PE=1 SV=1	15	6	70	6	456	51.3	5.01	114.55	6	0	443.1	568.6	603.9	526.9	694.4	530.4	946.5	483.8
P23257	Tubulin gamma-1 chain OS=Drosophila melanogaster OX=7227 GN=gammaTub23C PE=	8	3	11	2	475	53.3	5.94	5.86	3	0	18	29	28.1	18	20.8	34.9	27.2	20.7
P42271	Tubulin gamma-2 chain OS=Drosophila melanogaster OX=7227 GN=gammaTub37C PE=	6	3	13	2	457	51.3	6.32	7.99	3	1	94.9	123.9	147.8	109.6	131.3	142.3	175.5	127.7
A1ZBM2	Tubulin-binding cofactor B OS=Drosophila melanogaster OX=7227 GN=TBCB PE=1 SV=1	8	2	4	2	244	27	5.19	1.67	2	0	107.2	126.5	97.3	99	81.8	124.5	148.4	127.6
Q9V9U7	Tubulin-specific chaperone A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1890 f	27	3	7	3	110	12.9	5.71	10.36	3	0	229.9	259.3	257.1	228	185.4	194.8	222.8	218.9
Q9VVA7	Tumor suppressor protein 101 OS=Drosophila melanogaster OX=7227 GN=TSG101 PE=1	8	2	3	2	408	45.2	6.37	7.1	2	0	10.6	15.7	12.1	14.4	55.7	15.9	19.4	13.1
Q9VV60	Tyrosine--tRNA ligase OS=Drosophila melanogaster OX=7227 GN=TyrRS PE=1 SV=1	4	2	3	2	525	58.1	6.87	2.18	2	0	49.8	51	51.8	19	14.9	62	55.8	22.3
Q9W0G1	Tyrosine-protein phosphatase non-receptor type 61F OS=Drosophila melanogaster OX=72	7	4	6	4	548	62.1	5.55	4.02	4	0	69.6	87.7	94.1	77.9	74.2	90.6	107	73
M9PBM1	U2 small nuclear riboprotein auxiliary factor 38, isoform B OS=Drosophila melanogaster OX	8	2	9	2	264	29.9	8.91	10.34	2	0	202.7	217.8	198.3	185.1	119.5	258.2	246	217
Q9VLK1	U3 small nucleolar ribonucleoprotein protein MPP10 OS=Drosophila melanogaster OX=72	3	2	4	2	662	76.1	4.77	4.84	2	0	23.8	20.7	14	20.2	15.4	29.8	34.1	30.9
Q9W087	U6 snRNA-associated Sm-like protein LSm8 OS=Drosophila melanogaster OX=7227 GN=l	25	2	10	2	95	10.3	4.92	18.92	2	0	156.6	146.9	126.9	77.9	55.9	113.6	153.8	113.3
Q9VRP5	Ubiquitin carboxyl-terminal hydrolase 36 OS=Drosophila melanogaster OX=7227 GN=scny	1	2	6	2	1038	114	9.09	11.17	2	0	95.8	96.1	65.2	95.2	56.5	108.5	128.6	112.7
Q9VYQ8	Ubiquitin carboxyl-terminal hydrolase 7 OS=Drosophila melanogaster OX=7227 GN=Usp7	11	9	36	9	1129	130.4	6.04	54.67	9	0	266.5	271.9	294.9	205.9	176.3	377.5	364.5	427
Q9VWN5	Ubiquitin carboxyl-terminal hydrolase MINDY-3 homolog OS=Drosophila melanogaster OX=	7	4	6	4	560	61.7	5.92	5.95	4	0	80.3	102	113.2	94.6	82.6	94.8	136.1	74.5
M9MRD0	Ubiquitin carboxyl-terminal hydrolase OS=Drosophila melanogaster OX=7227 GN=Uch PE	22	5	64	5	227	25.8	5.49	37.14	5	0	554.2	795.7	584.9	534.7	410.2	638.2	732.2	550.2

Q9XZ61	Ubiquitin carboxyl-terminal hydrolase OS=Drosophila melanogaster OX=7227 GN=Uch-L5	16	4	25	4	324	37.6	5.21	35.71	4	0	465.1	537.9	520.2	455.3	355.9	579.1	664.7	527.8
Q9VZU7	Ubiquitin carboxyl-terminal hydrolase OS=Drosophila melanogaster OX=7227 GN=Usp5 PE	9	6	29	6	827	92	5.49	44.34	6	0	568.8	617.7	673.6	608.5	503.9	739.3	802.5	643.2
M9PBW0	Ubiquitin conjugating enzyme E2M, isoform B OS=Drosophila melanogaster OX=7227 GN=	12	2	11	2	181	20.7	7.15	23.92	2	0	240.2	251.1	259.6	227.5	177.5	280.9	323.4	252.5
Q7K4I5	UBX domain-containing protein 7 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG88	13	5	18	5	496	55.1	5.01	30.73	5	0	287.9	330.8	317.9	289.4	191.9	360.3	398.2	310
Q09332	UDP-glucose:glycoprotein glucosyltransferase OS=Drosophila melanogaster OX=7227 GN	4	4	5	4	1548	174.2	6.15	2.37	4	0	16.9	29	32.2	22	37.1	26.3	44.1	36
Q9VBI2	UMP-CMP kinase OS=Drosophila melanogaster OX=7227 GN=Dak1 PE=1 SV=1	15	3	13	3	253	27.8	8	20.44	3	0	299.8	267.1	249.4	172.9	154	322.8	300	193.9
Q9VCP1	Uncharacterized protein CG4449 OS=Drosophila melanogaster OX=7227 GN=CG4449 PE	13	5	10	5	424	47.7	6.57	12.44	5	0	100.4	112.1	101	90.7	99.4	133.7	144.5	113.5
A1A708	Uncharacterized protein CG4951 OS=Drosophila melanogaster OX=7227 GN=CG4951 PE	11	4	10	4	446	50.7	9.45	18.32	4	0	221.6	240.1	165.5	187.5	159.4	344.5	320.7	270.7
Q7YZA2	Uncharacterized protein CG7065 OS=Drosophila melanogaster OX=7227 GN=CG7065 PE	5	6	11	6	1231	136.7	9.23	6.74	6	0	100	112.1	86	103.6	80.9	122.2	140	116.1
Q9W0H6	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=ACAT PE=1 SV=2	7	2	6	2	392	41.1	7.05	10.69	2	0	41.1	39.9	37.3	31.4	25.4	48.4	46.6	28.1
Q9VJG2	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=cg12288 PE=1 SV=	5	2	3	2	435	47.9	10.04	2.34	2	0	36.1	46.5	27.4	37.7	28.2	57.6	41.2	38
B7Z0I8	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=CG14896 PE=1 SV=	6	16	25	16	3441	378.4	4.93	25.72	16	0	506.5	483.1	458.3	352.3	309.5	598.2	583.5	378.6
Q9VVV7	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=cg3808 PE=1 SV=3	3	2	7	2	615	68.6	6.23	10.61	2	0	125.2	169.3	177.1	159.7	132.1	166.5	196.7	159.5
Q9VD07	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12499 PE=	2	3	3	3	2059	237	6.76	6.43	3	0	51.8	41.8	31.2	29.5	34.3	91.2	56.2	47
Q9V9Z8	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG15561 PE=	15	4	4	4	357	39.9	9.17	2.48	4	0	60.6	39.9	34.5	24.2	20.2	68.7	53.7	32.9
A1ZAW6	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG30105 PE=	15	2	6	2	155	17.4	5.1	6.81	2	0	86.8	108.4	100.5	111.3	63.3	85.6	115.5	94.6
Q9VEP0	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3995 PE=1	6	2	2	2	322	37.4	6.55	1.68	2	0	71.5	59.1	51.5	55.9	46.1	61.1	75.3	54.6
Q9VBK9	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5913 PE=1	7	3	4	3	454	49.9	9.7	1.84	3	0	48.6	47.4	37.1	24.9	34.8	75.1	78.1	33.5
Q9W2N6	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9346 PE=1	6	6	8	6	957	108.4	8.53	2.01	6	0	106	126.2	124	113.1	83.3	157.7	165.3	129.3
Q9W246	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=GM01751p PE=1 SV	1	3	5	3	2733	311.7	7.74	1.84	3	0	14.9	17.1	17.8	14.8	13.6	24.6	24.2	15.3
A1Z6Z7	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=146745_e	5	3	6	3	586	63.9	4.55	5.21	3	0	156.7	159.8	153.6	147.2	92.1	198.5	194.5	167.3
Q9VEA6	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Aar2 PE=	4	2	2	2	379	42.4	5.44	3.73	2	0	43.6	44.3	39.5	45	30.1	47.2	60.4	40.4
Q9VTY2	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=anon-WO	13	3	10	3	317	35.8	6.11	12.03	3	0	162.5	149.6	117.9	86.3	66.4	157.3	171.7	99.6
Q86BM0	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=CG33085	7	2	3	2	209	22.9	5.44	1.75	2	0	24.6	27.4	29.2	27.5	24.8	29.9	31.4	26.4
Q9VRP2	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1	15	4	8	4	391	42.7	7.11	4.36	4	0	100.2	94.3	100.1	56.7	65	129.2	119.1	80
Q9VYA4	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1	18	5	17	5	340	37.6	8.95	17.84	5	0	239.4	288.5	285.7	244.2	139.2	359	321.1	257.7
A1ZBW6	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1	17	9	28	9	726	82.6	7.24	35.61	9	0	666.9	573.2	374.4	386.2	349.2	859.8	638.9	744.5
A1Z830	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1	5	3	4	3	485	53.8	7.27	4.19	3	0	93.7	80.6	72.4	73.9	59.9	125.3	103.6	114.7
Q9W3W6	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1	2	8	18	8	3313	371.1	7.77	27.44	8	0	321.3	347.7	301.7	371.7	257.1	381.9	403.1	346.4
Q9VRD4	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1	11	2	6	2	288	31.6	5.39	8.11	2	0	70.7	80.4	76.1	93.7	63.3	76.1	95	81.3
Q7PLL6	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1	1	4	4	4	2630	293.7	7.03	3.54	4	0	17.2	26.6	27.8	18.4	32.4	25.3	33.7	26.3
Q9VCD4	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1	20	3	5	3	144	16.9	9.83	6.91	3	0	134.8	114.1	108.8	85.9	76.4	244.2	390.5	294.2
Q9VZ60	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2	2	2	2	2	1128	122.6	9.6	2.17	2	0	34.5	42.8	42.2	45.4	26.8	35	41	39.6
Q9VB64	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4	18	2	3	2	212	23.6	5	2.79	2	0	8.8	12	6.6	6	5.5	7.8	9.4	8
Q9VXW9	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5	2	2	3	2	984	114.2	9.29	0	2	0	8.2	9.5	8.2	6.3	7.5	11.6	10.4	13.7
Q9VCR2	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6	4	2	5	2	401	45	5.62	4.53	2	0	105.3	113.9	129.8	107.9	84.4	107.7	142.3	95.4
Q9VEC4	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7	8	4	16	4	450	50.7	5.33	13.95	4	0	217.5	249.7	225	242.3	159.3	309.8	306.9	279.1
Q8IQM5	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7	7	2	3	2	317	34.7	4.4	0	2	0	31.8	34.1	34.2	34.7	24.4	36.7	45.5	34.6
Q0KHZ6	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7	12	3	7	3	253	27.2	8.05	7.78	3	0	62.1	71.9	82.9	68.3	93.2	103.9	113.9	80.2
Q9W039	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9	14	4	11	4	375	41.9	7.46	16.88	4	0	70.8	66.8	67.1	61.1	59.4	79.5	80.8	75.9
M9PFR8	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Arts PE=4	4	3	7	3	1080	120.8	4.86	7.25	3	0	27.6	23	27.2	12.8	11.5	25.5	28.9	11.9
Q9VID9	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=BEST:LD	2	5	9	5	2663	292.4	5.27	14.08	5	0	89.6	100.3	105.6	91.4	77.1	122.2	139.6	95.2
X2JKF2	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=CG32585	4	2	4	2	687	78.1	9.35	5.79	2	0	53	50.8	56.3	46.1	36.1	64	73	60.8
M9PGG8	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=CG40016	21	3	12	3	182	20.7	5.05	13.21	3	0	320.9	366.6	257.6	311.5	184	343.9	359.8	250.7
A1ZBJ2	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=cg7461 P	3	2	2	2	627	68.3	7.77	4.31	2	0	19.4	22.9	31.4	26.2	59.2	31.1	27.9	18
A0A0B4KFV4	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1	9	2	3	2	243	28.5	4.92	1.75	2	0	11.7	7	10.8	6.5	5.2	10.1	8.2	4.6
A0A0B4K6I6	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3	4	2	5	2	508	55.4	6.99	5.88	2	0	104.1	118.3	119.2	100.6	75.9	96.4	147	92.7
B7Z0N0	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5	10	3	9	3	355	39.8	6.4	14.94	3	0	247.8	225.5	186.1	158.9	144	300.8	241.2	197.5
Q9VT33	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6	7	2	2	2	388	42.7	7.4	2.15	2	0	52	71.8	75.8	52.9	58.2	66.4	88.2	62.1
B7Z0D7	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7	1	2	2	2	1676	190.9	8.84	2.25	2	0	40.1	43.5	42.8	38.2	28.5	61.2	53.9	45.2
M9MRG2	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Ndf PE=4	9	4	35	4	603	65.3	5.97	64.31	4	0	599	612.2	518.6	433.3	445.5	874.6	655.2	553.4
A0A0B4KFB8	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=CG33097	7	8	26	8	1123	129.7	8.27	28.25	8	0	431.2	505.2	403.4	379.3	278.6	563.7	644.8	429.2
Q0E8G6	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Cpsf5 PE	8	2	10	2	237	26.9	8.85	17.71	2	0	283.1	326.9	261.1	256	220.6	242.3	319.4	260.3
X2JAQ5	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1	19	3	8	3	214	24.4	7.37	11.58	3	0	68.2	78.4	70.3	46.7	58.1	60.3	79	50.5
E1JGL8	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3	8	9	30	9	1272	140.5	5.01	32.2	9	0	531.1	600.4	540	520.9	381.3	620	759.2	554.7
E1JIV0	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5	6	2	5	2	243	28.2	8.03	7.21	2	0	130.5	156.1	125.2	142	121.4	162.5	170	168.3
Q7KSN8	Uncharacterized protein, isoform D OS=Drosophila melanogaster OX=7227 GN=CG14730	9	14	28	14	1486	172.2	6.1	14.89	14	0	315.9	388.7	354.9	274.8	243.5	458.9	457.1	303.6
A0A023GRW3	Uncharacterized protein, isoform D OS=Drosophila melanogaster OX=7227 GN=cg4896 P	4	2	2	2	949	107.6	8.22	0	2	0								
X2JEJ0	Uncharacterized protein, isoform D OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1	3	2	8	2	551	62.5	7.11	9.5	2	0	142.9	202.4	199.5	144.4	176.4	193.4	223.7	147.4
M9ND57	Uncharacterized protein, isoform E OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7	2	2	2	2	1298	138	5.91	2.02	2	0	23.5	28.9	25.4	25.3	23.3	31.4	38.4	32
A8JNI2	Uncharacterized protein, isoform F OS=Drosophila melanogaster OX=7227 GN=anon-EST	1	2	4	2	1655	185.8	10.8	5.8	2	0	113.5	110.1	86.9	114.4	82.7	145.8	167.3	135.6
X2JF73	Uncharacterized protein, isoform H OS=Drosophila melanogaster OX=7227 GN=URE-B1 P	1	4	5	4	5151	557.3	5.45	7.23	4	0	129.5	143.4	136	126.5	88.5	126.9	142.3	119.1
M9PGK3	Uncharacterized protein, isoform I OS=Drosophila melanogaster OX=7227 GN=CG4564 P	3	4	10	4	1367	143.2	9.2	6.81	4	0	170.7	172.6	176.2	156.4	87.2	197	222	132.6
A0A0B4K897	Uncharacterized protein, isoform O OS=Drosophila melanogaster OX=7227 GN=BcDNA:R	5	2	3	2	369	41	5.05	1.98	2	0	18	27	23.8	15.9	29.4	21.5	44.4	25.7
A1Z9A2	UPF0587 protein CG4646 OS=Drosophila melanogaster OX=7227 GN=CG4646 PE=2 SV	12	2	3	2	163	18.6	4.96	2.54	2	0	71.1	70.8	69.5	65.9	51.8	79.6	93.4	65
Q01637	Uridine 5'-monophosphate synthase OS=Drosophila melanogaster OX=7227 GN=r-l PE=2	15	5	22	5	493	53.4	7.25	33.74	5	0	384.5	352.2	311.5	260	217.5	457	421.6	268.9
Q9V595	Uroporphyrinogen decarboxylase OS=Drosophila melanogaster OX=7227 GN=Updo PE=3	11	3	14	3	356	40	6.54	27.39	3	0	283.7	343.8	325.3	306	211.4	304	413.4	289.2
Q9VSW1	UTP--glucose-1-phosphate uridylyltransferase OS=Drosophila melanogaster OX=7227 GN	3	2	3	2	520	58.7	7.39	5.47	2	0	42.1	41.2	45.2	34.5	35.1	49.7	43.6	27.6
Q9VE75	V-type proton ATPase subunit a OS=Drosophila melanogaster OX=7227 GN=Vha100-2 P	2	2	2	2	834	94.8	6.68	0	2	0	11	19.5	21.4	21.9	41.6	18.4	33.4	25.8
Q9V7N5	V-type proton ATPase subunit C OS=Drosophila melanogaster OX=7227 GN=Vha44 PE=	6	5	10	5	836	92.3	7.56	9.06	5	0	85	102.3	118.6	98	101.4	95.3	158.7	90.2
Q9V7D2	V-type proton ATPase subunit D 1 OS=Drosophila melanogaster OX=7227 GN=Vha36-1 P	10	2	3	2	246	27.6	9.54	0	2	0								
P54611	V-type proton ATPase subunit E OS=Drosophila melanogaster OX=7227 GN=Vha26 PE=	8	2	10	2	226	26.1	6.15	5.79	2	0	255.8	309.5	306.2	250.6	235.1	297.7	355.9	244.2
E1JIJ5	Vacuolar H[+]-ATPase 55kD subunit, isoform C OS=Drosophila melanogaster OX=7227 GI	14	6	7	6	490	54.5	5.4	11.05	6	0	124.2	184.9	194.3	160.9	206.3	189.1	244.1	156.4
A0A0B4KF06	Valyl-tRNA synthetase, isoform C OS=Drosophila melanogaster OX=7227 GN=ValRS PE=	7	7	12	7	1055	118.7	6.68	19.58	7	0	171.9	255.5	295.1	236.7	256.7	233.7	295.6	232.5
M9PBB5	Vasa, isoform B OS=Drosophila melanogaster OX=7227 GN=vas PE=3 SV=1	8	6	15	6	661	72.3	5.66	12.91	6	0	255.6	278.3	264.6	235.1	149.7	342.7	344.2	237
P54351	Vesicle-fusing ATPase 2 OS=Drosophila melanogaster OX=7227 GN=Nsf2 PE=2 SV=2	2	2	2	2	752	83.4	6.74	0	2	0	37.5	43.8	52.9	42.3	46.7	48	53.2	39.9
Q9VBX3	Vig2, isoform B OS=Drosophila melanogaster OX=7227 GN=vig2 PE=1 SV=2	10	3	9	3	443	48.7	9.38	7.14	3	0	105.8	218.3	117.1	317.3	189.3	112.7	251.5	252.6
Q9VMV5	Viking, isoform A OS=Drosophila melanogaster OX=7227 GN=vkg PE=1 SV=1	2	4	4	4	1940	193.7	6.43	3.59	4	0	11.9	12	19.8	14.1	15.9	18.1	14.8	27
X2JAB9	Vinculin, isoform B OS=Drosophila melanogaster OX=7227 GN=Vinc PE=1 SV=1	8	6	10	6	961	106.2	6.7	7.75	6	0	45.1	46.4	47.3	41.2	46.4	53.4	54.8	35.7
Q8MR62	Viral IAP-associated factor homolog OS=Drosophila melanogaster OX=7227 GN=viaf PE=	10	2	4	2	240	27.4	4.86	2.22	2	0	73.7	75.6	77.4	62.1	65.9	106	108.1	92.1
P02843	Vitellogenin-1 OS=Drosophila melanogaster OX=7227 GN=Yp1 PE=1 SV=1	5	3	14	3	439	48.7	7.69	25.9	3	0	627.2	488.8	392.5	326.2	325.6	329.3	464	383.3
Q94920	Voltage-dependent anion-selective channel OS=Drosophila melanogaster OX=7227 GN=p	7	2	6	2	282	30.5	6.96	9.05	2	0	177.8	226.4	229.9	133.9	345.4	229.4	215.1	153.3
Q7K0L4	WD repeat-containing protein 26 homolog OS=Drosophila melanogaster OX=7227 GN=CG	2	2	3	2	630	69.6	5.63	3.6	2	0	58.7	68.1	63.1	38.6	50.8	87.2	84.9	45.3
Q8T088	WD repeat-containing protein 55 homolog OS=Drosophila melanogaster OX=7227 GN=CG	7	3	8	3	498	55.3	4.53	3.3	3	0	88.6	79.3	90.8	83.6	72.6	121.5	120.4	98.9
Q9VLN1	WD repeat-containing protein 82 OS=Drosophila melanogaster OX=7227 GN=Wdr82 PE=	9	2	4	2	317	35.3	7.24	6.53	2	0	50.6	39.1	25.9	14.1	6.6	57.3	43.7	13
A8JRE3	Without children, isoform B OS=Drosophila melanogaster OX=7227 GN=woc PE=1 SV=1	6	10	30	10	1703	188.6	4.75	33.21	10	0	545.2	585.2	505.8	490.8	437	772.6	841.9	595.6

E1JIP3	WRN exonuclease, isoform B OS=Drosophila melanogaster OX=7227 GN=WRNexo PE=4	9	2	15	2	354	40.4	9.14	12.6	2	0	104.9	126.2	119.5	108	92.6	227.8	161.6	153.6
Q9VJG0	Xaa-Pro aminopeptidase ApepP OS=Drosophila melanogaster OX=7227 GN=ApepP PE=	9	4	6	4	613	68.5	5.95	12.78	4	0	224.3	249.8	261.6	193.9	161.8	229.7	299.2	217.7
Q7KVP9	Xeroderma pigmentosum D OS=Drosophila melanogaster OX=7227 GN=Xpd PE=1 SV=1	5	4	6	4	769	88	6.77	6.07	4	0	103.7	121.5	121.7	100.7	80	146.4	151	98.5
A0A0B4KHA1	Yemanuclein, isoform B OS=Drosophila melanogaster OX=7227 GN=yem PE=1 SV=1	2	2	2	2	1101	119.2	8.54	2.33	2	0	6.9	10	8.8	6	6.9	9.4	10.5	9.5
X2JB25	Yolk protein 2, isoform B OS=Drosophila melanogaster OX=7227 GN=Yp2 PE=1 SV=1	20	6	27	6	442	49.6	7.96	30.48	6	0	775.8	775	674.2	607.1	574	435.5	853.5	579.5
X2JEX8	Yolk protein 3, isoform B OS=Drosophila melanogaster OX=7227 GN=Yp3 PE=1 SV=1	14	3	59	3	420	46.1	8.5	98.79	3	0	761	893.3	759.8	872.6	753.6	546.6	921.5	712.8
M9NGY4	ZAP3, isoform E OS=Drosophila melanogaster OX=7227 GN=ZAP3 PE=1 SV=1	2	3	3	3	1885	205.1	5.69	0	3	0	16.8	15.7	14.5	13.5	12.4	20.9	19.4	12.9
Q9V468	Zinc finger matrin-type protein CG9776 OS=Drosophila melanogaster OX=7227 GN=CG97	2	2	2	2	1260	140.2	9.35	2.08	2	0	28.8	28.6	22.7	23.6	17.7	28.4	39.3	20.7
Q9W3Y0	Zinc finger protein 593 homolog OS=Drosophila melanogaster OX=7227 GN=CG3224 PE	16	2	2	2	162	18.9	9.67	1.85	2	0	13.9	21.4	20.6	15.9	14.2	19	21.5	14.9
Q8IRH5	Zinc finger protein CG2199 OS=Drosophila melanogaster OX=7227 GN=CG2199 PE=1 S	14	7	16	7	733	81.9	8.56	19.89	7	0	120.1	114	90.9	88	92.7	201.2	117.5	154.7
P41073	Zinc finger protein on ecdysone puffs OS=Drosophila melanogaster OX=7227 GN=Pep PE	14	9	58	9	716	78	5.58	107.08	9	0	1770.7	1897.7	1809.5	1765.4	1140.8	1887.4	2258.6	1759.9
Q86BI3	Zinc-finger protein at 72D, isoform B OS=Drosophila melanogaster OX=7227 GN=Zn72D F	7	5	10	5	884	96	8.44	20.01	5	0	169.8	188.5	172.9	184.3	121.6	225	235.7	180.2

Supplemental Table 3-2: Normalized TMT Intensities for Pulse-Enriched Embryo iPOND Replicates

Accession	Description	EdU Pulse R1	Edu Pulse R2	EdU Pulse R3	EdU Pulse R4	Thy Chase R1	Thy Chase R2	Thy Chase R3	Thy Chase R4	Pulse Average	Thy Aver	Pulse - Chase	Fold Change	p-value
P92177	14-3-3 protein epsilon OS=Drosophila melanogaster OX=7227 GN=14-3-3epsilon I	10.93899144	10.64256968	10.89815458	10.20515716	9.681451497	10.23578733	10.04783018	10.37638281	10.67121822	10.08536296	0.585855261	1.500928508	0.041109
P29310	14-3-3 protein zeta OS=Drosophila melanogaster OX=7227 GN=14-3-3zeta PE=1	10.41098127	10.2072143	10.41135665	9.897173421	9.354331976	9.778135648	9.652773367	9.921832432	10.23168141	9.676768356	0.554913054	1.469080095	0.017666
P02572	Actin-42A OS=Drosophila melanogaster OX=7227 GN=Act42A PE=1 SV=3	10.92911043	10.69353466	11.08218439	10.63960726	10.73497517	10.4390432	10.27729013	10.44546426	10.83610918	10.47419319	0.361915996	1.285131506	0.04203
O16043	Anon1A4 OS=Drosophila melanogaster OX=7227 GN=Df31 PE=1 SV=1	8.721782768	8.016860587	8.044408486	7.730349416	7.088862243	7.072902438	7.513794616	7.548388815	8.128350314	7.305987028	0.822363286	1.768300283	0.015879
F0JAI1	Arginine methyltransferase 4, isoform B OS=Drosophila melanogaster OX=7227 GI	8.235535607	8.23313307	8.448973299	8.155863757	7.303298526	7.979640966	7.837686683	7.962875056	8.268376433	7.770875308	0.497501125	1.41176614	0.027038
Q9VGH5	AT27789p OS=Drosophila melanogaster OX=7227 GN=glo PE=1 SV=1	8.051480865	7.881435487	7.705253955	7.936771533	7.119952436	7.596639459	7.404862395	7.806299042	7.89373546	7.481938333	0.411797127	1.330341954	0.044642
A0A0B4LF57	Calmodulin, isoform C OS=Drosophila melanogaster OX=7227 GN=Cam PE=1 SV=	8.057450272	7.774889365	7.839222811	7.787800526	6.902052581	6.710296791	6.856590515	7.086337119	7.864804743	6.888819252	0.976021492	1.967033451	0.000073
O96989	CDC45L OS=Drosophila melanogaster OX=7227 GN=CDC45L PE=1 SV=1	6.614709844	7.162582078	7.425590449	6.69223141	5.297212997	6.040035532	5.74936151	5.83222662	6.973778445	5.729709165	1.24406928	2.368656968	0.002447
Q9VIH1	CG9273 protein OS=Drosophila melanogaster OX=7227 GN=RPA2 PE=1 SV=2	8.607330314	8.597458223	9.023238428	8.111232135	6.517651645	7.556727512	7.291613104	7.326255981	8.584814775	7.173062061	1.411752714	2.660602001	0.002954
A1Z898	Chromatin assembly factor 1, p105 subunit OS=Drosophila melanogaster OX=722	6.934280594	6.729255037	7.250335427	6.559817286	5.684621722	6.512318822	6.161990049	6.191499858	6.868422086	6.137607613	0.730814473	1.659575741	0.017886
Q9W3D1	Chromatin assembly factor 1, p180 subunit OS=Drosophila melanogaster OX=722	9.23457796	9.153856087	9.515965377	8.890329313	7.450039943	8.641814736	8.275687205	8.545705925	9.198682184	8.228311952	0.970370232	1.959343348	0.017765
Q494K2	Chromosome transmission fidelity 4 OS=Drosophila melanogaster OX=7227 GN=C	8.010108453	7.962216759	8.442611581	7.703911958	6.11169343	7.414926694	7.24700947	7.342321915	8.029712188	7.028987877	1.000724311	2.00100436	0.026927
Q8IRB5	Claspin OS=Drosophila melanogaster OX=7227 GN=Claspin PE=1 SV=1	9.168672118	8.893949366	9.204847647	8.452014586	7.657039458	8.447868346	8.23667226	8.494208591	8.929870929	8.208947164	0.720923765	1.648237072	0.031932
Q8IQ05	Cutlet OS=Drosophila melanogaster OX=7227 GN=cutlet PE=1 SV=2	7.99830835	7.988714568	8.423733958	7.528287091	6.246460674	7.289009634	7.053745385	7.224263411	7.984760992	6.953369776	1.031391216	2.043994361	0.0143
Q9VSD6	D-Importin 7/RanBP7 OS=Drosophila melanogaster OX=7227 GN=msk PE=1 SV=	9.429615964	9.280299206	9.486574556	9.219422183	8.424680869	9.048688479	8.983086975	9.092304513	9.353977977	8.887190209	0.466787768	1.382028884	0.031959
A0A0B4LEV2	DNA helicase OS=Drosophila melanogaster OX=7227 GN=dpa PE=1 SV=1	10.55669763	10.36113455	10.74960776	10.11902845	9.944458917	10.19375042	9.649175117	9.860154323	10.4466171	9.661884694	0.784732406	1.722772747	0.038241
P26019	DNA polymerase alpha catalytic subunit OS=Drosophila melanogaster OX=7227 G	9.21310422	9.150073895	9.626338263	8.72224869	7.061719707	8.294157828	8.02795424	8.16559135	9.177941267	7.887355781	1.290585486	2.446273119	0.008553
Q9VCN1	DNA polymerase epsilon catalytic subunit OS=Drosophila melanogaster OX=7227	9.946467699	10.03295591	10.50133462	9.617558126	8.101035787	9.085597842	8.830212373	8.904749718	10.02457909	8.73039893	1.294180158	2.452375945	0.003805
Q9VRQ7	DNA polymerase epsilon subunit OS=Drosophila melanogaster OX=7227 GN=DNA	6.563768278	6.718367084	6.875298315	6.143563784	5.064579328	5.713445629	5.785968419	5.671785583	6.575249365	5.55894474	1.016304625	2.022731217	0.004389
Q9VPH2	DNA primase large subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-al	9.37286506	9.456073642	9.842062899	9.005381351	7.32707851	8.356339119	8.178241983	8.287414941	9.419095738	8.037268638	1.3818271	2.605981966	0.003365
Q24317	DNA primase small subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-al	8.346513733	8.533386042	8.842997354	8.264385106	6.560211035	7.580711567	7.330623716	7.405410149	8.496820559	7.219239117	1.277581442	2.424322186	0.002662
P49735	DNA replication licensing factor Mcm2 OS=Drosophila melanogaster OX=7227 GN=	10.81322003	10.60015208	10.96606488	10.3176068	9.018944507	10.2969942	9.834603866	10.04384913	10.67426095	9.798597926	0.875663022	1.834851139	0.030247
Q9VGW6	DNA replication licensing factor Mcm5 OS=Drosophila melanogaster OX=7227 GN=	9.298520857	9.313347671	9.573323591	9.192515921	7.946720946	9.087135555	8.72099209	8.856628749	9.34442701	8.652869335	0.691557675	1.615026318	0.037593
Q9V461	DNA replication licensing factor Mcm6 OS=Drosophila melanogaster OX=7227 GN=	10.69165629	10.52849757	10.89133582	10.24505738	9.121555325	10.28868949	9.829743308	10.15549693	10.58913677	9.848871265	0.740265503	1.670483234	0.045675
Q9V3V0	DXl6 protein OS=Drosophila melanogaster OX=7227 GN=x16 PE=1 SV=1	7.669593751	7.421027343	7.055384722	7.261126945	6.296059817	7.076650795	6.851306298	6.950843487	7.35178319	6.793715099	0.558068091	1.472296349	0.041271
Q9VHJ3	Enhancer of variegation 3-9 OS=Drosophila melanogaster OX=7227 GN=E(var)3-9	6.708739041	6.661468858	6.726621236	6.480821682	5.640706051	6.338429922	6.340500934	6.341175562	6.644412705	6.165203117	0.479209588	1.393979734	0.040158
C9QP42	Eukaryotic translation initiation factor 4A, isoform E OS=Drosophila melanogaster C	10.65123112	10.57489196	10.83222642	10.47813017	9.825676318	10.37670481	10.19653147	10.41400507	10.63411992	10.20322942	0.430890499	1.348065409	0.031226
Q9XZU1	Exportin-2 OS=Drosophila melanogaster OX=7227 GN=Cse1 PE=2 SV=2	8.273329387	8.393002943	8.606115952	8.296082258	7.623671151	8.168297221	8.11004903	8.018966922	8.392132635	7.980246081	0.411886554	1.330424419	0.02904
Q9VN44	FI07923p OS=Drosophila melanogaster OX=7227 GN=Karybeta3 PE=1 SV=1	8.518062976	8.552162885	8.833057344	8.49218579	7.947753795	8.333947209	8.191272368	8.175075146	8.598867249	8.162012129	0.436855119	1.353650334	0.008088
Q9VZ00	FI19420p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1737 PE=1 SV=	8.479376091	8.329469919	8.527772894	8.389323497	7.796304349	8.286489086	8.134904901	8.26478303	8.4314856	8.120620342	0.310865259	1.24045144	0.04311
Q7K3Z3	GH01724p OS=Drosophila melanogaster OX=7227 GN=p47 PE=1 SV=1	7.725195817	7.665560782	7.674689231	7.441391653	6.655137684	7.172744334	7.458192257	7.332302695	7.626709371	7.154594242	0.472115129	1.38714166	0.045324
Q9VTB3	GH06691p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11811 PE=1 SV	3.263034406	3.26163525	3.075902853	3.119861636	3.602479443	3.391452073	3.638576638	3.510506401	3.180108536	3.535753639	-0.355645102	0.781520108	0.002849
Q9VPL0	GM13767p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3436 PE=1 SV=	7.682994584	7.557060687	7.694503933	7.367181444	6.827644198	7.383627408	7.215899044	7.334312379	7.575435162	7.190370757	0.385064405	1.305918085	0.03973
P48809	Heterogeneous nuclear ribonucleoprotein 27C OS=Drosophila melanogaster OX=7	6.968090752	7.095935583	7.255530956	6.991906226	6.47160866	6.884812764	6.821174933	6.845188874	7.077865879	6.755696308	0.322169572	1.250209241	0.03194
M9MSL3	Hsc70Cb, isoform G OS=Drosophila melanogaster OX=7227 GN=Hsc70Cb PE=1 S	9.930885147	9.828053464	10.06512006	9.638862304	8.881892906	9.591658119	9.466120168	9.531450285	9.865730244	9.36778037	0.497949874	1.412205337	0.037371
P52295	Importin subunit alpha OS=Drosophila melanogaster OX=7227 GN=Pen PE=1 SV=	9.154564982	9.115173588	9.227270173	8.965148761	7.814302677	8.633497875	8.449499035	8.626338585	9.115539376	8.380909543	0.734629833	1.663970473	0.010721
Q9W0I7	IP07275p OS=Drosophila melanogaster OX=7227 GN=Psf1 PE=1 SV=2	8.173427297	8.203102078	8.618432111	7.769592547	6.048875884	7.063864014	6.962254178	7.07829875	8.191138508	6.788323207	1.402815301	2.644170673	0.003548
Q4V3Z5	IP10727p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11788 PE=2 SV=	8.071998581	8.158929884	8.396877002	7.632154753	6.552395163	7.278078484	7.016987276	7.310681543	8.064990055	7.039535616	1.025454438	2.035600483	0.004956
Q9VBP5	Jing interacting gene regulatory 1, isoform A OS=Drosophila melanogaster OX=72	8.663202279	8.657621174	8.95087161	8.4417088	7.527708429	8.27039826	7.989701145	8.137862487	8.678350966	7.981417581	0.696933385	1.621055387	0.0111
A0A0B4KFY9	Lamin C, isoform B OS=Drosophila melanogaster OX=7227 GN=LamC PE=3 SV=1	6.432959407	6.394833366	6.473394523	6.225058484	6.134675092	6.09812893	6.22461941	6.027011745	6.381561445	6.121108794	0.260452651	1.197854477	0.008845
M9NE89	Lamin, isoform B OS=Drosophila melanogaster OX=7227 GN=Lam PE=3 SV=1	11.00133782	10.79283695	10.86461695	10.7909079	10.15468388	10.35885437	10.47327035	10.45881881	10.86242491	10.36140685	0.501018054	1.41521187	0.001306
Q9VPN5	LD03220p OS=Drosophila melanogaster OX=7227 GN=Stip1 PE=1 SV=1	7.38024459	7.397780864	7.554537734	7.147076626	6.646947816	7.137410456	7.146084265	7.000351955	7.369909954	6.982698623	0.387211331	1.307862915	0.035963
Q9VY91	LD21074p OS=Drosophila melanogaster OX=7227 GN=Pdcd4 PE=1 SV=2	8.121015401	8.277527526	8.365549011	8.047730192	7.534763177	7.837562855	7.877917019	8.070119642	8.202955533	7.830090673	0.37286486	1.294921695	0.030406
Q8SX76	LD24646p OS=Drosophila melanogaster OX=7227 GN=pch2 PE=1 SV=1	7.236492618	7.280430679	7.440087484	7.158992517	6.652413312	7.074403021	6.925273502	6.986633597	7.279000825	6.909680858	0.369319967	1.291743807	0.014508
Q9V3E7	LD24793p OS=Drosophila melanogaster OX=7227 GN=Ref1 PE=1 SV=1	7.9795681	7.771312341	7.744398235	7.579442951	6.779764897	7.410833871	7.387025583	7.577307072	7.768680407	7.288732856	0.479947551	1.394692961	0.047509
Q9W3M7	LD32873p OS=Drosophila melanogaster OX=7227 GN=mahe PE=1 SV=1	3.99095486	3.921817984	4.036720102	4.050945185	3.926642925	3.805079751	3.780038828	3.834873526	4.000109533	3.836658757	0.163450776	1.119962771	0.009184
Q9V3P3	LD45860p OS=Drosophila melanogaster OX=7227 GN=REG PE=1 SV=1	9.05853297	8.928811892	8.94271596	8.931659815	7.838053269	8.531314638	8.344932502	8.697046426	8.965430159	8.352836709	0.61259345	1.529005345	0.017527
P42283	Longitudinals lacking protein, isoform G OS=Drosophila melanogaster OX=7227 G	8.52160044	9.218968446	8.596387612	8.313727306	7.467913947	8.316005276	7.962714942	8.023438264	8.662670951	7.942518107	0.720152844	1.647356552	0.033608
Q9VCH5	Nuclear pore complex protein Nup98-Nup96 OS=Drosophila melanogaster OX=72	4.995484519	4.947450631	5.357716487	4.866333145	4.380359396	4.718607912	4.905715084	4.50732004	5.041746195	4.628000608	0.413745587	1.332139888	0.040425
P25007	Peptidyl-prolyl cis-trans isomerase OS=Drosophila melanogaster OX=7227 GN=Cyp	10.08520687	9.907726064	10.15653162	9.93204248	9.277740012	9.629428287	9.476144911	9.734878842	10.02037676	9.529548013	0.490828745	1.40525188	0.005505
A1Z8A6	Pipsqueak, isoform M OS=Drosophila melanogaster OX=7227 GN=psq PE=1 SV=	6.891176125	6.732504828	7.125277701	6.381888745	5.329468581	6.419683341	6.327684163	5.743757578	6.78271185	5.955148416	0.827563434	1.774685565	0.033086
Q9VXE0	Probable small nuclear ribonucleoprotein G OS=Drosophila melanogaster OX=722	5.786596362	5.873205897	5.8380019	5.745988028	4.718279059	5.190156481	5.661359399	5.36452388	5.810948047	5.233579705	0.577368342	1.49212494	0.027479
Q9VI10	Probable small nuclear ribonucleoprotein Sm D2 OS=Drosophila melanogaster OX	8.597680144	8.777100351	8.634580214	8.608933207	7.585839733	8.168297221	8.303224806	8.285403299	8.654573479	8.085691265	0.568882214	1.483373822	0.017171
P18053	Proteasome subunit alpha type-4 OS=Drosophila melanogaster OX=7227 GN=Pro	9.171176798	9.048544111	9.291459227	8.92857485	8.159555237	8.758436007	8.722715046	8.949589628	9.109938747	8.64757398	0.462364767	1.377798361	0.048493
Q9XZJ4	Proteasome subunit alpha type-6 OS=Drosophila melanogaster OX=7227 GN=Pro	9.144913113	9.203931297	9.278809491	8.825094511	8.299621353	8.845804979	8.844969108	8.775157246	9.113187103	8.691388172	0.421798932	1.33959689	0.043324
Q9VNA5	Proteasome subunit beta type-4 OS=Drosophila melanogaster OX=7227 GN=Pros	7.746850183	7.578980157	7.616217647	7.456789695	7.028539328	7.256605104	7.220887266	7.283168764	7.59970942	7.197300116	0.402409305	1.321713334	0.00286
Q8INX3	Protein TIPIN homolog OS=Drosophila melanogaster OX=7227 GN=CG10336 PE=	6.272396509	6.44098441	5.856618751	6.096696193	4.88565004	5.315986095	5.130947033	4.598142102	6.166673966	4.982681318	1.183992648	2.272046952	0.001023
M9PGH6	Regulator of telomere elongation helicase 1 homolog OS=Drosophila melanogaste	6.807354922	6.89275452	7.284618985	6.684455304	5.566876527	6.43176404	6.068657204	6.139886809	6.917295933	6.051796145	0.865499788	1.821970737	0.007935
Q9U9Q1	Replication factor C 38kD subunit, isoform A OS=Drosophila melanogaster OX=72	9.104598754	9.170562902	9.508009761	8.889875693	7.776886718	8.868453208	8.525842518	8.659208303	9.168261777	8.457597687	0.710664091	1.636557272	0.038924
P53034	Replication factor C subunit 2 OS=Drosophila melanogaster OX=7227 GN=RfC4 P	9.587964989	9.571290224	9.851283876	9.163774358	7.998402134	9.309256221	8.733005027	8.972594414	9.543578362	8.753314449	0.790263912	1.729390791	0.044571
Q9VKW3	Replication factor C subunit 3 OS=Drosophila melanogaster OX=7227 GN=RfC3 P	8.773139207	8.72714962	9.027967533	8.422454559	7.403242885	8.419991128	8.018832716	8.250059613	8.73767773	8.023031585	0.714646144	1.641080654	0.030911
Q24492	Replication protein A 70 kDa DNA-binding subunit OS=Drosophila melanogaster O	10.86758763	10.80178855	11.30645916	10.30850884	8.465213992	9.705758887	9.456017395	9.544285783	10.82108605	9.292819014	1.528267032	2.884391572	0.004557
A0A0B4KGW6	Sequence-specific single-stranded DNA-binding protein, isoform D OS=Drosophila	7.438791853	7.453575015	7.558734024	7.450394624	6.547486879	7.027097511	7.05431155	7.315440265	7.475373879	6.986084051	0.489289828	1.403753702	0.023625
Q9W457	Serine hydroxymethyltransferase OS=Drosophila melanogaster OX=7227 GN=Shn	8.737754352	8.823398772	9.071283159	8.823905485	8.265078365	8.664136058	8.491322436	8.685552881	8.864085442	8.526522435	0.337563007	1.26362029	0.031682
P26686	Serine-arginine protein 55 OS=Drosophila melanogaster OX=7227 GN=B52 PE=1	10.29599846	9.663614164	9.526329085	9.627984831	8.498189104	9.189722608	8.987561952	9.317627691	9.778481635	8.998275339	0.780206297	1.71737643	0.020896
Q9VXG8	Serine/threonine-protein kinase ATR OS=Drosophila melanogaster OX=7227 GN=	6.121015401	6.177092026	6.627986839	6.14685159	5.652302466	5.892789161	5.821571126	5.822226803	6.268236464	5.797222389	0.471014075	1.386083408	0.011375
Q9VXV3	Shattered OS=Drosophila melanogaster OX=7227 GN=shtd PE=1 SV=1	4.03562391	3.99378838	4.375450845	4.192477213	3.547667098	4.00525503	3.913965153	3.809135042	4.149335087	3.819005581	0.330329506	1.257300505	0.045792
M9ND86	Spellchecker1, isoform D OS=Drosophila melanogaster OX=7227 GN=spel1 PE=1	10.00351791	9.889844609	10.22678602	9.687929526	8.62187189	9.518923252	9.232071575	9.418335092	9.952019516	9.197800453	0.754219063	1.686718318	0.016925
O46106	Splicing factor 3A subunit 3 OS=Drosophila melanogaster OX=7227 GN=noi PE=1	7.553821257	7.688018072	7.676618896	7.418624967	6.8792428	7.391965389	7.322822781	7.057176691	7.584270798	7.162801915	0.421468883	1.339290462	0.02028

Q8INH7	Timeout OS=Drosophila melanogaster OX=7227 GN=timeout PE=1 SV=2	9.732506644	9.760091135	10.18368509	9.398512128	8.013884148	8.964827169	8.584432652	8.728046139	9.76869875	8.572797527	1.195901223	2.29087894	0.003582
B7Z126	Tousled-like kinase, isoform G OS=Drosophila melanogaster OX=7227 GN=Tlk PE	7.731997787	7.976853153	8.355216969	7.599157729	6.543547203	7.61792591	7.305213982	7.225712852	7.915806409	7.173099987	0.742706422	1.673311944	0.038221
A0A0B4JD97	Transforming acidic coiled-coil protein, isoform K OS=Drosophila melanogaster OX=	2.485426827	2.901662566	2.5475983	2.864278116	2.822194585	3.345724143	3.21438329	3.338877645	2.699741452	3.180294916	-0.480553464	0.716702621	0.025675
A1ZAW6	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG301	6.439623138	6.499797097	6.554914425	6.530252228	5.531534087	6.052808188	6.164239502	6.264736293	6.506146722	6.003329517	0.502817204	1.416977848	0.022586
Q0E8G6	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Cp	8.145167939	8.030934466	7.912411727	7.684559765	7.196462227	7.468165484	7.484463797	7.658472882	7.943268474	7.451891097	0.491377377	1.405786374	0.011588
X2JF73	Uncharacterized protein, isoform H OS=Drosophila melanogaster OX=7227 GN=UF	7.016808288	6.887926398	6.985017494	6.707653933	5.978439484	6.588368733	6.435075455	6.581860465	6.899351528	6.395936034	0.503415494	1.417565594	0.01968
P41073	Zinc finger protein on ecdysone puffs OS=Drosophila melanogaster OX=7227 GN=	10.79010409	10.47051959	10.66495841	10.36049579	9.387711669	10.26051505	10.02329556	10.29010457	10.57151947	9.990406711	0.581112758	1.496002678	0.045314

Supplemental Table 3-3: Unnormalized TMT Intensities for iPOND S2 Cell Replicates

Accession	Description	Sum PEP Score	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	# AAs	MW [kDa]	calc. pI	Score Sequest HT	# Peptides	# Razor Peptides	EdU Pulse R1	EdU Pulse R2	EdU Pulse R3	EdU Pulse R4	Thy Chase R1	Thy Chase R2	Thy Chase R3	Thy Chase R4
A1Z992	1,4-Alpha-Glucan branching enzyme OS=Drosophila melanogaster OX=7227 GN=AGBE PE=1 SV=1	19.66	7	5	5	5	685	79.1	6.25	15.37	5	0	958.6	449.6	729	934.8	377.2	379.8	394.3	459.1
P48375	12 kDa FK506-binding protein OS=Drosophila melanogaster OX=7227 GN=FK506-bp2 PE=3 SV=2	23.337	29	3	8	3	108	11.7	8.13	29.4	3	0	1299.2	566.8	905.1	1254.3	479.3	600.8	453.5	866.7
P92177	14-3-3 protein epsilon OS=Drosophila melanogaster OX=7227 GN=14-3-3epsilon PE=1 SV=2	44.025	29	7	16	6	262	29.8	4.78	48.14	7	0	2478.6	797.6	1499	1816.7	916.1	834.1	775.1	1718.2
P29310	14-3-3 protein zeta OS=Drosophila melanogaster OX=7227 GN=14-3-3zeta PE=1 SV=1	65.513	48	9	18	8	248	28.2	4.88	59.07	9	1	2603	1029.8	1745.4	1949.3	1019.1	983.5	1010.8	1512.3
Q9VFE9	2-(3-amino-3-carboxypropyl)histidine synthase subunit 2 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG	14.963	10	3	3	3	469	52.1	5.25	10.32	3	0	239.9	121.3	249	320.1	129.6	133.2	140.9	212.4
Q9VHB8	2-oxoisovalerate dehydrogenase subunit alpha OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8199 P	38.161	21	7	15	7	439	49.7	6.65	48.67	7	0	837.2	585.2	1529.3	1520.8	408.3	529.5	602.2	1112.7
P23226	205 kDa microtubule-associated protein OS=Drosophila melanogaster OX=7227 GN=Map205 PE=1 SV=2	59.568	15	12	17	12	1185	126.6	4.86	47.45	12	0	1329.8	576.7	1459.9	1282.3	503.3	662.6	855.6	739.4
Q9V3P6	26S proteasome non-ATPase regulatory subunit 1 OS=Drosophila melanogaster OX=7227 GN=Rpn2 PE=1 S	48.021	10	10	11	10	1020	113.1	5.19	33.2	10	0	1796	804.8	1221.2	1405.5	603.5	693.5	681.5	865.7
Q9VW54	26S proteasome non-ATPase regulatory subunit 2 OS=Drosophila melanogaster OX=7227 GN=Rpn1 PE=1 S	24.988	5	3	8	3	919	102.2	5.85	28.5	3	0	190.8	102.1	203.8	256.3	92.4	88	116.4	230
Q9V3G7	26S proteasome non-ATPase regulatory subunit 6 OS=Drosophila melanogaster OX=7227 GN=Rpn7 PE=2 S	23.871	14	6	7	6	389	45.4	6.48	22.8	6	0	903.8	390.4	770.9	932.5	357.7	358.3	355.6	1068.6
P26270	26S proteasome non-ATPase regulatory subunit 7 OS=Drosophila melanogaster OX=7227 GN=Rpn8 PE=1 S	23.462	18	3	4	3	338	38.1	6.71	21.92	3	0	357.3	192	330.2	363.9	157.2	182.7	193.7	230.3
Q9V436	26S proteasome regulatory complex subunit p30 OS=Drosophila melanogaster OX=7227 GN=Rpn12 PE=1 S	15.833	13	3	6	3	264	30.2	6.06	17.99	3	0	180.4	101.5	137.8	152.9	76.2	82.4	92.1	89.4
Q7KMP8	26S proteasome regulatory complex subunit p39A OS=Drosophila melanogaster OX=7227 GN=Rpn9 PE=1 S	4.442	7	2	2	2	382	43.7	5.26	4.68	2	0	10.5	6.1	16.6	16.2	7	10	8.2	13.3
Q9V405	26S proteasome regulatory complex subunit p48A OS=Drosophila melanogaster OX=7227 GN=Rpt3 PE=1 S	5.44	6	2	3	1	413	47	5.38	5.53	2	0	18.7	6.9	19.4	14	8.3	6.2	11.2	14.2
Q7KMQ0	26S proteasome regulatory complex subunit p48B OS=Drosophila melanogaster OX=7227 GN=Rpt1 PE=1 S	31.199	17	6	12	6	433	48.5	6.04	35.04	6	0	599.8	415.3	535.4	878.6	322.5	291.2	310.5	495
Q9V3V6	26S proteasome regulatory complex subunit p50 OS=Drosophila melanogaster OX=7227 GN=Rpt5 PE=1 SV	22.85	21	5	8	5	428	47.8	5.34	19.62	5	0	894.4	579.7	889.6	919	383.3	393.4	446.8	429.6
P48601	26S proteasome regulatory subunit 4 OS=Drosophila melanogaster OX=7227 GN=Rpt2 PE=1 SV=2	20.031	13	5	6	4	439	49.3	6.58	19.14	5	1	501.6	213.4	323.3	439	175.7	167.9	174.1	285.9
O18413	26S proteasome regulatory subunit 8 OS=Drosophila melanogaster OX=7227 GN=Rpt6 PE=1 SV=2	16.29	11	4	4	3	405	45.8	8.41	10.83	4	0	481.1	196.8	314.4	411	189.4	199.8	170.3	378.9
Q9VFB2	28S ribosomal protein S10, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpS10 PE=2 SV=2	24.999	25	4	5	4	173	20	9.42	19.72	4	0	623.1	348.8	847.9	737.7	228.6	309.7	463.8	523.2
Q8WTC1	28S ribosomal protein S15, mitochondrial OS=Drosophila melanogaster OX=7227 GN=bonsai PE=2 SV=2	22.771	15	3	4	3	280	33.5	9.2	14.85	3	0	266.5	148.3	565.8	411	96.2	158	306.6	253.2
Q7K4Q9	3-hydroxy-3-methylglutaryl coenzyme A synthase OS=Drosophila melanogaster OX=7227 GN=Hmgs PE=1 SV	13.425	9	3	4	3	465	51.1	6.32	11.12	3	0	455.8	224.7	361	393.2	212.4	215.8	214.4	238.8
O18404	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Drosophila melanogaster OX=7227 GN=scu PE=1 SV=1	86.326	42	8	29	8	255	26.9	9.03	103.42	8	0	1691.6	843.1	3450.2	3145.1	684	761.7	1358.7	2912.7
A0A0B4JCU8	3-hydroxyisobutyrate dehydrogenase OS=Drosophila melanogaster OX=7227 GN=Dmel\CG15093 PE=1 SV=	42.703	25	4	11	4	324	33.9	8.13	36.73	4	0	381.5	218.4	650.3	628.5	147.9	149.5	281.4	809.6
Q86BP1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=CT16187 PE=	36.387	18	5	24	5	386	42.8	8.35	80.49	5	0	1118.8	629.7	2210.1	1681.7	436.6	578.6	1034	1540.5
Q9VNF5	3-oxoacyl-[acyl-carrier-protein] synthase OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12170 PE=1 S	64.671	23	7	14	7	438	46.4	7.88	61.18	7	0	444.6	229.2	844.5	609.4	148.8	171.5	354.9	392.1
Q9W0F9	312, isoform A OS=Drosophila melanogaster OX=7227 GN=312 PE=1 SV=1	42.642	24	5	14	5	241	28.1	6.01	47.97	5	0	711.9	415.1	1459.3	928.3	236	354.9	649.8	577.1
Q9VFJ2	39S ribosomal protein L11, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpL11 PE=2 SV=1	25.666	12	3	9	3	196	21.6	9.63	32.99	3	0	665.7	441.3	1412.7	1152.6	228	330.7	705.1	598.6
Q9VJ38	39S ribosomal protein L13, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpL13 PE=2 SV=2	17.488	16	2	9	2	178	21.1	8.75	39.3	2	0	135.7	79.3	194.8	181.5	62.2	70.4	98.3	102.4
Q9VHN6	39S ribosomal protein L19, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpL19 PE=2 SV=1	39.392	31	7	23	7	306	36.2	8.82	83.11	7	0	1081.8	559.9	2261.3	2001.7	412.1	491.7	1053.3	1292.6
Q9W021	39S ribosomal protein L23, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpL23 PE=2 SV=1	18.254	20	3	11	3	150	17.9	9.61	33.37	3	0	1148.6	748	2500.1	1473.1	351	619.2	1222.6	846
Q9VMX0	39S ribosomal protein L28, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpL28 PE=2 SV=1	12.914	12	3	3	3	302	34.9	8.95	11	3	0	757.2	290.8	902.5	552.7	219	274.2	429.5	787.3
Q9V9Z1	39S ribosomal protein L32, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpL32 PE=2 SV=1	8.276	15	3	3	3	195	22.6	9.23	5.93	3	0	270.8	165.6	571.5	353.5	78.3	129.2	274.4	224.9
Q9VUJ0	39S ribosomal protein L39, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpL39 PE=2 SV=2	30.488	20	7	13	7	333	37.3	8.62	33.43	7	0	1008.5	455.5	1733.1	1337.1	389.6	488.8	706.8	902.1
Q7JZM8	39S ribosomal protein L41, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpL41 PE=2 SV=1	36.099	30	4	8	4	166	18.6	9.39	39.69	4	0	730.8	425.6	1444.4	878.4	301.7	404.9	735	602.5
Q9VLJ9	39S ribosomal protein L51, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpL51 PE=2 SV=2	13.837	16	2	4	2	174	20.2	10.54	12.96	2	0	252.9	103.9	281.3	282.6	107.3	112.5	153	433.8
Q9VE04	39S ribosomal protein L55, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpL55 PE=1 SV=1	16.514	27	2	4	2	107	12.6	10.18	15.87	2	0	238.2	129.3	512.4	417.9	131.3	190	305.8	504.4
Q9VF89	39S ribosomal protein L9, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpL9 PE=2 SV=1	6.047	8	2	3	2	248	28.8	9.26	8.21	2	0	288.1	218.3	615.5	386.7	106.6	226.7	340.3	246.3
Q0E9B6	40S ribosomal protein S11 OS=Drosophila melanogaster OX=7227 GN=RpS11 PE=1 SV=1	11.447	21	4	6	4	155	18.1	10.93	14.38	4	0	1296.4	469.9	1105.7	1256.5	445.8	548.4	727.9	1162.1
Q03334	40S ribosomal protein S13 OS=Drosophila melanogaster OX=7227 GN=RpS13 PE=1 SV=3	10.017	23	4	5	4	151	17.2	10.55	12.21	4	0	1054.2	377.4	913.7	1182.5	358.7	495.6	537.5	1164.3
C0HKA1	40S ribosomal protein S14b OS=Drosophila melanogaster OX=7227 GN=RpS14b PE=2 SV=1	23.472	17	3	7	3	151	16.3	10.35	22.8	3	0	371	168.1	474.4	469.9	181.6	215.9	247.1	352.8
P48149	40S ribosomal protein S15Aa OS=Drosophila melanogaster OX=7227 GN=RpS15Aa PE=1 SV=2	19.455	46	6	8	6	130	14.8	9.8	19.84	6	0	1702.2	465.7	1321.3	1359.9	604.3	527.1	706.8	2896
P17704	40S ribosomal protein S17 OS=Drosophila melanogaster OX=7227 GN=RpS17 PE=1 SV=2	20.768	35	4	5	4	131	15.3	9.94	16.23	4	0	509.2	223.1	492.8	470.4	198.6	252.7	290.8	273.8
P39018	40S ribosomal protein S19a OS=Drosophila melanogaster OX=7227 GN=RpS19a PE=1 SV=3	8.256	19	3	6	3	156	17.3	10.11	17.11	3	0	863.6	317.9	816.8	876.5	341.5	343.7	414.1	1101.7
P31009	40S ribosomal protein S2 OS=Drosophila melanogaster OX=7227 GN=RpS2 PE=1 SV=2	3.57	5	2	2	2	267	28.9	10.15	3.92	2	0	30.7	18	40.9	50.6	13.3	20.1	25.9	14.6
P55828	40S ribosomal protein S20 OS=Drosophila melanogaster OX=7227 GN=RpS20 PE=1 SV=1	10.106	21	2	26	2	120	13.5	10.33	17.03	2	0	321.2	163.5	396.2	362.4	180.1	189.4	220.1	278
M9PEA6	40S ribosomal protein S21 OS=Drosophila melanogaster OX=7227 GN=RpS21 PE=1 SV=1	23.994	53	4	5	4	83	9.2	5.91	21.47	4	0	851	349	672.6	666.5	358.8	375.8	455	335.3
Q9W229	40S ribosomal protein S24 OS=Drosophila melanogaster OX=7227 GN=RpS24 PE=1 SV=1	8.483	21	2	2	2	131	15	11.22	7.25	2	0	85.7	34.5	66.9	84.2	35.4	31.2	33.8	157.9
P48588	40S ribosomal protein S25 OS=Drosophila melanogaster OX=7227 GN=RpS25 PE=1 SV=3	4.787	14	2	5	2	117	13.2	10.27	10.98	2	0	889.1	298.4	663.2	966.4	328.4	358.4	348.3	928.1
P13008	40S ribosomal protein S26 OS=Drosophila melanogaster OX=7227 GN=RpS26 PE=1 SV=1	17.41	21	2	7	2	114	13.3	11.15	20.36	2	0	955.3	281.6	674.1	625.4	315.9	412.3	418.9	912.3
Q06559	40S ribosomal protein S3 OS=Drosophila melanogaster OX=7227 GN=RpS3 PE=1 SV=1	48.274	40	9	15	9	246	27.5	9.39	54.85	9	0	2081.1	660.4	1704.3	1708.8	690.3	818.6	980.9	2096.9
P55830	40S ribosomal protein S3a OS=Drosophila melanogaster OX=7227 GN=RpS3A PE=1 SV=4	62.35	38	11	29	11	268	30.3	9.61	105.07	11	0	2857.2	1000.5	2609.1	2745.8	873.7	1300.6	1671.6	2444.2
P41042	40S ribosomal protein S4 OS=Drosophila melanogaster OX=7227 GN=RpS4 PE=1 SV=2	19.134	27	8	11	8	261	29.1	10.18	25.12	8	0	1543.9	540	1225.8	1264.7	540.7	662	787.4	1215.7
Q24186	40S ribosomal protein S5a OS=Drosophila melanogaster OX=7227 GN=RpS5a PE=1 SV=1	10.884	12	2	3	2	228	25.4	8.63	9.26	2	0	229.8	89.9	191.8	227	68.2	96.9	113.8	255.6
P29327	40S ribosomal protein S6 OS=Drosophila melanogaster OX=7227 GN=RpS6 PE=1 SV=1	23.48	15	4	11	4	248	28.4	10.74	35.21	4	0	1812.1	675.6	1524.9	1078.2	581.8	881.2	1185.1	653.2
Q9VA91	40S ribosomal protein S7 OS=Drosophila melanogaster OX=7227 GN=RpS7 PE=1 SV=1	15.503	29	5	14	5	194	22.2	9.8	28.58	5	0	1378.7	592.3	1196.5	970.2	445.3	736.4	758.5	551.5
A0A0B4K6N1	40S ribosomal protein S8 OS=Drosophila melanogaster OX=7227 GN=RpS8 PE=3 SV=1	49.376	34	7	18	7	208	23.7	10.48	56.92	7	0	2331.4	701.8	1543.3	1484	797	1019.1	1012.8	1020.5
P38979	40S ribosomal protein SA OS=Drosophila melanogaster OX=7227 GN=sta PE=1 SV=3	74.681	43	7	25	7	270	30.2	4.87	93.28	7	0	752.2	334.2	878.3	872.2	281.1	368.5	449.2	567.7
M9PEY6	5'-3' exoribonuclease OS=Drosophila melanogaster OX=7227 GN=Rat1 PE=1 SV=1	20.496	5	4	4	4	908	103.9	7.05	13.94	4	0	426.2	191.1	177.5	237.8	197.6	152.1	116.8	124
P19889	60S acidic ribosomal protein P0 OS=Drosophila melanogaster OX=7227 GN=RpLP0 PE=1 SV=1	4.221	5	2	2	2	317	34.2	6.95	2.13	2	0	168.9	49	144.7	186.3	64.8	52.3	72.7	591.9
Q9VTP4	60S ribosomal protein L10a-2 OS=Drosophila melanogaster OX=7227 GN=RpL10Ab PE=1 SV=2	21.144	13	2	9	2	217	24.3	9.86	30.82	2	0	1481.8	498	1161	863.9	509.3	628.7	790.5	774.9
P41126	60S ribosomal protein L13 OS=Drosophila melanogaster OX=7227 GN=RpL13 PE=1 SV=1	15.733	17	4	5	4	218	24.9	10.99	15.7	4	0	669.6	228.2	587.9	453.7	153	320.1	469.5	409.4
Q9VNE9	60S ribosomal protein L13a OS=Drosophila melanogaster OX=7227 GN=RpL13A PE=1 SV=1	3.63	6	2	13	2	205	23.6	11.03	2.07	2	0	465.2	172.7	338.2	352.4	180.3	168.7	192.8	278.1
P55841	60S ribosomal protein L14 OS=Drosophila melanogaster OX=7227 GN=RpL14 PE=1 SV=1	20.111	19	3	8	3	166	19.2	11.18	27.53	3	0	1009.5	238.4	767.5	836.2	339.1	331.5	385.9	1240.1
O17445	60S ribosomal protein L15 OS=Drosophila melanogaster OX=7227 GN=RpL15 PE=1 SV=1	6.669	13	3	4	3	204	24.3	11.47	10.63	3	0	513.4	188.8	425.1	517.4	174.8	235.4	302.1	309.9
Q9W3W8	60S ribosomal protein L17 OS=Drosophila melanogaster OX=7227 GN=RpL17 PE=1 SV=1	7.14	9	2	3	2	186	21.6	10.3	8.95	2	0	414.7	122	303.3	358.5	145.2	161.9	191.9	1069.2
Q9VS34	60S ribosomal protein L18 OS=Drosophila melanogaster OX=7227 GN=RpL18 PE=1 SV=1	13.506	22	3	9	3	188	21.7	11.53	24.83	3	0	1265.5	434.9	1258.1	1279.5	608.5	690.3	802.9	1708.3
P41093	60S ribosomal protein L18a OS=Drosophila melanogaster OX=7227 GN=RpL18A PE=1 SV=1	26.832	23	5	8	5	177	21	10.62	25.66	5	0	1571.9	427.8	1244.9	1264.4	552.7	581.4	715.9	1745.9
P36241	60S ribosomal protein L19 OS=Drosophila melanogaster OX=7227 GN=RpL19 PE=1 SV=2	23.243	17	4	10	4	203	24	11	26.88	4	0	1241.1	461.1	1298.9	1569.3	475.6	594.2	841.8	1082.4
P50887	60S ribosomal protein L22 OS=Drosophila melanogaster OX=7227 GN=RpL22 PE=1 SV=2	13.761	8	2	6	2	299	30.6	10.11	18.38	2	0	923.2	326	772.9	910.6	335.8	437.2	489.6	589.5
P48159	60S ribosomal protein L23 OS=Drosophila melanogaster OX=7227 GN=RpL23 PE=1 SV=2	5.805	18	3	3	3	140	14.9	10.83	6.51	3	0	221.1	101.3	275.4	288.1	75.4	115.3	150.5	115.9
Q9VZS5	60S ribosomal protein L28 OS=Drosophila melanogaster OX=7227 GN=RpL28 PE=1 SV=1	4.738	6	2	2	2	144	16	11.09	6.25	2	0	231.2	95.5	277.6	330.7	93.6	80	145.3	393.9
O16797	60S ribosomal protein L3 OS=Drosophila melanogaster OX=7227 GN=RpL3 PE=1 SV=3	26.537	9	4	6	4	416	46.9	10.24	19.41	4	0	1046.6	307	735.6	599.6	383.1	435.7	589.2	440.2
Q9V597	60S ribosomal protein L31 OS=Drosophila melanogaster OX=7227 GN=RpL31 PE=1 SV=1	7.764	17	2	15	2	124	14.5	10.2	28.42	2	0	765.5	322.5	686	783.6	332.2	394.6	421.7	500.5
P09180	60S ribosomal protein L4 OS=Drosophila melanogaster OX=7227 GN=RpL4 PE=1 SV=2	23.794	14	5	22	5	401	45	11.47	49.03	5	0	1080.5	388.7	1160.1	1326.7	362.2	491.7	756.9	1413.6
Q9W5R8	60S ribosomal protein L5 OS=Drosophila melanogaster OX=7227 GN=RpL5 PE=1 SV=2	17.972	12	4	5	4	299	34	9.77	16.1	4	0	1238.4	391.5	818.1	765.1	419.9	422.7	575.4	594.8
Q9V3G1	60S ribosomal protein L8 OS=Drosophila melanogaster OX=7227 GN=RpL8 PE=1 SV=1	15.318	11	4	5	4	256	27.9	11.15	13.53	4	0	572.5	200.3	521.1	648.9	206.5	264.8	342.1	546.4
Q9VLL3	A-kinase anchor protein 200 OS=Drosophila melanogaster OX=7227 GN=Akap200 PE=1 SV=3	40.452	13	6	12	6	753	79	4.16	45.62	6	0	1136.7	719.3	2556.4	1552.4	401.1	587.4	1291.2	776
Q9W133	AarF domain containing kinase, isoform A OS=Drosophila melanogaster OX=7227 GN=Adck PE=1 SV=2	7.703	5	2	2	2	518	59.8	9.16	5.98	2	0	104.1	60.8	166.6	144.9	47.4	67.7	104	66.8
A1Z7K8	AaRS-interacting multifunctional protein 1 OS=Drosophila melanogaster OX=7227 GN=AIMP1 PE=1 SV=1	16.033	10	2	6	2	323	34.4	8.91	25.95	2	0	215.4	103.1	262.4	247.6	71.4	103.4	153.5	100.2
Q8T060	AaRS-interacting multifunctional protein 2, isoform B OS=Drosophila melanogaster OX=7227 GN=AIMP2 PE=	4.459	5	2	2	2	301	33.2	8.62	4.19	2	0	281	113.7	291.5	289.5	98.1	117.3	176.6	186.2
A0A0B4KH51	Abelson interacting protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Abi PE=1 SV=1	8.586	6	2	2	2	472	51.8	6.93	7.24	2	0	33.6	15.8	41.2	45.5	16.2	18.9	22.9	18.5
A1Z784	Acetyl-CoA carboxylase, isoform A OS=Drosophila melanogaster OX=7227 GN=ACC PE=1 SV=1	370.614	27	49	104	49	2482	278.4	6.24	380.69	49	0	7872	5065.4	8402.2	9029.1	3096.2	4886.5	3689	7886.1
Q9VJ12	Acinus, isoform A OS=Drosophila melanogaster OX=7227 GN=Acn PE=1 SV=1	21.901	7	4	5	4	739	83.7	6.7	16.14	4	0	1201.9	426.5	540.7	641.1	473.9	418.2	341.1	480.6
Q9VIE8	Aconitate hydratase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mAcon1 PE=1 SV=2	117.92	21	14	73	14	787	85.3	8.24	213.07	14	0	3869.4	2374.1	7794.4	6952.3	1466.5	1996.7	3510.2	5223.1
P02572	Actin-42A OS=Drosophila melanogaster OX=7227 GN=Act42A PE=1 SV=3	114.072	32	10	66	1	376	41.8	5.48	207.97	10	12	11381.3	4739.2	9951.9	10299.1	4379.5	5458.3	5334.5	7774.5
P10987	Actin-5C OS=Drosophila melanogaster OX=7227 GN=Act5C PE=1 SV=4	114.373	32	10	67	1	376	41.8	5.48	209.69	10	0	295.1	132.1	261.2	343.1	118.8	123	129.7	135.1
Q9VU68	Actin-interacting protein 1 OS=Drosophila melanogaster OX=7227 GN=flr PE=2 SV=1	17.76	12	6	7	6	608	66.5	6.73	15.64	6	0	963.7	534	1073.5	1381.6	368.4	486.1	552.7	640.7
P45889	Actin-related protein 1 OS=Drosophila melanogaster OX=7227 GN=Arp1 PE=2 SV=2	12.398	10	5	6	5	376	42.7	7.3	13.16	5	0	1203.7	524.1	1181.8	1243.1	373	544.8	718.9	683.4
P45888	Actin-related protein 2 OS=Drosophila melanogaster OX=7227 GN=Arp2 PE=2 SV=3	13.161	10	3	6	3	399	45.3	6.02	18.18	3	0	299.3	104	324.1	398.6	128.7	74.2	138.6	2385.9
Q9VF28	Actin-related protein 2/3 complex subunit 3 OS=Drosophila melanogaster OX=7227 GN=Arpc3A PE=1 SV=4	13.878	16	2	3	2	177	20.2	9.07	9.03	2	0	114.8	42.7	102	125.8	45.3	66.4	58.1	72.3
Q9VMH2	Actin-related protein 2/3 complex subunit 4 OS=Drosophila melanogaster OX=7227 GN=Arpc4 PE=1 SV=1	12.865	18	3	5	3	168	19.6	8.46	13.11	3	0	312.9	146	364.4	435.9	145.4	116.1	152.1	218.6
O97182	Actin-related protein 2/3 complex subunit OS=Drosophila melanogaster OX=7227 GN=Arpc1 PE=1 SV=1	15.064	10	3	3	3	377	41.6	8.35	11.63	3	0	278.7	96.9	282.5	394.2	88	106.3	149.8	232
P32392	Actin-related protein 3 OS=Drosophila melanogaster OX=7227 GN=Arp3 PE=2 SV=3	14.379	8	3	5	3	418	47	5.99	15.28	3	0	546.2	264.3	719.4	972	241.7	269.9	383.7	429.9
Q7KSM5	Activator of SUMO 1 OS=Drosophila melanogaster OX=7227 GN=Aos1 PE=1 SV=1	45.128	19	5	11	5	337	37.7	5.44	42.16	5	0	445.4	226	280.2	301.7	186.9	192.6	130.8	150.4
M9PDU4	Acyl carrier protein OS=Drosophila melanogaster OX=7227 GN=ND-ACP PE=1 SV=1	3.037	9	2	4	2	181	20.6	8.7	8.3	2	0	490.6	196.4	862.5	561.5	199.6	201.2	359	1345.5
A1Z7H3	Acyl-CoA synthetase long-chain, isoform C OS=Drosophila melanogaster OX=7227 GN=Acsl PE=1 SV=1	37.202	14	9	13	9	707	79.4	8.44	37.99	9	0	1806.9	895.2	2994.8	3065.4	495.4	801.7	1430.6	1750
Q9VIX4	Acyl-coenzyme A oxidase OS=Drosophila melanogaster OX=7227 GN=Dmel\CG17544 PE=1 SV=2	3.929	3	2	2	2	693	77.2	7.03	1.95	2	0	229.6	97.8	288.8	280.8	91.9	111.7	146.6	165.3
O62530	Adaptor protein complex 2, mu subunit, isoform A OS=Drosophila melanogaster OX=7227 GN=AP-2mu PE=1	5.634	6	2	2	2	437	49.8	9.48	6.2	2	0	132.5	64.7	124.1	163.4	52	63.8	64.7	71
A1Z8R2	ADD domain-containing protein 1, isoform A OS=Drosophila melanogaster OX=7227 GN=ADD1 PE=1 SV=1	11.77	3	3	3	3	1199	130.9	5.43	9.3	3	0	276.1	146.7	162.1	194.8	119	178.7	114.3	110.1
X2JF40	Adenosylhomocysteinase OS=Drosophila melanogaster OX=7227 GN=Ahcy PE=3 SV=1	26.243	15	4	8	4	432	47.3	6.2	26.16	4	0	705	226.7	431.2	432.7	234.1	266.8	206.2	489.9
Q9U915	Adenylate kinase OS=Drosophila melanogaster OX=7227 GN=Adk2 PE=1 SV=1	56.372	38	11	35	11	240	26.5	7.88	97.68	11	0	2393.8	1168.6	4671	3312.6	856.6	995.6	2119.6	2971
Q9Y0Y2	Adenylosuccinate synthetase OS=Drosophila melanogaster OX=7227 GN=AdSS PE=2 SV=1	10.465	10	3	3	3	447	48.9	6.84	6.88	3	0	59.7	34.7	43.2	58	25.8	33.1	26.3	24.3
Q9VPX7	Adenylyl cyclase-associated protein OS=Drosophila melanogaster OX=7227 GN=capt PE=1 SV=2	8.69	7	3	3	3	424	45.6	7.06	7.06	3	0	330.7	160.5	326.7	381.5	143.7	164.9	186.6	158.9
M9PCK7	Adenylyltransferase and sulfurtransferase MOCS3 homolog OS=Drosophila melanogaster OX=7227 GN=Uba	5.127	4	2	2	2	453	50.2	5.88	5.16	2	0	262.6	95.6	163.4	141	97	119.3	93.2	80.7
Q9VHV5	ADP-ribosylation factor-like protein 8 OS=Drosophila melanogaster OX=7227 GN=Gie PE=1 SV=1	12.834	12	2	3	2	186	21.2	7.21	8.37	2	0	43.7	33.7	130.9	153.6	17.6	35.2	65.6	77.8
Q26365	ADP,ATP carrier protein OS=Drosophila melanogaster OX=7227 GN=sesB PE=2 SV=4	40.746	33	12	57	12	312	34.2	9.8	150.16	12	0	3642.3	1864.1	8840.8	7754.8	1364.2	1543.4	3602.3	10704.7
Q9VLM8	Alanine--tRNA ligase, cytoplasmic OS=Drosophila melanogaster OX=7227 GN=AlaRS PE=2 SV=1	20.004	8	5	7	5	966	107.7	6.13	19.78	5	0	482.2	182.6	462.9	374.4	172	174.6	237	241.4
Q9VRJ1	Alanine--tRNA ligase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=AlaRS-m PE=2 SV=1	29.801	6	4	6	4	1012	113	6.62	14.97	4	0	150.9	97.6	295.4	266.8	68.1	127.1	160	157.1
Q9VLC5	Aldehyde dehydrogenase OS=Drosophila melanogaster OX=7227 GN=Aldh PE=1 SV=1	111.628	25	11	108	11	520	57	6.8	331	11	0	6817.1	4381.7	16204.7	12266.6	2990.8	3750.5	7272.8	8291.6
A0A0B4KEL0	Aldehyde dehydrogenase OS=Drosophila melanogaster OX=7227 GN=Aldh-III PE=1 SV=1	18.62	12	6	9	6	498	55.8	8.07	26.75	6	0	591.1	386.2	1457.6	1123.8	201.2	339.1	630.8	1301.2
Q9VB05	ALG-2 interacting protein X OS=Drosophila melanogaster OX=7227 GN=ALiX PE=1 SV=1	9.974	3	2	2	2	836	92.5	5.45	5.25	2	0	272.1	111.4	263.1	247.3	105.6	99.2	135.1	122.2
M9PGV6	Alpha spectrin, isoform B OS=Drosophila melanogaster OX=7227 GN=alpha-Spec PE=4 SV=1	132.092	12	22	32	22	2457	282.4	5.2	111.67	22	0	3460.6	1396.8	3682.8	3797.9	1274.9	1538.2	2107.9	2678.2
Q23983	Alpha-soluble NSF attachment protein OS=Drosophila melanogaster OX=7227 GN=alphaSnap PE=1 SV=1	4.964	7	2	2	2	292	33	5.45	5.14	2	0	389.5	135.6	245.5	264.2	132.8	112.9	120.5	188
Q9VAK1	Alphabet, isoform A OS=Drosophila melanogaster OX=7227 GN=alph PE=1 SV=1	11.267	9	4	5	4	368	40.9	5.3	11.28	4	0	1590.6	717.3	1244.4	1392.3	587.8	627.2	639.3	672.7
Q9VEH0	Aluminum tubes, isoform A OS=Drosophila melanogaster OX=7227 GN=alt PE=1 SV=1	58.737	16	10	14	10	842	95	7.09	57.23	10	0	840.1	410.3	1384.3	1224.8	335.8	470.1	809.5	732.9
Q27601	Amidophosphoribosyltransferase OS=Drosophila melanogaster OX=7227 GN=Prat PE=1 SV=2	11.2	7	2	2	2	546	59.5	6.67	5.94	2	0	121.8	58.8	101.9	127.9	45.9	57.1	59.6	54.7
X2JEY5	AMP deaminase OS=Drosophila melanogaster OX=7227 GN=AMPdeam PE=1 SV=1	14.197	4	2	2	2	798	91.5	6.1	6.86	2	0	262.7	109.4	286.7	287.5	98.7	102.8	127.6	139
Q9V3Y2	Anamorsin homolog OS=Drosophila melanogaster OX=7227 GN=CIAPIN1 PE=2 SV=1	13.503	13	2	2	2	248	27.1	5.21	7.09	2	0	336.4	139.6	195	146.3	125.7	125	121.1	92.6

Q9V4P1	Anillin OS=Drosophila melanogaster OX=7227 GN=scra PE=1 SV=3	9.2	3	3	3	3	1239	135.9	6.24	6.92	3	0	248.6	88.6	178.1	161.3	93.4	91.7	104.6	106.5
P22465	Annexin B10 OS=Drosophila melanogaster OX=7227 GN=AnxB10 PE=2 SV=3	20.276	8	2	5	2	321	35.7	4.74	21.79	2	0	287	151.9	373.2	349.1	116.1	139.9	143.9	172.9
A0A0B4KH34	Annexin OS=Drosophila melanogaster OX=7227 GN=AnxB9 PE=1 SV=1	35.701	31	10	18	10	324	35.9	5.06	44.12	10	0	1329.2	443.9	1490.1	1133.7	475	394.5	654.7	2034.4
O16043	Anon1A4 OS=Drosophila melanogaster OX=7227 GN=Df31 PE=1 SV=1	21.714	22	4	4	4	183	18.8	4.27	14.8	4	0	1507.6	605.8	392.2	365.1	432.9	425	231.3	338.2
Q9VN55	Antimeros, isoform A OS=Drosophila melanogaster OX=7227 GN=atms PE=1 SV=1	12.054	9	4	4	4	538	60.8	9.29	10.59	4	0	1218.8	574.1	626.2	799.7	497.6	608.5	392.6	538
Q24253	AP complex subunit beta OS=Drosophila melanogaster OX=7227 GN=AP-1-2beta PE=1 SV=1	7.664	3	2	2	2	921	101.1	5.11	5.89	2	0	206.9	99.6	296.2	387.6	86.2	107.5	139.9	235.9
Q7KVR8	AP-1 complex subunit gamma OS=Drosophila melanogaster OX=7227 GN=AP-1gamma PE=1 SV=1	8.851	5	4	4	4	982	106.9	5.68	7.26	4	0	177.9	88.6	252	335.5	81.1	104.8	128.1	213.7
P91926	AP-2 complex subunit alpha OS=Drosophila melanogaster OX=7227 GN=AP-2alpha PE=1 SV=1	12.556	4	3	4	3	940	105.6	7.18	12.16	3	0	538.6	223.8	640.8	528.7	214.4	226.4	337.4	516
M9PBQ4	Apoptosis inducing factor, isoform C OS=Drosophila melanogaster OX=7227 GN=AIF PE=1 SV=1	68.146	17	11	23	11	738	81.1	6.2	78.8	11	0	1377	804	3303.2	2619.5	502.8	664.7	1498.3	1929.8
Q9V431	Apoptosis inhibitor 5 homolog OS=Drosophila melanogaster OX=7227 GN=Aac11 PE=2 SV=1	20.988	11	4	4	4	536	59.9	6.76	18.41	4	0	950.5	294.8	497	591.8	334.2	282.7	270.2	681.6
Q9VDT1	Arc42 OS=Drosophila melanogaster OX=7227 GN=Arc42 PE=1 SV=1	53.806	21	6	28	6	405	43.6	7.88	78.74	6	0	2809.5	1433.2	5479.3	4879.1	979.4	1110.6	2275.1	2792
Q9VGW7	Arginine methyltransferase 1 OS=Drosophila melanogaster OX=7227 GN=Art1 PE=1 SV=1	11.153	9	3	7	3	376	42.8	5.15	18.46	3	0	1125.8	403.8	490.1	510.7	413.4	391.2	260.1	254.8
Q8SXK2	Arginyl-tRNA synthetase, mitochondrial, isoform A OS=Drosophila melanogaster OX=7227 GN=ArgRS-m PE=	11.031	7	4	4	4	594	68.3	8.28	9.96	4	0	229.1	127.4	482.5	420.6	81.5	99.3	204.4	310.9
Q9VPU7	Arouser, isoform C OS=Drosophila melanogaster OX=7227 GN=aru PE=1 SV=1	7.436	3	2	2	2	778	85.1	6.54	5.18	2	0	79.9	41.9	129.1	123.3	312	33.7	134.5	101.2
X2JAI2	Arp2/3 complex 34 kDa subunit OS=Drosophila melanogaster OX=7227 GN=Arpc2 PE=3 SV=1	6.211	6	2	2	2	301	35.1	7.91	4.98	2	0	219.3	70.5	170.1	237.1	67.7	83.1	91.5	163.4
A0A0B4KEI5	Arsenic resistance protein 2, isoform E OS=Drosophila melanogaster OX=7227 GN=Ars2 PE=1 SV=1	28.236	7	8	8	8	935	106.2	5.59	19.81	8	0	1673	606.3	756.1	921.8	679.4	626.4	466.8	846.3
Q9V434	Asparaginyl-tRNA synthetase, isoform A OS=Drosophila melanogaster OX=7227 GN=AsnRS PE=1 SV=1	58.443	25	8	15	8	558	63.9	5.96	52.7	8	0	654.2	324.1	980.5	1062.5	356.6	325.9	529.2	611.1
Q9VQ61	Aspartate aminotransferase OS=Drosophila melanogaster OX=7227 GN=Got2 PE=1 SV=1	100.195	22	8	52	8	424	47.2	8.78	174.75	8	0	1450.2	798.1	2718.8	2169.7	585.7	644.9	1100.7	1489.9
Q7K0E6	Aspartyl-tRNA synthetase, isoform A OS=Drosophila melanogaster OX=7227 GN=AspRS PE=1 SV=1	62.193	16	5	14	5	531	59	6.81	57.24	5	0	689.3	312.1	908.9	868.6	302.6	350.3	434.4	643
Q9VJH2	Aspartyl-tRNA synthetase, mitochondrial, isoform A OS=Drosophila melanogaster OX=7227 GN=AspRS-m PE	88.17	15	13	24	13	1082	121.4	5.82	93.62	13	0	3606.6	1665.1	4222.3	3639	1314.1	2012.4	2044	2410.5
A0A0B4KF31	Asrij, isoform B OS=Drosophila melanogaster OX=7227 GN=asrij PE=4 SV=1	42.467	24	4	11	4	258	28.7	6.43	41.33	4	0	279.7	151.2	603.9	514.2	68.8	116.9	299.4	307.1
Q7K3V6	AT01345p OS=Drosophila melanogaster OX=7227 GN=mEFTu2 PE=1 SV=1	58.296	20	7	17	7	456	49.6	7.69	55.3	7	0	596.5	286	910.2	838.8	272.1	311.4	428.9	793.9
Q6AWD5	AT02057p OS=Drosophila melanogaster OX=7227 GN=FCHo PE=1 SV=1	17.132	5	3	3	3	1220	129.8	8.32	10.09	3	0	284.6	133.5	270.2	278.5	109.3	139.5	165.1	206.8
Q9VV75	AT02348p OS=Drosophila melanogaster OX=7227 GN=UQCR-C2 PE=1 SV=1	145.833	45	15	56	15	440	45.4	9.44	234.26	15	0	3148.8	1763.4	9698.3	7571.7	1241.6	1510.9	3785.1	7966.5
Q9VYD9	AT04676p OS=Drosophila melanogaster OX=7227 GN=ALT PE=1 SV=3	51.066	16	8	21	8	575	64	9.1	62.04	8	0	1408.2	628	2160.6	1702.8	585.6	634.7	893.8	2379.8
A8JV22	AT08049p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1440 PE=1 SV=1	17.232	9	4	4	4	511	57.7	6.24	12.47	4	0	458.8	222.2	656.2	683.9	171.2	189.9	261.6	529.3
Q9VL10	AT10584p OS=Drosophila melanogaster OX=7227 GN=Mulk PE=1 SV=2	9.017	11	2	2	2	408	45.7	8.37	3.66	2	0	25.9	15.7	38	19	13.8	23.1	14.8	18.7
Q9VJZ4	AT12494p OS=Drosophila melanogaster OX=7227 GN=ND-B22 PE=1 SV=1	18.843	25	5	10	5	144	17.4	9.5	30.13	5	0	866.8	476.3	1652.9	1426.5	368.5	462.1	775	1423.3
Q9VXF9	AT13091p OS=Drosophila melanogaster OX=7227 GN=mgo PE=1 SV=1	57.357	25	7	10	7	458	50.5	5.16	39.85	7	0	654.1	292.6	421.4	535.3	298.9	355	314.7	365
Q9VVH5	AT13736p OS=Drosophila melanogaster OX=7227 GN=UQCR-Q PE=1 SV=1	6.36	19	3	7	3	89	10.1	10.08	5.68	3	0	686.7	388.8	1844.7	1031.3	188.3	288	834.7	519.2
Q9VMX4	AT19154p OS=Drosophila melanogaster OX=7227 GN=Scox PE=1 SV=1	23.352	18	3	7	3	251	28.2	8.28	26.26	3	0	504.7	303.7	1375.4	1127.1	173	253.2	569.4	697
Q8T8W3	AT21416p OS=Drosophila melanogaster OX=7227 GN=Past1 PE=1 SV=1	28.682	12	8	12	8	540	61.5	6.42	34.35	8	0	847.9	388.2	769.8	733.2	322.4	417.5	408.7	452.4
Q9VFT4	AT27578p OS=Drosophila melanogaster OX=7227 GN=rin PE=1 SV=1	22.624	7	5	9	5	690	74.9	7.37	24.64	5	0	1046.8	505.7	1397.3	1273.3	397.4	551.6	727.3	540.9
Q9VGH5	AT27789p OS=Drosophila melanogaster OX=7227 GN=glo PE=1 SV=1	41.163	14	7	14	7	586	61.4	6.04	51.76	7	0	3412.4	1213.5	1626.7	1629.5	1339.6	1151.5	919.1	1124.3
Q8T3V6	AT29239p OS=Drosophila melanogaster OX=7227 GN=mRpL47 PE=1 SV=1	14.529	9	4	4	4	271	31.7	9.89	11.67	4	0	326.6	139.7	539.9	546.1	121.3	158.1	262.6	411.4
A0A0B4LH64	Ataxin-2, isoform D OS=Drosophila melanogaster OX=7227 GN=Atx2 PE=4 SV=1	14.347	3	3	5	3	1023	111.3	8.03	15.04	3	0	563.3	255.1	702.3	829.6	268.4	284	367	553.3
Q7KVB1	ATP binding cassette subfamily B member 7, isoform B OS=Drosophila melanogaster OX=7227 GN=ABCB7 F	53.928	16	7	15	7	709	76.7	9.26	52.48	7	0	636.7	335.4	1504.9	1113.4	227.6	311.2	653.2	779.9
P35381	ATP synthase subunit alpha, mitochondrial OS=Drosophila melanogaster OX=7227 GN=blw PE=1 SV=2	215.294	43	23	193	23	552	59.4	9.01	541.98	23	0	9041.2	4970.8	22908.5	19806.7	4150.8	4113	11014.3	14600.4
Q94516	ATP synthase subunit b, mitochondrial OS=Drosophila melanogaster OX=7227 GN=ATPsynB PE=2 SV=2	45.51	31	8	17	8	243	27.3	8.72	52.52	8	0	839.1	477.6	2466.8	2177.9	273.5	386.4	1279.6	2153.3
Q05825	ATP synthase subunit beta, mitochondrial OS=Drosophila melanogaster OX=7227 GN=ATPsynbeta PE=1 SV	261.632	51	17	186	17	505	54.1	5.27	654.48	17	0	4947.3	2603.8	12418.2	10314.2	2209.1	2544.9	5164.3	9514.4
A0A0B4LHL7	ATP synthase subunit d, mitochondrial OS=Drosophila melanogaster OX=7227 GN=ATPsynD PE=3 SV=1	39.711	37	6	26	6	178	20.2	6.55	76.44	6	0	2667.9	1468.3	7315.6	4438.7	1039.6	1311.1	3493.6	2906.4
O01666	ATP synthase subunit gamma, mitochondrial OS=Drosophila melanogaster OX=7227 GN=ATPsyngamma PE	60.263	35	10	116	10	297	32.9	9.22	219.72	10	0	2976.4	1950.5	6347.2	4993.7	1899.7	2253	4014.1	5849.3
Q24439	ATP synthase subunit O, mitochondrial OS=Drosophila melanogaster OX=7227 GN=ATPsynO PE=2 SV=2	14.835	18	4	6	4	209	22.4	9.63	16.26	4	0	311.8	172.2	871.3	668.7	118.5	127	365.7	2227.6
D1Z3A2	ATP synthase-coupling factor 6, mitochondrial OS=Drosophila melanogaster OX=7227 GN=ATPsynCF6 PE=	8.155	18	2	4	2	106	11.9	9.04	10.3	2	0	108	71.8	348.4	410.6	36.6	43.1	155.9	354.7
Q9W2X6	ATP synthase, delta subunit, isoform A OS=Drosophila melanogaster OX=7227 GN=ATPsyndelta PE=1 SV=	68.838	47	5	44	5	157	16.7	5.99	190.09	5	0	1163.8	833.9	3208.2	1991.8	495.7	575	1243.1	1605.9
Q6NN09	ATP synthase, subunit C, isoform A OS=Drosophila melanogaster OX=7227 GN=ATPsynC PE=2 SV=1	4.706	12	2	6	2	138	14.4	10.27	13.79	2	0	936.3	630.5	3282.7	2117	221.9	507.9	1527.4	974.6
Q9VKM3	ATP synthase, subunit G, isoform A OS=Drosophila melanogaster OX=7227 GN=ATPsynG PE=1 SV=1	4.751	22	2	4	2	99	10.9	9.76	7.34	2	0	22.4	14.7	65.4	65.7	4.4	10.7	22.6	54.4
Q7KN85	ATP-citrate synthase OS=Drosophila melanogaster OX=7227 GN=ATPCL PE=1 SV=1	43.813	6	6	14	6	1112	121.3	7.31	55.29	6	0	1186.3	555.1	964.3	962.4	482.9	591.9	584.4	756.5
Q9VVW8	ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Drosophila melanogaster OX=7227 GN=CG10424 PE	18.273	14	3	5	3	300	32.1	7.44	14.77	3	0	215.8	99.3	338.2	280.1	83.9	69.9	139.7	299.5
Q9V9T4	ATP-dependent chromatin assembly factor large subunit OS=Drosophila melanogaster OX=7227 GN=Acf PE	15.945	3	5	7	5	1476	170.3	6.87	18.43	5	0	1731.7	841.3	818.2	955.7	683.2	558.9	376.9	410.7
Q9VKY3	ATP-dependent Clp protease proteolytic subunit OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5045 I	8.455	10	4	10	4	253	27.6	7.8	25.28	4	0	1162.2	473.8	2298.4	2050.1	419.5	362.9	846	1999.5
P25439	ATP-dependent helicase brm OS=Drosophila melanogaster OX=7227 GN=brm PE=1 SV=2	30.285	7	10	12	10	1638	185	7.56	31.67	10	0	1532.5	604.8	899.8	889.7	586.1	498.1	517.9	556.8
Q9VHP0	ATP-dependent RNA helicase bel OS=Drosophila melanogaster OX=7227 GN=bel PE=1 SV=1	87.495	18	10	26	9	798	85	7.53	97.5	10	0	1620.9	719.5	1837.5	1694.4	652	815.5	1172.4	900.3
Q9VNV3	ATP-dependent RNA helicase Ddx1 OS=Drosophila melanogaster OX=7227 GN=Ddx1 PE=2 SV=1	11.128	4	3	3	3	727	80.8	6.87	9.29	3	0	792.6	340.6	560.9	651.8	297.6	337.8	307	477.3
A1Z9L3	ATP-dependent RNA helicase DHX8 OS=Drosophila melanogaster OX=7227 GN=pea PE=1 SV=1	5.36	2	2	2	2	1242	141.8	8.76	3.89	2	0	226.9	101.6	195.8	232.3	119.4	108	117.4	163
P19109	ATP-dependent RNA helicase p62 OS=Drosophila melanogaster OX=7227 GN=Rm62 PE=1 SV=3	102.958	23	16	53	13	719	78.5	9.6	152.93	16	5	6015.1	2722.2	5395.5	5915.9	2511.2	2816.9	2739.5	4040
Q9VN03	ATP-dependent RNA helicase SUV3 homolog, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Su	30.51	10	6	11	6	763	86.6	7.68	21.55	6	0	595.4	300.6	939.3	1007	270.2	393.7	470.1	768.3
Q27268	ATP-dependent RNA helicase WM6 OS=Drosophila melanogaster OX=7227 GN=Hel25E PE=1 SV=1	67.13	19	7	26	7	424	48.6	5.66	95.36	7	0	2179.3	942.1	1344.1	1393.1	882.5	853	703.4	836.6
Q9VEX6	ATPase family AAA domain-containing protein 3A homolog OS=Drosophila melanogaster OX=7227 GN=bor F	187.657	38	25	131	25	604	68.3	9.17	392.94	25	0	6743.3	3952.9	17030.7	14023.6	2357.5	3661.7	8414.5	10281.8
B7Z0R7	Autophagy-related 16, isoform F OS=Drosophila melanogaster OX=7227 GN=Atg16 PE=1 SV=2	7.089	5	2	2	2	612	68.2	7.37	4.67	2	0	234.7	114.5	289	276.9	120.5	133.5	142.6	137.6
M9PER1	Autophagy-related 18a, isoform E OS=Drosophila melanogaster OX=7227 GN=Atg18a PE=1 SV=1	8.818	7	2	2	2	447	47.9	6.74	6.65	2	0	306	173.4	256.8	319.5	194.4	174.5	127.4	200.2
A4V3G8	Ballchen, isoform B OS=Drosophila melanogaster OX=7227 GN=ball PE=1 SV=1	18.022	8	5	6	5	599	66	9.86	18.14	5	0	5018.4	1245.9	804.5	1099.8	1695.6	2255.4	817.5	1071.6
Q9VLU0	Barrier-to-autointegration factor OS=Drosophila melanogaster OX=7227 GN=baf PE=1 SV=1	14.774	36	2	5	2	90	10.1	5.16	15.99	2	0	356.9	106.6	208	325.1	135.4	118.7	128.1	552
Q9Y166	BcDNA.GH02431 OS=Drosophila melanogaster OX=7227 GN=Dic1 PE=1 SV=1	19.242	13	3	5	3	280	30.7	10.02	20.37	3	0	224.1	68.2	545	626.1	71.7	43.6	178.1	814.6
Q9Y162	BcDNA.GH02678 OS=Drosophila melanogaster OX=7227 GN=Vps4 PE=1 SV=1	6.118	6	3	3	3	442	49.6	6.96	7.39	3	0	1404	526.6	866.5	841.5	476.5	495.9	546	843.2
Q7KMM4	BcDNA.GH04962 OS=Drosophila melanogaster OX=7227 GN=GCS2alpha PE=1 SV=1	55.622	12	9	13	9	924	105.7	6.51	44.11	9	0	665.9	319.5	2502	2160.2	227.1	230.1	1009.1	895.3
Q9Y114	BcDNA.GH10229 OS=Drosophila melanogaster OX=7227 GN=BcDNA:GH10229 PE=1 SV=1	11.698	5	3	3	3	656	71.2	6.74	10.84	3	0	236.5	140.2	335.4	295.5	115.3	137.9	174.2	142.7
O96676	BcDNA.GH12350 OS=Drosophila melanogaster OX=7227 GN=CBP PE=1 SV=1	3.787	6	2	2	2	298	34	7.08	4.45	2	0	120.9	59.5	264.2	234.3	51.9	54.2	92.5	169.4
Q9V397	BcDNA.GH12558 OS=Drosophila melanogaster OX=7227 GN=Mtpalpha PE=1 SV=1	104.851	24	17	48	17	783	84	9.17	165.01	17	0	3738.4	1848.4	8354.8	5994	1236.4	1818.9	3500.2	7457
Q7KLW9	BcDNA.LD02793 OS=Drosophila melanogaster OX=7227 GN=Prp19 PE=1 SV=1	20.886	10	4	6	4	505	55.2	6.9	18.04	4	0	753.2	339	541.7	637.1	323	328.2	292.5	376.5
Q7KMI3	BcDNA.LD23371 OS=Drosophila melanogaster OX=7227 GN=BcDNA.LD23371 PE=2 SV=1	26.796	9	6	6	6	1004	113.7	7.81	15.78	6	0	811.4	333.8	438.6	553.4	336.1	420.2	354.5	371.3
Q9V3Y5	BcDNA.LD23634 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4119 PE=1 SV=1	10.881	4	5	5	5	998	112.6	6.49	11.46	5	0	1153.1	546.2	892.4	917.2	485.7	504.3	522.6	617
Q9V3H9	BcDNA.LD27873 OS=Drosophila melanogaster OX=7227 GN=Nab2 PE=1 SV=1	17.4	4	3	3	3	1004	112.9	9.58	10.85	3	0	738.7	357.4	523.3	609.1	315.9	360.4	341.1	353.1
Q9VHH8	Beag OS=Drosophila melanogaster OX=7227 GN=beag PE=1 SV=1	21.76	9	3	3	3	557	61.4	6.86	15.08	3	0	632.9	260	386.3	401.2	246	282.9	249.4	297.2
Q9Y118	BG:DS07295.3 OS=Drosophila melanogaster OX=7227 GN=Pol32 PE=1 SV=1	36.792	7	3	5	3	431	47	9.28	23.91	3	0	1687.5	876.5	953.5	863.9	588.2	356.8	260.7	296.1
M9PDL9	Bicaudal D, isoform C OS=Drosophila melanogaster OX=7227 GN=BicD PE=1 SV=1	3.099	2	2	2	2	782	88.9	5.16	2.1	2	0								
Q9VJ86	Bicoid stability factor OS=Drosophila melanogaster OX=7227 GN=bsf PE=1 SV=2	129.107	19	25	50	25	1412	157.2	7.14	156.83	25	0	4090.4	2109.6	7354	5943.7	1384.9	2206.2	3679.7	8050.8
Q9VD28	Bifunctional arginine demethylase and lysyl-hydroxylase PSR OS=Drosophila melanogaster OX=7227 GN=PS	10.187	6	2	3	2	408	47	9.06	9.27	2	0	191.5	86.8	124.9	130.3	83.3	100.7	67.9	110
P28668	Bifunctional glutamate/proline--tRNA ligase OS=Drosophila melanogaster OX=7227 GN=GluProRS PE=1 SV=	22.665	5	8	8	8	1714	189.3	8.63	15.29	8	0	597.2	271.8	726	959.6	216	299.6	395.5	647
Q04448	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial OS=Drosophila melano	29.867	19	6	10	6	309	33.5	7.52	35.59	6	0	1596.9	682.2	2312.4	1673.8	582.4	621.6	1078	1146.3
Q9VRP4	Bifunctional phosphopantetheine adenylyltransferase-Dephospho-CoA kinase OS=Drosophila melanogaster (	7.381	5	3	3	3	518	57.6	7.2	7.03	3	0	96.4	49.4	138.2	133.3	35.1	42.3	62.2	77.5
Q9VRL8	Blanks OS=Drosophila melanogaster OX=7227 GN=blanks PE=1 SV=1	24.15	19	6	6	6	324	35.6	8.27	14.27	6	0	1862.6	742.5	836.3	740.8	623.1	664	502	716.5
O97365	BM-40 OS=Drosophila melanogaster OX=7227 GN=SPARC PE=1 SV=1	11.522	10	3	4	3	304	35.2	4.64	10.93	3	0	268.1	129.8	2308.1	1065.6	3	49.3	1144.5	486.3
A0A0B4KGE5	Bonus, isoform C OS=Drosophila melanogaster OX=7227 GN=bon PE=1 SV=1	5.732	2	3	4	3	1207	130.1	6.55	8.42	3	0	1300.9	558.2	793.5	801.8	524.3	553.4	451.1	491.9
Q7JN06	Boundary element associated factor OS=Drosophila melanogaster OX=7227 GN=BEAF-32 PE=1 SV=1	9.05	7	3	3	3	283	31.6	6.54	5.86	3	0	997.1	270.2	281.5	305.5	330.6	381.7	226.5	311.2
P52172	Box A-binding factor OS=Drosophila melanogaster OX=7227 GN=srp PE=1 SV=2	22.458	3	4	7	4	1264	134.1	7.02	20.75	4	0	2560.3	994.1	1161	1231.6	951.2	939.6	724.4	1032.3
Q9W384	Brahma associated protein 111kD OS=Drosophila melanogaster OX=7227 GN=Bap111 PE=1 SV=1	28.12	8	3	5	3	749	78.6	7.52	20.24	3	0	247.1	123.5	156.9	185.8	108.2	106.2	114.4	110.5
A1Z6M0	Brahma associated protein 170kD OS=Drosophila melanogaster OX=7227 GN=Bap170 PE=1 SV=1	12.137	2	3	3	3	1688	182.9	8.46	9.71	3	0	382.1	186.7	278	341.3	151.8	137.2	141	147.3
Q7K012	Brahma associated protein 55kD OS=Drosophila melanogaster OX=7227 GN=Bap55 PE=1 SV=1	18.756	14	5	6	5	425	47.3	5.49	13.44	5	0	1298.2	511.8	665.3	758.7	532.5	434.3	369.1	455.3
Q9VYG2	Brahma-associated protein of 60 kDa OS=Drosophila melanogaster OX=7227 GN=Bap60 PE=1 SV=1	17.304	10	5	5	5	515	58.1	9.32	12.54	5	0	356.1	169.4	226.1	304.1	172.7	136.7	137.5	251.9
Q9VYD5	Branched-chain-amino-acid aminotransferase OS=Drosophila melanogaster OX=7227 GN=cg1673 PE=1 SV=	17.192	10	5	6	5	443	49.5	7.09	13.07	5	0	227.6	178.9	463.3	392.9	99.8	142.4	199.7	336.6
Q7JVP4	Bromodomain-containing protein, 140kD, isoform A OS=Drosophila melanogaster OX=7227 GN=Br140 PE=1	5.047	2	2	2	2	1430	157	7.14	5.25	2	0	275.2	131.4	223.6	254.2	284.5	139.5	121.8	127.7
Q9VC96	BRWD3 OS=Drosophila melanogaster OX=7227 GN=BRWD3 PE=1 SV=2	41.354	6	9	9	9	2232	248.5	6.61	23.27	9	0	1649.9	876.1	1058.8	1564.1	732.2	534.8	445	848.4
contaminant_INT-S	BSA	125.129	37	20	181	20	607	69.2	6.11	424.66	20	0	19034.2	7655.8	8354.6	11322.7	8338	10695.2	8438.8	14889.9
M9PH51	BTB-protein-VII, isoform I OS=Drosophila melanogaster OX=7227 GN=BtbVII PE=4 SV=1	8.302	3	2	2	2	747	78.8	7.21	5.43	2	0	490.9	165.4	227.5	345.6	176.9	182	151.6	245.2
Q9VAJ2	Bub3, isoform A OS=Drosophila melanogaster OX=7227 GN=Bub3 PE=1 SV=1	11.818	7	3	4	3	326	37.4	6.54	12.22	3	0	351.1	139.3	193.4	249.1	124.2	137.3	103.2	185.8
Q9VIE7	Burgundy, isoform B OS=Drosophila melanogaster OX=7227 GN=bur PE=1 SV=3	36.671	12	6	7	6	683	76.7	6.8	23.99	6	0	752.4	337	551.3	513.7	285.1	314.5	244.1	317.8
M9PGQ6	Bx42, isoform B OS=Drosophila melanogaster OX=7227 GN=Bx42 PE=4 SV=1	24.493	9	3	5	3	547	61.1	9.38	19.65	3	0	1145.4	548.6	748	887	524.3	560.8	496.4	717.6
P51406	Bystin OS=Drosophila melanogaster OX=7227 GN=bys PE=1 SV=2	17.158	9	3	3	3	436	49.9	8.46	9.92	3	0	986.4	426.4	435.7	491.9	384.3	402	258.9	275
A0A0B4KGG9	C-terminal binding protein, isoform F OS=Drosophila melanogaster OX=7227 GN=CtBP PE=1 SV=1	16.501	9	3	5	3	383	41.9	6.98	11.34	3	0	1435.2	486.7	541.1	561.9	472.3	456.8	338.7	330
Q9W347	C12.2, isoform A OS=Drosophila melanogaster OX=7227 GN=c12.2 PE=1 SV=3	27.239	6	8	10	8	1386	155.6	7.09	28.23	8	0	534.1	291.9	881.1	809.1	242.5	296.5	393.1	624.2
M9PH94	Cabeza, isoform D OS=Drosophila melanogaster OX=7227 GN=caz PE=4 SV=1	76.055	29	7	16	7	355	34.3	9.39	74.4	7	0	1553.3	732.6	942.8	1004.4	628.5	660.2	539.4	482.9
Q9VR99	Cactin OS=Drosophila melanogaster OX=7227 GN=cactin PE=1 SV=3	4.766	3	2	2	2	720	86.5	7.94	5.57	2	0	83.4	46.6	132.4	121.3	46.3	46.8	62.4	98.5
P05990	CAD protein OS=Drosophila melanogaster OX=7227 GN=r PE=1 SV=3	18.413	3	4	8	4	2224	246.5	6.64	26.92	4	0	358.1	185.8	464.6	511.2	178	204.1	263.3	294.4
Q8IQ70	Calcium uniporter protein, mitochondrial OS=Drosophila melanogaster OX=7227 GN=CG18769 PE=2 SV=2	12.468	9	4	6	4	366	42.5	8.53	15.13	4	0	386.1	258.4	838.2	597.4	163.6	240.9	434.1	344.8
Q9VA73	Calcium-binding mitochondrial carrier protein Aralar1 OS=Drosophila melanogaster OX=7227 GN=aralar1 PE=	27.227	10	7	14	7	695	76.7	8.72	35.95	7	0	977.4	461.6	2341.6	2206	368.5	361.2	867.5	2568.2
Q7KUD4	Calcium-independent phospholipase A2 VIA, isoform B OS=Drosophila melanogaster OX=7227 GN=iPLA2-V	21.908	6	4	4	4	887	97.7	6.99	15.01	4	0	304.1	143.2	284.5	246.7	101.5	158.7	156.6	196.1
A0A0B4LGB7	Calcium-transporting ATPase OS=Drosophila melanogaster OX=7227 GN=SERCA PE=1 SV=1	65.861	13	10	20	10	999	109.3	5.45	61.71	10	0	1818.2	915.8	2875.8	2454.4	689.7	888.4	1352.3	1512.4
A0A0B4LF57	Calmodulin, isoform C OS=Drosophila melanogaster OX=7227 GN=Cam PE=1 SV=1	28.424	40	6	9	6	149	16.8	4.22	22.27	6	0	1945.1	850.7	1088.8	1182.5	640	750.1	601.5	845.1
Q9VAL7	Calnexin 99A, isoform A OS=Drosophila melanogaster OX=7227 GN=Cnx99A PE=1 SV=2	9.45	4	2	4	2	605	68	4.84	9.89	2	0	708.8	309.4	934.8	691.7	244.5	321.1	463.4	336.9
P29413	Calreticulin OS=Drosophila melanogaster OX=7227 GN=Calr PE=1 SV=2	39.932	20	6	19	6	406	46.8	4.58	56.11	6	0	523.3	237.4	2532.9	1684.9	97.6	141.1	1148.7	628.4
Q9VM49	Caper, isoform A OS=Drosophila melanogaster OX=7227 GN=Caper PE=1 SV=1	10.778	4	2	3	2	594	66.4	10.01	9.6	2	0	886.3	293	372.8	473.6	310.3	271.6	265.9	505.7
Q9I7D3	Caprin homolog OS=Drosophila melanogaster OX=7227 GN=Capr PE=1 SV=1	19.795	6	5	5	5	961	103.5	6.51	13.34	5	0	309.3	130.9	288.1	251.7	105.7	142.9	163.7	132.5
Q9VHJ5	Carbonic anhydrase OS=Drosophila melanogaster OX=7227 GN=CAHbeta PE=3 SV=1	38.787	22	9	22	9	255	30	6.99	64	9	0	1603.5	573.6	2000.3	2222.3	743.7	620.9	886.6	2595.6
Q9VIB5	Carboxylic ester hydrolase OS=Drosophila melanogaster OX=7227 GN=alpha-Est7 PE=1 SV=1	5.998	7	2	2	2	572	65.4	6.49	7.6	2	0	87.1	40.5	100.1	104.2	53.3	52.7	49.7	63.8
Q0KIA8	Carnitine O-Acetyl-Transferase, isoform B OS=Drosophila melanogaster OX=7227 GN=CRAT PE=1 SV=1	30.972	9	4	8	4	657	74.3	8.38	21.34	4	0	478.9	271.8	1085	869.5	186.3	219.4	426.7	510.9
Q9VZW7	Carnitine palmitoyltransferase 2 OS=Drosophila melanogaster OX=7227 GN=CPT2 PE=1 SV=1	36.056	13	8	10	8	667	75.1	8.35	29.94	8	0	872.5	422.6	1837.4	1389.7	299.2	309.5	748.9	1376.9
A0A0B4LFH2	Caspar, isoform C OS=Drosophila melanogaster OX=7227 GN=casp PE=1 SV=1	8.109	4	2	2	2	690	77.9	4.89	6.26	2	0	66.8	43.8	99.2	75.6	38.8	35.2	42.4	51.4
P17336	Catalase OS=Drosophila melanogaster OX=7227 GN=Cat PE=1 SV=2	19.49	7	3	4	3	506	57.1	8.18	12.56	3	0	186.4	123.5	217.3	222.8	88.8	118.2	115.5	118.5
Q9VRE0	Catalytic subunit 3A of the oligosaccharyltransferase complex, isoform A OS=Drosophila melanogaster OX=72	6.967	4	3	4	3	713	80.6	7.88	7.57	3	0	575.9	208.9	696.9	739.8	163.6	211.6	298.4	734.9

Q9XZ53	Catalytic subunit 3B of the oligosaccharyltransferase complex OS=Drosophila melanogaster OX=7227 GN=St	6.101	4	2	3	2	774	87.6	9	5.02	2	0	319.2	143.3	510.6	442.7	91.4	164.8	292.9	201
Q95029	Cathepsin L OS=Drosophila melanogaster OX=7227 GN=Cp1 PE=2 SV=2	27.407	10	5	6	5	371	41.6	7.21	21.34	5	0	640.1	279.4	1676.2	1383.8	174.3	245	684.7	507.6
Q9VKJ6	Cation-transporting ATPase OS=Drosophila melanogaster OX=7227 GN=dCOD1 PE=1 SV=1	25.988	6	4	5	4	1225	136.3	7.74	20.78	4	0	229	112.9	378.2	340.3	112.7	136	201.8	210.9
A0A0B4JD46	CCHC-type zinc finger nucleic acid binding protein, isoform B OS=Drosophila melanogaster OX=7227 GN=CN	16.274	22	2	2	2	165	17.6	8.65	11.54	2	0	336.2	131.9	195	272.2	136.5	76.7	121.4	137.2
Q9VKV5	CD2 antigen cytoplasmic tail-binding protein 2 homolog OS=Drosophila melanogaster OX=7227 GN=holn1 PE	7.932	8	2	2	2	319	36.8	4.91	3.78	2	0	56.4	25.4	30.2	29.4	21.7	20.2	17.2	32.6
M9NFF8	Cdc42, isoform C OS=Drosophila melanogaster OX=7227 GN=Cdc42 PE=4 SV=1	11.336	11	2	3	2	191	21.4	7.14	9.49	2	0	185.4	99.5	353.3	225.2	27.5	66	169.3	106
Q9VZ27	CDK2-associated protein 1, isoform A OS=Drosophila melanogaster OX=7227 GN=CDK2AP1 PE=1 SV=2	23.623	14	4	4	4	281	29.2	9.47	15.83	4	0	1567.4	740.8	852.7	769.5	555.4	521.6	499.2	377.2
Q9W0R0	Cell division cycle 5, isoform A OS=Drosophila melanogaster OX=7227 GN=Cdc5 PE=1 SV=2	42.002	13	6	6	6	814	93	8.19	22.41	6	0	363.6	142.1	198.5	278.8	119.4	124.4	114.5	144.9
Q9VHP9	Centromeric protein-C, isoform A OS=Drosophila melanogaster OX=7227 GN=Cenp-C PE=1 SV=4	7.046	2	2	3	2	1411	157.6	8.41	8.34	2	0	875.7	326.6	404.5	467.3	359.5	543.6	302.9	360.7
Q24478	Centrosome-associated zinc finger protein CP190 OS=Drosophila melanogaster OX=7227 GN=Cp190 PE=1	35.954	8	7	10	7	1096	121.6	4.67	36.55	7	0	3591.6	1088.6	1395.2	1344.5	1222	1455.6	1054.1	970.1
Q9VXT3	Cervantes, isoform A OS=Drosophila melanogaster OX=7227 GN=cerv PE=1 SV=2	8.384	13	3	3	3	230	26.1	5.53	8.41	3	0	1296.9	612.2	625.2	739.1	459.6	757.7	444.2	502.5
Q9VM69	CG10206-PA OS=Drosophila melanogaster OX=7227 GN=nop5 PE=1 SV=2	30.688	21	7	10	7	511	57.1	8.59	34.42	7	0	1960.8	745.5	906.6	944.4	763.9	654.2	502.7	609.6
Q7K0D3	CG12909 protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12909 PE=1 SV=1	7.739	8	2	2	2	281	32.1	8.95	6.25	2	0	785.5	264.5	319.4	418.6	293.4	229.7	210.1	475.3
Q9VYG8	CG15717-PA OS=Drosophila melanogaster OX=7227 GN=Dmel\CG15717 PE=1 SV=1	8.676	11	3	5	3	252	27.7	6.29	10.3	3	0	669.9	340.6	496.3	488.6	271.3	356.3	325.4	292.3
C0MJA0	CG17950-PA OS=Drosophila melanogaster OX=7227 GN=HmgD PE=1 SV=1	9.321	21	2	6	1	112	12.4	9.2	19.94	2	0	1005.2	245	358.7	379.5	396	325.8	211.8	265
Q9W2T3	CG2124 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2124 PE=2 SV=1	8.244	4	2	3	2	629	73.5	8.6	5.64	2	0	47.1	36.7	68.2	79.9	34.2	31.7	41.9	46.3
F6J1D0	CG3595 OS=Drosophila melanogaster OX=7227 GN=sqh PE=1 SV=1	9.473	13	2	3	2	174	19.9	4.81	8.32	2	0	684.8	232	525.5	479.7	206.7	273	304.8	475.8
Q7K511	CG3835-RA OS=Drosophila melanogaster OX=7227 GN=D2hgdh PE=1 SV=1	28.391	18	6	16	6	533	58.3	6.93	41.76	6	0	851	490.8	1861.2	1354.6	322.6	394	745.1	860.8
O76742	CG5915 protein OS=Drosophila melanogaster OX=7227 GN=Rab7 PE=1 SV=1	11.927	19	4	5	4	207	23.3	5.47	13.64	4	0	349.4	215.7	761.7	586.7	103.5	210.6	385.8	336.5
Q9VDC2	CG5919 protein OS=Drosophila melanogaster OX=7227 GN=Idi PE=2 SV=1	16.427	13	3	5	3	256	29.8	7.12	17.59	3	0	152.2	101.1	266.1	302.9	67.8	117.3	106.5	228.8
Q7JXC4	CG6459 protein OS=Drosophila melanogaster OX=7227 GN=P32 PE=1 SV=1	63.101	25	5	33	5	263	29	5.08	105.58	5	0	753.1	423.4	1813.8	1186.1	302.5	348.6	793.5	2405.4
Q9VVJ7	CG7484 protein OS=Drosophila melanogaster OX=7227 GN=BcDNA:SD16138 PE=1 SV=2	8.406	18	2	2	2	178	19.9	5.66	6.76	2	0	103	61.7	182.4	175	51.8	61.3	86.9	101.8
Q9VQR2	CG8844 protein OS=Drosophila melanogaster OX=7227 GN=ND-PDSW PE=1 SV=1	50.693	37	8	38	8	159	18.9	7.01	122.27	8	0	2278.2	1422.1	5693.5	4683.2	908.9	1304.3	2769.6	3437.5
Q9VMI5	CG9135 protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9135 PE=1 SV=1	3.088	3	2	2	2	487	53.4	7.18	2.17	2	0	175.7	68	85.8	127	59.9	65.1	47.1	109.3
Q9VIH1	CG9273 protein OS=Drosophila melanogaster OX=7227 GN=RPA2 PE=1 SV=2	10.782	11	3	7	3	246	26.4	5.08	20.9	3	0	2074.3	1047	1007.4	897	727.5	387.6	260.1	364
A4V391	Chaperonin containing TCP1 subunit 1, isoform B OS=Drosophila melanogaster OX=7227 GN=CCT1 PE=1 S	34.586	17	7	11	7	557	59.5	6.39	34.95	7	0	1010.7	382	965.4	1052	348.2	415.3	510.8	926
Q9W392	Chaperonin containing TCP1 subunit 2 OS=Drosophila melanogaster OX=7227 GN=CCT2 PE=1 SV=2	46.424	23	9	22	9	535	58	5.85	65.58	9	0	1227.3	616.2	1389.7	1853.8	484.2	593.5	688	1357.8
Q9VXQ5	Chaperonin containing TCP1 subunit 6 OS=Drosophila melanogaster OX=7227 GN=CCT6 PE=1 SV=1	26.568	12	6	10	6	533	58.2	6.62	27.5	6	0	1125.9	493	1037.8	1194.7	390.6	458.5	577.2	733.5
Q7K3J0	Chaperonin containing TCP1 subunit 8 OS=Drosophila melanogaster OX=7227 GN=CCT8 PE=1 SV=1	67.685	28	12	19	12	546	59.4	5.31	59.22	12	0	3439.5	1525.6	3360	3373.8	1251.4	1495.8	1758.9	2234.2
A0A0B4KHN1	Cheerio, isoform N OS=Drosophila melanogaster OX=7227 GN=cher PE=1 SV=1	159.355	17	28	56	28	2404	259.5	6.16	179.03	28	0	5186.8	2036	5316.5	5405.8	1920.3	2259.8	3114.7	3520.6
Q9VY78	Chloride intracellular channel, isoform A OS=Drosophila melanogaster OX=7227 GN=Clic PE=1 SV=1	11.258	15	3	6	3	260	30.2	6.29	16.81	3	0	670.1	257.5	430.4	485.5	259.4	193.3	217.2	578.6
Q9W4K0	CHOp24, isoform A OS=Drosophila melanogaster OX=7227 GN=CHOp24 PE=1 SV=1	13.464	12	2	3	2	208	23.2	5.76	10.31	2	0	89.3	63	149.6	236.9	38.4	58	74.4	244.8
A1Z898	Chromatin assembly factor 1, p105 subunit OS=Drosophila melanogaster OX=7227 GN=Caf1-105 PE=1 SV=	22.188	7	5	5	5	747	83.3	8.22	14.48	5	0	1073.1	667.7	683.1	890.7	520.8	172.5	159.8	209.9
Q9W3D1	Chromatin assembly factor 1, p180 subunit OS=Drosophila melanogaster OX=7227 GN=Caf1-180 PE=1 SV=	24.116	6	7	12	7	1183	133.4	7.03	37.77	7	0	2827.4	1893.8	1917.7	2549	1291.5	528.7	453.7	693.4
Q24368	Chromatin-remodeling complex ATPase chain Iswi OS=Drosophila melanogaster OX=7227 GN=Iswi PE=1 SV	39.888	11	11	14	11	1027	118.8	8.29	45.3	11	0	4630.5	1842.7	1939.4	2316.6	1711.9	1622.7	1054	1261.2
Q86BS3	Chromator, isoform A OS=Drosophila melanogaster OX=7227 GN=Chro PE=1 SV=1	65.258	10	6	11	6	926	101	7.17	59.03	6	0	1039.1	513.9	585.7	525.4	501.8	694	573.5	197.4
Q7KU24	Chromodomain-helicase-DNA-binding protein 1 OS=Drosophila melanogaster OX=7227 GN=Chd1 PE=1 SV=	12.353	2	3	3	3	1883	211.7	6.38	8.74	3	0	971.3	392.8	444.8	466.3	369.1	393.9	309.6	242.6
O16102	Chromodomain-helicase-DNA-binding protein 3 OS=Drosophila melanogaster OX=7227 GN=Chd3 PE=2 SV=	10.426	5	4	4	2	892	103	8.48	12	4	0	74.8	28.5	99.4	113.2	31.9	45.1	41.5	76.3
Q9V3I5	Chromosomal serine/threonine-protein kinase JIL-1 OS=Drosophila melanogaster OX=7227 GN=JIL-1 PE=1 S	29.698	7	6	8	6	1207	137	6.6	27.61	6	0	1714.2	583.9	829.7	862.8	657.2	857	573.8	734.3
Q494K2	Chromosome transmission fidelity 4 OS=Drosophila melanogaster OX=7227 GN=Ctf4 PE=1 SV=1	31.373	8	4	5	4	895	96.6	5.34	18.71	4	0	323.5	168.4	239.7	267.4	136.4	117.5	79.9	138.9
A0A0B4KI32	CIN85 and CD2AP related, isoform E OS=Drosophila melanogaster OX=7227 GN=cindr PE=1 SV=1	24.979	6	3	5	3	848	88.4	9.26	21.8	3	0	466.8	238.5	555.8	562	193.9	249.6	339.1	183.5
Q8IRB5	Claspin OS=Drosophila melanogaster OX=7227 GN=Claspin PE=1 SV=1	8.797	2	3	3	3	1465	165.2	4.79	6.59	3	0	1622.5	945.6	981.9	904.3	608.5	384.8	241.3	276.2
X2JC31	Clathrin heavy chain OS=Drosophila melanogaster OX=7227 GN=Chc PE=3 SV=1	69.177	7	10	21	10	1678	191.1	5.72	71.22	10	0	900.5	415.8	1167.5	1192.9	376.5	472.7	663.3	798.2
Q9V726	Cleavage and polyadenylation specificity factor subunit 1 OS=Drosophila melanogaster OX=7227 GN=Cpsf16	9.117	2	3	3	3	1455	164.6	6.2	8.78	3	0	667.2	339.3	435.9	462.1	288.1	340.4	269.9	349.6
Q9V9V0	Cleavage stimulation factor 50 kD subunit OS=Drosophila melanogaster OX=7227 GN=CstF50 PE=1 SV=1	6.837	6	3	3	3	424	46.9	5.95	7.25	3	0	432.1	159.1	255.4	255.5	151.7	167.3	132.1	173.1
Q9VE52	Cleavage stimulation factor 64 kD subunit OS=Drosophila melanogaster OX=7227 GN=CstF64 PE=1 SV=2	5.401	4	2	2	2	419	46.2	5.78	5.8	2	0	634.1	275.2	393.3	399.9	282.7	300.5	239.9	248.8
Q9W0B8	Coatomer subunit alpha OS=Drosophila melanogaster OX=7227 GN=alphaCOP PE=1 SV=1	23.918	5	6	8	6	1234	139.2	7.65	17.75	6	0	600.2	300.5	656.1	766.5	251	321.5	352	468.1
P45437	Coatomer subunit beta OS=Drosophila melanogaster OX=7227 GN=betaCOP PE=2 SV=2	38.735	6	4	5	4	964	107.3	6.32	23.11	4	0	401.1	155.1	509.9	531.8	138.3	156.6	247.5	551.3
O62621	Coatomer subunit beta' OS=Drosophila melanogaster OX=7227 GN=beta'COP PE=2 SV=2	44.882	11	7	11	7	914	102.6	5.26	36.92	7	0	1102.7	479	1096	1181.6	421	718.7	694.7	641.6
Q9W555	Coatomer subunit delta OS=Drosophila melanogaster OX=7227 GN=deltaCOP PE=1 SV=1	12.639	8	3	3	3	532	57.9	6.2	10.65	3	0	184.4	87	207.8	225.2	88.5	86.2	102.9	145.7
Q9Y0Y5	Coatomer subunit epsilon OS=Drosophila melanogaster OX=7227 GN=epsilonCOP PE=1 SV=1	9.36	7	2	2	2	306	34.6	4.87	8.23	2	0	272.5	112.6	297.7	255.7	98.7	103.6	167.3	287.6
Q8I0G5	Coatomer subunit gamma OS=Drosophila melanogaster OX=7227 GN=gammaCOP PE=2 SV=1	10.059	4	3	6	3	883	97.6	5.67	11.66	3	0	260.6	136.7	300	341.5	107.2	145.9	168.3	196.2
P45594	Cofilin/actin-depolymerizing factor homolog OS=Drosophila melanogaster OX=7227 GN=tsr PE=1 SV=1	31.593	33	6	18	6	148	17.1	7.17	52.29	6	0	3370.4	1442.7	2148.4	2360.4	1285	1223.3	1181.4	2192.1
Q9VKJ9	Coiled-coil and C2 domain-containing protein 1-like OS=Drosophila melanogaster OX=7227 GN=l(2)gd1 PE=1	8.484	4	3	3	3	816	89	5.39	4.84	3	0	223.8	80.1	168.9	181.1	75.3	107.2	92.3	140.2
Q9VA18	Coiled-coil-helix-coiled-coil-helix domain containing 3 OS=Drosophila melanogaster OX=7227 GN=Chchd3 PE	16.737	13	2	4	2	223	24.2	8.97	15.11	2	0	481.7	251.8	751.8	505.1	140.1	245.4	413.4	380.4
P08120	Collagen alpha-1(IV) chain OS=Drosophila melanogaster OX=7227 GN=Col4a1 PE=1 SV=3	78.844	8	11	35	11	1779	174.2	8.6	115.91	11	0	2076.4	870.2	10087.2	6635.4	600.5	808.8	4020.6	2001.3
Q9VAI1	Complex I intermediate-associated protein 30, mitochondrial OS=Drosophila melanogaster OX=7227 GN=CIA	7.655	9	3	3	3	296	34.2	9.01	8.07	3	0	266.4	143.2	668.7	572.8	84.7	111.7	242.3	433.7
Q9VAJ1	Condensin complex subunit 1 OS=Drosophila melanogaster OX=7227 GN=Cap-D2 PE=1 SV=1	20.402	3	5	5	5	1380	157.4	5.86	15.03	5	0	1019.3	531.4	588.4	627.6	464.3	540.5	354.4	384.6
Q9VIP9	Condensin complex subunit 2 OS=Drosophila melanogaster OX=7227 GN=barr PE=1 SV=1	25.896	10	5	6	5	735	82.7	5.58	21.2	5	0	959.4	418.7	467.4	613.7	449.5	441.5	310.4	361.1
Q9VAD6	Conserved oligomeric Golgi complex subunit 7 OS=Drosophila melanogaster OX=7227 GN=Cog7 PE=2 SV=2	9.59	3	2	2	2	742	84	5.85	5.47	2	0	259.8	130.3	289.9	319	112.9	137.3	153.8	185.1
contaminant_KER/	contaminant_KERATIN02	186.834	42	22	89	22	622	62	5.24	359.29	22	0	7363.3	3905.6	3055.8	5782	5048.2	6379.7	3105.7	17376.7
contaminant_KER/	contaminant_KERATIN03	291.841	51	29	105	24	593	59.5	5.21	390.62	29	5	9167.7	3167.6	5231.6	6739.6	5294	5089.1	3084.2	15606.1
contaminant_KER/	contaminant_KERATIN04	28.893	15	7	9	3	458	49.6	4.93	27.4	7	0	303	49.6	90.4	134.6	70.5	147.5	61.1	127.4
contaminant_KER/	contaminant_KERATIN05	116.225	47	20	41	9	471	51.5	5.16	132.26	20	9	2992.5	1403.1	1645.6	2466.6	1540.5	1864.4	1056.9	3390.6
contaminant_KER/	contaminant_KERATIN07	23.778	14	6	12	1	473	50.9	5.53	34.74	6	0	42.4	18.2	38.7	42	19.4	21.7	15.3	60.1
contaminant_KER/	contaminant_KERATIN08	84.674	34	14	24	8	469	50.5	5	78.84	14	0	2864.7	735.8	1032.1	1656.6	806.5	1030.6	537	1488.6
contaminant_KER/	contaminant_KERATIN12	47.885	22	12	22	4	431	47.9	5.02	61.7	12	0	511.8	173.8	331.2	366.7	199.7	162.2	181.7	581.1
contaminant_KER/	contaminant_KERATIN13	199.422	36	18	144	14	643	65.5	6.62	479.46	18	1	15177	6855.2	6559	10424.7	10115	11526.7	5378.1	18827.7
contaminant_KER/	contaminant_KERATIN15	17.549	8	4	10	2	629	64.5	6.48	30.95	4	0	635.6	75.1	129	288.9	187.3	229.9	67.6	116.6
contaminant_KER/	contaminant_KERATIN17	99.379	30	18	41	11	590	62.4	8.06	120.24	18	3	3191.5	1476.8	1661.7	2377.3	1634	2244.5	1277.3	2819.7
contaminant_KER/	contaminant_KERATIN18	115.252	33	17	41	9	562	59.8	7.94	128.1	17	0	2608	901.6	1123.3	1657.4	736.2	1146.7	762.4	1401.1
contaminant_KER/	contaminant_KERATIN20	15.703	6	3	50	1	483	53.7	5.43	118.42	3	0	195	37.1	60	78.5	99.8	36	25.3	364.2
contaminant_KER/	contaminant_KERATIN22	177.149	40	22	106	14	645	65.8	8	373.53	22	8	6695.8	2662.9	4031.7	5742.1	4626.4	4000.5	2354.3	10854.9
Q9V345	COP9 signalosome complex subunit 4 OS=Drosophila melanogaster OX=7227 GN=CSN4 PE=1 SV=1	6.377	5	2	2	2	407	46.4	6.32	6.44	2	0	444	208.1	377.4	405	199.4	198.7	182.9	244.2
C7LAG1	CoRest, isoform G OS=Drosophila melanogaster OX=7227 GN=CoRest PE=1 SV=1	27.954	8	5	9	5	824	87.3	6.47	26.34	5	0	1883.9	812.4	995.4	943.1	695.9	706.5	615.5	619.6
A0A0B4KEU5	Coronin OS=Drosophila melanogaster OX=7227 GN=coro PE=1 SV=1	10.268	5	3	4	3	534	58	6.48	10.94	3	0	831.7	311.7	959	925.6	329	312.8	487.6	756.1
A8JV09	Coronin OS=Drosophila melanogaster OX=7227 GN=pod1 PE=1 SV=1	13.397	3	3	4	3	1255	139	6.76	11.87	3	0	308.4	128.1	309.5	408.1	126.7	154.2	154	265.8
Q9VP13	CR6-interacting factor OS=Drosophila melanogaster OX=7227 GN=CRIF PE=1 SV=1	26.077	17	4	11	4	232	26.8	9.54	46.21	4	0	527	320.3	961.5	746.9	184.5	300.5	474	417.4
Q9W2F4	Cricklet OS=Drosophila melanogaster OX=7227 GN=clt PE=1 SV=1	42.854	13	6	8	6	562	63.7	6.84	28.68	6	0	464.5	304.2	912.5	656.2	195.3	266.7	416.9	350.7
H9XVM7	Crk oncogene, isoform D OS=Drosophila melanogaster OX=7227 GN=Crk PE=1 SV=1	7.088	10	2	2	2	184	21.4	5.72	5.25	2	0	414.2	242.6	388.2	471.8	207	231.5	207	283.8
Q7K0X3	Ctr9, isoform A OS=Drosophila melanogaster OX=7227 GN=Ctr9 PE=1 SV=1	16.398	3	3	3	3	1150	130.4	9.55	10.47	3	0	221.8	93.2	134.8	172.7	79.7	91.2	76.8	93.1
Q9V9R2	Cullin 2, isoform A OS=Drosophila melanogaster OX=7227 GN=Cul2 PE=1 SV=3	16.9	4	3	4	3	753	87.3	6.92	9.11	3	0	482.6	197.9	331.7	318.6	176.5	178.8	203	237.6
Q5BI50	Cullin 4, isoform A OS=Drosophila melanogaster OX=7227 GN=Cul4 PE=1 SV=1	27.212	10	6	6	6	821	94.3	8.66	16.62	6	0	930.4	523.9	606.5	577.6	389.5	361.2	317.9	232.3
M9PB90	Cullin-associated and neddylation-dissociated 1, isoform B OS=Drosophila melanogaster OX=7227 GN=Cand	14.442	5	4	4	4	1248	139.3	5.87	8.62	4	0	271	85.4	164.4	248.2	91.6	91.4	65	296.9
Q8IQ05	Cutlet OS=Drosophila melanogaster OX=7227 GN=cutlet PE=1 SV=2	21.424	10	7	7	7	993	111.7	8.51	15.81	7	0	824.6	507.3	558.1	691.7	356	186.4	144.5	162.2
P23572	Cyclin-dependent kinase 1 OS=Drosophila melanogaster OX=7227 GN=Cdk1 PE=1 SV=1	11.803	7	2	2	2	297	34.4	6.87	7.07	2	0	789.3	377.8	382	461.9	301.8	334	206.7	244.1
Q9VMS1	Cyclope, isoform A OS=Drosophila melanogaster OX=7227 GN=cype PE=1 SV=3	10.858	31	2	3	2	77	8.3	9.92	9.45	2	0	161.3	76.1	738	439.1	37.4	64.7	319	572.8
A0A0B4LF45	Cyp12d1-p, isoform B OS=Drosophila melanogaster OX=7227 GN=Cyp12d1-p PE=3 SV=1	69.262	32	14	23	1	521	60.2	9.1	66.69	14	13	1237.1	720.7	2125.8	1725.9	551.7	689.8	908	1777.7
Q9VRD9	Cystathionine beta-synthase OS=Drosophila melanogaster OX=7227 GN=Cbs PE=1 SV=1	11.042	7	2	2	2	522	56.8	7.06	9.91	2	0	40.4	20.6	44.5	44.9	17.3	20.6	17.7	37.5
Q7K3P0	Cysteinyl-tRNA synthetase, mitochondrial, isoform A OS=Drosophila melanogaster OX=7227 GN=CysRS-m PE	23.634	10	4	8	4	558	63.5	7.99	28.94	4	0	105.3	63.3	206.4	155.5	65.4	68.7	109.3	112.8
Q9VQ29	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Drosophila melanogaster OX=7227 GN=RFeSP	13.285	14	4	11	4	230	24.9	8.68	34.11	4	0	1087.4	673.1	2708.9	2037.8	334.6	502.2	1115.7	1034
Q9VD55	Cytochrome c heme lyase OS=Drosophila melanogaster OX=7227 GN=Cchl PE=1 SV=1	3.765	5	2	2	2	281	32	7.21	4	2	0	315.5	109.1	337.1	194.3	109.7	158.2	181.3	113.8
P0DKM0	Cytochrome c oxidase assembly factor 3, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Ccdc56 I	8.77	21	2	4	2	87	9.9	9.28	9.05	2	0	502.4	239.9	1265.7	1144	188.1	168.2	486.4	1051.5
Q9W5N0	Cytochrome c oxidase assembly factor 7 homolog OS=Drosophila melanogaster OX=7227 GN=CG13865 PE=	23.249	17	4	7	4	266	29.6	7.77	20.24	4	0	1177.9	538.3	2076.3	1487.4	323.2	463	964.7	1187.2
P00399	Cytochrome c oxidase subunit 1 OS=Drosophila melanogaster OX=7227 GN=mt:CoI PE=2 SV=2	6.151	8	2	4	2	511	56.3	6.61	7.5	2	0	67	42.3	218.3	231.6	15.7	22.2	86.1	358.8
P00408	Cytochrome c oxidase subunit 2 OS=Drosophila melanogaster OX=7227 GN=mt:CoII PE=3 SV=1	7.085	11	3	5	3	228	26.2	5.1	9.64	3	0	195.1	143.9	905.4	702.9	37.2	109.2	329.1	775.9
Q9VIQ8	Cytochrome c oxidase subunit 4, isoform A OS=Drosophila melanogaster OX=7227 GN=COX4 PE=1 SV=1	54.363	32	6	41	6	182	20.5	8.25	141.31	6	0	1153.8	724.1	3280	2458.6	412.4	568.3	1431	1408.5
Q94514	Cytochrome c oxidase subunit 5A, mitochondrial OS=Drosophila melanogaster OX=7227 GN=COX5A PE=2 S	9.46	13	3	14	3	149	16.6	5.68	35.3	3	0	1627.1	1049.9	4382.1	3358.2	612.4	781.2	1893.5	2598.8
Q9VMB9	Cytochrome c oxidase subunit 5B, isoform A OS=Drosophila melanogaster OX=7227 GN=COX5B PE=1 SV=	13.35	20	2	7	2	120	13.6	8.69	23.32	2	0	1294	852.1	3403.9	2498.4	719.4	884.1	1400.5	1517.5
Q9VWD1	Cytochrome c oxidase subunit OS=Drosophila melanogaster OX=7227 GN=COX6B PE=1 SV=2	12.361	40	5	10	5	96	11.4	8.7	22.74	5	0	698.3	386.8	1350.1	1189.4	256.7	299.9	636.7	916.8
P84029	Cytochrome c-2 OS=Drosophila melanogaster OX=7227 GN=Cyt-c-p PE=1 SV=2	12.921	25	2	5	2	108	11.7	9.57	15.93	2	0	403.6	245.3	1059.1	802.3	108.5	240	535.9	640.3
Q9VRL0	Cytochrome c1, isoform A OS=Drosophila melanogaster OX=7227 GN=Cyt-c1 PE=1 SV=1	36.088	18	4	18	4	307	33.7	8.53	66.21	4	0	1212.2	752.8	3449.2	2292.2	447.9	588.4	1485.9	1321
Q9VF87	Cytoplasmic FMR1-interacting protein OS=Drosophila melanogaster OX=7227 GN=Sra-1 PE=1 SV=1	12.416	3	4	4	4	1291	149.2	7.12	10.22	4	0	524.2	255.7	692.7	728.3	196.1	260.1	381.1	312
E1JHJ9	Cytoplasmic linker protein 190, isoform M OS=Drosophila melanogaster OX=7227 GN=CLIP-190 PE=1 SV=2	6.843	2	3	3	3	1668	186.6	4.96	4.5	3	0	694.7	290.9	473.4	583.7	274.7	459.5	339.1	322.3
Q9VIV3	Cytoplasmic tRNA 2-thiolation protein 2 OS=Drosophila melanogaster OX=7227 GN=CG10189 PE=2 SV=1	9.527	8	2	2	2	405	44.7	6.33	8.23	2	0	144.9	65.5	170.6	146	53.5	80.4	71.4	81.1
A4V2K7	D1 chromosomal protein, isoform C OS=Drosophila melanogaster OX=7227 GN=D1 PE=1 SV=1	56.549	34	6	16	6	355	37	6.64	49.96	6	0	3084.5	958.8	850	909.8	1239	1460.6	691	706.7
Q9VPT3	DEAD box protein 21E2 OS=Drosophila melanogaster OX=7227 GN=Dbp21E2 PE=1 SV=1	17.263	9	5	6	5	536	59.6	9.38	18.41	5	0	606.3	347.6	1290.7	1109.4	224.8	316.4	524.3	874.5
Q7K3M5	DEAH-box helicase 15, isoform A OS=Drosophila melanogaster OX=7227 GN=Dhx15 PE=1 SV=1	8.013	3	2	3	2	729	82.6	7.06	8.52	2	0	1262.1	621	730.6	593.9	510.6	538.6	455.3	309
Q9Y140	Dehydrogenase/reductase SDR family protein 7-like OS=Drosophila melanogaster OX=7227 GN=CG7601 PE	2.567	4	2	2	2	326	35.7	9.26	3.7	2	0	171.3	94.1	232.4	307	68.8	75.7	112.8	384.8
Q8T0D3	Dek, isoform B OS=Drosophila melanogaster OX=7227 GN=Dek PE=1 SV=1	26.45	7	3	5	3	669	72.5	4.88	21.49	3	0	1066.7	428.3	549.6	781.4	360.3	303.1	289.1	1146.1
Q9VNX4	Delta-1-Pyrroline-5-carboxylate dehydrogenase 1, isoform A OS=Drosophila melanogaster OX=7227 GN=P5C	23.765	15	7	9	7	574	63.6	8.22	23.91	7	0	853.7	387.3	1345.8	1252	363.5	350.1	577.6	1897.2
Q9XZT6	Deoxynucleoside kinase OS=Drosophila melanogaster OX=7227 GN=dnk PE=1 SV=1	10.022	11	2	2	2	250	29.1	8.06	7.45	2	0	228.6	133.1	243.8	193.9	87.9	98.5	89.5	107.3
Q8IPB1	Deoxyuridine triphosphatase, isoform B OS=Drosophila melanogaster OX=7227 GN=dUTPase PE=1 SV=1	22.483	30	4	6	4	174	18.5	5.43	19.69	4	0	1247.7	627.9	589.8	637.5	535.8	504.7	309.1	282
Q9VEU2	Derlin OS=Drosophila melanogaster OX=7227 GN=Der-2 PE=1 SV=1	15.389	19	2	2	2	261	29.8	6.77	8.18	2	0	89.6	28.4	77.1	93	40.6	39.6	34.2	136.6
Q94515	Des-1 protein OS=Drosophila melanogaster OX=7227 GN=ifc PE=1 SV=1	11.975	11	2	2	2	321	37.2	9.11	8.04	2	0	24.8	16.7	31.2	41.2	14.8	24.4	25.4	31.9
Q7K4Y0	Desaturase 1, isoform A OS=Drosophila melanogaster OX=7227 GN=Desat1 PE=1 SV=1	5.63	4	2	2	2	383	43.4	8.82	5.33	2	0	425.8	155.5	403.7	386.5	127.2	119.5	233.6	293.6
A1ZAW0	Dicer-2, isoform A OS=Drosophila melanogaster OX=7227 GN=Dcr-2 PE=1 SV=1	7.899	2	2	2	2	1722	197.6	6.86	6.28	2	0	241	116	368.9	353.9	114.1	139.3	156.3	264.6
Q9VXY3	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex OS=Drosophila melanog	11.834	9	3	3	3	462	50	6.61	9.77	3	0	61.8	29	82.7	97.1	33.4	37.4	39.3	96.7
Q9VVL7	Dihydrolipoyl dehydrogenase OS=Drosophila melanogaster OX=7227 GN=E3 PE=1 SV=1	84.487	19	8	26	8	504	53.1	6.87	90.67	8	0	2294.8	1073.9	4185.5	2751.3	817.5	1005.8	1994.6	2363.1
P32748	Dihydroorotate dehydrogenase (quinone), mitochondrial OS=Drosophila melanogaster OX=7227 GN=Dhod P	20.044	13	4	5	4	405	44.3	9.25	18.68	4	0	480.2	243.3	998.4	737.7	149.3	220.7	476.8	711.4

Q9VSU6	Dihydropteridine reductase OS=Drosophila melanogaster OX=7227 GN=Dhpr PE=1 SV=1	27.738	25	4	10	4	235	24.5	6.34	28.74	4	0	937.6	555.3	1304.4	1104	332	408.1	496.8	465.7
Q9W374	Dihydropyrimidine dehydrogenase [NADP(+)] OS=Drosophila melanogaster OX=7227 GN=su(r) PE=1 SV=2	26.34	5	5	7	5	1031	111.2	6.8	21.05	5	0	230.7	131.7	246.9	316	82.1	135.7	125.3	122.3
Q9VH38	Dimethyladenosine transferase 2, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mtTFB2 PE=2 S	17.237	8	3	4	3	452	52.1	7.46	13.68	3	0	130.5	70.4	287	154.5	43.3	64.4	128	88
Q9VFQ9	Dipeptidase B, isoform A OS=Drosophila melanogaster OX=7227 GN=Dip-B PE=1 SV=2	84.579	24	10	32	10	508	55.5	6.76	107.75	10	0	1553.9	747.5	2547	2355.7	709.8	844.9	1132.3	1648.3
Q9VHR8	Dipeptidyl peptidase 3 OS=Drosophila melanogaster OX=7227 GN=DppIII PE=2 SV=2	52.656	17	11	14	11	786	89.1	6.43	41.96	11	0	2886.2	1324.9	2807	2431.5	994.7	985.6	1160.6	2294.6
Q9W0T7	Dis3 like 3'-5' exoribonuclease 2, isoform A OS=Drosophila melanogaster OX=7227 GN=Dis3l2 PE=1 SV=2	8.157	3	2	2	2	1032	116.8	8.18	6.03	2	0	36.7	16.1	35.8	41.9	17.7	26.8	22.3	21.3
Q9VC93	Dis3, isoform A OS=Drosophila melanogaster OX=7227 GN=Dis3 PE=1 SV=1	22.518	8	6	7	6	982	112.1	6.68	18.49	6	0	766.4	350.7	526.8	594.6	304.9	292.6	260.4	326.8
M9NGZ2	Discs large 1, isoform Q OS=Drosophila melanogaster OX=7227 GN=dlg1 PE=1 SV=1	12.313	6	3	3	3	975	104	7.14	10.53	3	0	156.2	73.1	148.1	173.6	80.7	81.4	69.3	92.2
Q9XYZ5	DNA damage-binding protein 1 OS=Drosophila melanogaster OX=7227 GN=pic PE=1 SV=1	91.875	18	12	29	12	1140	126	5.36	98.06	12	0	3241.4	1483.7	1918.4	2365.3	1341.4	1160.8	933.9	1484.5
A0A0B4LEV2	DNA helicase OS=Drosophila melanogaster OX=7227 GN=dpa PE=1 SV=1	55.693	17	12	20	12	866	96.6	7.52	61.4	12	0	4329.2	1635.5	2094.2	2834.9	1661.9	1330.5	943.4	2443.7
X2JAI4	DNA helicase OS=Drosophila melanogaster OX=7227 GN=Mcm3 PE=1 SV=1	74.868	20	14	23	14	818	90.7	6.33	78.25	14	0	3294.2	1373.3	1850.6	2299.7	1258.6	1050.5	807.8	1599.1
Q9W1H4	DNA ligase 1 OS=Drosophila melanogaster OX=7227 GN=DNAlig1 PE=1 SV=2	21.737	9	5	7	5	747	84.7	6.62	18.03	5	0	1148.3	591.7	822.4	1115.3	540.7	483.5	365.3	518.1
M9NEY8	DNA N6-methyl adenine demethylase OS=Drosophila melanogaster OX=7227 GN=Tet PE=1 SV=1	17.534	1	3	3	3	2860	306.5	7.74	11.54	3	0	775.9	353.7	509.5	605.1	319.4	310.8	313.4	336.3
P26019	DNA polymerase alpha catalytic subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-alpha180 PE=1	26.406	6	6	7	6	1488	169.8	8.02	20.15	6	0	837.3	384.8	520.3	566.6	326.5	217.3	196.3	391.2
P54358	DNA polymerase delta catalytic subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-delta PE=2 SV=	38.435	8	8	11	8	1092	124.8	6.92	30.19	8	0	1433.2	804.9	850	726.2	590.5	291.3	184	259
Q9W088	DNA polymerase delta small subunit OS=Drosophila melanogaster OX=7227 GN=CG12018 PE=2 SV=1	26.447	15	5	10	5	431	48	6.52	43.02	5	0	1214.8	612.3	694.6	780.1	485.2	267.1	170.4	294.6
Q9VCN1	DNA polymerase epsilon catalytic subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-epsilon255 PE	20.44	3	6	7	6	2236	256.5	6.47	19.06	6	0	1293.1	700.6	778.8	1199.3	570.9	334.4	270.6	606.1
Q9VRQ7	DNA polymerase epsilon subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-epsilon58 PE=3 SV=1	5.456	4	2	2	2	525	58.7	6.48	5.11	2	0	228	118.1	159.8	165.3	87.8	74.9	55.8	69.2
Q9VJV8	DNA polymerase gamma 35kD OS=Drosophila melanogaster OX=7227 GN=DNApol-gamma35 PE=2 SV=2	19.894	16	4	4	4	361	41	7.39	13.55	4	0	193.9	103.1	298.3	266.6	96.5	103.5	159.9	205.7
Q27607	DNA polymerase subunit gamma-1, mitochondrial OS=Drosophila melanogaster OX=7227 GN=tam PE=1 SV=	15.498	3	4	4	4	1145	129.7	7.46	11.58	4	0	315.9	170.9	606.5	517.9	130.9	141.9	273.1	470.5
Q9VPH2	DNA primase large subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-alpha60 PE=1 SV=2	27.053	13	6	8	6	533	61.4	6.96	25.12	6	0	1548.7	777.4	905.1	981.3	683.1	404.4	275.5	424
Q24317	DNA primase small subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-alpha50 PE=2 SV=2	4.399	3	2	2	2	438	50.2	7.5	4.68	2	0	410.9	207.5	305.2	389.5	147.5	83.1	75.6	304.5
Q24595	DNA repair protein complementing XP-C cells homolog OS=Drosophila melanogaster OX=7227 GN=Xpc PE=	8.087	1	2	2	2	1293	144.1	9.29	5.43	2	0	401.6	190.5	427.4	530.2	180.3	198.2	212.3	224.1
P49735	DNA replication licensing factor Mcm2 OS=Drosophila melanogaster OX=7227 GN=Mcm2 PE=1 SV=1	34.315	11	9	14	9	887	100.4	5.11	29.53	9	0	1201.1	580.5	973.5	1081.4	516.9	484.1	421	728.9
Q9VGW6	DNA replication licensing factor Mcm5 OS=Drosophila melanogaster OX=7227 GN=Mcm5 PE=1 SV=1	71.753	24	13	27	13	733	82.2	7.84	93.79	13	0	3123.1	1425.5	1906.3	2325.9	1288.2	1102.6	869.5	1463.5
Q9V461	DNA replication licensing factor Mcm6 OS=Drosophila melanogaster OX=7227 GN=Mcm6 PE=1 SV=1	52.743	15	10	15	10	817	92.3	5.38	53.72	10	0	2463.1	1041	1376.3	1840	902.4	686.6	583.4	1121.4
Q9XYU0	DNA replication licensing factor Mcm7 OS=Drosophila melanogaster OX=7227 GN=Mcm7 PE=1 SV=1	41.596	14	8	13	8	720	81.2	6.99	38	8	0	1672.5	708	1006.6	1351	629.9	528.6	441.2	1323
Q94883	DNA replication-related element factor, isoform A OS=Drosophila melanogaster OX=7227 GN=Dref PE=1 SV=	25.941	7	5	7	5	709	80.7	5.86	21.85	5	0	3796.2	1082	1339.8	1620.4	1307.3	1335.2	947.1	2092.8
P15348	DNA topoisomerase 2 OS=Drosophila melanogaster OX=7227 GN=Top2 PE=1 SV=1	247.598	32	43	77	43	1447	164.3	8.22	246.54	43	0	20245	8159	7085.9	8581.4	7691.6	5744.9	3222.3	5405.9
Q9NG98	DNA topoisomerase 3-alpha OS=Drosophila melanogaster OX=7227 GN=Top3alpha PE=2 SV=2	15.104	5	6	8	6	1250	136.1	8.31	18.66	6	0	1067.2	432.1	1550.7	1184	287.4	326.4	636.6	982.7
O96651	DNA topoisomerase 3-beta OS=Drosophila melanogaster OX=7227 GN=Top3beta PE=2 SV=2	8.816	2	2	2	2	875	96.9	8.19	6.37	2	0	482.6	205.6	544.7	578.1	170.9	229.1	299.7	312.6
P13469	DNA-binding protein modulo OS=Drosophila melanogaster OX=7227 GN=mod PE=1 SV=2	41.328	17	7	15	7	542	60.3	5.43	48.08	7	0	2538.7	871.1	1077.4	1384.8	1145.2	1019	641.1	1943.5
P91875	DNA-directed RNA polymerase I subunit RPA1 OS=Drosophila melanogaster OX=7227 GN=RpI1 PE=1 SV=2	9.213	2	2	3	1	1642	185.3	7.64	8.18	2	0	65.7	30.3	52.7	41.3	17.7	33.4	22.2	57.3
P20028	DNA-directed RNA polymerase I subunit RPA2 OS=Drosophila melanogaster OX=7227 GN=RpI135 PE=1 SV	21.151	6	5	6	4	1129	128.4	8.41	20.38	5	0	359.4	142	205.3	225.4	136.9	132.6	115	212.9
P04052	DNA-directed RNA polymerase II subunit RPB1 OS=Drosophila melanogaster OX=7227 GN=RpII215 PE=3 S	44.514	7	14	16	13	1887	209	7.81	40.98	14	1	2764.5	957.7	1238	1539.8	981.3	1121.7	849.4	1268.1
P08266	DNA-directed RNA polymerase II subunit RPB2 OS=Drosophila melanogaster OX=7227 GN=RpII140 PE=2 S	14.57	4	5	5	4	1176	134	7.05	12.84	5	1	2226.1	853.6	860.6	957.2	798.6	980.8	766.1	593.5
Q9VEA5	DNA-directed RNA polymerase II subunit Rpb4 OS=Drosophila melanogaster OX=7227 GN=Rpb4 PE=2 SV=	6.038	12	2	2	2	139	16.2	4.82	5.3	2	0	409.7	128.4	171.7	265.6	150	136.6	115.4	263.1
A8JUY3	DNA-directed RNA polymerase subunit OS=Drosophila melanogaster OX=7227 GN=RpIIIC160 PE=1 SV=2	4.332	1	2	2	2	1383	154.5	8.57	2.55	2	0	642.7	176.1	325.6	341.5	206	247.2	194.6	492.4
Q9VPQ2	DnaJ homolog shv OS=Drosophila melanogaster OX=7227 GN=shv PE=1 SV=1	29.594	17	4	12	4	354	40.2	5.67	41.23	4	0	343.2	204.2	1020.3	1121.5	185	206.6	479.4	495
Q9VFV9	DnaJ-like-2, isoform A OS=Drosophila melanogaster OX=7227 GN=Droj2 PE=1 SV=1	67.101	30	8	13	8	403	45.2	6.48	56.1	8	0	2754.7	1232.7	2037.7	1791.8	1004.6	1152.6	1194.7	980.3
Q7KN75	Dodeca-satellite-binding protein 1, isoform A OS=Drosophila melanogaster OX=7227 GN=Dp1 PE=1 SV=1	64.064	11	11	19	11	1301	144.2	6.2	59.43	11	0	1535.7	676.4	1493.1	1593.9	572.9	795.5	845.4	892.8
Q24319	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Drosophila melanogaster	20.59	13	5	9	5	449	50	5.59	27.12	5	0	586.4	272.1	782.5	841.3	213.7	278.5	361.9	976.3
Q76NQ0	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Drosophila melanogaster OX=7	15.65	10	4	4	4	458	51.7	8.05	11.99	4	0	232.8	94	365.5	487.3	96.6	92.6	173.8	1028.1
Q9VLQ1	Dolichyl-phosphate beta-glucosyltransferase OS=Drosophila melanogaster OX=7227 GN=wol PE=1 SV=1	5.084	5	2	2	2	326	37.1	8.06	4.36	2	0	85.5	38.2	130.7	157.1	41.8	36.2	62.5	108.6
Q8MLW2	Domino, isoform D OS=Drosophila melanogaster OX=7227 GN=dom PE=1 SV=1	20.401	2	4	4	4	3183	348.2	8.87	10.66	4	0	353.2	170.2	374.9	319.7	165.2	181.1	204.7	166.9
B7Z0Z0	Dorsal switch protein 1, isoform F OS=Drosophila melanogaster OX=7227 GN=Dsp1 PE=1 SV=1	27.822	10	2	5	2	397	45.3	8.41	19.02	2	0	286.4	69.9	101.5	86.8	107.4	50.5	57.5	37.5
P24785	Dosage compensation regulator OS=Drosophila melanogaster OX=7227 GN=mle PE=1 SV=2	28.386	6	6	7	6	1293	143.6	7.23	23.93	6	0	1181.3	359.2	421.7	417.3	439.1	381.2	304.3	317
O18335	Drab11 OS=Drosophila melanogaster OX=7227 GN=Rab11 PE=1 SV=1	17.242	24	6	7	6	214	24.2	5.73	19.61	6	0	1085.7	548.1	1800.8	1596.7	309.8	512.6	917.5	1108.4
Q9V3I2	Drab5 OS=Drosophila melanogaster OX=7227 GN=Rab5 PE=1 SV=1	8.455	14	2	2	2	219	23.9	8.41	6.12	2	0	150.3	110.7	222.5	222	125.7	101.9	92.1	143.1
Q7KHK9	DREAM OS=Drosophila melanogaster OX=7227 GN=Strica PE=1 SV=1	5.475	3	2	2	2	527	57.4	9.8	4.9	2	0	153.7	81.1	195.6	123.3	65.1	105.6	99.6	59.5
Q8STG9	DSec61alpha OS=Drosophila melanogaster OX=7227 GN=Sec61alpha PE=1 SV=1	13.299	6	3	5	3	476	52.2	8.24	16.69	3	0	288.1	109.2	296.4	353.8	118.3	105.3	152.2	289.2
Q9V3V0	DXl6 protein OS=Drosophila melanogaster OX=7227 GN=x16 PE=1 SV=1	16.427	17	3	7	3	258	27.9	11.56	22.58	3	0	597.4	221.8	311.4	336.5	268.9	272.5	217.6	227.2
Q7KNA0	Dymeclin OS=Drosophila melanogaster OX=7227 GN=CG8230 PE=1 SV=1	7.36	3	2	2	2	699	79.1	6.01	3.04	2	0	44.1	27.1	64	71.2	24.7	31.9	31.2	34.1
Q7K130	Dynactin 4, p62 subunit OS=Drosophila melanogaster OX=7227 GN=DCTN4-p62 PE=1 SV=1	12.304	7	3	3	3	514	57.9	8.22	10.23	3	0	294.8	171.2	386.9	434.6	116	155.2	237.1	178.1
P13496	Dynactin subunit 1 OS=Drosophila melanogaster OX=7227 GN=DCTN1-p150 PE=1 SV=2	11.962	2	3	3	3	1265	141.1	5.62	8.23	3	0	218.2	120.7	275.4	297.7	93.2	119.5	152.7	144
M9PBF6	Dynamin associated protein 160, isoform G OS=Drosophila melanogaster OX=7227 GN=Dap160 PE=1 SV=1	8.566	2	2	2	2	1088	119.8	5.16	6.23	2	0	221.9	109.8	283.9	309.4	106.4	125.9	155.6	133.8
Q9VQE0	Dynamin related protein 1, isoform A OS=Drosophila melanogaster OX=7227 GN=Drp1 PE=1 SV=1	23.301	6	5	6	5	735	82.5	6.98	19.1	5	0	452.8	231.6	550.8	453.9	151.4	260	296.5	283.4
M9PEC8	Dynein heavy chain 64C, isoform G OS=Drosophila melanogaster OX=7227 GN=Dhc64C PE=1 SV=1	47.376	3	11	11	11	4648	530.8	6.33	35.46	11	0	722.8	350.3	962.3	945.4	314.1	391	445.7	479.5
Q9VZ20	Dynein light intermediate chain, isoform A OS=Drosophila melanogaster OX=7227 GN=Dlic PE=1 SV=2	14.335	7	3	3	3	493	54.4	6.02	9.95	3	0	338	157.2	344.1	351.7	136.8	159.3	207.5	218.8
A0A0B4K7J2	E3 SUMO-protein ligase RanBP2 OS=Drosophila melanogaster OX=7227 GN=Nup358 PE=1 SV=1	7.596	1	2	2	2	2718	298.7	6.11	6.59	2	0	754.2	236	554.8	493.5	201.7	288.8	343	257.3
Q95RX5	E3 ubiquitin-protein ligase Kcmf1 OS=Drosophila melanogaster OX=7227 GN=Kcmf1 PE=1 SV=1	21.95	5	3	5	3	599	62.4	5.72	20.63	3	0	49.1	23	60.4	62.2	21.2	39.8	50.1	40.1
P50534	E3 ubiquitin-protein ligase msl-2 OS=Drosophila melanogaster OX=7227 GN=msl-2 PE=1 SV=2	9.631	5	2	3	2	773	84.8	4.94	7.93	2	0	57.4	28.1	62.1	59.8	25.4	32.7	47.3	65.5
B7YZY9	E3 ubiquitin-protein ligase OS=Drosophila melanogaster OX=7227 GN=Su(dx) PE=1 SV=1	3.156	2	2	2	2	949	107.9	7.21	4.57	2	0	294.6	148.5	250.5	335.7	119.1	150.1	132.8	152
Q9XZ57	Eb1, isoform E OS=Drosophila melanogaster OX=7227 GN=Eb1 PE=1 SV=1	17.366	19	4	5	4	290	32.5	5.34	14.38	4	0	646	264.9	489	457.1	206.3	273.3	321.2	303.1
Q9VJ26	EF-hand domain-containing protein D2 homolog OS=Drosophila melanogaster OX=7227 GN=Swip-1 PE=2 S	9.144	11	2	2	2	217	25.1	5.14	6.31	2	0								
O76876	EG:132E8.1 protein OS=Drosophila melanogaster OX=7227 GN=ssx PE=1 SV=1	5.885	5	2	2	2	485	53.4	7.01	6.21	2	0	402.6	188.8	237.8	263.4	166.1	163.2	124.9	160.4
O46048	EG:133E12.4 protein OS=Drosophila melanogaster OX=7227 GN=east PE=1 SV=1	15.97	2	3	3	3	2342	250	6.23	9.57	3	0	703.5	326.2	406.3	412.2	282.3	293.6	243.7	241.4
O97418	EG:152A3.7 protein OS=Drosophila melanogaster OX=7227 GN=ND-B14.5A PE=1 SV=1	12.106	30	3	7	3	103	11.5	7.34	21.1	3	0	461.1	276.7	1338.5	845.9	146.4	211.1	673.7	622.1
O46067	EG:25E8.1 protein OS=Drosophila melanogaster OX=7227 GN=EG:25E8.1 PE=1 SV=1	53.432	12	10	23	10	923	103.4	5.12	76.47	10	0	1419.3	611.1	4926.2	4031.9	447.9	473.1	2048.9	2620.5
O77434	EG:34F3.8 protein OS=Drosophila melanogaster OX=7227 GN=Sec22 PE=1 SV=2	11.195	14	2	2	2	211	24.6	9.29	6.64	2	0	105.8	40.9	96.5	102.2	34.1	61.5	45.7	82.1
Q9W4Z2	EG:BACH48C10.6 protein OS=Drosophila melanogaster OX=7227 GN=mRpL14 PE=2 SV=1	11.303	22	3	6	3	161	17.7	10.35	18.7	3	0	1106.2	976.8	1845.3	1249.1	404.5	505.8	815.5	998.5
Q9W592	EG:BACN32G11.3 protein OS=Drosophila melanogaster OX=7227 GN=Lrpprc2 PE=1 SV=1	47.223	12	8	20	8	1072	120.1	8.22	65.72	8	0	605.9	390.9	1216.9	1268.5	268.5	340.9	547.2	767.7
Q9XZ29	EG:BACR25B3.9 protein OS=Drosophila melanogaster OX=7227 GN=Klp3A PE=1 SV=1	18.533	4	4	4	4	1212	135.7	7.01	10.01	4	0	606.9	199.2	224	313.2	239.5	219.3	159.3	162.6
Q7JXZ2	Eip55E, isoform A OS=Drosophila melanogaster OX=7227 GN=Eip55E PE=1 SV=1	11.953	6	2	3	2	393	43	7.62	8.72	2	0	131.9	76.3	109.9	124.9	63.4	64.3	57.7	84.2
Q7JWF1	Electron transfer flavoprotein-ubiquinone oxidoreductase, isoform A OS=Drosophila melanogaster OX=7227 (	42.57	16	8	19	8	604	65.9	6.64	58.01	8	0	1189.1	609.8	2321	1998.3	439.9	1305	1022.9	1859.4
P08736	Elongation factor 1-alpha 1 OS=Drosophila melanogaster OX=7227 GN=eEF1alpha1 PE=1 SV=2	17.045	10	5	9	5	463	50.3	9.07	23.96	5	0	2137.8	754.7	2399	2324.4	615.3	810.1	1429.5	3440.2
Q9NJH0	Elongation factor 1-gamma OS=Drosophila melanogaster OX=7227 GN=eEF1gamma PE=2 SV=2	38.539	22	6	11	6	431	48.9	7.05	34.35	6	0	1197.6	510.2	1252.6	999.3	434.2	517.9	743.3	787.6
P13060	Elongation factor 2 OS=Drosophila melanogaster OX=7227 GN=EF2 PE=1 SV=4	109.558	29	18	61	18	844	94.4	6.6	186.8	18	0	6848.7	2702.5	6305.3	6095.7	2445.9	3102.8	3725.6	4904.9
Q9VM33	Elongation factor G, mitochondrial OS=Drosophila melanogaster OX=7227 GN=ico PE=2 SV=2	53.577	19	14	27	14	745	83.5	6.73	68.85	14	0	2304.2	1166.5	4551.3	4606.3	849.5	1001.6	1926.2	4725.2
Q9VJC7	Elongation factor Ts, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mEFTs PE=2 SV=1	9.73	10	4	11	4	318	35.4	6.87	26.31	4	0	1038.8	520.3	2224.5	1982.1	331.8	432.9	829.6	1403.2
A1Z9E3	Elongation factor Tu OS=Drosophila melanogaster OX=7227 GN=mEFTu1 PE=1 SV=1	151.34	37	12	142	12	489	54	8.03	526.12	12	0	4201.1	2103.4	7301	6811.8	1771.5	2175.5	3404.8	6320.4
A0A0B4LFX0	Enabled, isoform G OS=Drosophila melanogaster OX=7227 GN=ena PE=4 SV=1	10.453	6	2	2	2	664	69.6	9.33	8.05	2	0	85	47	103.6	116.1	33.9	52.1	55	47.2
Q9V3V9	Endonuclease G inhibitor, isoform A OS=Drosophila melanogaster OX=7227 GN=EndoGI PE=1 SV=1	32.797	22	6	8	6	359	40.6	4.6	27.11	6	0	1731.8	558.6	696.6	791.4	649.3	460.6	388	1857.2
Q9VIH0	Endonuclease III homolog OS=Drosophila melanogaster OX=7227 GN=NTH1 PE=3 SV=2	10.776	9	2	2	2	388	43.5	9.51	8.34	2	0	89.6	49.5	125.3	136.4	41.9	59.2	49.8	77.9
P29844	Endoplasmic reticulum chaperone BiP OS=Drosophila melanogaster OX=7227 GN=Hsc70-3 PE=1 SV=2	120.904	28	16	144	15	656	72.2	5.36	463.59	16	0	3723.1	1824.6	16028.3	16242.3	1313.4	1689.4	6820.9	7429.6
M9PE12	Enhancer of bithorax, isoform I OS=Drosophila melanogaster OX=7227 GN=E(bx) PE=1 SV=1	39.794	4	9	11	9	2668	300.4	8.54	32.8	9	0	2334	892.2	973.8	1396.5	864.3	982.8	696.9	935.9
Q9VKK1	Enhancer of mRNA-decapping protein 4 homolog OS=Drosophila melanogaster OX=7227 GN=Ge-1 PE=1 S\	6.748	2	3	3	3	1354	149.2	5.9	7.4	3	0	322.1	188.8	433.1	493.3	132.8	214.1	259.9	257.5
M9PHZ0	Enhancer of yellow 3, isoform D OS=Drosophila melanogaster OX=7227 GN=e(y)3 PE=4 SV=1	30.753	4	8	8	8	2011	213.3	7.52	23.18	8	0	1704.4	766.9	971	1017.6	661.4	664.6	556.3	561.7
Q5U117	Enigma OS=Drosophila melanogaster OX=7227 GN=Egm PE=1 SV=1	106.89	31	16	45	16	639	70.8	6.44	146.31	16	0	2120.6	1184.2	4801.1	4042.4	880.4	1045.9	2016.1	4653.8
P15007	Enolase OS=Drosophila melanogaster OX=7227 GN=Eno PE=1 SV=2	93.52	29	11	72	11	500	54.3	8.53	243.96	11	0	4017.7	1859.7	4476.8	4422.1	1553.1	1806.7	2444.7	2850
Q9V6U9	Enoyl-[acyl-carrier-protein] reductase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=CG16935 PE	14.038	10	3	7	3	357	39.1	9.11	12.67	3	0	180	92.4	314	255.6	87.4	89.2	157	293.6
M9PBN6	Ensconsin, isoform J OS=Drosophila melanogaster OX=7227 GN=ens PE=1 SV=1	14.848	4	3	5	3	968	106.2	8.66	17.01	3	0	859.9	362.1	785.7	751.5	332	395.6	461.8	454.6
Q9VHY6	ER membrane protein complex 1, isoform A OS=Drosophila melanogaster OX=7227 GN=EMC1 PE=1 SV=1	18.667	7	5	7	5	915	100.9	8.13	18.5	5	0	525	276.6	695	796.9	219	278	370.3	559
Q9V3A8	Ergic53, isoform A OS=Drosophila melanogaster OX=7227 GN=ergic53 PE=1 SV=1	8.425	4	2	2	2	512	57.5	6.07	6.89	2	0	322.8	127.5	395.4	358.8	119.7	132	208.5	315.9
Q9VDL1	Esterase CG5412 OS=Drosophila melanogaster OX=7227 GN=CG5412 PE=2 SV=1	14.09	10	2	3	2	279	30.6	5.29	8.78	2	0	373	216.9	338.2	389.2	145.8	170	175.8	155.4
Q9VHS8	Eukaryotic initiation factor 4A-III OS=Drosophila melanogaster OX=7227 GN=CG7483 PE=1 SV=1	8.217	6	2	2	1	399	45.6	6.02	6.18	2	0	164.9	76.2	104.6	146.8	68.4	82.1	62.9	73.8
A0A0B4LFL3	Eukaryotic translation elongation factor 1 beta, isoform C OS=Drosophila melanogaster OX=7227 GN=eEF1b	19.086	23	4	6	4	222	24.2	4.58	19.09	4	0	240	66.1	366	280	76.1	68.5	143.4	882.7
P41374	Eukaryotic translation initiation factor 2 subunit 1 OS=Drosophila melanogaster OX=7227 GN=eIF2alpha PE=	34.158	26	9	12	9	341	38.6	4.94	37.92	9	0	1969	861.2	1693.3	1982.9	804.2	831.4	974.2	1299.6
A0A0B4KGP8	Eukaryotic translation initiation factor 2 subunit gamma, isoform D OS=Drosophila melanogaster OX=7227 GN	23.826	15	7	12	7	475	51.5	8.73	35.73	7	0	2084.8	790.1	1764.1	1808	669	970.3	1028.8	1180.8
Q9W1Q8	Eukaryotic translation initiation factor 2B subunit delta, isoform A OS=Drosophila melanogaster OX=7227 GN=	8.472	4	2	2	2	626	67.6	9.44	6.99	2	0	393.4	169.1	460.8	443.3	148.7	204	257.2	290.2
Q9W541	Eukaryotic translation initiation factor 2B subunit epsilon, isoform A OS=Drosophila melanogaster OX=7227 G	7.997	5	2	2	2	669	75	5.07	5.78	2	0	59.3	33	82.4	90.8	32.5	41.9	36.8	62.2
Q9VN25	Eukaryotic translation initiation factor 3 subunit A OS=Drosophila melanogaster OX=7227 GN=eIF3a PE=1 S\	77.374	18	18	22	18	1140	133.8	9.01	69.03	18	0	3622.8	1537.9	3700.8	3875.1	1737.2	1708.7	2178.3	2948.6
E2QCG7	Eukaryotic translation initiation factor 3 subunit B OS=Drosophila melanogaster OX=7227 GN=eIF3b PE=1 S\	46.361	16	9	16	9	690	80.4	6.28	50.25	9	0	1675.1	675.8	1699.2	1875.9	643.8	827.9	876.1	1361
A0A0B4LFL2	Eukaryotic translation initiation factor 3 subunit C OS=Drosophila melanogaster OX=7227 GN=eIF3c PE=3 S\	42.212	13	9	12	9	910	105.6	6.06	37.82	9	0	1450.6	576.3	1575.5	1723.9	544.8	642.7	863.6	1383.1
Q9U9Q4	Eukaryotic translation initiation factor 3 subunit H OS=Drosophila melanogaster OX=7227 GN=eIF3h PE=1 S\	6.809	6	2	3	2	338	38.4	6.1	9.16	2	0	334.7	163.4	373	417.7	135.1	170.3	234.9	170.2
O02195	Eukaryotic translation initiation factor 3 subunit I OS=Drosophila melanogaster OX=7227 GN=eIF3i PE=1 SV=	37.014	21	5	13	5	326	36.1	5.34	41.65	5	0	1740.1	720	1415.5	1365	660.6	843.4	806.5	767.9
Q9W2D9	Eukaryotic translation initiation factor 3 subunit K OS=Drosophila melanogaster OX=7227 GN=eIF3k PE=2 S\	12.967	18	3	5	3	222	25.6	6.43	16.33	3	0	266.8	106.1	241.6	301.4	89.8	113.6	140	206.7
Q9VTU4	Eukaryotic translation initiation factor 3 subunit L OS=Drosophila melanogaster OX=7227 GN=eIF3l PE=2 SV	6.53	5	2	2	2	539	63.2	5.96	5.85	2	0	333.1	120.1	271.8	241	126.5	134.4	205.6	181.1
Q7JVI3	Eukaryotic translation initiation factor 3 subunit M OS=Drosophila melanogaster OX=7227 GN=eIF3m PE=2 S	8.913	6	2	2	2	387	44.1	5.71	6.88	2	0	478	233.1	522.9	586.1	192.6	274.9	329.9	396.2
C9QP42	Eukaryotic translation initiation factor 4A, isoform E OS=Drosophila melanogaster OX=7227 GN=eIF4A PE=1	82.152	32	10	47	9	403	45.8	5.66	140.44	10	1	4695.3	1768.9	3387.8	4425.8	1686	1943.9	1837.2	3922.1
A8DZ29	Eukaryotic translation initiation factor 4G1, isoform B OS=Drosophila melanogaster OX=7227 GN=eIF4G1 PE	105.048	13	18	30	18	1919	211	8.35	90.49	18	0	3030.3	1386.4	3251.3	3186.6	1122.3	1633.3	1957.3	1841.3
X2JC79	Eukaryotic translation initiation factor 4H1, isoform D OS=Drosophila melanogaster OX=7227 GN=eIF4H1 PE	20.443	10	3	10	3	388	41.7	9.79	31.58	3	0	766.2	364.8	729.9	685.6	309.6	352.4	437.8	296.6
Q9GU68	Eukaryotic translation initiation factor 5A OS=Drosophila melanogaster OX=7227 GN=eEF5 PE=2 SV=2	30.187	41	6	7	6	159	17.6	5.15	22.73	6	0	2590.4	949.9	1552.6	1282.9	913.2	1066.1	936	1319.2
M9NFL1	Eukaryotic translation initiation factor 5B, isoform D OS=Drosophila melanogaster OX=7227 GN=eIF5B PE=1	27.553	3	2	2	2	1090	121	5.5	11.39	2	0	254.5	121.3	296.4	251.2	81.1	150.3	180.5	107.9
P56538	Eukaryotic translation initiation factor 6 OS=Drosophila melanogaster OX=7227 GN=eIF6 PE=2 SV=3	7.053	17	2	2	2	245	26.5	4.73	5.86	2	0	119.8	80.3	176.6	188.7	85.5	71.4	82.5	134
M9PFR9	Eukaryotic translation release factor 1, isoform I OS=Drosophila melanogaster OX=7227 GN=eRF1 PE=1 SV=	9.402	9	2	3	2	447	49.7	7.46	5.9	2	0	145.6	61.5	153.2	167.3	52.4	79	69.8	111
Q9U6M0	Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial OS=Drosophila melanogaster O	36.951	24	6	14	6	409	47	6.73	49.36	6	0	519.8	307.1	1100	823.8	259.3	305.8	488.9	843.5
Q9TVM2	Exportin-1 OS=Drosophila melanogaster OX=7227 GN=emb PE=1 SV=1	26.497	8	6	10	6	1063	122.7	5.87	32.24	6	0	639.2	237.2	397.2	448.5	229.2	283	240.1	329.5
A0A0B4K6F9	Extended synaptotagmin-like protein 2, isoform C OS=Drosophila melanogaster OX=7227 GN=Esyt2 PE=1 S	47.674	13	6	9	6	853	94.8	6.15	39.06	6	0	511.7	236.4	794	641.6	178.4	238.8	376.1	397.3
Q9W2N0	F-actin-capping protein subunit alpha OS=Drosophila melanogaster OX=7227 GN=cpa PE=2 SV=1	14.414	18	3	4	3	286	32.7	5.94	13.42	3	0	913.2	418.3	732.7	777.8	351.6	433.8	403	499.6

P48603	F-actin-capping protein subunit beta OS=Drosophila melanogaster OX=7227 GN=cpb PE=2 SV=1	3.23	8	2	3	2	276	31.3	5.44	3.87	2	0	277.8	106.4	255.1	354.7	101.2	129.1	122.6	203.2
Q8IRG6	FACT complex subunit spt16 OS=Drosophila melanogaster OX=7227 GN=dre4 PE=1 SV=2	58.556	9	9	17	9	1083	123.5	6.29	65.72	9	0	6747.1	3052	2811	3044.8	2572.7	1555.6	1002	1329.2
Q05344	FACT complex subunit Ssrp1 OS=Drosophila melanogaster OX=7227 GN=Ssrp PE=1 SV=2	50.088	16	10	21	10	723	81.5	5.63	59.35	10	0	4801.7	1938.6	2279.1	2963.1	1796.2	1100	797	1654.3
Q8MYL1	Fancd2 OS=Drosophila melanogaster OX=7227 GN=Fancd2 PE=2 SV=1	5.744	1	2	2	2	1478	167.4	6.89	5.02	2	0	482.9	197	347.7	629.4	160.1	213	173.2	530.1
Q7KN61	Farnesyl pyrophosphate synthase OS=Drosophila melanogaster OX=7227 GN=Fpps PE=1 SV=1	26.664	12	5	10	5	419	47.9	6.92	29.38	5	0	684.9	313.7	1152.3	877.2	289.4	331.1	512.2	1415
Q9VR31	Farnesyl transferase alpha, isoform A OS=Drosophila melanogaster OX=7227 GN=Fnta PE=1 SV=1	10.951	7	2	3	2	331	38.9	5.17	11.07	2	0	425.4	239.3	301.3	402.6	166.2	206.1	168.5	188.3
Q9VJ58	Fas-associated factor 2, isoform A OS=Drosophila melanogaster OX=7227 GN=Faf2 PE=1 SV=1	12.527	5	3	3	3	464	52.9	5.38	9.22	3	0	231.9	130.2	314.8	308.9	108.9	137.7	154.9	131.3
Q9VKU1	Fatty acid (Long chain) transport protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Fatp1 PE=1	12.809	6	3	3	3	626	70.1	8.84	6.74	3	0	161.7	99.5	333.9	355.7	86.8	116	169.7	133
Q9VGM2	Fatty acid binding protein, isoform B OS=Drosophila melanogaster OX=7227 GN=fabp PE=1 SV=1	22.573	37	4	10	4	130	14.5	5.66	35.9	4	0	2247.3	977.4	1159.5	1208.5	767.4	878.7	571.5	714.9
Q9VQL7	Fatty acid synthase 1, isoform A OS=Drosophila melanogaster OX=7227 GN=FASN1 PE=1 SV=1	169.513	18	28	48	28	2438	266.3	6.37	162.44	28	0	4466.4	1941.2	3871.5	4421.6	1544.8	2046.1	2195.5	3666.1
M9MRX8	Ferredoxin 1, isoform B OS=Drosophila melanogaster OX=7227 GN=Fdx1 PE=4 SV=1	12.106	11	2	3	2	172	19.7	7.03	10.51	2	0	46.6	26.4	78	63	20.3	33.5	40.5	40.1
Q8SZA8	Ferredoxin 2 OS=Drosophila melanogaster OX=7227 GN=Fdx2 PE=1 SV=1	18.157	33	3	7	3	152	16.4	5.35	19.12	3	0	265.4	150.3	402.5	412.7	441.3	179.8	354.3	364.7
H1UUD2	Ferritin OS=Drosophila melanogaster OX=7227 GN=Fer1HCH PE=1 SV=1	7.817	14	2	2	2	169	19.2	6.11	4.28	2	0	18.9	9.2	90.7	83.3	11.7	15.1	40.4	34.2
Q9V9S8	Ferrochelatase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=FeCh PE=2 SV=1	25.394	13	5	13	5	384	43.6	8.4	39.69	5	0	333.8	208	870.2	652.6	159.2	166	367.8	388.8
Q0E8X8	FI01416p OS=Drosophila melanogaster OX=7227 GN=SK[[66]] PE=1 SV=1	10.971	19	3	9	3	107	11.9	9	18.33	3	0	574	315.6	1090.1	634.3	227.7	237.2	630.5	461.8
O18332	FI01544p OS=Drosophila melanogaster OX=7227 GN=Rab1 PE=1 SV=1	25.877	27	4	13	3	205	22.7	5.47	41.46	4	0	439.1	243.9	953	938.8	214.8	282.3	408.8	616.9
Q9W0A8	FI01658p OS=Drosophila melanogaster OX=7227 GN=RpL23A PE=1 SV=1	21.4	10	3	7	3	277	29.4	10.95	22.64	3	0	756.4	333.1	764.8	466.5	264.5	406.2	648.2	242.5
Q9W4I3	FI01736p OS=Drosophila melanogaster OX=7227 GN=mRpL30 PE=1 SV=1	28.424	37	8	13	8	180	21	9.73	38.78	8	0	1161.7	594.9	1986.4	1456.5	384.3	586	920.8	1019.9
Q9VVM8	FI02004p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5290 PE=1 SV=1	6.86	4	3	3	3	798	92.1	6.06	3.13	3	0	681.2	359.8	579.8	690.8	320.7	344.6	432.6	484.3
Q9VWC7	FI02109p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12702 PE=1 SV=1	10.436	3	2	3	2	870	97.1	6.71	11.36	2	0	38.7	19.6	44	43.1	19.6	24.9	25	26.6
Q9VBH8	FI02850p OS=Drosophila melanogaster OX=7227 GN=RpL34a PE=1 SV=2	4.194	9	2	2	2	162	18.1	11.44	4.27	2	0	212.3	79	161.8	201.8	81.2	111.1	125	109.4
A1Z803	FI02892p OS=Drosophila melanogaster OX=7227 GN=Marc PE=1 SV=1	25.146	20	5	5	5	340	38.1	8.54	20.15	5	0	371.6	291.7	1055.7	555.8	80.7	199.3	492.5	312.3
Q9W3R9	FI03239p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1677 PE=1 SV=2	9.394	3	3	3	3	1000	109	5.76	9.32	3	0	757.9	281.1	447.9	462	299.2	338.1	277.7	362
Q9N6D7	FI03258p OS=Drosophila melanogaster OX=7227 GN=hrg PE=1 SV=1	20.598	12	5	6	5	659	74.5	7.09	18.89	5	0	1171.3	532.2	707.5	772.8	473.2	477.8	330.4	413.4
Q9VKC8	FI03495p OS=Drosophila melanogaster OX=7227 GN=Tom70 PE=1 SV=2	43.904	13	8	15	8	589	66.3	6.21	50.3	8	0	1162.1	751.7	1687.7	1345.3	410.8	791.2	848.7	861.7
C8VV60	FI03659p OS=Drosophila melanogaster OX=7227 GN=CG10616-RA PE=1 SV=1	11.968	8	2	2	2	492	54.6	5.01	8.7	2	0	117.9	70	167.4	220.6	69	85.9	90	232.9
Q9VXR9	FI03680p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8128 PE=2 SV=1	21.421	10	5	5	5	330	38.1	8.92	15.41	5	0	289.9	168.4	515.6	430	139.8	148.8	221.3	227.6
Q9VVL8	FI03887p OS=Drosophila melanogaster OX=7227 GN=TrpRS-m PE=1 SV=1	22.189	8	4	7	4	665	72.8	9.22	22.91	4	0	103.2	68.2	219.4	187.1	50.2	54.5	88.3	131.1
Q9Y095	FI04011p OS=Drosophila melanogaster OX=7227 GN=XRCC1 PE=1 SV=1	7.493	4	2	2	2	614	68.7	9.22	5.47	2	0	574.7	262	309.9	394.5	228.6	229.4	157.5	241.8
Q9VQR9	FI04424p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG17593 PE=1 SV=1	14.923	7	2	3	2	476	54.1	5.3	10.06	2	0	74.8	41.9	89.3	74.6	38.7	38.7	40.4	73.1
Q9W149	FI04483p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11414 PE=1 SV=1	11.865	4	2	2	2	867	95.9	8.82	7.8	2	0	524.5	238.7	657.4	678.7	188.9	298.2	382.9	287.4
Q8SXC2	FI04487p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6950 PE=1 SV=1	20.501	12	4	11	4	450	51.2	7.72	27.38	4	0	524.5	311.6	1049.7	925.8	229.1	240.5	397.8	435.8
Q9VBQ7	FI04601p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5116 PE=1 SV=2	30.333	6	3	9	3	526	59.2	8.78	33.53	3	0	147.8	104.1	195.6	213.6	90.3	105.9	102.8	119.2
Q9W074	FI04779p OS=Drosophila melanogaster OX=7227 GN=HBS1 PE=1 SV=2	7.836	4	2	3	2	670	74.1	6.7	9.54	2	0	130.2	71.5	148.9	166.2	53.6	75.7	85.8	68
Q95WY3	FI04781p OS=Drosophila melanogaster OX=7227 GN=Nop56 PE=1 SV=1	5.89	5	2	2	2	496	54.8	9.28	5.29	2	0	297.2	100.5	154.1	207.8	113.1	94	75.9	207.4
Q9VJ28	FI05204p OS=Drosophila melanogaster OX=7227 GN=L2HGDH PE=1 SV=1	72.523	18	7	22	7	455	50.1	8.59	65.16	7	0	661.7	333.1	1490	1056.8	237	308.1	594.3	710
Q9VYE9	FI05227p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1622 PE=1 SV=1	37.235	18	5	6	5	398	45.4	9.39	26.72	5	0	1151.6	456.8	517.1	579	443.5	490.6	352.9	397
Q9VAZ0	FI05230p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5003 PE=1 SV=1	5.306	4	2	2	2	713	80.4	5.71	6.01	2	0	151	82.2	177.7	172.6	91.2	93.4	80.5	186.3
Q9W3X6	FI05334p OS=Drosophila melanogaster OX=7227 GN=Fum1 PE=1 SV=3	49.553	21	9	16	9	495	53.5	8.44	54.44	9	0	1083.2	518.5	1932.3	1288.9	340.6	382.4	822.7	1928.3
Q9VSW4	FI06490p OS=Drosophila melanogaster OX=7227 GN=mRRF1 PE=1 SV=1	7.484	7	2	2	2	254	28.5	9.79	6.03	2	0	88.1	45.3	214.2	191.5	23.2	26.4	87.4	136.5
Q9VIK0	FI06578p OS=Drosophila melanogaster OX=7227 GN=Amacr PE=2 SV=1	11.864	7	2	3	2	373	41.6	6.55	7.22	2	0	343	132.8	514.9	450.3	112.8	154.3	247.4	240.1
Q9VPF6	FI06804p OS=Drosophila melanogaster OX=7227 GN=mRpL15 PE=1 SV=1	9.491	16	3	3	3	286	32.6	9.36	8.17	3	0	146.6	72.2	198	153.5	58.5	73.2	113	78
Q9VGZ2	FI06805p OS=Drosophila melanogaster OX=7227 GN=Rrp46 PE=1 SV=3	6.844	9	2	2	2	233	25.7	5.33	5.96	2	0	586.5	267.9	544.9	740	241.3	232.5	262.8	556.5
Q9W396	FI06908p OS=Drosophila melanogaster OX=7227 GN=HP1b PE=1 SV=1	7.433	8	2	4	2	240	26	4.77	11.99	2	0	1098.1	554.3	647.9	698.1	450.7	567.3	422.4	319.6
Q9VD00	FI07666p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5377 PE=1 SV=1	46.254	13	5	15	5	278	31.7	8.27	50.14	5	0	1571.3	836.1	2948	2418.6	505	643.6	1263.5	1447
Q9VN44	FI07923p OS=Drosophila melanogaster OX=7227 GN=Karybeta3 PE=1 SV=1	6.874	2	2	2	2	1105	123.5	4.73	5.12	2	0	147.5	75.2	120.4	149.3	50.1	69.6	60.8	102.7
Q9VL66	FI09311p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4592 PE=1 SV=2	9.291	10	2	3	2	287	31.9	8.02	9.16	2	0	135.4	87.8	308.8	229	39.2	51.8	124.7	99.6
Q9VKI2	FI09336p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4788 PE=1 SV=1	6.472	7	2	3	2	252	26.6	9.29	9.45	2	0	1303.8	548.7	559.3	848.1	569.2	556.6	294.8	398.8
Q9VVU1	FI09602p OS=Drosophila melanogaster OX=7227 GN=CT12987 PE=1 SV=1	48.984	24	7	17	7	414	45.3	6.71	57.35	7	0	1158.4	675.8	2268.2	2433.8	387	373.2	817.2	2523
Q8INW7	FI11475p OS=Drosophila melanogaster OX=7227 GN=Pax PE=1 SV=1	8.046	6	2	2	2	557	62	6.51	4.06	2	0	101.1	58.4	214.9	348	54.7	72.7	91.1	149.3
O96689	FI11703p OS=Drosophila melanogaster OX=7227 GN=vtd PE=1 SV=1	8.51	4	3	3	3	715	79.9	5	7.8	3	0	547.3	182.2	251.8	395.7	212.4	267.3	136	360.3
Q9VW41	FI17101p1 OS=Drosophila melanogaster OX=7227 GN=Ccdc58 PE=1 SV=2	30.897	24	4	5	4	136	15.8	7.78	21.93	4	0	292.1	176.1	654.4	531.7	121.9	154.7	283.1	240
Q9V3E9	FI17138p1 OS=Drosophila melanogaster OX=7227 GN=spag PE=1 SV=1	8.982	4	2	2	2	534	59.6	8.34	6.06	2	0	254.1	131.5	316.9	321.8	103.4	129.2	153.7	199.6
H0RNI8	FI17821p1 OS=Drosophila melanogaster OX=7227 GN=CG3760-RB PE=1 SV=1	31.517	31	6	9	6	265	29	5.31	32.81	6	0	408.9	243.6	417.2	445.5	183.4	210.9	206	253.9
H5V8D0	FI18307p1 OS=Drosophila melanogaster OX=7227 GN=SCAR PE=1 SV=1	19.227	8	4	5	4	641	70.1	6.92	17.3	4	0	651.1	328.9	935.2	966.6	223	348.8	517.8	431.4
A1Z9G2	FI18620p1 OS=Drosophila melanogaster OX=7227 GN=fand PE=1 SV=1	13.013	3	2	2	2	883	103.3	5.64	7.92	2	0	535	262.1	325.4	366.1	208.2	243.1	177.5	148.2
A1Z936	FI18626p1 OS=Drosophila melanogaster OX=7227 GN=ZnT49B PE=1 SV=1	10.575	6	5	7	5	655	72.3	8.56	14.3	5	0	443.3	356.6	834.8	682.8	208.6	257.7	459.9	359.8
Q9VB46	FI18644p1 OS=Drosophila melanogaster OX=7227 GN=Hmu PE=1 SV=1	18.133	8	4	8	4	579	63.4	9.35	26.21	4	0	789	420.6	1474.5	1472.2	331.1	433.1	783.9	667.3
Q9VUK8	FI18749p1 OS=Drosophila melanogaster OX=7227 GN=GlyRS PE=1 SV=1	13.732	5	3	5	3	765	85.1	7.74	16.43	3	0	675.6	321.7	777.8	859.6	336.1	311.2	383.8	819.2
Q9V9X7	FI18849p1 OS=Drosophila melanogaster OX=7227 GN=PNPase PE=2 SV=2	68.795	22	15	25	15	771	84.9	7.66	76.79	15	0	1318.8	650.4	2286.9	1720.5	514.7	623	1074.3	1425.6
Q8IQZ7	FI19014p1 OS=Drosophila melanogaster OX=7227 GN=Fim PE=1 SV=1	14.35	7	4	4	4	641	72	5.55	9.26	4	0	356.2	123.3	241.4	340.7	140.3	147.3	154	219.3
Q9VZ00	FI19420p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1737 PE=1 SV=1	30.643	10	8	10	8	943	102.1	9.95	31.64	8	0	1522.9	590.1	1195.6	1267.5	638.4	724.6	725	924
A1Z7V9	FI20020p1 OS=Drosophila melanogaster OX=7227 GN=45551045 PE=1 SV=1	17.724	10	5	6	5	548	63.6	8.18	19.39	5	0	602.1	263.8	991.1	757.2	182.2	240	507.1	593.6
Q9VIF6	FI20110p1 OS=Drosophila melanogaster OX=7227 GN=DmRH24 PE=1 SV=1	16.822	7	3	3	3	507	56.5	6.81	11.96	3	0	732.8	271.8	348	395.2	269.5	280	185	254.8
Q24113	FI21126p1 OS=Drosophila melanogaster OX=7227 GN=nonA-l PE=1 SV=2	9.785	4	2	2	1	630	69.6	8.62	8.14	2	0	66.2	32.3	77.7	80.7	34.8	27.1	41.1	40.4
Q9VHC7	FI21236p1 OS=Drosophila melanogaster OX=7227 GN=rump PE=1 SV=1	45.753	11	5	13	5	632	66.7	7.85	42.82	5	0	1162.1	410.2	700.6	736.4	463.5	434.4	370.2	863.5
Q9W413	FI21245p1 OS=Drosophila melanogaster OX=7227 GN=mldr PE=2 SV=1	10.971	8	5	7	5	544	62.1	8.72	15.89	5	0	429	220.4	928.3	854	162.7	213.8	366.4	818.9
A1Z6L9	FI21274p1 OS=Drosophila melanogaster OX=7227 GN=Trap1 PE=1 SV=1	115.11	29	16	40	15	691	77.9	7.59	131.61	16	1	3990.6	1883.2	5663.6	6031.9	1456.8	1748.9	2510.8	7648.5
Q9VJZ1	FI21342p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9302 PE=1 SV=1	3.869	4	2	2	2	510	57.9	8.78	1.66	2	0	261.4	116.3	272	322.5	97	109.5	141.5	272.6
Q9VAV2	FI21480p1 OS=Drosophila melanogaster OX=7227 GN=mIF2 PE=1 SV=2	66.901	22	11	20	11	696	76.7	7.14	65.23	11	0	670.7	399.5	1350.7	1073.5	302.3	388.5	645.1	757.4
Q9W0D6	FI22004p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7879 PE=1 SV=1	10.43	4	4	6	4	985	109.5	9.2	12.66	4	0	714	337.8	699.4	699.6	272.5	322.4	353.9	442.4
Q9W4K8	FI22513p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3626 PE=1 SV=3	42.253	10	8	17	8	939	106.3	6.81	47.52	8	0	847	472.8	1305	1288.4	387.9	395.1	568.7	706.2
Q9VZY9	FI22774p1 OS=Drosophila melanogaster OX=7227 GN=ProRS-m PE=1 SV=1	14.231	8	3	3	3	458	50.6	7.66	10.4	3	0	434.9	265.8	994.5	563.1	168.8	189.8	463.6	279.1
Q9VYT3	FI23714p1 OS=Drosophila melanogaster OX=7227 GN=Nrd1 PE=1 SV=2	9.912	2	2	2	2	1147	132.7	5.15	6.09	2	0	141.7	71.3	172.2	199.5	57.2	72.1	83.9	132.5
Q9VES0	FI23980p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10324 PE=1 SV=1	10.434	9	2	2	2	543	61.8	9.63	8.05	2	0	131.9	58.2	64.7	48.2	45.7	49	42.6	18.7
A1Z9I5	FI24033p1 OS=Drosophila melanogaster OX=7227 GN=tum PE=1 SV=1	16.529	7	4	5	4	625	69.7	9.01	14.21	4	0	569.1	207	350.4	401.8	226	197.6	195.5	260.9
Q9VL78	FK506-binding protein 59 OS=Drosophila melanogaster OX=7227 GN=FKBP59 PE=1 SV=1	25.172	15	6	12	6	439	48.8	5.41	30.63	6	0	1243.9	549.2	917.3	835.1	497.6	491.4	494.7	458.3
Q9VWN4	Fl(2)d-associated complex component OS=Drosophila melanogaster OX=7227 GN=Flacc PE=1 SV=1	13.191	4	3	3	3	1150	128.9	9.25	6.88	3	0	310	142.8	197.1	200.2	134.7	169.5	125	148
Q7K7A9	Flap endonuclease 1 OS=Drosophila melanogaster OX=7227 GN=Fen1 PE=2 SV=1	24.856	19	6	7	6	385	42.9	8.53	21.68	6	0	1456	616.1	939.4	984.6	521.9	509.6	383.7	788.7
E1JJL2	Flotillin 2, isoform G OS=Drosophila melanogaster OX=7227 GN=Flo2 PE=1 SV=1	10.24	10	3	4	3	340	37.6	6.14	11.08	3	0	254	124.8	358.1	375.9	107.8	153.1	247	359.9
O61491	Flotillin-1 OS=Drosophila melanogaster OX=7227 GN=Flo1 PE=2 SV=1	10.357	9	4	4	4	426	47.1	5.64	8.35	4	0	722.2	348.3	1108.2	1092.1	262.5	368.9	545.9	652.6
A0A0B4K618	Fmr1, isoform G OS=Drosophila melanogaster OX=7227 GN=Fmr1 PE=1 SV=1	34.508	10	7	9	7	729	81	8.7	23.23	7	0	1006.5	430.9	1033.2	1129.5	378.3	503.5	632.9	614
Q9VYL1	Folylpolyglutamate synthase OS=Drosophila melanogaster OX=7227 GN=Fpgs PE=3 SV=2	12.516	5	2	2	2	572	64.3	7.74	8.46	2	0	59.1	26.5	86.9	92.4	29.6	31.6	52.8	76.3
Q0E8F8	Fork head transcription factor long isoform OS=Drosophila melanogaster OX=7227 GN=FoxK PE=1 SV=1	21.484	6	3	5	3	740	80	7.88	20.88	3	0	3136.1	948	991	982.1	1064.1	979.8	739.8	582.9
Q9VUC6	Formin-like protein OS=Drosophila melanogaster OX=7227 GN=Frl PE=1 SV=3	15.18	4	3	3	3	1183	133.1	8.09	10.24	3	0	78.1	46.7	88.2	79.8	38.2	45	54.4	39.8
C8VV14	Fructose-bisphosphate aldolase OS=Drosophila melanogaster OX=7227 GN=Ald1 PE=1 SV=1	41.605	25	7	11	7	361	39	7.4	38.24	7	0	525.1	306.1	648.8	701.5	273.2	327.6	322.6	457.3
A0A0B4KG97	Fruitless, isoform O OS=Drosophila melanogaster OX=7227 GN=fru PE=1 SV=1	31.752	10	4	4	4	882	97.7	7.27	18.67	4	0	533.9	245.2	370.5	466.1	259.3	262.3	204.4	335.4
P16378	G protein alpha o subunit OS=Drosophila melanogaster OX=7227 GN=Galphao PE=1 SV=1	9.195	5	2	2	2	354	40.5	5.53	5.61	2	0	156.4	109.1	235.1	260.1	96.2	89	142.2	137.9
A4V4I0	G protein beta-subunit 13F, isoform C OS=Drosophila melanogaster OX=7227 GN=Gbeta13F PE=1 SV=1	8.645	9	2	2	2	340	37.1	6.44	7.06	2	0	70.6	35.9	83.1	113.6	28.3	30	52.9	57.3
Q7K0S5	GDI interacting protein 3, isoform B OS=Drosophila melanogaster OX=7227 GN=Gint3 PE=1 SV=1	22.734	10	4	6	4	441	50	7.11	25.33	4	0	346.5	172.4	553.5	579	146.5	137.1	273.3	254.4
Q9VMW9	GDP-mannose 4,6 dehydratase OS=Drosophila melanogaster OX=7227 GN=Gmd PE=1 SV=2	13.304	8	2	2	2	395	44.8	7.3	8.01	2	0	54.2	28	48.6	56.7	28	31.4	21.5	46.2
Q07171	Gelsolin OS=Drosophila melanogaster OX=7227 GN=Gel PE=1 SV=2	2.82	2	2	2	2	798	88.3	5.1	4.37	2	0	234.2	112.2	294.1	365.4	95.1	102.8	154	138.1
Q05913	General transcription factor IIF subunit 1 OS=Drosophila melanogaster OX=7227 GN=TfIIFalpha PE=1 SV=3	9.695	5	2	2	2	577	64.4	7.88	6.55	2	0	154.2	72.1	108.9	133.8	55.4	67.4	49	74.4
Q9W022	GEO01508p1 OS=Drosophila melanogaster OX=7227 GN=8993 PE=1 SV=1	33.068	29	2	18	2	142	15.8	8.46	73.84	2	0	672.6	328.6	1016.9	696.1	237.7	267.8	459.2	517.8
Q9W551	GEO02601p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG14817 PE=2 SV=1	6.879	19	2	2	2	106	12.8	10.05	6.47	2	0	166.4	89.4	268.3	294.4	84.1	88.9	123.8	271.2
E1JGR3	GEO02620p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG42497 PE=2 SV=1	14.604	23	2	2	2	65	7.5	9.98	9.58	2	0	174.3	118.1	794.3	349.7	52.6	70	315.3	139
Q9V3L7	GEO04710p1 OS=Drosophila melanogaster OX=7227 GN=NP15.6 PE=1 SV=1	25.555	39	5	29	5	150	17	5.14	82.76	5	0	451.3	290	1338	968.8	186.2	239.2	580.9	482.7
Q8T9H0	GEO06673p1 OS=Drosophila melanogaster OX=7227 GN=38E.22 PE=1 SV=1	7.431	19	2	3	2	143	16	8.15	3.33	2	0	215	111.4	148.2	163.1	82.8	90.5	81.2	77.3
Q9VU46	GEO07182p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11279 PE=1 SV=1	4.777	14	2	3	2	102	11.1	10.58	6.77	2	0	129.4	43	44	73.3	45.9	51.6	20.6	31.4
X2JEM4	GEO07185p1 OS=Drosophila melanogaster OX=7227 GN=RpS28b PE=2 SV=1	23.429	38	3	10	3	65	7.5	10.37	34.14	3	0	1280.4	541.8	1688.6	1694.3	542.1	593.6	993.5	523
Q9VL93	GEO07195p1 OS=Drosophila melanogaster OX=7227 GN=BcDNA:SD27505 PE=1 SV=1	5.393	20	2	2	2	110	12.1	8.19	5.31	2	0	225.8	129.3	347.4	233	95.4	150.6	235.2	133.5
Q9VVU2	GEO07453p1 OS=Drosophila melanogaster OX=7227 GN=RpL26 PE=1 SV=1	17.535	16	3	9	3	149	17.3	10.95	21.51	3	0	585.4	291.7	760.3	621.4	254	438.8	444.8	441.5
Q9W199	GEO07594p1 OS=Drosophila melanogaster OX=7227 GN=mRpS17 PE=2 SV=1	7.341	17	3	5	3	155	18	8.75	7.54	3	0	339.3	175.6	509.6	524.6	206.6	226.8	298	545.7
Q9W1B9	GEO07602p1 OS=Drosophila melanogaster OX=7227 GN=RpL12 PE=1 SV=1	20.084	30	3	6	3	165	17.7	9.07	27.38	3	0	333.6	121.9	300.9	277	126.7	150.1	174.9	300.6
X2JE06	GEO07624p1 OS=Drosophila melanogaster OX=7227 GN=RpL24 PE=1 SV=1	5.499	10	2	3	2	155	17.5	11.06	8.85	2	0	641	216.7	573.1	425.9	194.1	352.6	425.9	414.1
A0A0B4LG52	GEO08239p1 OS=Drosophila melanogaster OX=7227 GN=RpS16 PE=2 SV=1	11.354	23	4	8	4	148	16.8	10.17	19.06	4	0	1081.8	396.6	963.6	1100.7	381.4	431.2	578.9	922.2
Q9VJI7	GEO08441p1 OS=Drosophila melanogaster OX=7227 GN=LSm7 PE=1 SV=1	17.067	36	3	4	3	110	12.2	6.7	14.03	3	0	519	178	253.3	252	179.6	146.9	159.4	154.8
Q9VC65	GEO08971p1 OS=Drosophila melanogaster OX=7227 GN=BcDNA:GH27470 PE=1 SV=2	11.37	18	2	2	2	139	15.2	5.95	7.09	2	0	179	97.1	314.6	257	62.9	77	144.9	160.7
Q7JVK8	GEO08987p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5323 PE=1 SV=1	17.161	25	3	3	3	146	16.6	7.24	10.43	3	0	51.2	38.2	152.3	164.7	14.2	32.3	87.6	93.5
Q9VG00	GEO09174p1 OS=Drosophila melanogaster OX=7227 GN=l(3)87Df PE=2 SV=1	3.983	15	2	2	2	110	12.6	8.34	4.51	2	0	106.5	59.2	571.9	449.2	6.3	16.4	189.4	326.3
X2JB87	GEO09348p1 OS=Drosophila melanogaster OX=7227 GN=Tim8 PE=2 SV=1	6.818	24	2	3	2	88	10.1	5.16	8.76	2	0	95.1	42.7	220.8	146.5	28.5	43.6	122.8	274.1
Q8SYJ2	GEO09626p1 OS=Drosophila melanogaster OX=7227 GN=ND-MLRQ PE=1 SV=1	6.911	40	4	7	4	83	9.4	9.26	10.72	4	0	535	263.7	1307.7	1050.8	184.2	251.4	519	851
Q6NP72	GEO09659p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG13220 PE=1 SV=1	8.129	12	2	2	2	153	16.4	9.44	6.09	2	0	332.8	165.2	707.1	377.2	64	119.4	352.5	321
Q9VA81	GEO10172p1 OS=Drosophila melanogaster OX=7227 GN=mRpS18C PE=2 SV=2	9.499	22	3	3	3	140	16.2	9.07	9.21	3	0	167.2	82.1	295.8	239.6	67.4	77.8	146.5	201.5
Q9VWQ7	GEO10539p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6891 PE=1 SV=1	12.544	12	3	3	3	163	18.5	4.98	8.72	3	0	612.3	302.7	335.7	378.2	221.2	291.9	178.8	261.5
M9PCI2	GEO11453p1 OS=Drosophila melanogaster OX=7227 GN=NHP2 PE=2 SV=1	14.064	28	4	5	4	160	17.7	8.1	12.39	4	0	1007.4	366.4	444.5	944.4	402.8	355	234	627.1
Q9W256	GEO12186p1 OS=Drosophila melanogaster OX=7227 GN=Mes4 PE=1 SV=1	3.587	20	2	3	2	155	17.4	4.31	4.74	2	0	176.4	101.5	113.3	128.8	68.7	59.7	53.4	71
Q0KI97	GEO13368p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG34117 PE=2 SV=1	9.953	27	2	4	2	101	11.6	9.58	15.33	2	0	221.5	86	312.3	157.5	67.1	85.3	115.1	169.6
Q9VFF0	GH01077p OS=Drosophila melanogaster OX=7227 GN=UQCR-C1 PE=1 SV=2	105.328	32	12	177	12	470	51.8	6	671.35	12	0	3361	1852.8	6370.4	5776.1	1734.4	2064.8	2911.8	4610.9
Q9I7T5	GH01116p OS=Drosophila melanogaster OX=7227 GN=mge PE=1 SV=1	8.694	22	2	2	2	122	13.4	4.75	6.61	2	0								

Q7KRS9	GH01331p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1815 PE=1 SV=1	6.517	1	2	2	2	1664	181.8	8.35	5.32	2	0	351.3	148.2	213.9	233	140.7	161.8	125.1	155.4
O18333	GH01619p OS=Drosophila melanogaster OX=7227 GN=Rab2 PE=1 SV=1	11.257	18	3	6	3	213	23.5	6.39	14.32	3	0	152.5	87.6	234.8	297.2	76.6	91.3	117.2	323.1
Q9VB10	GH01709p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5590 PE=1 SV=1	59.887	25	7	22	7	412	44.3	8.02	82.01	7	0	1460.9	617.9	2358.2	1616	582.6	617.9	1000.4	1303.9
Q7K3Z3	GH01724p OS=Drosophila melanogaster OX=7227 GN=p47 PE=1 SV=1	58.219	25	6	11	6	407	43.4	5.62	43.94	6	0	894	442.4	586.8	589.8	365	412.8	308.6	332.1
Q9VZJ3	GH01794p OS=Drosophila melanogaster OX=7227 GN=Rcd5 PE=1 SV=1	12.317	9	4	4	4	578	63.5	9.44	11.82	4	0	438.6	182.5	280.5	382.5	190.9	212	175	261.5
Q9VCW6	GH03051p OS=Drosophila melanogaster OX=7227 GN=Gclm PE=1 SV=1	4.558	7	2	2	2	285	31.5	5.74	4.65	2	0	224	103.9	182.6	220.8	80.7	103.6	83.4	106.5
Q9VEP9	GH03554p OS=Drosophila melanogaster OX=7227 GN=Sf3a1 PE=1 SV=1	19.057	7	6	8	6	784	88	6.37	21.91	6	0	2001.9	766.2	1070.1	1139.3	721.3	837.5	680.8	653
Q9VNH5	GH04919p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2091 PE=1 SV=1	6.608	9	2	2	2	374	43	5.3	4.39	2	0	16.4	11	9.9	16.4	9.3	9.9	6.2	7.9
Q9VIV6	GH04973p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10194 PE=2 SV=1	26.044	16	5	13	5	351	40.3	6.92	35.58	5	0	449.3	277.2	916	825.4	181.4	267.7	468.7	476.2
Q8SXQ1	GH05218p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9629 PE=1 SV=1	89.085	36	14	69	14	540	58.3	7.44	168.95	14	0	3089.6	1707.8	6275.1	4496.1	1047.6	1431.1	2723.8	3523.8
Q9VXP3	GH05406p OS=Drosophila melanogaster OX=7227 GN=mRpS30 PE=1 SV=1	56.402	20	9	18	9	557	65.1	8.47	60.8	9	0	537.2	319.6	1325.2	1084.6	245	360.8	598.4	1015
Q7K5M2	GH05836p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10139 PE=2 SV=1	31.046	30	4	6	4	224	25.5	7.33	17.07	4	0	818.2	286.7	332.6	411.2	333.1	403	251.3	288.2
Q9VLM9	GH05949p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG17294 PE=1 SV=1	13.978	17	3	4	3	255	28	5.95	13.58	3	0	160.7	81	254.9	271.2	69.9	53.7	107.3	172.5
Q95U54	GH06271p OS=Drosophila melanogaster OX=7227 GN=Mms19 PE=1 SV=1	8.133	4	2	2	2	959	107	5.91	3.64	2	0	95.8	44	80.2	76.5	37.4	38.3	39.2	51
Q9VTB3	GH06691p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11811 PE=1 SV=1	13.077	8	3	4	3	233	25.9	7.44	13.01	3	0	722.7	401.7	1039.9	826.6	233.8	362.3	479.5	580.3
Q9VMC6	GH06693p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9547 PE=1 SV=1	54.976	28	9	38	9	419	45.7	8.51	82.76	9	0	1076.4	720.7	1866.8	1918.5	696.6	678.3	1017.2	1707.8
Q9VZ55	GH07148p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1582 PE=1 SV=2	4.446	1	2	2	2	1288	146	7.4	4.7	2	0	204.9	119.3	220.8	276.2	159.4	149	125.5	178.2
Q9VD14	GH07286p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG13850 PE=1 SV=3	57.75	20	9	17	9	564	61.8	9.13	58.47	9	0	1925.6	811.6	2891.1	1914.2	635.3	830.6	1212.3	2243.9
Q9VWL4	GH07340p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7556 PE=1 SV=1	8.666	4	2	4	2	522	60	7.33	12.37	2	0	904.8	357.1	1085.8	763.8	313.6	371.6	632.2	343.1
O97183	GH07456p OS=Drosophila melanogaster OX=7227 GN=RpII33 PE=1 SV=1	19.337	13	4	7	4	275	31.2	4.82	20.19	4	0	1625	683.2	916.5	1197.7	675.4	833.2	675.3	732.3
Q9VEK8	GH07711p OS=Drosophila melanogaster OX=7227 GN=sds22 PE=1 SV=1	11.66	8	2	2	2	326	37.8	5.03	9.27	2	0	208.5	75.9	123.3	138.5	77	81.2	60.9	159.1
Q9VAY9	GH07821p OS=Drosophila melanogaster OX=7227 GN=mRpS22 PE=1 SV=1	24.778	14	5	12	5	393	45.8	7.74	37.63	5	0	1053.3	634.2	2475.4	1631.6	323.4	531.6	1143	1241.7
Q9VL02	GH08677p OS=Drosophila melanogaster OX=7227 GN=nmd PE=2 SV=1	15.943	5	3	3	3	369	41.5	8.22	9.32	3	0	150.6	82	172.6	184.1	66.4	87.1	92.3	83.1
Q24090	GH08712p OS=Drosophila melanogaster OX=7227 GN=Snr1 PE=1 SV=2	19.766	10	3	5	3	370	41.9	5.27	17.17	3	0	745.4	368.6	489.7	548.5	340.9	346	275.1	323.5
Q7K1H0	GH09096p OS=Drosophila melanogaster OX=7227 GN=CG6491 PE=1 SV=1	13.177	10	3	3	3	324	36.5	6.65	8.83	3	0	302.2	104.6	209.7	250.8	119.4	113.4	121.7	321.7
Q95TA3	GH09289p OS=Drosophila melanogaster OX=7227 GN=Tm1 PE=1 SV=1	25.575	10	4	5	1	441	48	5.48	19.95	4	0	14.4	8.2	16.3	18.9	4.9	7	8.1	11.7
Q7K3W2	GH09295p OS=Drosophila melanogaster OX=7227 GN=CG8728-RA PE=1 SV=1	103.979	29	13	59	13	556	61	7.12	159.5	13	0	2886.6	1547	5644.4	4705.9	1751.7	1517.6	2615.7	4240.7
Q9VE08	GH10002p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6013 PE=1 SV=1	9.625	10	2	2	2	213	24.8	9.55	7.03	2	0	294.2	148.1	334.7	370.3	111	156.4	207.8	265.4
Q9VY45	GH10289p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1434 PE=1 SV=2	11.213	8	2	2	2	473	52.7	8.24	4.93	2	0								
Q8MZI3	GH10652p OS=Drosophila melanogaster OX=7227 GN=p90 PE=1 SV=1	21.347	6	4	12	1	818	88.2	9.36	25.22	4	0	171	72.2	215.7	248.8	66.9	79.3	93.2	231.5
Q9VGV9	GH11067p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6567 PE=1 SV=1	4.665	9	2	2	2	235	26.2	8.15	4.51	2	0	34.3	18	44.6	53.7	13.3	15	21.2	70.3
O96880	GH11150p OS=Drosophila melanogaster OX=7227 GN=TfIIEalpha PE=1 SV=1	13.664	11	3	3	3	429	48.3	5	8.71	3	0	150.2	70.9	104.8	108.2	77.6	71.2	56.8	75.2
Q7JRM9	GH11283p OS=Drosophila melanogaster OX=7227 GN=Nmda1 PE=2 SV=1	7.107	3	2	2	2	324	35.5	7.18	6.64	2	0	41.3	61	126.4	158	22.5	51	73.7	70
Q9V3Z4	GH11341p OS=Drosophila melanogaster OX=7227 GN=Rpn5 PE=1 SV=1	6.123	4	3	5	3	502	57.7	5.8	10.66	3	0	674.1	279.4	448.2	587.5	253.2	253.7	218	503.6
Q9VNC0	GH11824p OS=Drosophila melanogaster OX=7227 GN=POLDIP2 PE=1 SV=1	72.536	35	9	23	9	410	46.3	7.14	92.92	9	0	1889.4	969.8	3372.5	2920.6	743.5	884	1366.9	2309.1
Q9W1H8	GH13256p OS=Drosophila melanogaster OX=7227 GN=Thiolase PE=1 SV=1	50.919	19	8	23	8	469	50.6	9.14	62.61	8	0	1027.7	572.9	2426.4	2032.7	376.1	500.3	1026.8	1692.4
Q8T0Q4	GH13992p OS=Drosophila melanogaster OX=7227 GN=shrb PE=1 SV=1	23.51	33	5	7	5	226	25.4	4.81	20.27	5	0	1335.3	449.8	881.5	1011	456.2	415.4	414.3	899
Q9VHN4	GH14121p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8043 PE=1 SV=1	42.182	21	5	13	5	348	39.5	8.68	46.86	5	0	621.9	339.1	1352	1085.3	255.9	277.7	551.9	1130.2
B7Z0C9	GH15104p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG42307 PE=2 SV=1	11.626	33	3	3	3	95	11	9.98	9.97	3	0	281.3	132.6	698.4	490.4	62.2	92.5	297.6	234.5
Q8MRM6	GH15213p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12065 PE=1 SV=1	20.268	9	4	4	4	641	71.1	7.39	12.85	4	0	236.7	83.5	202.5	229	99.5	83.6	79.8	277.3
Q9VMU1	GH16729p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4230 PE=1 SV=1	16.668	15	3	4	3	323	36.6	5.55	11.4	3	0	356.8	157.6	425.3	391.7	111.9	148.4	203.1	289.9
Q8MRM0	GH16740p OS=Drosophila melanogaster OX=7227 GN=GstT4 PE=1 SV=1	21.817	22	5	7	5	237	27.6	8.79	21.14	5	0	124.8	53.9	245.3	233.6	48.7	49.8	96.7	611.9
Q7K332	GH17623p OS=Drosophila melanogaster OX=7227 GN=CG3364 PE=2 SV=1	13.12	10	3	6	3	239	27.6	9.89	15.49	3	0	346.4	185.1	821.1	591.4	88.9	145.6	376	697.9
Q9VQ34	GH17801p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG17660 PE=1 SV=3	8.588	8	2	2	2	536	60.1	5.99	3.88	2	0	52.7	54.4	131.9	113.5	20	37.5	56.6	60.3
Q9W127	GH17932p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3663 PE=1 SV=1	21.982	20	3	5	3	208	23.3	7.69	16.04	3	0	243.7	131.2	382.9	419.7	138.7	132.3	195.2	269.1
Q9W5W7	GH19483p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9581 PE=1 SV=1	38.402	11	4	13	4	545	60.8	6.9	41.91	4	0	628.4	343.7	1132.2	1077.7	284.8	356.2	506.4	725.4
Q9VYL5	GH19726p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1824 PE=1 SV=1	18.718	7	4	5	4	761	83.5	7.81	11.35	4	0	113.4	56.3	316.8	254	37.3	50.3	133.7	147.6
Q9VNA3	GH21273p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11999 PE=1 SV=1	20.44	22	4	5	4	216	23.6	6.8	14.08	4	0	246.7	108	775.3	968	64.5	78.9	366.7	478
Q9VBP6	GH21316p OS=Drosophila melanogaster OX=7227 GN=Ssadh PE=1 SV=1	13.84	12	3	3	3	509	54.9	8.21	11.28	3	0	91.6	47.8	109.4	124.9	39.6	40.9	51.7	107.5
Q9VIM6	GH22016p OS=Drosophila melanogaster OX=7227 GN=FBgn0032858 PE=2 SV=1	6.216	5	2	3	1	459	53.1	5.45	7.67	2	1	129.4	58.3	60.4	84.5	42	67.9	25.2	41
Q95T49	GH22139p OS=Drosophila melanogaster OX=7227 GN=Dromel_CG8026_FBtr0088611_mORF PE=2 SV=1	5.139	5	2	2	2	304	34.1	9.57	4.91	2	0	97.5	51.1	327	257.1	31.5	40.8	133.4	140
Q95SI7	GH23390p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6028 PE=1 SV=1	15.29	16	3	4	3	293	32.3	6.57	11.94	3	0	142.6	68.4	205.9	169.9	66.3	63	96	131.2
Q9VEQ2	GH23451p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3678 PE=1 SV=2	16.586	16	3	4	3	282	32.7	7.05	6.16	3	0	157.7	74.8	190.4	247.6	65.1	72.7	100.5	143.8
Q7K1C0	GH23780p OS=Drosophila melanogaster OX=7227 GN=ND-15 PE=1 SV=1	7.916	22	3	3	3	101	12	7.72	4.4	3	0	250.7	135.3	528.2	396.3	96	103.2	235	274.5
Q9W245	GH24245p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4610 PE=2 SV=1	48.071	19	10	13	10	661	73.6	8.5	46.72	10	0	968.1	498.4	1171.2	944.3	355.3	406.8	533.4	512.3
Q8T0L3	GH24511p OS=Drosophila melanogaster OX=7227 GN=Uba1 PE=1 SV=1	38.489	9	9	12	9	1191	130.7	5.29	35.67	9	0	3536.6	1572.6	1943.7	1963.9	1358.9	1349.5	1028	1105.1
Q9V3Q4	GH25379p OS=Drosophila melanogaster OX=7227 GN=Jafrac2 PE=1 SV=1	16.908	12	3	7	3	242	26.7	6.8	20.07	3	0	323.7	137.6	1524.5	1784.3	92.5	103.2	582.6	630.6
Q9VK60	GH25425p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6180 PE=1 SV=2	6.725	9	3	3	3	257	28.7	8.82	6.62	3	0	637.8	228	690.4	498	211.8	249.8	297.3	633.6
Q9VD58	GH26270p OS=Drosophila melanogaster OX=7227 GN=Idh3b PE=1 SV=1	17.932	10	4	10	4	370	40.4	8.54	25.46	4	0	509	338.3	1069.1	1056.7	205.3	245.6	438.3	662.9
Q9VSM4	GH26459p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5989 PE=2 SV=1	6.545	5	2	2	2	436	50.3	9.67	6.63	2	0	73.8	48.6	180.3	133.6	27.9	38.5	79.6	75.8
Q9VG07	GH26602p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7488 PE=2 SV=2	12.945	13	2	3	2	373	41.6	9.36	13.92	2	0	96.6	50.9	116.1	107	40.4	60.5	54.7	109.3
Q9VVA4	GH26789p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9674 PE=1 SV=2	71.838	7	13	17	13	2114	231.9	6.42	56.48	13	0	2268.7	1005.8	2519.3	2502.3	863.7	991.5	1325.4	1288.8
Q9V3D8	GH27579p OS=Drosophila melanogaster OX=7227 GN=grsm PE=1 SV=1	15.36	6	2	2	2	558	60.1	6.79	8.99	2	0	440.5	199.6	412.8	314.7	171	157.6	201.1	247.8
Q9VJD1	Glucosidase 2 beta subunit, isoform A OS=Drosophila melanogaster OX=7227 GN=GCS2beta PE=1 SV=1	77.961	22	13	23	13	548	61.5	4.46	68.54	13	0	1328.4	634.6	5419.1	5196	473.8	510.4	2295.8	1585.6
P33438	Glutactin OS=Drosophila melanogaster OX=7227 GN=Glt PE=1 SV=2	16.401	5	3	3	3	1026	118.7	4.77	13.12	3	0	136.8	77.5	492.3	440.1	72.4	80.8	219.4	99.3
Q9VGF7	Glutamate carrier 1, isoform A OS=Drosophila melanogaster OX=7227 GN=GC1 PE=1 SV=1	17.72	18	5	8	5	321	34.5	9.55	17.54	5	0	626.1	292.1	1476.9	1458.9	256.4	249.8	576.5	1270
P54385	Glutamate dehydrogenase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Gdh PE=1 SV=2	33.957	14	7	11	7	562	62.5	8.27	26.45	7	0	1108.4	546.4	1737.4	1590.3	431.7	481.9	671.1	2126.8
Q7JQK6	Glutaminase, isoform A OS=Drosophila melanogaster OX=7227 GN=GLS PE=1 SV=1	148.734	33	15	49	15	706	78.5	7.24	181.21	15	0	2711.1	1276.7	5046.5	3702.8	1045	1163.4	2147.7	5102.6
E1JHQ1	Glutamine synthetase OS=Drosophila melanogaster OX=7227 GN=Gs1 PE=1 SV=1	4.922	6	2	2	2	399	44.4	6.46	5.07	2	0	95.4	75.6	131.8	162.1	59.7	70.4	64.7	123.9
Q9VV59	Glutamyl-tRNA synthetase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=GluRS-m PE=3 SV=1	7.976	5	2	3	2	511	58.5	7.75	9.75	2	0	171.9	73.5	266.9	275.8	62.4	72.2	126.5	231.6
Q9VE09	Glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial OS=Drosophila melanogaster OX=7227 GN=g	53.867	21	11	15	11	508	55.8	6.68	49.51	11	0	971.3	546.7	1662.7	1563.7	386.5	492.3	749.2	932.8
Q9VCD0	Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial OS=Drosophila melanogaster OX=7227 GN=G	30.728	12	5	7	5	516	57.3	7.25	27.57	5	0	1048.8	487.5	1601.3	1146.2	352.7	482	699.7	785.1
Q9VZQ8	Glutathione peroxidase OS=Drosophila melanogaster OX=7227 GN=PHGPx PE=1 SV=1	23.595	31	5	8	5	169	18.7	7.83	27.74	5	0	1496.3	579.5	2233.2	1808.6	456.6	543	1037.9	1638.6
A1ZB72	Glutathione S transferase E7 OS=Drosophila melanogaster OX=7227 GN=GstE7 PE=1 SV=1	9.272	11	2	3	2	223	25.5	6.57	5.75	2	0	248.7	126	120.8	195.7	99	93.5	60.2	98.7
Q7K0B6	Glutathione S transferase T1 OS=Drosophila melanogaster OX=7227 GN=GstT1 PE=1 SV=1	26.859	26	5	12	5	228	26.6	8.97	45.85	5	0	1001.6	544	1988.9	1613	402.8	441.1	769.9	2823.1
A1Z7X7	Glutathione S transferase T2 OS=Drosophila melanogaster OX=7227 GN=GstT2 PE=1 SV=2	29.682	20	3	7	3	228	26.6	8.88	27.02	3	0	368.8	165.9	603.1	640.9	177.2	173.6	254.7	670.9
P07486	Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Drosophila melanogaster OX=7227 GN=Gapdh1 PE=2 S	25.022	18	6	11	1	332	35.3	8.18	27.94	6	0	357.2	143.2	314.6	354.1	117.4	143.1	163.9	392.3
M9PJN8	Glyceraldehyde-3-phosphate dehydrogenase OS=Drosophila melanogaster OX=7227 GN=Gapdh2 PE=3 SV	48.842	26	7	14	2	332	35.3	8.44	46.4	7	5	2126.5	786.2	1829.3	2153.5	761.8	591.4	798.1	3243
Q7K569	Glycerol-3-phosphate dehydrogenase OS=Drosophila melanogaster OX=7227 GN=Gpo1 PE=1 SV=1	54.61	16	9	24	9	724	80.4	7.65	77.49	9	0	906.2	586.7	2004	2005.8	561.4	501.3	819	2322.1
Q9U616	Glycine cleavage system H protein, mitochondrial OS=Drosophila melanogaster OX=7227 GN=ppl PE=2 SV=	17.302	24	3	4	3	165	18	5.2	14.91	3	0	283.3	159.3	553.8	365.6	130.4	149.9	243.8	230.9
A1Z6H7	Glycoprotein 210 kDa, isoform A OS=Drosophila melanogaster OX=7227 GN=Gp210 PE=1 SV=1	53.321	8	13	16	13	1876	209.7	6.47	51.23	13	0	1969	486.3	998.8	1162.6	458.6	561.5	517.5	562.5
Q9VAY2	Glycoprotein 93 OS=Drosophila melanogaster OX=7227 GN=Gp93 PE=1 SV=1	144.974	29	20	45	20	787	90.2	5.02	160.01	20	0	2087.1	1042.2	9984.3	9207.5	632.3	735.8	4451.2	5056.2
Q9VGQ1	GM01350p OS=Drosophila melanogaster OX=7227 GN=alpha-KGDHC PE=1 SV=1	96.76	18	7	66	7	468	49.9	9.47	241.84	7	0	2661.4	1362.9	5192.5	4197.7	996	1293.8	2028	4850.4
Q9VIF2	GM01519p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9248 PE=1 SV=1	8.183	6	2	2	2	494	55.6	6.14	7.58	2	0	77.6	43	113.2	126.8	51.2	63.3	52.8	75.5
Q9VF27	GM02062p OS=Drosophila melanogaster OX=7227 GN=ND-23 PE=1 SV=1	27.44	28	5	13	5	217	24.6	5.88	31.65	5	0	1415.4	601	2107	1396.8	475.1	557.1	1040.4	1228.7
Q9VXQ8	GM02445p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11679 PE=2 SV=1	26.106	13	5	15	5	420	48.3	6.13	46.98	5	0	339.7	173.6	785.2	734.4	150.6	147.2	296.7	750.6
Q9VSR5	GM03767p OS=Drosophila melanogaster OX=7227 GN=mRpL12 PE=1 SV=1	12.262	12	2	6	2	182	19.6	8.75	18.75	2	0	641.2	423.4	1727.2	926.5	321.2	376.7	854.4	449.7
Q9VSN9	GM04779p OS=Drosophila melanogaster OX=7227 GN=SrpRbeta PE=1 SV=2	8.337	10	2	2	2	244	27.1	8.97	7.59	2	0	145.6	61.8	183	191.5	46.8	62.5	89.4	140.5
Q9VMR0	GM05057p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7382 PE=1 SV=1	31.418	25	4	7	4	236	26.6	9.98	27.4	4	0	458.6	300.3	1358.7	723.1	179.3	232.2	592.3	334.5
Q9V3E3	GM06185p OS=Drosophila melanogaster OX=7227 GN=mRpL50 PE=1 SV=1	16.602	20	2	4	2	189	20.9	9.48	17.88	2	0	81.8	35.8	185.9	137.3	38.4	41.9	80.8	143.8
Q9VSC5	GM09977p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8209 PE=1 SV=1	5.565	8	3	3	3	331	36.7	6.1	4.96	3	0	195.1	78.7	128.6	128	73.7	67.4	66.7	78.6
Q9VAI4	GM12182p OS=Drosophila melanogaster OX=7227 GN=Naa40 PE=1 SV=1	14.748	13	3	6	3	202	23.4	8.56	12.81	3	0	2349.4	1027.8	1476.3	1327.1	848.3	899.4	880.2	717.5
Q9VNH2	GM13341p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2100 PE=1 SV=1	6.482	4	2	2	2	477	55.3	9.01	5.28	2	0	221.6	89	233.3	189.7	76.2	84.2	109.6	262.7
Q9VPL0	GM13767p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3436 PE=1 SV=1	7.454	6	2	2	2	347	38.8	6.92	6.73	2	0	281.9	120.1	172.3	178.5	132.4	143	99.7	114.4
O76994	GM13959p OS=Drosophila melanogaster OX=7227 GN=Ip259 PE=2 SV=1	7.391	8	2	2	2	259	30	10.49	5.42	2	0	290.5	113	104.9	111.6	126.3	124.8	75.8	80.2
Q9W3Q1	GM14286p OS=Drosophila melanogaster OX=7227 GN=Pdp PE=1 SV=1	34.592	28	8	13	8	475	53.5	6.05	32.86	8	0	516	252.7	854.6	860.7	233.7	241.5	495.4	737.4
Q9W4J4	GM14292p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11444 PE=1 SV=1	11.075	16	2	2	2	215	22.9	9.38	6.99	2	0	533.2	194.5	351.8	325.8	158.2	225	220.7	293
Q9VAC1	GM14349p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7920 PE=1 SV=1	81.526	23	7	150	7	477	51.8	8.12	462.75	7	0	2728.3	1346.6	4755.6	4711	1138.2	1409.1	2028.5	4141.6
Q9V9T5	GM14617p OS=Drosophila melanogaster OX=7227 GN=Mccc1 PE=1 SV=2	295.344	48	29	320	29	698	76.5	6.2	1094.14	29	0	8553.8	5536.6	16061.7	20850.2	4610.6	6240.6	7605.2	13123
Q9V3W2	GM23292p OS=Drosophila melanogaster OX=7227 GN=ND-B17 PE=1 SV=1	20.195	27	6	13	6	167	19	9.82	30.63	6	0	360.7	239.6	788.1	744.7	217.7	247.3	385.2	447
Q7JVK6	GM27569p OS=Drosophila melanogaster OX=7227 GN=trsn PE=1 SV=1	9.926	10	2	3	2	235	27	5.5	7.51	2	0	149.5	70.6	129.6	154.6	59.5	58.8	70.3	122.5
Q9W1R3	Golgin-245 OS=Drosophila melanogaster OX=7227 GN=Golgin245 PE=1 SV=2	6.953	2	2	4	2	1489	170	5.2	10.15	2	0	170.1	97.4	350.2	286.3	103.5	117.6	147.6	551.8
A0A0B4JD02	Groucho, isoform F OS=Drosophila melanogaster OX=7227 GN=gro PE=1 SV=1	16.234	6	3	4	3	719	78.9	7.12	14.14	3	0	372.4	173.2	227	257.6	143.1	156.6	113.4	107.5
P48604	GrpE protein homolog, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Roe1 PE=2 SV=2	38.134	28	6	18	6	213	23.9	8.5	50.72	6	0	1981.9	899.6	3786.3	2630.6	664	729.1	1704.8	3309.5
A4V4A5	GTP-binding nuclear protein OS=Drosophila melanogaster OX=7227 GN=Ran PE=1 SV=1	13.927	18	3	5	3	216	24.7	7.81	17.81	3	0	846.5	309.2	438	471.9	305.9	327.1	273.1	303
P32234	GTP-binding protein 128up OS=Drosophila melanogaster OX=7227 GN=128up PE=2 SV=2	13.279	11	3	3	3	368	41.1	8.6	10.49	3	0	158.6	67.1	210.4	234.2	61.1	70.7	102.3	126.5
Q9VGU6	GTP:AMP phosphotransferase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Adk3 PE=1 SV=1	28.985	17	4	20	4	216	24.1	9.32	46.97	4	0	410.9	221	606.4	592.6	168.6	214	245.1	361.1
O18640	Guanine nucleotide-binding protein subunit beta-like protein OS=Drosophila melanogaster OX=7227 GN=Rac	37.673	22	6	13	6	318	35.6	7.47	45	6	0	1586.3	610.4	1661.7	1584.7	606.1	711.8	872.9	1217.5
Q9VWP5	Hat-trick, isoform D OS=Drosophila melanogaster OX=7227 GN=htk PE=1 SV=4	44.887	5	9	10	9	2486	259.3	8.94	31.92	9	0	2567.7	1088.5	1397.4	1612.6	890.9	1090.4	845.3	843.3
P11146	Heat shock 70 kDa protein cognate 2 OS=Drosophila melanogaster OX=7227 GN=Hsc70-2 PE=1 SV=2	17.732	7	3	10	1	633	69.7	7.18	25.42	3	0	153.2	96.9	320.7	355.1	53.3	101.8	145.7	284.2
P11147	Heat shock 70 kDa protein cognate 4 OS=Drosophila melanogaster OX=7227 GN=Hsc70-4 PE=1 SV=3	160.062	40	18	194	15	651	71.1	5.52	751.34	18	3	10914.6	4785.3	9507.5	10333.7	3765.7	4632.3	5006.8	5109.1
P29845	Heat shock 70 kDa protein cognate 5 OS=Drosophila melanogaster OX=7227 GN=Hsc70-5 PE=1 SV=2	209.638	40	24	176	24	686	74	6.35	590.7	24	0	12352.5	6619.3	20611.2	15161	4511.5	6583.6	9415.7	12654.1
P02515	Heat shock protein 22 OS=Drosophila melanogaster OX=7227 GN=Hsp22 PE=1 SV=4	26.855	22	4	7	4	174	19.8	5.27	23.51	4	0	214.4	337	653.5	577.4	78.7	237.5	266.9	271.5
O02649	Heat shock protein 60A OS=Drosophila melanogaster OX=7227 GN=Hsp60A PE=1 SV=3	236.811	47	24	131	24	573	60.8	5.49	442.54	24	0	8258.4	3822.4	17891.1	12886.8	2519.7	3059.8	7234.2	15898.3
M9PBL3	Heat shock protein 83, isoform B OS=Drosophila melanogaster OX=7227 GN=Hsp83 PE=3 SV=1	121.797	33	16	60	15	717	81.8	5.02	179.89	16	0	5949.1	2104.6	4276.4	4778.4	1977.9	2238.1	2375.5	4853.3
Q9VF20	Heavy metal tolerance factor 1 OS=Drosophila melanogaster OX=7227 GN=Hmt-1 PE=1 SV=1	13.209	4	2	2	2	866	97.8	8.37	9.48	2	0	94.9	55	154.8	164.2	46.6	79.9	79.9	74.4
P05205	Heterochromatin protein 1 OS=Drosophila melanogaster OX=7227 GN=Su(var)205 PE=1 SV=2	73.315	56	9	19	9	206	23.2	5.08	66.03	9	0	3201.7	1329.3	1460.6	1583.8	1415.9	1805.1	928.9	1242.4
Q9VYY7	Heterochromatin protein 5, isoform B OS=Drosophila melanogaster OX=7227 GN=HP5 PE=1 SV=1	27.488	7	5	10	5	837	92.6	5.97	29.94	5	0	758.3	290	360.9	423.4	307.3	447	232.2	235.9
P48809	Heterogeneous nuclear ribonucleoprotein 27C OS=Drosophila melanogaster OX=7227 GN=Hrb27C PE=1 SV	36.07	19	4	16	4	421	44.7	6.8	47.76	4	0	1982.3	606.2	1102.1	848.8	742.6	706.1	703.4	454.4
P48810	Heterogeneous nuclear ribonucleoprotein 87F OS=Drosophila melanogaster OX=7227 GN=Hrb87F PE=2 SV	19.496	16	5	13	4	385	39.5	9.03	36.47	5	0	889.7	302.2	365.6	332	314.4	296.1	225	285.6

A4V3J6	Heterogeneous nuclear ribonucleoprotein at 98DE, isoform F OS=Drosophila melanogaster OX=7227 GN=Hrl	41.857	26	6	19	5	361	38.5	9.16	61.98	6	1	4217.3	1480.8	2491.2	2486.6	1597.4	1477.8	1307.7	2054
E1JGN7	Heterogeneous nuclear ribonucleoprotein K, isoform E OS=Drosophila melanogaster OX=7227 GN=HnRNP-K	55.982	19	9	15	9	493	49.8	8.35	48.5	9	0	1526	707.2	1252.7	1309	616.6	741.1	734.6	1536.1
Q8IQX8	Histidyl-tRNA synthetase, isoform D OS=Drosophila melanogaster OX=7227 GN=HisRS PE=1 SV=2	49.377	21	10	16	10	564	62.3	7.47	53.85	10	0	1533.5	716.4	2771.2	2506.8	587.2	604.6	1179.5	1663.3
Q9W1A9	Histone acetyltransferase OS=Drosophila melanogaster OX=7227 GN=enok PE=1 SV=2	10.574	1	2	2	2	2291	254.5	8.43	7.44	2	0	320	115.1	202	240.3	137.5	118.8	109.3	164.6
Q0KIB3	Histone acetyltransferase type B catalytic subunit OS=Drosophila melanogaster OX=7227 GN=Hat1 PE=1 SV	14.108	12	4	4	4	405	47.9	6.73	10.81	4	0	1062.7	403	517.5	658.2	411.7	342.1	275.6	489
Q9VYF3	Histone deacetylase OS=Drosophila melanogaster OX=7227 GN=HDAC4 PE=1 SV=3	15.627	3	3	3	3	1252	134.1	7.75	10.16	3	0	388.3	193.5	446.6	539.8	136.8	195.7	247	272.5
Q94517	Histone deacetylase Rpd3 OS=Drosophila melanogaster OX=7227 GN=Rpd3 PE=1 SV=2	19.588	8	3	4	3	521	58.3	5.76	16.87	3	0	392.6	107.7	149.6	189.6	128.4	96.1	79.3	119.8
Q4ABD8	Histone H1 OS=Drosophila melanogaster OX=7227 GN=His1:CG33807 PE=3 SV=1	3.834	5	2	3	2	256	26.3	10.49	7.04	2	0	1404	357.6	347.5	403.4	532	686.6	340.4	635
Q4AB57	Histone H2A OS=Drosophila melanogaster OX=7227 GN=His2A:CG33859 PE=3 SV=1	25.013	41	4	15	3	124	13.4	10.56	43.41	4	0	1840.2	327.1	542.6	481.5	728.4	572.7	331.8	1994.8
A0A0B4KH25	Histone H2A OS=Drosophila melanogaster OX=7227 GN=His2Av PE=3 SV=1	16.494	27	5	10	4	141	15	10.24	21.93	5	1	2308.1	696.1	700.7	1136	922	1167.2	630.5	1203.1
P02283	Histone H2B OS=Drosophila melanogaster OX=7227 GN=His2B PE=1 SV=2	54.666	42	7	116	7	123	13.7	10.35	280.04	7	0	3657.1	908.4	1303.6	1894.1	1397.3	1976.1	1179.9	5885.2
C0HL66	Histone H3.3A OS=Drosophila melanogaster OX=7227 GN=His3.3A PE=1 SV=1	9.168	18	4	31	4	136	15.3	11.27	47.55	4	0	4323.3	1022.3	1124.5	1993	1456.8	1995.3	810.2	3208.4
P84040	Histone H4 OS=Drosophila melanogaster OX=7227 GN=His4 PE=1 SV=2	17.205	37	5	28	5	103	11.4	11.36	47.73	5	0	3271.2	1172.2	1446.8	1911.5	1332.1	1956.1	1170.6	7408.9
Q9VNI3	Histone PARylation factor 1-like OS=Drosophila melanogaster OX=7227 GN=CG1218 PE=1 SV=2	14.896	11	4	5	4	449	51.1	7.03	10.44	4	0	591.1	276.7	686.3	575.1	224.3	222	316.6	982.9
Q32KD2	Histone-lysine N-methyltransferase eggless OS=Drosophila melanogaster OX=7227 GN=egg PE=1 SV=1	13.934	3	2	2	2	1262	141.9	5.49	10.03	2	0	58.7	29.6	39.9	57.9	23.4	25.8	29	20.6
Q7JVK1	HL07956p OS=Drosophila melanogaster OX=7227 GN=mRpL18 PE=2 SV=1	7.341	10	2	2	2	186	21.2	9.29	5.56	2	0	148.4	71.6	311.5	260.4	42.1	60.3	124.2	256.7
Q9VL70	HL08109p OS=Drosophila melanogaster OX=7227 GN=yip2 PE=1 SV=1	54.393	22	5	33	5	398	41.6	8.51	97.37	5	0	738.9	403.8	1116.7	947.6	328.4	395.5	555.7	699.7
A0A0B4LG36	HMG protein Z, isoform C OS=Drosophila melanogaster OX=7227 GN=HmgZ PE=4 SV=1	12.533	18	2	5	1	111	12.6	9.29	17.47	2	1	1359.4	391.3	417	471.4	492.9	453.3	296.2	428.6
D2NUK9	Hoi-polloi, isoform B OS=Drosophila melanogaster OX=7227 GN=hoip PE=1 SV=1	14.773	16	2	3	2	127	13.9	7.09	10.81	2	0	618.5	297.4	314.9	350.1	301.6	252.4	179.1	194.1
A0A0B4LGS6	Holocarboxylase synthetase, isoform D OS=Drosophila melanogaster OX=7227 GN=Hcs PE=1 SV=1	8.873	4	2	2	2	999	110.9	7.2	6.77	2	0	23.9	13.2	32.1	39.2	13.1	20	15.2	35.5
P13709	Homeotic protein female sterile OS=Drosophila melanogaster OX=7227 GN=fs(1)h PE=1 SV=2	26.626	5	7	9	7	2038	205.2	9.16	18.76	7	0	621.7	202.8	334.1	368.6	223.1	226.8	202.4	385.1
O96607	Homer OS=Drosophila melanogaster OX=7227 GN=homer PE=1 SV=1	4.901	4	2	2	2	394	42.7	7.49	4.91	2	0	118.8	46.4	109.8	113.8	44.9	53	75.8	60.2
Q9V4C8	Host cell factor OS=Drosophila melanogaster OX=7227 GN=Hcf PE=1 SV=2	29.953	5	5	6	5	1500	160.1	7.68	30.02	5	0	1165.1	490.4	644.1	781.9	469.7	544.2	405.9	490.6
M9PG82	HP1 and insulator partner protein 1, isoform B OS=Drosophila melanogaster OX=7227 GN=HIPP1 PE=1 SV=	29.764	10	6	7	6	924	99.7	6.89	24.32	6	0	1269.3	508.4	610.1	546.1	475	579	403.7	367.5
E2QD63	Hsc/Hsp70-interacting protein related, isoform B OS=Drosophila melanogaster OX=7227 GN=HIP-R PE=4 SV	22.268	10	4	4	4	377	41	5.35	14.46	4	0	202.5	85.9	113.2	88.8	69.1	62.1	62.5	38.8
Q9VUC1	Hsc70Cb, isoform A OS=Drosophila melanogaster OX=7227 GN=Hsc70Cb PE=1 SV=1	46.493	13	10	16	10	804	88.4	5.43	47.21	10	0	2442.5	1095.7	1584.9	2038.2	837.2	897.9	889.8	1613.3
Q24276	Hsp90 co-chaperone Cdc37 OS=Drosophila melanogaster OX=7227 GN=Cdc37 PE=1 SV=1	28.858	18	5	7	5	389	45.1	5.06	24	5	0	928.8	411.2	759.3	735.7	351.4	416.6	404.5	457.7
A0A0B4K7A5	Hu li tai shao, isoform Q OS=Drosophila melanogaster OX=7227 GN=hts PE=1 SV=1	41.211	14	6	10	6	739	81.5	7.24	40.36	6	0	247.6	142	291.1	350.9	148.5	155	207.7	299.1
A0A126GUQ3	Humpty dumpty, isoform B OS=Drosophila melanogaster OX=7227 GN=hd PE=4 SV=1	9.196	4	2	2	2	568	63.4	6.62	5.77	2	0	629.6	418.6	586.9	593.4	297.8	147.1	221.3	216.8
A0A0B4LGZ6	Hyperplastic discs, isoform B OS=Drosophila melanogaster OX=7227 GN=hyd PE=1 SV=1	13.161	1	3	3	3	2887	318.9	5.96	8.73	3	0	425.6	197.8	227.3	229.1	147.1	150.7	105.9	128.3
Q9VHI1	Hyrax OS=Drosophila melanogaster OX=7227 GN=hyx PE=2 SV=1	6.622	4	2	2	2	538	61.3	9.63	3.28	2	0	212	107.4	171.5	166	88.5	112.7	105.5	78.3
Q9V455	Importin subunit alpha OS=Drosophila melanogaster OX=7227 GN=Kap-alpha3 PE=1 SV=1	8.627	5	3	6	3	514	57	5.26	10.69	3	0	409.7	182.2	239.9	293.7	148.9	174	119.8	169.9
P52295	Importin subunit alpha OS=Drosophila melanogaster OX=7227 GN=Pen PE=1 SV=2	40.775	19	5	8	5	522	57.8	5.35	35.66	5	0	379.9	128.6	281.2	337.7	145.6	140.5	127.5	259.8
O77460	Inorganic pyrophosphatase OS=Drosophila melanogaster OX=7227 GN=Nurf-38 PE=1 SV=3	22.749	12	3	8	3	338	37.9	7.01	27.91	3	0	1395.1	674.8	1373.3	1428.2	587.1	583.3	587.4	802.4
Q9VMW7	Inosine triphosphate pyrophosphatase OS=Drosophila melanogaster OX=7227 GN=CG8891 PE=2 SV=1	14.684	14	2	4	2	191	21.4	6.92	12.58	2	0	181.4	98.3	280.5	275.5	102.6	105.4	115.7	208.3
O97477	Inositol-3-phosphate synthase OS=Drosophila melanogaster OX=7227 GN=Inos PE=1 SV=1	34.941	16	6	12	6	565	62.2	6.23	41.47	6	0	1343.9	577.7	971.3	1030.5	947.4	565	487.6	711.2
Q9VHG5	Insulator binding factor 1, isoform A OS=Drosophila melanogaster OX=7227 GN=Ibf1 PE=1 SV=1	32.856	26	7	8	7	242	27.7	6.44	25.83	7	0	2428.7	795.2	721.1	1004	915.4	1186.6	620.8	924
Q9VHG6	Insulator binding factor 2 OS=Drosophila melanogaster OX=7227 GN=Ibf2 PE=1 SV=1	19.414	23	3	4	3	195	21.9	8.03	18.24	3	0	758.3	222.6	247.5	277.1	286.6	321.4	202.5	215.6
P22817	Insulin-degrading enzyme OS=Drosophila melanogaster OX=7227 GN=Ide PE=1 SV=4	18.665	6	4	4	4	990	113.6	6.27	13.78	4	0	187.1	90.4	306.7	265.1	76.2	87.6	149.6	168.2
A0AVU6	IP06021p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10375 PE=2 SV=1	7.625	12	2	2	2	160	19.4	9.64	5.27	2	0	375.4	169.7	294.8	363.7	162.5	159.2	145.9	197.1
Q059A4	IP07454p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4627 PE=2 SV=1	11.654	15	2	5	2	204	22.8	9.52	13.14	2	0	94.2	68.7	180.3	172	64.8	75.4	105.8	119
Q4V619	IP07950p OS=Drosophila melanogaster OX=7227 GN=mIF3 PE=2 SV=1	16.474	20	3	8	3	232	25.8	10.42	15.52	3	0	165.2	101.9	293.3	289.1	90.9	107.4	117.6	170.8
Q9VGV0	IP09589p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG14695 PE=1 SV=1	7.132	12	2	2	2	289	33.5	6.93	4.9	2	0								
Q9VEB1	IP09655p OS=Drosophila melanogaster OX=7227 GN=Mdh2 PE=1 SV=1	56.314	30	9	38	9	336	35.3	9.11	114.21	9	0	3455.3	1779	6953	5338.1	1100.1	1400.2	2559	6506.8
Q9W019	IP09724p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG15877 PE=1 SV=1	13.833	13	4	5	4	277	32	9.35	12.82	4	0	929.8	411.6	453	607	354.8	493.2	287.3	320.3
Q4QQ70	IP09819p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG15602 PE=1 SV=1	10.942	8	2	2	2	342	38.6	5.11	9.14	2	0	57.2	27.7	62.7	61.9	25.6	37.7	29.5	36.8
Q4V3Z5	IP10727p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11788 PE=2 SV=1	22.74	13	3	3	3	425	48.8	5.11	12.99	3	0	691.8	361.9	393.5	350.5	247.3	139.5	108.2	69.9
Q9VB17	IP11341p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5611 PE=2 SV=1	21.929	21	7	8	7	326	35.6	7.01	17.79	7	0	788.7	397	1484.1	1073.2	238.1	284.1	613.3	670.5
Q9W4C1	IP13321p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG15784 PE=1 SV=1	40.9	10	4	11	4	554	62.3	10.33	36.69	4	0	249.5	84.2	212.9	168	83.2	110.7	155.4	120.2
Q8IML6	IP14839p OS=Drosophila melanogaster OX=7227 GN=Pdhb PE=1 SV=1	51.487	15	5	13	1	273	31.2	10.29	45.5	5	0								
Q9W1F7	IP15825p OS=Drosophila melanogaster OX=7227 GN=Stoml2 PE=1 SV=2	62.39	25	10	25	10	366	40.5	8.84	85.6	10	0	1517.3	727	2787.3	1984.1	569.7	748.2	1231.1	2175.5
Q9W0H8	IP16409p OS=Drosophila melanogaster OX=7227 GN=scf PE=1 SV=2	22.416	21	5	5	5	329	38	4.69	17.03	5	0	190	130.1	876.3	818.6	73.2	90.8	384.3	306.9
Q9VKC1	IP16805p OS=Drosophila melanogaster OX=7227 GN=RpL7-like PE=1 SV=2	5.816	10	2	3	2	257	29.1	10.1	9.9	2	0	1242.8	457.5	491.6	436.9	501.6	559.1	328.5	281.9
Q9VLT7	IP17351p OS=Drosophila melanogaster OX=7227 GN=RpL36A PE=1 SV=2	3.561	13	2	2	2	104	12.5	10.8	2.29	2	0	325.4	139.5	250.2	223.2	90.2	173.4	252.2	109.5
Q9W0S6	IP18235p OS=Drosophila melanogaster OX=7227 GN=mRpL17 PE=1 SV=2	33.101	43	8	16	8	176	20.9	9.95	40.94	8	0	1008.2	509.7	2047.5	1683.3	368.3	500.1	772.2	1738.8
C6SV36	IP19903p OS=Drosophila melanogaster OX=7227 GN=CG3884-RB PE=1 SV=1	11.918	14	5	5	5	297	32	8.24	12.07	5	0	1392	564.9	925.5	1101.3	438.4	532.2	522.8	716.2
Q9VCV4	Iron regulatory protein 1A OS=Drosophila melanogaster OX=7227 GN=Irp-1A PE=1 SV=1	12.343	4	3	4	1	902	98.7	5.78	7.74	3	3	602.6	328.7	346	356.7	223.6	291	212.7	256
Q9VGZ3	Iron regulatory protein 1B OS=Drosophila melanogaster OX=7227 GN=Irp-1B PE=1 SV=1	13.248	4	3	4	1	899	98.5	5.95	7.68	3	0								
Q8T3X9	Iron-sulfur cluster assembly 1 homolog, mitochondrial OS=Drosophila melanogaster OX=7227 GN=MagR PE=	18.731	36	4	5	4	130	14.1	9.13	15.69	4	0	229.6	144.6	468	407.2	91	123.9	178.8	206.4
Q7KUB1	Isocitrate dehydrogenase [NADP] OS=Drosophila melanogaster OX=7227 GN=Idh PE=1 SV=1	41.193	20	8	19	8	469	52.6	7.5	55.68	8	0	1092	510.9	1576.5	1357.4	388.3	439.9	662.9	1815.7
Q8MSW0	Isoleucyl-tRNA synthetase, isoform A OS=Drosophila melanogaster OX=7227 GN=IleRS PE=1 SV=1	41.195	8	9	18	9	1229	141	7.52	48.12	9	0	1505.2	703.7	1995.6	2451	653.8	805.3	1090.4	1309.1
Q9VUY4	Isoleucyl-tRNA synthetase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=IleRS-m PE=1 SV=2	32.983	7	5	11	5	941	107.5	7.34	44.53	5	0	691.3	388.9	1356.5	1366.2	264.4	342.5	557.8	790.8
Q9VGR7	J domain-containing protein CG6693 OS=Drosophila melanogaster OX=7227 GN=CG6693 PE=1 SV=1	15.214	12	3	4	3	299	34.9	8.59	14.22	3	0	795.4	391.1	413.9	547	312.4	325.9	231.9	252.5
Q9VBP5	Jing interacting gene regulatory 1, isoform A OS=Drosophila melanogaster OX=7227 GN=jigr1 PE=1 SV=1	7.73	7	2	2	1	336	38.8	6.18	6.36	2	0	133	68.6	67.6	77.2	56.6	75.9	29.6	27.9
Q9VT00	Jumonji, AT rich interactive domain 2 OS=Drosophila melanogaster OX=7227 GN=Jarid2 PE=1 SV=3	15.556	1	3	3	3	2351	252.4	9.11	9.13	3	0	1122.1	427.4	529.7	572.5	409.9	501.3	338.7	386.9
A8JNJ6	Karst, isoform E OS=Drosophila melanogaster OX=7227 GN=kst PE=1 SV=2	183.812	10	31	43	31	4337	497.2	6.47	152.3	31	0	3456.7	1491.9	4524.6	4458.7	1217.9	1604.1	2770.8	2578.3
A0A0B4LHU8	Kayak, isoform G OS=Drosophila melanogaster OX=7227 GN=kay PE=1 SV=1	18.169	10	4	5	4	646	68.6	6.11	19.72	4	0	339.2	118	179.8	179.1	124.4	135	104.4	123.4
Q8MLQ5	Kazachoc, isoform D OS=Drosophila melanogaster OX=7227 GN=kcc PE=1 SV=1	4.514	1	2	2	2	1074	119.2	6.68	4.64	2	0	79.4	56.8	274.1	458.2	26.1	17.6	122	358.5
A4UZI0	Kinesin heavy chain 73, isoform C OS=Drosophila melanogaster OX=7227 GN=Khc-73 PE=1 SV=1	5.897	2	2	2	2	1899	212.3	6	3.17	2	0	12.7	10	22.7	19.5	9.1	6.6	11.8	16.2
P17210	Kinesin heavy chain OS=Drosophila melanogaster OX=7227 GN=Khc PE=1 SV=2	44.506	12	11	15	11	975	110.3	5.77	37.84	11	0	698.3	320.9	762.2	872.2	271.1	358.4	428.4	482.7
M9PF24	Kinesin light chain, isoform B OS=Drosophila melanogaster OX=7227 GN=Klc PE=4 SV=1	13.436	8	4	4	4	508	58	6.25	10.61	4	0	675.4	290.8	700.4	704.2	249.8	299.4	410.5	412.9
P46863	Kinesin-like protein Klp61F OS=Drosophila melanogaster OX=7227 GN=Klp61F PE=1 SV=2	14.681	3	3	4	2	1066	121.1	6.43	10.78	3	1	261.4	103.9	250.7	275.8	105.1	105.3	126.4	170.8
A4V4A1	Kinesin-like protein OS=Drosophila melanogaster OX=7227 GN=Klp10A PE=1 SV=1	16.928	5	3	3	3	805	88.6	7.21	9.8	3	0	428.6	169.5	238.1	289.9	188.9	221.4	167.8	214.4
A0A0B4LI25	Kinesin-like protein OS=Drosophila melanogaster OX=7227 GN=ncd PE=1 SV=1	39.909	15	8	13	8	700	77.4	9.17	41.35	8	0	3962.1	1729	1957.7	2607.1	1830.2	1621.2	1382.9	2352.5
Q9VZF5	Kinesin-like protein OS=Drosophila melanogaster OX=7227 GN=pav PE=1 SV=1	12.58	5	4	4	4	887	100.6	9.23	12.81	4	0	914	354.6	619.4	629.3	358.9	343.6	312.8	475.8
A0A0B4LGW1	Kinesin-like protein OS=Drosophila melanogaster OX=7227 GN=sub PE=3 SV=1	14.868	6	3	4	3	628	71.3	5.48	9.64	3	0	512.9	242.6	269.4	330	195.5	225.3	145.4	161.7
M9NEL3	Kismet, isoform F OS=Drosophila melanogaster OX=7227 GN=kis PE=1 SV=1	21.476	1	4	5	4	5191	560.6	5.77	14.76	4	0	612.6	214	290	248	229.8	209.5	170.2	164.9
A1Z6Q1	Klaroid, isoform B OS=Drosophila melanogaster OX=7227 GN=koi PE=1 SV=2	26.937	7	4	5	4	881	100.1	7.01	15.8	4	0	568.8	139.9	296.3	280.3	142	172.1	148.7	197.5
X2J4W8	Kruppel homolog 2, isoform C OS=Drosophila melanogaster OX=7227 GN=Kr-h2 PE=1 SV=1	9.189	10	3	3	3	276	31.2	9.77	5.5	3	0	143.5	69.9	231.7	270.8	60.1	62.9	105	489
Q9Y134	L.2.35Df OS=Drosophila melanogaster OX=7227 GN=Mtr4 PE=1 SV=1	17.451	4	4	4	4	1055	118.9	6.77	12.42	4	0	573.2	223.3	277.2	380	184.7	188.7	149.2	224.5
Q8IPN8	L82C OS=Drosophila melanogaster OX=7227 GN=mtd PE=1 SV=1	8.458	2	2	2	2	869	94.4	5.19	3.54	2	0	80.1	35.3	81	85.6	32.7	27.2	37.5	51.6
P40796	La protein homolog OS=Drosophila melanogaster OX=7227 GN=La PE=1 SV=2	38.614	23	7	12	7	390	44.9	7.58	41.84	7	0	5498.6	1637.2	1621.1	1913.7	1655.5	1228.4	797	1742.2
Q9VAW5	La-related protein 1 OS=Drosophila melanogaster OX=7227 GN=larp PE=1 SV=5	66.476	8	10	13	10	1673	178	9.6	48.37	10	0	1338.8	693.9	1581.3	1379.8	485.2	716.5	799.2	716.7
Q9I7T7	La-related protein Larp4B OS=Drosophila melanogaster OX=7227 GN=Larp4B PE=1 SV=2	8.49	3	2	2	2	1531	161.9	8.75	5.11	2	0	42.3	22	68.4	50.5	16.3	20.8	36.7	22
Q8MLV1	Lamin-B receptor OS=Drosophila melanogaster OX=7227 GN=LBR PE=1 SV=1	32.865	10	5	8	5	741	83.1	9.79	30.15	5	0	1704.4	606.1	1261.6	1435.9	485.1	710.4	651.9	719.7
M9NE89	Lamin, isoform B OS=Drosophila melanogaster OX=7227 GN=Lam PE=3 SV=1	160.242	43	28	62	28	622	71.3	6.47	211.1	28	0	15094.4	3431.6	6390.6	7408.4	3538.2	4309.2	3296.8	6614.5
Q00174	Laminin subunit alpha OS=Drosophila melanogaster OX=7227 GN=LanA PE=1 SV=2	61.904	5	13	15	13	3712	410.9	5.22	56.26	13	0	609.7	343.3	2528.6	2839.4	201.3	216.1	997.7	1142.3
P11046	Laminin subunit beta-1 OS=Drosophila melanogaster OX=7227 GN=LanB1 PE=1 SV=4	84.989	11	15	21	15	1788	198.2	5.33	72.17	15	0	1118.6	571.8	4577.4	4628.6	382.3	422.1	1911.4	1929.4
P15215	Laminin subunit gamma-1 OS=Drosophila melanogaster OX=7227 GN=LanB2 PE=2 SV=2	43.977	10	13	15	13	1639	182.2	5.38	49.25	13	0	803.8	490.4	2588.2	2251.4	322	414.3	1058.7	951.5
X2JAF1	Lava lamp, isoform D OS=Drosophila melanogaster OX=7227 GN=lva PE=4 SV=1	21.817	2	4	4	4	2779	315.7	4.86	13.39	4	0	331.4	148.4	367	443.2	167.9	180.9	200.6	270
Q95RY2	LD01461p OS=Drosophila melanogaster OX=7227 GN=CG17014 PE=1 SV=1	16.876	27	4	4	4	262	29.3	5.62	13.2	4	0	63.4	35.5	46.9	45.9	36.9	33.9	25	33.3
Q7PLS1	LD01937p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12567 PE=1 SV=2	7.131	6	2	3	2	349	39.6	6.64	9.51	2	0	552.4	273.9	838	835.4	188.1	229.9	325.8	416.8
Q7K180	LD02709p OS=Drosophila melanogaster OX=7227 GN=Map60 PE=1 SV=1	8.398	5	2	6	2	440	47.6	6.77	14.6	2	0	377.7	174	257.2	274.7	180.9	188.5	145.3	164.4
Q9VXR5	LD02975p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9281 PE=1 SV=1	18.12	9	5	6	5	611	69.5	7.53	15.01	5	0	923.6	383.6	1070.3	1006.6	315.6	434.8	547	854.8
Q9VPN5	LD03220p OS=Drosophila melanogaster OX=7227 GN=Stip1 PE=1 SV=1	10.951	5	2	4	2	490	55.7	6.81	15.37	2	0	1493.7	672.2	1245.5	1059.3	509.5	672.4	757.2	527.5
Q9W1I8	LD03592p OS=Drosophila melanogaster OX=7227 GN=Snap29 PE=1 SV=1	5.957	7	2	2	2	284	31.6	5.17	4.72	2	0	432.5	223.8	507.5	414.4	145.3	231.3	275.1	200.7
Q9VVU6	LD04472p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6841 PE=1 SV=2	8.06	2	2	2	2	931	105.2	7.44	7.06	2	0	327.6	137.1	162.1	206.2	109	131.9	93.5	105.7
Q7K2E1	LD05247p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8839 PE=1 SV=1	33.558	19	6	6	6	529	58.2	7.75	21.15	6	0	33.3	16.9	47.1	41.7	17.7	25.7	22.2	34.5
Q8SX78	LD05679p OS=Drosophila melanogaster OX=7227 GN=CG8446-RB PE=1 SV=1	24.643	13	5	10	5	396	44.1	9.1	30.11	5	0	503.1	258.1	817.8	904.2	239.4	243.7	302.3	842.3
Q9VZX6	LD06441p OS=Drosophila melanogaster OX=7227 GN=mRpS35 PE=1 SV=1	38.42	17	6	16	6	326	37.6	9.03	45.07	6	0	846.8	479	1530.3	1141.8	334.2	501.1	775.6	653.3
Q9VYT5	LD06533p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10347 PE=1 SV=1	5.034	3	2	2	2	580	65.3	5.78	4.16	2	0	160.2	81.2	117.2	140.7	66.9	70.8	51.7	104
Q9VQB4	LD06553p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3609 PE=1 SV=1	14.164	10	2	3	2	335	37.3	7.52	13.45	2	0	947.9	522	551.9	523.2	304.7	476	281.9	292.2
Q7K159	LD06557p OS=Drosophila melanogaster OX=7227 GN=mip40 PE=1 SV=1	10.288	10	3	3	3	267	30.1	9.86	9.03	3	0	1292.1	377.8	510.1	623.9	473.6	481.1	375.2	784.5
Q9V426	LD07162p OS=Drosophila melanogaster OX=7227 GN=vig PE=1 SV=1	27.771	13	5	10	5	490	52.7	9.74	28.2	5	0	1153	420.3	1112	806.1	413.4	502.8	744.4	404.6
Q9W542	LD07342p OS=Drosophila melanogaster OX=7227 GN=mip130 PE=1 SV=3	14.025	3	2	2	2	986	110.4	5.27	6.37	2	0	275.4	89.4	90.9	129.7	100.3	100.5	59.2	87.9
Q8IH18	LD07709p OS=Drosophila melanogaster OX=7227 GN=4E-T PE=1 SV=1	10.602	4	3	3	3	1010	113.8	8.46	6.35	3	0	326.5	140.4	488.4	386.8	143.3	177.2	214	612.2
Q9VBU5	LD07939p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10425 PE=1 SV=1	13.382	9	3	3	3	336	36.5	8.07	8.67	3	0	437.9	264.8	762.7	570.8	118	258.9	478.8	349.8
Q9W3C3	LD10016p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2004 PE=1 SV=1	13.058	10	3	5	3	425	48.3	5.21	17.23	3	0	114.3	41.6	62.6	96.5	37.5	32.8	26.9	94.3
Q9VX08	LD10434p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6769 PE=1 SV=1	9.892	7	2	2	2	409	47	6.44	7.45	2	0	139.6	63.6	149.9	197.9	65.3	71	84	104.4
Q9V9M6	LD10456p OS=Drosophila melanogaster OX=7227 GN=Tif-IA PE=2 SV=3	4.816	3	2	2	2	611	70.7	6.65	4.69	2	0	207	85.8	158.7	201.3	83.5	93.2	84.5	161.9
Q9VIJ9	LD10773p OS=Drosophila melanogaster OX=7227 GN=Ns4 PE=1 SV=1	7.665	4	2	2	2	575	66.6	6.51	6.25	2	0	75.6	36.6	66.8	94.5	46.1	49.3	50.9	59.2
A1Z9W4	LD11480p OS=Drosophila melanogaster OX=7227 GN=Pcf11 PE=1 SV=2	8.071	1	2	2	2	1953	212.6	6.23	6.31	2	0	55.7	31.6	31.8	36.9	28.6	28.1	24.5	19.6
O76268	LD11641p OS=Drosophila melanogaster OX=7227 GN=NTPase PE=1 SV=1	10.372	8	2	2	2	461	50.8	8.15	6.13	2	0	224.3	81.6	284.8	333.4	60.4	68.9	120.7	485.1
Q7YU03	LD11744p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3632 PE=1 SV=1	9.497	2	2	2	2	1250	138.5	5.96	5.52	2	0	203.1	110.1	224.9	216.7	74.6	116.3	119.9	139.6
Q9VCX7	LD12377p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG31156 PE=2 SV=3	5.889	2	2	2	2	948	106.4	8.87	4.68	2	0	202.1	79	130.7	132.1	84	83.9	74.7	134.6
C6SUW3	LD13662p OS=Drosophila melanogaster OX=7227 GN=RpS9 PE=1 SV=1	18.494	30	8	13	8	195	22.6	10.61	27.37	8	0	3020.2	925.7	2108.4	2221.9	809.5	1234.6	1405.1	2528.4
Q9W3Y3	LD13807p OS=Drosophila melanogaster OX=7227 GN=Q9W3Y3 PE=1 SV=1	7.534	9	2	2	2	230	25.8	6.96	5.67	2	0	378.5	140.9	212.1	218.2	125.9	116.1	134.8	145.4
Q9VRY6	LD14015p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10103 PE=1 SV=1	5.031	5	2	2	2	417	45.6	5.96	5.28	2	0	336.7	144.6	388	387.7	165.4	146.5	166.3	343.3
Q9VK57	LD15349p OS=Drosophila melanogaster OX=7227 GN=Pih1D1 PE=1 SV=1	8.797	8	2	2	1	335	38	7.84	6.89	2	0								
Q95RQ8	LD15650p OS=Drosophila melanogaster OX=7227 GN=pita PE=1 SV=1	12.54	5	2	4	2	683	78.3	7.28	14.76	2	0	814	317.1	482	587.2	339	446.5	343.5	339.5

Q9VP57	LD15904p OS=Drosophila melanogaster OX=7227 GN=pzg PE=1 SV=1	76.639	14	7	17	7	996	105	4.89	74.52	7	0	2535.6	850.5	1010.6	935.5	839.5	1148	837.3	622
Q9VW59	LD16419p OS=Drosophila melanogaster OX=7227 GN=RhoGDI PE=1 SV=1	12.863	23	4	4	4	201	23.2	5.64	9.79	4	0	537.1	216.6	464.9	504.5	213.6	190.7	238.4	288.4
Q7K264	LD16826p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8569 PE=2 SV=1	5.786	3	2	2	2	608	68.8	8.51	4.1	2	0	1204.2	375.9	491.4	589.8	442.5	503.9	305.8	437.8
Q9VUE5	LD17962p OS=Drosophila melanogaster OX=7227 GN=stwl PE=1 SV=1	39.302	12	9	10	9	1037	112.8	9.39	35.18	9	0	1078.7	467.1	688.4	717.5	417.7	558.1	397.1	647.6
Q8SWW9	LD18126p OS=Drosophila melanogaster OX=7227 GN=EG:171D11.2 PE=1 SV=1	23.427	7	2	4	2	692	75.7	9.38	17.41	2	0	12.9	4.9	27.5	16.8	4.5	3.4	11.6	7.5
Q9VK20	LD18447p OS=Drosophila melanogaster OX=7227 GN=mRF1 PE=2 SV=1	23.382	9	3	9	3	392	44.6	6.77	28.39	3	0	142.6	110.6	297.2	251.5	88.6	91.9	211.6	164.5
Q7K110	LD18774p OS=Drosophila melanogaster OX=7227 GN=OstDelta PE=1 SV=1	19.097	10	5	6	5	634	69.2	9.17	17.77	5	0	758.2	317.4	979.9	961	247.2	289	459.6	852.2
Q9VIL2	LD19544p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2608 PE=1 SV=1	8.703	9	2	3	2	255	29.1	5.99	9.83	2	0	218.7	82.6	122.8	148.5	81.4	84.5	81.9	118.6
Q9VT75	LD19812p OS=Drosophila melanogaster OX=7227 GN=vnc PE=1 SV=1	8.212	12	2	2	2	196	22.3	6.95	6.29	2	0	183.1	97.6	186.2	193.6	100	110.8	110.7	98
Q9VTT2	LD20590p OS=Drosophila melanogaster OX=7227 GN=vers PE=1 SV=1	24.441	16	5	9	5	391	44.8	5.81	30.9	5	0	941.2	342.2	389.3	458.4	364.6	437.5	283.8	309.3
Q7K231	LD20635p OS=Drosophila melanogaster OX=7227 GN=CYC4 PE=1 SV=1	8.186	4	2	3	2	517	58.9	8.13	6.07	2	0	288.5	150.7	171.6	190.3	135.5	131.3	93.3	86
Q9VY91	LD21074p OS=Drosophila melanogaster OX=7227 GN=Pdcd4 PE=1 SV=2	6.911	5	3	4	3	509	56.3	5.97	9.51	3	0	673.7	232.5	433.7	539.2	294.5	237.3	242.6	494.4
Q8T092	LD21421p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4282 PE=2 SV=1	13.556	3	2	2	2	652	75.2	7.34	9.36	2	0	109.8	52.8	90.4	91.7	42	45.8	45.3	58.4
Q9W1G7	LD21576p OS=Drosophila melanogaster OX=7227 GN=Nap1 PE=1 SV=1	18.843	9	2	4	2	370	42.7	4.79	18.15	2	0	522	245.1	630.4	624.1	238.9	268.5	255	344.5
Q9W5X0	LD21953p OS=Drosophila melanogaster OX=7227 GN=Rab35 PE=1 SV=1	10.095	10	2	5	1	201	22.8	8.54	10.52	2	0	103.8	63.9	188.6	202.6	55.7	58.8	89.6	85.1
Q8MQJ5	LD22337p OS=Drosophila melanogaster OX=7227 GN=CG7687 PE=2 SV=1	5.712	4	2	2	2	524	57.3	5.72	5.2	2	0	338.3	151.4	294.9	379.8	152.9	121.3	135.2	392.8
Q7KUA4	LD22577p OS=Drosophila melanogaster OX=7227 GN=Uba2 PE=1 SV=1	12.37	6	4	5	4	700	77.6	5.02	12.91	4	0	1086.9	572	493.3	494.6	471	435.2	300.9	261.4
Q9VLX2	LD22651p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7154 PE=1 SV=1	16.054	6	3	3	3	861	95.9	6.1	8.35	3	0	55.6	26.1	57.7	55.6	23.3	29.6	29.2	55.7
Q9VL91	LD23102p OS=Drosophila melanogaster OX=7227 GN=zf30C PE=1 SV=2	10.708	3	2	3	2	777	88.3	8.13	10.43	2	0	680.8	286.6	334.2	401.3	259.3	307.1	203.6	232.2
Q9W2M0	LD23155p OS=Drosophila melanogaster OX=7227 GN=Rbpn-5 PE=1 SV=2	20.985	6	2	3	2	647	74.9	5.38	12.27	2	0								
Q9VCF8	LD23561p OS=Drosophila melanogaster OX=7227 GN=anon-WO0118547.306 PE=1 SV=1	10.557	7	2	5	2	371	41.8	5.62	17.96	2	0	265.6	94.2	193.5	187.3	99.8	191.1	186.4	406.4
Q9VK59	LD23647p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5787 PE=1 SV=2	88.079	16	10	22	10	950	100.2	9.74	87.44	10	0	6439.8	2462.5	3255.3	2943.2	2325.8	2526.2	2033.4	1784.9
Q9VAA9	LD23804p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7946 PE=1 SV=1	35.254	18	6	11	6	475	52.8	8.18	29.03	6	0	469.6	173	283.6	331.4	210.9	207.3	163.6	351.8
Q7K4T8	LD23856p OS=Drosophila melanogaster OX=7227 GN=FBgn 33734 PE=1 SV=1	18.209	6	2	7	2	458	52.4	8.06	28.75	2	0	344.8	168.8	641.4	638.1	168.6	209	431.8	468.3
Q9VP77	LD23875p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10565 PE=1 SV=1	14.73	7	4	5	4	646	73.6	8.97	17.19	4	0	387.7	216.8	421.3	459.6	151.2	238.5	235.3	241.4
Q9VYI6	LD23884p OS=Drosophila melanogaster OX=7227 GN=Coq8 PE=1 SV=2	98.6	31	17	26	17	661	74.4	8.18	78.43	17	0	1491.1	806.9	2874.3	2691.7	599.1	756.8	1372.5	1745.8
Q9W3N9	LD24105p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10932 PE=1 SV=1	46.733	17	4	13	4	410	43.4	8.68	52.98	4	0	1037.2	549.4	2002.1	1654.2	375.3	473.3	895.1	1714
Q7JR58	LD24265p OS=Drosophila melanogaster OX=7227 GN=Echs1 PE=1 SV=1	70.193	39	9	23	9	295	31.6	8.63	70.83	9	0	1168.5	669.6	2665.5	1996.5	384	618.6	1228	1961.2
O77477	LD24471p OS=Drosophila melanogaster OX=7227 GN=GM14313 PE=1 SV=1	15.677	10	4	9	4	406	45.7	8.56	27.62	4	0	906.3	499.8	1740.9	1348.4	337.4	523.2	883.3	847.7
Q9W0X3	LD24657p OS=Drosophila melanogaster OX=7227 GN=Jhebp29 PE=1 SV=1	3.964	9	2	2	2	263	30.3	6.81	4.66	2	0	160.8	76	248.6	265.7	55.2	65.7	105.3	176.7
Q9VYQ9	LD24662p OS=Drosophila melanogaster OX=7227 GN=Tango4 PE=1 SV=1	13.145	8	2	2	2	482	52.7	9.31	7.79	2	0	378.4	131.9	231.8	238.1	139.9	124.3	134.1	133
Q9VHX4	LD24679p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2767 PE=1 SV=1	25.017	20	5	43	5	329	36.8	5.99	50.19	5	0	1576	908.7	1097.3	1107	889.9	894.8	828.3	1133.4
Q7JVH6	LD24696p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9436 PE=1 SV=1	6.024	5	2	2	2	311	35.4	6.76	5.88	2	0	1103.3	496.6	605.2	638.4	404	400.5	339	386.5
Q9VQK5	LD24714p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3542 PE=1 SV=1	6.028	3	2	2	2	806	91.3	8.84	3.81	2	0	348.8	120.9	167.5	197.2	124.3	150.2	104.8	207.4
Q9VJD4	LD24721p OS=Drosophila melanogaster OX=7227 GN=Sgt PE=1 SV=1	20.33	8	3	3	3	331	36.2	4.64	11.79	3	0	802	392.7	741.5	589.7	294.7	373.1	451.5	243.2
Q9VY54	LD24737p OS=Drosophila melanogaster OX=7227 GN=l(1)G0007 PE=1 SV=2	9.198	3	3	3	3	1222	139.5	7.4	7.64	3	0	885.2	395.1	586.9	587.9	351.8	392.7	331.5	347.8
Q9V3E7	LD24793p OS=Drosophila melanogaster OX=7227 GN=Ref1 PE=1 SV=1	21.68	11	3	6	3	266	27.8	10.55	23.98	3	0	984.4	383.1	494.3	709.2	373	408.7	278	413.6
Q9VK44	LD24832p OS=Drosophila melanogaster OX=7227 GN=ufd2 PE=1 SV=1	7.785	2	2	3	2	1217	138.5	5.87	8.2	2	0	286.6	142.7	254.5	287.6	105.8	124.9	133.8	191.6
Q9W403	LD24968p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3847 PE=2 SV=1	6.081	4	2	2	2	380	43.6	4.83	5.26	2	0	405.3	135.1	175.3	242.3	141	152.2	110.5	189.3
Q9VGW9	LD25118p OS=Drosophila melanogaster OX=7227 GN=mRpL37 PE=1 SV=3	30.274	21	8	28	8	408	45.7	9.52	41.74	8	0	836.3	370.8	1439.6	1201.3	274.3	361.5	595.9	1793.3
Q9VZU4	LD25561p OS=Drosophila melanogaster OX=7227 GN=ND-30 PE=1 SV=1	57.876	35	9	22	9	265	30	7.84	67.17	9	0	1042.8	604.2	2480.2	1890.7	375.1	533.3	1021	1429.5
Q9VHA8	LD25575p OS=Drosophila melanogaster OX=7227 GN=P58IPK PE=1 SV=1	29.128	24	7	11	7	498	56.8	6.29	29.34	7	0	648.2	341.2	2692.7	2981.7	165.8	204.3	1037.1	1090
Q9VIZ3	LD25692p OS=Drosophila melanogaster OX=7227 GN=l(2)37Cb PE=1 SV=1	13.085	4	4	4	4	894	102.8	6.52	11.29	4	0	1161.6	498	773.7	1022.8	496.5	493.5	417.6	671.6
Q9VPB3	LD26447p OS=Drosophila melanogaster OX=7227 GN=tzn PE=1 SV=2	12.883	12	3	3	3	305	34.2	6.64	11.43	3	0	385.5	181.9	530.5	496.5	157.8	160.5	241.5	322.3
Q9W335	LD26546p OS=Drosophila melanogaster OX=7227 GN=l(1)G0320 PE=1 SV=1	18.274	8	2	4	2	302	33	4.84	17.32	2	0	90.1	42.8	135.1	121.1	39.8	52.5	77.7	53.6
Q9VYI5	LD26737p OS=Drosophila melanogaster OX=7227 GN=Fad1 PE=2 SV=2	3.545	5	2	2	2	322	37	7.08	4.48	2	0	193.6	110.1	457	494.8	62	92	198.5	265.4
Q9VT61	LD27033p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8108 PE=1 SV=1	18.175	7	6	8	6	919	102.9	6.21	20.93	6	0	940	384.8	468.6	440.9	338.2	411.5	319.8	308.8
Q7K0W1	LD27406p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8531 PE=1 SV=1	20.824	10	6	6	6	545	60.9	8.16	17.64	6	0	431.2	261.8	835.5	816.2	129.5	226.9	406.9	649.9
Q9VZS1	LD28127p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG17746 PE=1 SV=1	11.711	11	3	3	3	371	41	4.89	8.82	3	0	230.3	111.5	190.9	233.4	86.1	118.1	103	113.9
Q9VAX8	LD28793p OS=Drosophila melanogaster OX=7227 GN=Snu114 PE=1 SV=1	37.158	7	7	10	7	975	110.6	5.03	29.6	7	0	1475.1	678.7	1158.6	1132.6	624.4	688.4	664.7	735.9
Q9VH64	LD29322p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8507 PE=1 SV=1	20.008	9	4	7	4	379	44.6	8.15	21.08	4	0	417.1	157	1655.8	1538	81.3	97.2	693.3	1099.4
Q9VLS5	LD29542p OS=Drosophila melanogaster OX=7227 GN=Rbsn-5 PE=1 SV=1	8.44	6	2	2	2	505	56.9	6.83	7.12	2	0								
Q9VL71	LD29830p OS=Drosophila melanogaster OX=7227 GN=Srp54 PE=1 SV=1	21.428	8	3	6	3	513	58.3	11.33	22.71	3	0	432.8	201	314.9	344.3	185.6	223.6	174.8	253.4
Q9VN21	LD30155p OS=Drosophila melanogaster OX=7227 GN=lost PE=1 SV=1	98.79	29	13	22	13	545	59.7	9.06	84.15	13	0	1435	661.8	1777.7	1520.7	463.4	690.8	1040.6	1067
Q9VXW3	LD30439p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12608 PE=1 SV=2	7.548	4	2	4	2	443	49.1	8.03	9.83	2	0	1344.3	576.5	566.8	884.5	520.8	533.4	295	477.6
Q9VHM3	LD30467p OS=Drosophila melanogaster OX=7227 GN=M1BP PE=1 SV=1	5.89	5	2	3	2	418	48.1	5.52	7.1	2	0	308.5	120.4	172.5	224	118.3	154.3	100.6	161.5
Q9VJJ8	LD30602p OS=Drosophila melanogaster OX=7227 GN=CT15043 PE=1 SV=2	10.168	3	2	2	2	1413	153.2	7.93	7.33	2	0	125.7	61.8	155.4	159.3	58.5	86.4	82.4	74.3
Q9VHE4	LD31229p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8132 PE=1 SV=1	40.321	24	5	12	5	283	31.9	7.15	53.51	5	0	509.3	304.5	907.3	761.2	208.2	277.4	384.7	417.1
Q9VXK7	LD31474p OS=Drosophila melanogaster OX=7227 GN=ND-20 PE=2 SV=1	23.27	13	4	7	4	221	24.6	9.74	20.28	4	0	300.6	147.5	714.6	629.1	103.7	115.5	249.3	1712.4
Q9VHT5	LD31571p OS=Drosophila melanogaster OX=7227 GN=mRpL1 PE=1 SV=2	9.572	6	3	16	3	354	40.3	9.42	14.12	3	0	333.7	173.3	648.7	538.8	119.7	160.5	292.2	443.1
Q9VTC1	LD32732p OS=Drosophila melanogaster OX=7227 GN=DmRH27 PE=1 SV=1	37.04	9	6	6	6	791	87.2	6.99	22.09	6	0	1597.7	599.1	730.8	965.4	646.6	497.1	382.2	753.3
Q9W3M7	LD32873p OS=Drosophila melanogaster OX=7227 GN=mahe PE=1 SV=1	47.734	12	8	16	6	945	100.4	9.14	45.11	8	0	451.7	216.3	436.2	466	214.7	256.5	260.7	254.6
Q9V3D0	LD33485p OS=Drosophila melanogaster OX=7227 GN=mRpL4 PE=1 SV=1	19.391	13	3	7	3	296	32.8	9.22	25.3	3	0	398	246	858.2	652.8	174.6	232.4	320.1	1185.8
Q9VB22	LD33695p OS=Drosophila melanogaster OX=7227 GN=pins PE=1 SV=1	9.03	6	3	5	3	658	71.4	6.74	12.72	3	0	376.7	197.1	370.5	384.7	173.9	177.3	194.3	320.9
Q7K4L8	LD33749p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7878 PE=1 SV=1	12.991	3	2	7	1	703	78.5	6.7	12.1	2	0	95.7	49.2	87.2	90.1	37.8	58.3	52.7	39.1
Q9VM62	LD34181p OS=Drosophila melanogaster OX=7227 GN=SA PE=1 SV=2	10.494	2	2	3	2	1127	130	5.4	9.98	2	0	1176.3	512.8	411.7	600.7	490.6	728.5	323.2	270.9
Q95RF6	LD34461p OS=Drosophila melanogaster OX=7227 GN=Tom20 PE=1 SV=1	32.728	39	4	10	4	171	18.8	7.24	30.63	4	0	532.8	228.9	808	568.1	210.4	225.4	394.9	621
Q9VX15	LD35209p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8142 PE=1 SV=2	27.14	12	5	9	5	353	39.5	7.87	30.13	5	0	1494.7	668.5	736.1	916.3	615.5	343	227.9	548.3
Q7K1W5	LD35843p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8187 PE=1 SV=1	21.215	17	6	7	6	376	41.6	7.66	18.94	6	0	349.3	172.7	505.1	410.9	139.4	164.9	247.2	319
Q9VWQ3	LD35981p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6961 PE=2 SV=2	26.002	14	4	6	4	474	53	9.74	32.46	4	0	422.1	192.6	398.2	436.4	165.7	194.4	201.4	323.2
Q9V3F2	LD36009p OS=Drosophila melanogaster OX=7227 GN=lace PE=1 SV=1	5.99	4	2	2	2	597	66	7.81	5.05	2	0	289.3	135.3	351.6	349.7	129	212.9	206.9	188.7
Q9VQ76	LD36155p OS=Drosophila melanogaster OX=7227 GN=tho2 PE=1 SV=2	36.458	5	7	8	7	1641	188.4	8.82	30.18	7	0	833.9	446.4	703.6	881.5	360.3	410.8	368	435.7
Q9W3H4	LD36273p OS=Drosophila melanogaster OX=7227 GN=sni PE=1 SV=1	32.449	30	4	13	4	247	26.5	8.65	40.16	4	0	773.3	396.7	1503.5	1551.1	313.4	313.4	620.1	837.8
Q9W158	LD36772p OS=Drosophila melanogaster OX=7227 GN=cg4612 PE=1 SV=1	3.755	6	2	2	2	307	33.6	9.28	4.75	2	0	104.1	58.2	167.5	167.2	53.3	71.6	92.1	183.6
Q9VK18	LD36945p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG16812 PE=2 SV=1	22.893	11	4	5	4	455	49.8	9.99	18.42	4	0	733.7	344.2	470.3	599.6	291.7	411.9	242.3	395.2
Q9VC06	LD37516p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11771 PE=1 SV=1	49.711	16	11	17	11	730	81.3	7.08	45.14	11	0	1339.6	707.9	2756.6	2069.3	465	573	1149	1575.6
Q95RE4	LD37574p OS=Drosophila melanogaster OX=7227 GN=yps PE=1 SV=1	27.705	26	6	9	6	352	38.2	9.85	23.57	6	0	476.2	201.4	516.1	584.3	197.7	238.4	232.6	309.4
Q9W379	LD37736p OS=Drosophila melanogaster OX=7227 GN=Zpr1 PE=1 SV=1	10.733	12	3	3	3	457	51.3	4.74	6.17	3	0	362.4	190.1	329.1	437	188.9	190.3	202.3	241.2
Q9VXL4	LD38104p OS=Drosophila melanogaster OX=7227 GN=Rrp47 PE=1 SV=1	5.556	15	2	2	2	159	18.1	6.2	5.38	2	0	285.7	123.2	186.2	242.5	128.4	105.6	102.1	143.9
Q9VWD9	LD38919p OS=Drosophila melanogaster OX=7227 GN=Ubqn PE=1 SV=1	38.632	19	6	9	6	547	58.8	5.11	28.37	6	0	692.1	325.8	667.8	703.9	312.5	326.4	348.4	453.4
M9NEW0	LD39232p2 OS=Drosophila melanogaster OX=7227 GN=CG9243 PE=2 SV=1	12.566	18	2	4	2	150	17.6	8.95	16.63	2	0	375	233.4	865.5	525.6	120.9	175.9	414.1	279.7
Q960Q8	LD39850p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3511 PE=1 SV=1	11.483	8	4	4	4	637	71.7	7.14	10.2	4	0	679.4	310.7	441.7	591.7	267.7	296.8	230.4	775
Q9VS47	LD39967p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8602 PE=2 SV=1	13.677	9	3	3	3	478	53.3	6.39	9.98	3	0	217.7	149.6	423.8	451.7	104.9	166	195.6	210
O15971	LD39986p OS=Drosophila melanogaster OX=7227 GN=Rab10 PE=1 SV=1	8.437	9	2	4	1	204	23.3	8.05	10.08	2	0	153.1	81.4	321.4	326.8	51.1	76.3	163.3	230.9
Q7K3B7	LD40177p OS=Drosophila melanogaster OX=7227 GN=Hacl PE=1 SV=1	16.022	8	3	4	3	568	62.2	7.47	7.25	3	0	290.5	121	278.8	268.4	132.1	144.7	174.7	178.6
Q7JQY8	LD40262p OS=Drosophila melanogaster OX=7227 GN=p190 PE=2 SV=1	3.736	1	2	2	2	1309	145.9	6.19	2.39	2	0	461.4	186.3	189.4	341.1	188.9	235.3	135.9	201.3
Q9VPX3	LD40271p OS=Drosophila melanogaster OX=7227 GN=l(2)10685 PE=1 SV=1	33.191	19	7	11	7	503	57.5	7.15	35.05	7	0	589.3	327.2	1159.8	744.1	208	281.5	533.1	388.2
Q9V3W7	LD40489p OS=Drosophila melanogaster OX=7227 GN=SF2 PE=1 SV=1	26.844	29	6	12	6	255	28.3	9.91	29.2	6	0	2071.9	940.2	1250.1	1457.8	814.5	947.7	761.7	802.9
Q9W253	LD41023p OS=Drosophila melanogaster OX=7227 GN=mRpS29 PE=1 SV=1	17.047	11	3	3	3	392	44.3	8.41	9.64	3	0	159.7	78.5	293.1	221.7	79.8	112.8	134.3	189.7
Q9VXW2	LD41277p OS=Drosophila melanogaster OX=7227 GN=Prp5 PE=1 SV=1	9.273	2	2	2	2	1224	136.2	8.07	6.01	2	0	287.7	112.8	168.1	211.5	117.6	106.2	77.9	165.6
Q7JQT8	LD41464p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG17002 PE=1 SV=1	12.9	9	3	4	3	421	46.5	9.48	11.3	3	0	592.7	242.9	341.1	368.3	242.3	233.3	177.8	173.5
Q95TL8	LD41494p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9911 PE=1 SV=1	10.443	9	4	4	4	412	47	5.97	9.25	4	0	103.6	51.3	399.9	496.5	53.9	42.5	192.5	584.4
Q9VKW1	LD41958p OS=Drosophila melanogaster OX=7227 GN=Wdfy2 PE=1 SV=1	13.726	14	4	4	4	408	46.2	7.37	9.67	4	0	824	341	661.5	734	288.7	340.1	398.4	588.3
Q9V3Y4	LD43650p OS=Drosophila melanogaster OX=7227 GN=Mtch PE=1 SV=1	14.647	10	3	7	3	316	35	9.06	15.9	3	0	64.3	53.5	193.5	190.1	20.1	34.9	73.6	188.8
Q9V9Q4	LD43819p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1416 PE=1 SV=2	10.281	6	2	2	2	354	40.1	6.57	4.62	2	0	208.5	110.6	200.4	205.1	85.8	104.7	118.6	77
Q9W2K4	LD44216p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4266 PE=1 SV=2	17.86	5	3	3	3	1215	130.3	8.22	8.48	3	0	198.9	90.9	149.8	176.6	76.3	107	95.2	88
Q8MR14	LD44235p OS=Drosophila melanogaster OX=7227 GN=velo PE=1 SV=1	7.058	4	2	2	2	711	78.9	5.55	5.03	2	0								
Q9VZ82	LD44376p OS=Drosophila melanogaster OX=7227 GN=LeuRS-m PE=1 SV=1	61.942	17	11	18	11	869	99.2	8.05	58.64	11	0	1174.3	661.9	2461.8	2410.5	456.4	553.3	997.2	1424
O18338	LD44762p OS=Drosophila melanogaster OX=7227 GN=Rab8 PE=1 SV=1	13.964	14	2	3	1	207	23.7	8.48	10.2	2	0	17	9.8	21.9	19.8	5.7	4.6	6	23.3
Q95TK5	LD44914p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1635 PE=1 SV=1	36.485	13	5	12	5	448	51.1	9.06	42.33	5	0	959.4	504.5	1570	1519.2	533.5	464.9	739.4	877.5
Q9VQK7	LD45152p OS=Drosophila melanogaster OX=7227 GN=Sf3b2 PE=1 SV=2	15.935	5	2	2	2	749	84.7	5.34	8.01	2	0	16	7.1	17.7	22.4	5.4	7.3	12	10.5
Q9VZY0	LD45195p OS=Drosophila melanogaster OX=7227 GN=Non2 PE=1 SV=1	9.646	12	2	3	2	244	27.5	6.32	7.92	2	0	201.1	83.6	192.8	230.3	102.4	105.3	101.1	288.2
Q9V9U3	LD45254p OS=Drosophila melanogaster OX=7227 GN=Anon1A3 PE=1 SV=1	97.192	35	9	14	9	489	51.6	4.56	59.6	9	0	2200.3	908.6	926.3	928.7	851.5	865.1	554.5	665.7
Q960M4	LD45324p OS=Drosophila melanogaster OX=7227 GN=Prx5 PE=1 SV=1	33.681	36	4	42	4	190	19.9	8.68	143.5	4	0	906.1	453.8	1536.9	1258.3	402.8	426.6	683.1	991.6
Q7KTG0	LD45607p OS=Drosophila melanogaster OX=7227 GN=CG31879 PE=1 SV=1	36.472	10	5	12	5	570	64.3	7.44	42.16	5	0	678.9	475.1	1466.1	1009.2	310.7	461.4	676.7	584.6
Q9VN88	LD45836p OS=Drosophila melanogaster OX=7227 GN=Vps37B PE=1 SV=1	17.387	24	4	6	4	214	24.2	5.17	13.93	4	0	234	110.8	226.9	266.9	106.2	123.3	126.3	123.9
Q9V3P3	LD45860p OS=Drosophila melanogaster OX=7227 GN=REG PE=1 SV=1	30.263	26	4	12	4	245	28.1	6.05	38.84	4	0	475.1	172.8	203.2	235.3	154.5	137.6	130.4	292.3
Q7K4C7	LD46058p OS=Drosophila melanogaster OX=7227 GN=Pcyt1 PE=1 SV=1	33.614	13	4	5	4	526	58.2	5.99	16.15	4	0	1267.4	561.3	612.2	778.2	538.1	497.3	357	370.9
Q7KSQ0	LD46175p OS=Drosophila melanogaster OX=7227 GN=sea PE=1 SV=1	8.05	5	2	7	2	317	34.1	9.42	21	2	0	865	387.4	2995.1	1735.4	482.9	389.5	1255.3	1852.5
Q9W3S4	LD46272p OS=Drosophila melanogaster OX=7227 GN=CC28 PE=2 SV=2	37.671	15	5	7	5	418	45.7	9.48	21.66	5	0	457.2	200.3	299	366	185.9	212.5	192.3	217.8
Q9VDI1	LD46328p OS=Drosophila melanogaster OX=7227 GN=Synd PE=1 SV=2	12.888	8	3	3	3	494	55.9	5.63	8.49	3	0	290.6	166	391	430.3	116.4	152.3	231.8	149.5
Q95RB1	LD46870p OS=Drosophila melanogaster OX=7227 GN=cg14641 PE=1 SV=1	25.255	12	5	6	5	418	47.1	8.57	18.66	5	0	788.8	358	563.5	697.6	336.2	366.6	331.7	376.6
Q9VHI7	LD47007p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11982 PE=1 SV=1	25.875	14	3	3	3	380	40.3	4.79	17.05	3	0	91.3	41.8	77.6	88.6	38.2	47.8	39.3	57.6
Q9V4E0	LD47962p OS=Drosophila melanogaster OX=7227 GN=ND-49 PE=1 SV=2	89.348	20	8	54	8	468	52.9	6.67	160.8	8	0	1393.1	755.9	2952.4	2779.3	643.5	825.7	1304.2	4985.2
Q8T9B6	LDLR chaperone boca OS=Drosophila melanogaster OX=7227 GN=boca PE=1 SV=2	7.722	16	3	5	3	180	21	4.91	7.73	3	0	172	70.5	442.9	405.8	42.9	65.5	200.9	367.8
Q9VLW1	Lectin type C OS=Drosophila melanogaster OX=7227 GN=lectin-28C PE=1 SV=2	5.133	7	2	2	2	265	29.9	5.85	5.14	2	0	140.7	65.8	839	833.5	21.6	21.3	340.7	214.2
Q709R6	LEM domain-containing protein Bocksbeutel OS=Drosophila melanogaster OX=7227 GN=bocks PE=1 SV=1	11.091	9	3	3	3	399	44.2	9.23	9.92	3	0	862.8	296.7	675.4	848	325.2	402.9	404.3	395
Q7KVT8	Lethal (1) G0193, isoform B OS=Drosophila melanogaster OX=7227 GN=l(1)G0193 PE=1 SV=1	4.926	3	2	2	2	646	75.3	7.71	4.76	2	0	202.3	115.1	306.2	366.8	119.1	155.5	153.4	201.6
Q9VJ10	Lethal (2) 37Bb OS=Drosophila melanogaster OX=7227 GN=l(2)37Bb PE=1 SV=1	34.444	18	6	12	6	515	56.7	6.84	29.55	6	0	492.7	320.9	1085.4	906.8	251.4	352.5	548.5	577
A0A023GQA5	Lethal (2) 37Cc, isoform D OS=Drosophila melanogaster OX=7227 GN=l(2)37Cc PE=1 SV=1	138.389	49	13	304	13	276	30.4	5.73	1007.85	13	0	6652.7	4004.8	14202.6	11123.5	2626.6	3484	7182.5	8574.3

M9PBJ2	Lethal (2) giant larvae, isoform K OS=Drosophila melanogaster OX=7227 GN=l(2)gl PE=4 SV=1	15.974	3	3	3	3	1093	119.7	6.11	10.96	3	0	384.3	189.8	464.6	577.3	167.1	187.4	238.7	310.1
Q8MLS7	Lethal (2) k09913, isoform D OS=Drosophila melanogaster OX=7227 GN=l(2)k09913 PE=1 SV=1	13.238	11	4	10	4	316	36.5	9.38	19.92	4	0	1615.4	816.9	2570.6	2208.7	643.5	927	1145.3	2381.3
Q9VID7	Lethal (2) k14505, isoform A OS=Drosophila melanogaster OX=7227 GN=l(2)k14505 PE=1 SV=1	42.297	25	5	19	5	279	31.8	7.2	78.98	5	0	1622.7	883.6	2790.3	1674.3	663.6	818.4	1286.9	1602
A0A0B4K7M9	Lethal (2) tumorous imaginal discs, isoform D OS=Drosophila melanogaster OX=7227 GN=l(2)tid PE=1 SV=1	148.039	33	14	37	1	514	55.6	9.1	152.27	14	15	3691.8	1840.3	6107.6	4653.2	1349.7	1706.7	2665	3769.5
O62602	Licorne OS=Drosophila melanogaster OX=7227 GN=lic PE=1 SV=1	10.851	12	4	5	4	334	38.2	6.39	9.75	4	0	292.7	125.2	237.2	255.8	134.1	136.8	115.6	222.2
Q8I7C3	LIM and SH3 domain protein Lasp OS=Drosophila melanogaster OX=7227 GN=Lasp PE=1 SV=2	23.373	12	6	7	6	657	74.2	7.88	16.86	6	0	486.9	206.9	654.6	685.2	226.7	245.6	330.7	408.3
A0A0B4K7U5	Lingerer, isoform H OS=Drosophila melanogaster OX=7227 GN=lig PE=1 SV=1	84.429	13	10	13	10	1330	134.3	6.92	58.22	10	0	1321.1	601.8	1436.6	1329	614.9	630.1	855.9	691.4
Q7JQW6	Lipoyl synthase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Las PE=2 SV=2	11.17	10	2	2	2	377	42.7	7.65	6.36	2	0	68.6	45.5	169.2	177.5	22.5	36.6	59.5	72.6
M9PCR7	Liprin-alpha, isoform D OS=Drosophila melanogaster OX=7227 GN=Liprin-alpha PE=1 SV=1	5.583	2	2	3	2	1205	135	6.28	6.88	2	0	620.3	257.7	582.2	504.1	231.8	271.7	336.8	487.4
M9NEV0	Little imaginal discs, isoform C OS=Drosophila melanogaster OX=7227 GN=lid PE=4 SV=1	71.123	7	8	11	8	1838	203.9	6.62	43.88	8	0	620.5	260.9	472.2	509.5	273.4	311.5	262.3	367.6
Q7KUT2	Lon protease homolog, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Lon PE=1 SV=1	112.962	23	13	32	13	1024	115	7.59	109.4	13	0	1238	574.8	2091	1522.6	458.8	483	981.1	1484
P82890	Low molecular weight phosphotyrosine protein phosphatase 1 OS=Drosophila melanogaster OX=7227 GN=p	10.166	17	2	4	2	155	17.5	7.27	15.42	2	0	449.4	246.2	600.5	566.1	179.7	190.4	280.4	245.7
Q7K0L7	LP01207p OS=Drosophila melanogaster OX=7227 GN=Tpc1 PE=1 SV=1	15.115	11	3	5	3	332	36.7	9.76	20.58	3	0	293.3	170.3	555.4	385.5	154.6	175.2	265.7	225
Q9VG69	LP03547p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5844 PE=1 SV=1	34.168	20	4	6	4	378	41.6	5.68	27	4	0	262.7	128.3	466	359.4	113.9	117.2	217.3	331
Q9VQI5	LP04564p OS=Drosophila melanogaster OX=7227 GN=CG3098 PE=1 SV=2	11.683	7	3	5	3	425	47.3	6.28	7.44	3	0	285.7	116.8	200.5	301	118.1	140.5	142.2	141
Q9VU36	LP04985p OS=Drosophila melanogaster OX=7227 GN=mRpL20 PE=1 SV=1	16.541	24	4	9	4	150	17.4	10.56	17.62	4	0	574.8	279.9	933.8	837.5	223.4	279.2	414.8	853.1
Q9VEV3	LP07287p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG14894 PE=1 SV=2	5.397	11	3	3	3	263	29.4	4.64	7.52	3	0	343.7	169.5	419.8	426.6	155.3	187.7	195.2	305.8
Q9VKW5	LP07359p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5355 PE=1 SV=2	47.376	20	10	17	10	756	86.3	6.19	57.16	10	0	1408.6	663.5	1353.8	1103.3	515.7	576.7	626.4	702.5
Q9VGP4	LP08082p OS=Drosophila melanogaster OX=7227 GN=Ranbp9 PE=1 SV=1	9.359	4	2	2	2	1018	114.3	4.87	4.29	2	0	12.2	9.2	14.6	20.3	5.1	9.8	7.2	15.8
Q9VKZ8	LP08774p OS=Drosophila melanogaster OX=7227 GN=Usp14 PE=1 SV=1	17.769	6	2	3	2	475	53.7	6.25	11.12	2	0	174.2	70.4	151.4	211.6	57.4	68.7	73.7	121.9
Q9VY79	LP09908p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11095 PE=1 SV=1	18.637	14	3	7	3	283	32	9.35	23.29	3	0	278.5	152.1	512.5	520.4	205.9	196.9	249.3	303.5
Q9VIN9	LP10852p OS=Drosophila melanogaster OX=7227 GN=mRpS18B PE=1 SV=1	14.945	26	5	9	5	204	23.2	8.68	21.54	5	0	802.5	468.2	1613.7	1152.2	362.2	484.2	861.7	667.5
Q9W0M4	LP10861p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG13887 PE=1 SV=1	31.196	17	5	9	5	228	26.1	9.32	34.33	5	0	713.8	441.3	1088.1	968.8	241.8	493.4	591.4	453.1
Q9VQL1	LP20978p OS=Drosophila melanogaster OX=7227 GN=SerRS PE=1 SV=1	15.986	7	3	6	3	501	56.4	6.49	16.22	3	0	808.2	466.3	903.6	945.3	372	324.4	464.8	372.1
Q8IRH0	LP21249p OS=Drosophila melanogaster OX=7227 GN=Psa PE=1 SV=1	54.104	12	14	18	14	1053	120.2	6.47	53.38	14	0	1801.3	927.1	1928.7	1912.3	684.4	815.8	913	1570.4
E2QCZ3	LP22035p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7705 PE=2 SV=1	12.055	4	2	2	2	592	68.1	5.54	7.44	2	0	232.9	175.7	362.1	286.7	77.4	178.5	196.1	145.6
E1JH52	Lysine (K)-specific demethylase 4B, isoform B OS=Drosophila melanogaster OX=7227 GN=Kdm4B PE=1 SV=	10.319	5	2	2	2	590	66.4	7.46	7.13	2	0	771.5	371.1	441.9	531.6	323.4	366.1	238.6	260.5
Q9VLX0	Lysine ketoglutarate reductase/saccharopine dehydrogenase, isoform A OS=Drosophila melanogaster OX=72	201.694	24	21	137	21	928	103.1	6.79	397.33	21	0	5242.1	3569.6	11581.8	8998.5	1974.3	3064	4981	6302.1
Q9W327	Lysine--tRNA ligase OS=Drosophila melanogaster OX=7227 GN=LysRS PE=1 SV=2	22.581	8	6	9	6	607	68.5	7.08	24.19	6	0	1167.4	1138.7	920.6	856.3	960.4	401.3	370.3	543.7
A0A0B4K8A5	Mahjong, isoform B OS=Drosophila melanogaster OX=7227 GN=mahj PE=4 SV=1	6.544	1	2	2	2	1544	172	5	6.09	2	0	419.5	196.1	372.5	438.9	175	183	180.5	197
P02825	Major heat shock 70 kDa protein Ab OS=Drosophila melanogaster OX=7227 GN=Hsp70Ab PE=2 SV=3	27.871	10	5	12	1	642	70.1	5.77	38.76	5	1	55.4	25.5	98.7	108.8	18	23	46.1	75
O02193	Males-absent on the first protein OS=Drosophila melanogaster OX=7227 GN=mof PE=1 SV=1	19.354	7	4	5	4	827	92.6	4.79	20.91	4	0	245.4	113.7	243.7	229.8	108.2	111.6	118.9	204.5
Q9VG32	Malic enzyme OS=Drosophila melanogaster OX=7227 GN=Men PE=1 SV=1	43.797	13	9	19	9	759	84.3	7.21	57.89	9	0	1111.5	539.8	1611.8	1449.4	439	460.7	739.9	864.6
Q9VB69	Malic enzyme OS=Drosophila melanogaster OX=7227 GN=Men-b PE=1 SV=1	85.937	24	13	39	13	617	68.6	6.71	125.21	13	0	2693.1	1336.8	4581.2	4037.4	1008.7	1044.3	1824.2	4253.6
Q9VGA4	MBD-R2 OS=Drosophila melanogaster OX=7227 GN=MBD-R2 PE=1 SV=2	28.004	4	4	7	4	1169	130.1	8.03	23.52	4	0	738.8	300.2	408.6	530.3	317.7	339.1	258.9	473.6
Q9VWL0	Mec2 OS=Drosophila melanogaster OX=7227 GN=Mec2 PE=1 SV=1	36.24	30	8	10	8	350	38.6	5.25	34.11	8	0	569.6	386.2	1094	1296.5	214.8	373.2	459.4	731.7
Q9VP05	Mediator of RNA polymerase II transcription subunit 1 OS=Drosophila melanogaster OX=7227 GN=MED1 PE=	16.952	3	2	2	2	1475	149.4	9.33	10.49	2	0	759.7	390.2	412.8	438.6	269.6	313.7	233.8	186.8
A0A0B4KFE9	Megator, isoform B OS=Drosophila melanogaster OX=7227 GN=Mtor PE=1 SV=1	42.34	5	10	10	10	2346	262.2	5.1	28.6	10	0	1241	484.8	847.2	1067.3	418.3	474.3	430.1	695.7
P55162	Membrane-associated protein Hem OS=Drosophila melanogaster OX=7227 GN=Hem PE=2 SV=1	4.398	1	2	2	2	1126	129.3	6.81	3.89	2	0	72.7	39	93.5	130.1	36.6	43.7	66.4	61.3
Q0E8J0	MEP-1, isoform A OS=Drosophila melanogaster OX=7227 GN=MEP-1 PE=1 SV=1	9.645	4	3	3	3	1152	124	5.03	8.92	3	0	284.4	129.7	310.3	352.4	121.8	131.9	169.5	248.9
Q9VNF7	Metastasis associated 1-like, isoform B OS=Drosophila melanogaster OX=7227 GN=MTA1-like PE=1 SV=2	24.649	6	4	5	4	844	92.7	9.35	16.4	4	0	571.1	295.2	418.6	483.5	246.9	265.9	222.2	240.9
Q9VKV9	Methionine aminopeptidase OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5188 PE=3 SV=2	19.598	15	4	6	4	317	34.8	5.82	19.22	4	0	261.8	118.6	270.1	300	123.2	134.3	157.6	281.8
Q9VC48	Methionine aminopeptidase OS=Drosophila melanogaster OX=7227 GN=MAP1A PE=1 SV=1	11.651	6	2	3	2	374	41.7	6.93	9.7	2	0	436.3	195.7	328.6	397.9	167.2	166.5	177.7	168.9
Q9VFL5	Methionine--tRNA ligase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Aats-met-m PE=2 SV=2	54.584	20	9	18	9	582	66	8	63.08	9	0	1095.1	626.3	2198.2	1828.5	348.9	505.1	1082.6	1328.2
A1ZBE9	Methionyl-tRNA synthetase OS=Drosophila melanogaster OX=7227 GN=MetRS PE=1 SV=1	22.629	7	5	7	5	1022	112.4	8.51	20.56	5	0	431.1	191.2	518.3	504.7	182.4	202.8	318.5	285.9
M9PIA6	Mi-2, isoform D OS=Drosophila melanogaster OX=7227 GN=Mi-2 PE=1 SV=1	65.75	8	14	16	12	1973	223	5.76	50.32	14	2	3262.1	1436.2	1806.9	2161.8	1350.4	1190.7	1022.3	1528.1
A0A0B4KHL7	MICOS complex subunit MIC60 OS=Drosophila melanogaster OX=7227 GN=Mitofilin PE=3 SV=1	75.616	22	15	22	15	739	82	8.94	73.11	15	0	1037.2	608.8	2648.7	2060.6	308.5	550	1509.8	1762.7
Q9W062	Microfibrillar-associated protein 1 OS=Drosophila melanogaster OX=7227 GN=Mfap1 PE=1 SV=1	10.96	5	2	2	2	478	56.1	5.35	5.88	2	0	286.3	101	131.8	123.1	100.5	113.1	93	126.8
Q9I7K0	Microtubule-associated protein Jupiter OS=Drosophila melanogaster OX=7227 GN=Jupiter PE=1 SV=2	28.101	25	4	7	4	208	22.3	10.14	26.65	4	0	2100.5	828.3	1307.9	1024.8	722.1	799.9	772.2	648.7
Q7KTK9	Midline uncoordinated, isoform A OS=Drosophila melanogaster OX=7227 GN=muc PE=1 SV=1	38.603	23	9	20	9	421	44.1	8.82	53.78	9	0	1589.8	850.9	3461.9	2959.9	612.8	803.6	1457.4	3184.7
Q9VG06	MIP04754p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG17327 PE=1 SV=2	21.065	21	3	7	3	139	15	9.61	27.53	3	0	955.2	451.6	1193.2	1115.7	358.9	438.4	556.8	574.5
Q9VAX9	MIP05919p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4884 PE=2 SV=1	10.064	12	2	3	2	189	21.3	9.57	9.87	2	0	364	206.7	696.1	577.5	122	178.9	287.6	342.1
C0PDF4	MIP06482p OS=Drosophila melanogaster OX=7227 GN=CG18815-RA PE=1 SV=1	7.444	12	2	2	2	221	23.7	6.42	4.89	2	0	274.3	136.1	377.2	348.6	124.5	121.9	178.3	189.3
Q0E8E8	MIP08013p1 OS=Drosophila melanogaster OX=7227 GN=Mpcp2 PE=1 SV=1	25.601	14	5	9	5	356	38.8	8.88	29.68	5	0	624.6	295.3	3452.3	2281.6	152.9	130.8	1391	2887.7
A4V0N4	MIP16230p OS=Drosophila melanogaster OX=7227 GN=Vha68-2 PE=1 SV=1	38.574	12	6	10	3	614	68.3	5.34	32.36	6	4	707	423.5	853.9	1131.7	259.5	280.9	442.1	844.5
H5V8B8	MIP33436p1 OS=Drosophila melanogaster OX=7227 GN=Pp2A-29B PE=1 SV=1	12.146	5	3	5	3	650	71.8	4.91	15.75	3	0	818.6	323.2	685.1	929.4	274.6	262.6	329.3	820.2
X2JG23	Misato, isoform B OS=Drosophila melanogaster OX=7227 GN=mst PE=4 SV=1	10.634	6	3	3	3	574	64.7	5.03	8.02	3	0	481.9	237.3	478.9	511.7	197.2	224.1	260.9	307.2
Q9W002	Misshapen, isoform A OS=Drosophila melanogaster OX=7227 GN=msn PE=1 SV=3	30.552	5	5	6	5	1504	162.3	9.33	22.97	5	0	688.2	347.1	905.5	916.3	292.5	363.7	492	585.6
Q9VQ37	Mitochondrial carrier protein Rim2 OS=Drosophila melanogaster OX=7227 GN=Rim2 PE=2 SV=2	10.35	9	2	2	2	365	40.5	9.76	6.49	2	0	215.7	106.7	530.8	391.1	64.8	92.4	220.8	185.7
Q9VL76	Mitochondrial DNA helicase OS=Drosophila melanogaster OX=7227 GN=mtDNA-helicase PE=4 SV=1	12.257	8	5	6	5	613	70	9.25	13.82	5	0	575.5	286.6	957.5	968.3	240.8	298.1	422.5	542
Q9VZJ9	Mitochondrial E3 ubiquitin protein ligase 1 OS=Drosophila melanogaster OX=7227 GN=Mul1 PE=1 SV=1	10.958	9	2	7	2	338	37.8	8.31	17.89	2	0	139	104	239.2	218.9	80.7	93.6	101.5	201.6
Q9VF08	Mitochondrial import inner membrane translocase subunit Tim16 OS=Drosophila melanogaster OX=7227 GN=	43.901	43	7	14	7	141	15.7	9.6	50.89	7	0	585.2	290	1303	1056.6	191.8	232	636.6	777.1
Q9VDZ7	Mitochondrial import inner membrane translocase subunit TIM44 OS=Drosophila melanogaster OX=7227 GN=	74.924	28	13	24	13	459	52.8	8.38	61.48	13	0	1547.8	747.2	3313.6	2236.9	506.1	691.7	1591	1729
Q9W4V8	Mitochondrial import inner membrane translocase subunit TIM50-C OS=Drosophila melanogaster OX=7227 G	32.927	16	6	13	6	428	49.6	7.44	41.04	6	0	641.9	360.6	1442.4	1063.3	295.6	360.8	610.5	987.2
Q9U4L6	Mitochondrial import receptor subunit TOM40 homolog 1 OS=Drosophila melanogaster OX=7227 GN=Tom40	24.896	16	5	12	5	344	36.3	7.09	20.2	5	0	463.9	343.8	934.9	1017.8	328	394.8	442.5	1199.7
Q9VJD0	Mitochondrial inner membrane protease ATP23 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5131 P	22.294	17	4	5	4	283	31.9	7.08	16.71	4	0	314.9	164.2	746.7	537.4	164.9	179.2	303.9	518.7
P91927	Mitochondrial proton/calcium exchanger protein OS=Drosophila melanogaster OX=7227 GN=Letm1 PE=2 SV	47.91	12	11	15	11	1013	113.5	6.84	47.73	11	0	955.1	523.1	2014.6	1502.4	375.6	520.1	932.2	952.1
Q7JUX9	Mitochondrial ribonuclease P protein 1 homolog OS=Drosophila melanogaster OX=7227 GN=trmt10c PE=1 S	14.546	8	3	6	3	446	52.5	9.42	18.15	3	0	331.1	181.2	578.2	450.3	126.3	174	271.7	288.3
Q9VVX4	Mitochondrial ribosomal protein L21, isoform A OS=Drosophila melanogaster OX=7227 GN=mRpL21 PE=1 S	12.831	14	2	7	2	201	22.6	10.15	21.12	2	0	678.4	490.4	1441.4	1209.9	335.6	505.1	739.7	839.3
Q9VXQ0	Mitochondrial ribosomal protein L3 OS=Drosophila melanogaster OX=7227 GN=mRpL3 PE=1 SV=2	16.31	6	2	4	2	362	40.5	10.07	15.23	2	0	326.4	175.7	732.3	686.9	96.2	133.6	320.2	403.2
Q9VY48	Mitochondrial ribosomal protein L38 OS=Drosophila melanogaster OX=7227 GN=mRpL38 PE=1 SV=2	18.621	13	5	7	5	416	47.7	9.07	20.18	5	0	259.8	141.6	659.1	554.2	110.7	130.6	266.7	1083.2
Q9VGP7	Mitochondrial ribosomal protein L40 OS=Drosophila melanogaster OX=7227 GN=mRpL40 PE=1 SV=1	10.05	17	2	4	2	196	22.5	9.45	13.71	2	0	80.7	51.9	166.1	151.6	31.6	47.9	79.9	112.3
Q9W1L1	Mitochondrial ribosomal protein L43 OS=Drosophila melanogaster OX=7227 GN=mRpL43 PE=1 SV=1	26.583	23	4	7	4	192	22	9.26	26.35	4	0	558.2	307.9	1149.2	831.4	194.1	272.5	498	1177.6
Q9VNC1	Mitochondrial ribosomal protein L44 OS=Drosophila melanogaster OX=7227 GN=mRpL44 PE=1 SV=1	33.766	24	6	14	6	321	36.2	8.25	56.58	6	0	562.2	287.2	933.7	744.4	255.9	290.7	592.8	748.3
Q9W086	Mitochondrial ribosomal protein L46 OS=Drosophila melanogaster OX=7227 GN=mRpL46 PE=1 SV=1	13.776	11	3	5	3	258	29.7	8.31	15.37	3	0	617.4	321.6	1070.7	789.1	249.1	283.4	468.1	835.7
Q9VQ35	Mitochondrial ribosomal protein L48, isoform A OS=Drosophila melanogaster OX=7227 GN=mRpL48 PE=1 S	43.818	36	5	6	5	181	20.9	5.47	27.2	5	0	307.3	177.7	594.9	441.1	123.5	142.5	253.3	385.3
Q8MSS7	Mitochondrial ribosomal protein S2 OS=Drosophila melanogaster OX=7227 GN=mRpS2 PE=2 SV=1	19.042	13	3	6	3	264	30.2	9.14	22.11	3	0	376.7	172.6	541.3	494	147.4	191.9	254.5	435.5
Q8IP62	Mitochondrial ribosomal protein S23 OS=Drosophila melanogaster OX=7227 GN=mRpS23 PE=1 SV=1	30.143	32	6	15	6	189	21.5	5.73	47.4	6	0	938.4	496.9	1808.3	1349.9	345.4	457.2	855.7	1486.7
Q9VUX1	Mitochondrial ribosomal protein S31 OS=Drosophila melanogaster OX=7227 GN=mRpS31 PE=1 SV=1	24.996	21	5	8	5	376	42.4	7.18	23.09	5	0	405.3	251.5	802.3	588.3	163.3	245.4	440.2	300.5
Q9VV39	Mitochondrial ribosomal protein S34 OS=Drosophila melanogaster OX=7227 GN=mRpS34 PE=1 SV=2	18.138	18	3	5	3	188	21.6	9.52	17.45	3	0	275.1	140.5	497.4	338.2	104.1	142.2	224.3	227.5
Q8SYP9	Mitochondrial ribosomal protein S5, isoform A OS=Drosophila melanogaster OX=7227 GN=mRpS5 PE=1 SV=	22.46	7	2	4	2	407	46	10.2	17.61	2	0	139.9	88.1	322.9	232.4	57.7	81.2	120.8	134
Q8SXF0	Mitochondrial ribosomal protein S9 OS=Drosophila melanogaster OX=7227 GN=mRpS9 PE=1 SV=1	19.815	17	6	6	6	395	45.2	8.91	14.45	6	0	227.1	118.6	410.2	360	78.6	114.4	165	388.7
Q9VCU5	Mitochondrial ribosome-associated GTPase 1 OS=Drosophila melanogaster OX=7227 GN=CG17141 PE=1 S	7.481	7	2	3	2	323	36.5	9.55	8.1	2	0	337.7	166.4	454.9	457.8	174.6	206.6	214.4	276.6
Q86BR8	Mitochondrial transcription factor A, isoform B OS=Drosophila melanogaster OX=7227 GN=TFAM PE=1 SV=1	39.801	22	8	13	8	284	33	9.96	41.77	8	0	1606.2	804.7	3370.9	2133	507.9	686.6	1405.3	2241.5
P40417	Mitogen-activated protein kinase ERK-A OS=Drosophila melanogaster OX=7227 GN=rl PE=1 SV=3	7.97	10	2	2	2	376	43.1	6.07	6.25	2	0	47	22.2	93	72.8	17.1	19.6	37.9	39.1
A0A0B4LFQ3	Mitogen-activated protein kinase kinase kinase kinase OS=Drosophila melanogaster OX=7227 GN=hppy PE=	8.835	5	2	3	2	934	103.6	7.87	9.27	2	0	47.2	23.9	57.6	71.4	17.1	36.2	34.9	24.8
E1JHD6	Mitogen-activated protein kinase OS=Drosophila melanogaster OX=7227 GN=bsk PE=1 SV=1	8.193	9	3	4	3	372	43	6.42	6.49	3	0	195.9	109.7	241	219.3	87.4	83.7	127.8	148.6
Q9VAW1	Moca-cyp, isoform A OS=Drosophila melanogaster OX=7227 GN=Moca-cyp PE=1 SV=1	14.417	5	6	7	5	970	112.7	10.56	18.09	6	1	1841.9	831.3	1102.8	1166.7	699.4	851.5	741.3	941.2
Q86B87	Modifier of mdg4 OS=Drosophila melanogaster OX=7227 GN=mod(mdg4) PE=1 SV=1	23.333	6	2	5	2	610	67.1	5.07	18.83	2	0	454	172.8	290	297.1	168.7	207.9	159	214.9
M9PHG2	Moesin, isoform M OS=Drosophila melanogaster OX=7227 GN=Moe PE=1 SV=1	78.837	25	17	26	17	584	68.8	5.99	74.07	17	0	2425.4	1083.8	2482.5	2453.6	863.8	1137.1	1372.9	1388.7
A0A0B4JDA0	Moira, isoform B OS=Drosophila melanogaster OX=7227 GN=mor PE=1 SV=1	23.271	7	6	7	6	1145	124.8	5.63	20.7	6	0	497.6	232.6	333	328.6	200.8	197	190.3	197.4
Q7K003	MRG/MORF4L binding protein OS=Drosophila melanogaster OX=7227 GN=MrgBP PE=1 SV=1	11.332	15	2	2	2	201	22.3	8.12	7.42	2	0	234.9	107.3	96.2	103.1	77.3	84.9	61.1	59.3
Q9VY44	mRNA-capping enzyme OS=Drosophila melanogaster OX=7227 GN=mRNA-cap PE=2 SV=1	4.076	2	2	2	2	649	74.7	6.95	4.51	2	0	440.4	156.7	192.9	312.5	173.2	158.2	131.1	229.9
Q9VGM1	Multidrug resistance protein 4 OS=Drosophila melanogaster OX=7227 GN=Mrp4 PE=1 SV=2	10.126	3	3	3	3	1316	147.8	7.59	4.22	3	0	14	8.2	18.5	14.2	9.7	11.7	9.8	17.9
Q9VK56	Multidrug-Resistance like protein 1, isoform A OS=Drosophila melanogaster OX=7227 GN=MRP PE=1 SV=4	23.446	6	6	6	6	1549	173.3	6.44	19.8	6	0	444.9	268.1	617.4	691.7	162.6	245.1	310.2	357.9
Q9I7S8	Multifunctional protein ADE2 OS=Drosophila melanogaster OX=7227 GN=ade5 PE=2 SV=2	28.964	22	7	12	7	429	47.3	8.07	35.58	7	0	1726.1	790.7	1742.5	1640.1	698.9	740.9	858.8	955.6
A0A0B4KHR8	Multiple ankyrin repeats single KH domain, isoform E OS=Drosophila melanogaster OX=7227 GN=mask PE=4	16.873	1	3	3	3	4000	422.8	5.69	9.62	3	0	418.4	234.9	313.8	388.5	215.3	212.6	167.9	187.1
M9MRJ4	Muscle-specific protein 300 kDa, isoform G OS=Drosophila melanogaster OX=7227 GN=Msp300 PE=1 SV=1	35.031	1	9	10	9	13540	1506.8	4.63	30.29	9	0	967.4	509.2	1050.4	933.7	337.6	526.4	549.3	535.1
Q9VY97	Mutagen-sensitive 101 OS=Drosophila melanogaster OX=7227 GN=mus101 PE=1 SV=1	10.476	3	3	3	3	1425	158.3	6.51	3.4	3	0	132.3	61.7	104.8	103.9	56.2	56.2	49.5	94.6
Q9W5E4	Myb-binding protein 1A OS=Drosophila melanogaster OX=7227 GN=Mybbp1A PE=1 SV=1	3.228	1	2	2	2	1133	127.8	7.55	3.97	2	0	182.9	65.7	100.7	117.4	103	92.6	67.4	106.6
M9NDS8	Myosin binding subunit, isoform N OS=Drosophila melanogaster OX=7227 GN=Mbs PE=1 SV=1	16.868	4	4	4	4	1245	133.9	6.23	13.1	4	0	543.2	200.5	476.1	474.5	195.8	261.1	259.2	287
E1JHJ3	Myosin heavy chain, isoform O OS=Drosophila melanogaster OX=7227 GN=Mhc PE=1 SV=1	18.472	3	7	7	7	1962	224.4	6.19	12.59	7	0	397.9	289	849.5	813.2	212.4	274.9	256.3	1078.1
Q23978	Myosin-IA OS=Drosophila melanogaster OX=7227 GN=Myo31DF PE=2 SV=1	7.925	2	2	3	2	1011	117	9.42	8.55	2	0	189.8	93.6	228.7	253.3	77.5	103.1	120.8	193.6
Q23979	Myosin-IB OS=Drosophila melanogaster OX=7227 GN=Myo61F PE=1 SV=3	17.88	6	4	5	4	1035	118.9	9.04	19.66	4	0	113.8	56.2	144.9	171.4	49.6	64.3	97.4	126.4
Q9VWI2	N(Alpha)-acetyltransferase 15/16, isoform A OS=Drosophila melanogaster OX=7227 GN=Naa15-16 PE=1 SV	9.03	3	3	3	3	890	103	7.27	7.98	3	0	386.8	163.1	540.1	612.9	218.3	320.6	262.7	497.9
Q9VLP7	N6-adenosine-methyltransferase non-catalytic subunit OS=Drosophila melanogaster OX=7227 GN=Mettl14 P	11.371	9	3	3	3	397	44.8	8.68	8.54	3	0	187.4	83.5	107.5	118.5	76.8	87.7	62	58.3
Q7JW73	NAD kinase 2, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8080 PE=1 SV=1	56.461	26	7	19	7	413	46.8	8.22	56.8	7	0	564.2	324.3	1096.7	995.3	257.9	295.2	507.4	606.7
Q9VTB4	NADH dehydrogenase (Ubiquinone) 13 kDa B subunit OS=Drosophila melanogaster OX=7227 GN=ND-13B P	16.362	35	4	6	4	124	13.8	9.39	22.77	4	0	303.8	130.2	759.9	479.6	71.1	112.7	301.3	802.3
Q9VWI0	NADH dehydrogenase (Ubiquinone) 18 kDa subunit OS=Drosophila melanogaster OX=7227 GN=ND-18 PE=	42.01	17	2	11	2	183	20.7	9.8	47.66	2	0	905.9	500.4	1640.9	1372.5	337.5	443.5	747.4	761.6
Q9VX36	NADH dehydrogenase (Ubiquinone) 24 kDa subunit, isoform A OS=Drosophila melanogaster OX=7227 GN=N	18.076	21	4	25	4	242	26.8	6.9	25.36	4	0	790.9	547	1060.1	769.6	571.5	574	700.3	860.1
Q9VPE2	NADH dehydrogenase (Ubiquinone) 39 kDa subunit, isoform A OS=Drosophila melanogaster OX=7227 GN=N	32.34	13	6	18	6	416	46.8	9.39	45	6	0	1525.6	730	2994.6	2701.2	562.2	692.5	1254.2	2126.3
A4V449	NADH dehydrogenase (Ubiquinone) 75 kDa subunit, isoform B OS=Drosophila melanogaster OX=7227 GN=N	113.897	29	16	89	16	731	78.6	6.84	312.48	16	0	2566.8	1516.4	6217.4	4246.1	935.2	1409.4	2947.4	2931.1
Q9W2E8	NADH dehydrogenase (Ubiquinone) B12 subunit, isoform A OS=Drosophila melanogaster OX=7227 GN=ND-I	6.205	16	2	2	2	110	12.1	8.27	4.9	2	0	125.9	62.4	266.5	203	32.3	53.8	133.6	216.3
Q7JZK1	NADH dehydrogenase (Ubiquinone) B14 subunit, isoform A OS=Drosophila melanogaster OX=7227 GN=ND-I	3.236	10	2	2	2	124	14.9	9.5	4.63	2	0	195.2	78	453.7	245.7	37.3	49.4	137.7	741.5
Q6IDF5	NADH dehydrogenase (Ubiquinone) B15 subunit OS=Drosophila melanogaster OX=7227 GN=ND-B15 PE=1	24.45	25	2	6	2	113	13.1	9.82	19.29	2	0	425.2	208.4	1083.4	704.2	161.2	204.9	433.9	599
Q9W402	NADH dehydrogenase (Ubiquinone) B16.6 subunit, isoform A OS=Drosophila melanogaster OX=7227 GN=NI	16.332	17	4	11	4	154	17.7	9.39	36.73	4	0	329	177.9	621.2	509.3	146	188.7	332.8	344.5
Q9VYS5	NADH dehydrogenase (ubiquinone) complex I, assembly factor 6 homolog OS=Drosophila melanogaster OX=	16.224	17	6	11	6	334	38.2	9.54	27.41	6	0	520.2	260.1	1013.3	1076	201.8	286.6	502.1	721.4
Q9VTU2	NADH dehydrogenase (Ubiquinone) SGDH subunit, isoform A OS=Drosophila melanogaster OX=7227 GN=NI	22.219	19	6	13	6	186	22	8.51	37.69	6	0	975.4	719.7	2601.7	2061.2	386.6	605.6	1305.2	1305
P91929	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Drosophila melanoga:	69.647	27	10	49	10	407	46.9	6.8	105.08	10	0	1930.7	1145.3	4547.6	3364.1	815	968.7	2175.2	3116.8
Q9VQD7	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Drosophila melanogaster OX=7227	16.943	21	3	6	3	142	16.8	9.23	16.32	3	0	443.3	206.2	1039.2	743.3	155.2	196	401.5	2445.4

Q9W125	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=Drosophila melanogaster OX=7227 G	17.365	25	2	9	2	175	19.8	6.87	42.63	2	0	208.2	110.5	409.1	333.6	81.4	104.2	177.9	365.1
Q9W3X7	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial OS=Drosophila melanogaste	17.463	14	2	11	2	175	20.2	8.09	36.96	2	0	835.4	472.6	1562.2	1341.9	322.4	375.9	649.1	838.9
Q9VMI3	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Drosophila melanogaster OX=7227 GN	51.848	15	6	12	6	474	51.8	8.47	39.31	6	0	1028.4	574.8	2393.5	1731.4	331.6	509.7	1144	1301.9
M9PCQ1	NADPH--cytochrome P450 reductase OS=Drosophila melanogaster OX=7227 GN=Cpr PE=1 SV=1	12.391	7	4	5	4	679	76.3	5.9	10.23	4	0	514.3	257.6	828	848	190.5	249.8	450.1	385.4
Q9V3T9	NADPH:adrenodoxin oxidoreductase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=dare PE=2 S	54.296	20	6	13	6	466	51.3	8.38	61.2	6	0	589.9	345	1344	1160.2	242.8	274.5	572.3	529.7
A0A0B4LEY6	Nascent polypeptide associated complex protein alpha subunit, isoform D OS=Drosophila melanogaster OX=7	28.373	28	4	8	4	217	23	4.74	25.61	4	0	3155.6	1110.9	3068.9	2230.2	1048.1	1068.2	1879.7	1712.9
A1Z968	NAT1, isoform D OS=Drosophila melanogaster OX=7227 GN=NAT1 PE=1 SV=1	55.115	6	7	10	7	1488	162.8	8.53	40.56	7	0	448.5	220.7	508.9	565.6	177.5	229.3	287.8	444.5
Q9VXB0	NECAP-like protein CG9132 OS=Drosophila melanogaster OX=7227 GN=CG9132 PE=2 SV=1	9.624	10	3	3	3	246	26.6	8.81	8.7	3	0	1166.7	407.6	556.7	703	386.1	371.9	311.8	613.6
A0A0B4LIF3	Negative elongation factor A, isoform C OS=Drosophila melanogaster OX=7227 GN=Nelf-A PE=4 SV=1	29.855	6	4	7	4	1250	134.7	9.91	30.68	4	0	777	337.7	566	518.9	308.4	349.1	308	330
P92204	Negative elongation factor E OS=Drosophila melanogaster OX=7227 GN=Nelf-E PE=1 SV=1	9.263	9	2	2	2	280	31.8	9.47	6.36	2	0	163.7	71.5	103.2	121.5	64.9	103.5	61.6	81.9
Q9W321	Nejire, isoform B OS=Drosophila melanogaster OX=7227 GN=nej PE=1 SV=2	4.909	1	2	2	2	3276	340.5	8.69	4.67	2	0	433.1	207.2	243.2	286.2	162.3	180.3	166.1	124.8
Q9W376	Neuferricin homolog OS=Drosophila melanogaster OX=7227 GN=CG12056 PE=2 SV=1	20.842	21	2	3	2	287	32.6	5.58	14.83	2	0	30.8	21.9	56	52.3	21.2	17.4	26.1	30
Q8IQQ0	Neural conserved at 73EF, isoform F OS=Drosophila melanogaster OX=7227 GN=Nc73EF PE=1 SV=1	110.451	23	23	120	4	1017	113.6	6.99	317.05	23	21	5318.9	3049.6	9615.2	8510.6	2939.4	2535.9	4185.2	6421.9
A8JNU6	Neural conserved at 73EF, isoform I OS=Drosophila melanogaster OX=7227 GN=Nc73EF PE=1 SV=1	102.544	20	21	112	2	1105	122.8	6.93	294.87	21	0	139.3	98.3	325.2	268.9	73	79.7	138.4	170.7
Q8SY96	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial OS=Drosophila melanogaster OX=7227 GN=CG3250	26.131	12	2	5	2	283	31.3	5.4	19.64	2	0	132.8	58	204.4	165.7	46.9	50.8	71.1	119.6
A0A0B4KF23	Nipped-B protein OS=Drosophila melanogaster OX=7227 GN=Nipped-B PE=1 SV=1	18.577	3	4	4	4	1957	223.2	6.51	14.74	4	0	392.9	173.7	292.7	315	146.6	194	169	205.6
O76464	Nitrilase and fragile histidine triad fusion protein NitFhit OS=Drosophila melanogaster OX=7227 GN=NitFhit PE	35.058	15	6	12	6	460	52.2	7.61	26.95	6	0	513.9	325.8	1073.8	978.2	251.6	282.3	471.7	605.3
Q9VFK4	NK7.1, isoform A OS=Drosophila melanogaster OX=7227 GN=NK7.1 PE=4 SV=2	10.854	3	2	3	2	721	78.9	7.59	9.92	2	0	216.6	108.1	129.7	158.9	81.4	83.6	76.4	93.6
M9PE74	No circadian temperature entrainment, isoform D OS=Drosophila melanogaster OX=7227 GN=nocte PE=1 SV	52.367	4	7	10	7	2305	234.9	9.25	36.49	7	0	967.4	504.7	1255	1319.9	348.3	512.4	755.1	521.2
X2JFR1	No on or off transient A, isoform D OS=Drosophila melanogaster OX=7227 GN=nonA PE=1 SV=1	87.004	24	13	19	12	700	76.9	9.35	70.73	13	1	2312	935.9	1368.6	1530	920.6	1064.6	802.1	1077
Q7JNE1	Non-histone chromosomal protein Prod OS=Drosophila melanogaster OX=7227 GN=prod PE=1 SV=1	25.054	18	4	7	4	346	39.4	5.3	27.54	4	0	1867.7	771.7	752.3	657.6	779.1	1352.3	559.9	563.5
E2QD16	Non-specific lethal 1, isoform M OS=Drosophila melanogaster OX=7227 GN=nsl1 PE=1 SV=1	17.978	4	4	4	4	1570	169.7	6.81	12.79	4	0	1529.7	537.1	649.2	827.2	612.2	543.4	435.1	568.3
M9PFZ1	Nopp140, isoform E OS=Drosophila melanogaster OX=7227 GN=Nopp140 PE=1 SV=1	4.337	2	2	2	2	773	78.1	9.16	4.37	2	0	417.2	141.8	155.3	182.6	186.8	154.6	96	101.4
Q9VVK7	NUCB1 OS=Drosophila melanogaster OX=7227 GN=NUCB1 PE=1 SV=3	8.383	4	2	2	2	569	67.3	5.3	6.34	2	0	174	100.8	572.7	510.9	24	45.1	248.2	223
Q7K4N3	Nuclear cap-binding protein subunit 1 OS=Drosophila melanogaster OX=7227 GN=Cbp80 PE=1 SV=1	14.011	4	2	2	2	800	93.2	6.55	9.1	2	0								
Q9V3L6	Nuclear cap-binding protein subunit 2 OS=Drosophila melanogaster OX=7227 GN=Cbp20 PE=1 SV=1	9.982	9	2	2	2	154	17.7	7.78	7.1	2	0	324.8	146.2	168.2	191.5	127.8	143.1	95.2	170
Q9VVA6	Nuclear migration protein NudC OS=Drosophila melanogaster OX=7227 GN=nudC PE=1 SV=2	12.845	9	3	4	3	332	37.8	5.64	14.39	3	0	559	272.1	514.5	488.3	200.4	266.9	319.9	240.2
Q9V466	Nuclear pore complex protein Nup107 OS=Drosophila melanogaster OX=7227 GN=Nup107 PE=1 SV=1	22.763	7	4	5	4	845	97.3	5.94	16.91	4	0	411.2	180.7	413	451.1	148.3	200.9	218.2	224.9
Q9VCW3	Nuclear pore complex protein Nup133 OS=Drosophila melanogaster OX=7227 GN=Nup133 PE=2 SV=2	8.99	2	2	3	2	1200	135.1	5.63	8.39	2	0	101.4	84.6	63.7	77.7	36.2	40	30	45.1
Q9VXE6	Nuclear pore complex protein Nup153 OS=Drosophila melanogaster OX=7227 GN=Nup153 PE=1 SV=4	9.582	2	3	3	3	1883	196.5	8.13	8.64	3	0	568.1	215.2	448.9	495.3	172	225	276.6	248.6
Q9V463	Nuclear pore complex protein Nup154 OS=Drosophila melanogaster OX=7227 GN=Nup154 PE=1 SV=1	3.241	1	2	3	2	1365	153.8	6.58	3.58	2	0	273.5	83.6	185.4	299.6	107.4	117.4	122	178
Q8IQV9	Nuclear pore complex protein Nup205 OS=Drosophila melanogaster OX=7227 GN=Nup205 PE=2 SV=1	9.058	2	2	2	2	2090	235	6.65	4.38	2	0	142.3	65.9	161.9	184.4	59.9	81.3	88.4	108.7
Q7K0D8	Nuclear pore complex protein Nup50 OS=Drosophila melanogaster OX=7227 GN=Nup50 PE=2 SV=1	19.992	12	5	5	5	564	59.4	8.43	17.7	5	0	1235.4	446.1	771	928.2	430.4	447.9	447.6	524.4
A1YK02	Nuclear pore complex protein Nup75 OS=Drosophila melanogaster OX=7227 GN=Nup75 PE=2 SV=1	11.583	4	2	4	2	668	76.8	6.05	13.36	2	0	115.9	37.1	83.2	92.5	37.3	48.9	59.5	65.9
Q9XZ06	Nuclear pore complex protein Nup93-1 OS=Drosophila melanogaster OX=7227 GN=Nup93-1 PE=1 SV=1	21.766	8	5	5	5	823	93.8	6.27	17.37	5	0	718.3	259.4	437.2	618.4	235.8	251.4	238.6	340
Q9VCH5	Nuclear pore complex protein Nup98-Nup96 OS=Drosophila melanogaster OX=7227 GN=Nup98-96 PE=1 SV	25.453	3	5	5	5	1960	210	6.52	21.17	5	0	510	197.5	474.1	525.4	171.5	228.8	277.4	234.8
Q9VBP9	Nuclear protein localization protein 4 homolog OS=Drosophila melanogaster OX=7227 GN=Npl4 PE=1 SV=3	13.889	8	4	4	4	652	73.3	7.24	10.16	4	0	805.2	457.1	1020.5	1040.3	359.1	423.7	518	563.6
Q9U1H9	Nuclear RNA export factor 1 OS=Drosophila melanogaster OX=7227 GN=sbr PE=1 SV=2	5.578	3	2	2	2	672	76.2	9	5.5	2	0	452.6	221	350.7	377.6	188.4	214.2	189.6	203.3
A0A0B4LEY9	Nucleolar GTP-binding protein 1 OS=Drosophila melanogaster OX=7227 GN=Non1 PE=1 SV=1	14.491	6	3	4	3	652	75.3	9.54	16.5	3	0	1188.8	401.1	520.2	641.9	466.1	493.8	352.2	561.9
A0A0B4KI24	Nucleoplasmin, isoform B OS=Drosophila melanogaster OX=7227 GN=Nlp PE=4 SV=1	26.333	22	3	8	3	152	17	4.61	28.14	3	0	4148.6	1337.5	1372.6	1365.9	1401.7	1211.8	689.4	848.1
A0A0B4LJ12	Nucleoside diphosphate kinase OS=Drosophila melanogaster OX=7227 GN=awd PE=1 SV=1	19.783	17	2	4	2	153	17.2	8.12	13.48	2	0	744.1	391.8	626.6	968.8	259.5	320.7	312.2	548.2
Q9VY27	Nucleoside diphosphate kinase OS=Drosophila melanogaster OX=7227 GN=nmdyn-D6 PE=2 SV=2	16.736	23	3	7	3	151	17.2	8.46	22.54	3	0	346.9	152.4	572.6	542.2	119.7	159	230.4	376.1
Q9VBV5	Nucleotide exchange factor SIL1 OS=Drosophila melanogaster OX=7227 GN=CG10420 PE=2 SV=1	6.136	6	2	2	2	429	47.9	5.33	6.72	2	0	151.2	97.1	776.1	841	38.1	67.7	276.5	256
E6PBV6	Obg-like ATPase 1 OS=Drosophila melanogaster OX=7227 GN=CG1354-RA PE=1 SV=1	7.993	8	3	4	3	397	44.9	6.71	9.96	3	0	202.6	88.4	180.9	222.1	72.3	82.7	89.4	129.4
A0A0B4LGF5	Optic atrophy 1, isoform C OS=Drosophila melanogaster OX=7227 GN=Opa1 PE=1 SV=1	97.19	21	19	34	19	969	111.5	8.59	105.07	19	0	1761.9	948.8	3929.6	3099.8	577.2	875.3	1726.1	3285.4
A0A0B4KHD4	Organic cation transporter 2, isoform B OS=Drosophila melanogaster OX=7227 GN=Orct2 PE=4 SV=1	8.012	4	2	2	2	567	63.1	6.46	5.89	2	0	38.5	45	160.1	158.1	8.8	20.3	90.6	78.8
Q24169	Origin recognition complex subunit 5 OS=Drosophila melanogaster OX=7227 GN=Orc5 PE=1 SV=1	5.042	5	2	2	2	460	52.1	6.55	5.88	2	0	17.9	10.1	18.4	20.1	5.5	10.7	9.9	11.1
Q9VW26	Ornithine aminotransferase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Oat PE=2 SV=1	31.576	20	7	15	7	431	47.3	7.05	38.53	7	0	670.3	486	1051.4	793.2	304.8	438.6	454.3	745.2
P20240	Otefin OS=Drosophila melanogaster OX=7227 GN=Ote PE=1 SV=2	42.254	21	6	11	6	424	46.6	9.55	44.99	6	0	4588	1077.4	2011.8	2030.9	1052	1452.9	1041.8	1214.1
A1ZAW9	Oxpecker OS=Drosophila melanogaster OX=7227 GN=Oxp PE=4 SV=1	6.547	20	2	4	2	84	9.9	7.93	11.48	2	0	1060.2	374.4	736.1	718.6	428.9	379.9	382.5	484
Q9V3D2	Oxygen-dependent coproporphyrinogen-III oxidase OS=Drosophila melanogaster OX=7227 GN=Coprox PE=	45.495	23	8	17	8	390	44.4	8.72	67.65	8	0	898	450.5	2185.5	1493.6	250.3	369.5	859.9	1074.7
A0A0B4JDG2	Oxysterol-binding protein OS=Drosophila melanogaster OX=7227 GN=CG5077 PE=1 SV=1	28.25	10	7	10	7	956	104.5	7.9	28.75	7	0	1034.9	427.3	1329.8	1544.3	393.5	447.3	720.2	921
A1ZAK8	P-element somatic inhibitor, isoform C OS=Drosophila melanogaster OX=7227 GN=Psi PE=1 SV=1	23.857	5	3	5	3	797	81.7	8.13	19.82	3	0	1332	492.4	694.9	728	532.3	499.6	424.5	430.4
Q7K2V5	Palmitoyltransferase OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1407 PE=2 SV=1	3.339	4	2	2	2	338	39.7	7.59	4.66	2	0	204.5	142.4	423.6	421.8	61.4	119.7	221.1	173.8
Q963E5	Par-1, isoform T OS=Drosophila melanogaster OX=7227 GN=par-1 PE=1 SV=1	13.491	3	2	3	2	1058	114.8	9.88	8.73	2	0	174.3	84.1	193.1	187.9	67.7	81.6	103.3	119.8
Q0KI94	Pasilla, isoform I OS=Drosophila melanogaster OX=7227 GN=ps PE=1 SV=1	11.649	8	3	4	1	519	54.4	6.74	9.08	3	0								
A0A0B4LI06	Pasilla, isoform T OS=Drosophila melanogaster OX=7227 GN=ps PE=1 SV=1	24.239	7	4	7	2	616	63.3	7.02	24.52	4	2	360	169.6	317.6	298.6	148.6	146.3	156.2	163.9
Q7KTI8	PDGF-and VEGF-receptor related, isoform E OS=Drosophila melanogaster OX=7227 GN=Pvr PE=1 SV=1	29.102	6	5	5	5	1503	169.4	5.85	17.97	5	0	374.5	180.6	503.8	543.9	118.9	147.6	289.9	250.1
Q9V3G3	Peptidyl-prolyl cis-trans isomerase E OS=Drosophila melanogaster OX=7227 GN=cyp33 PE=1 SV=1	11.887	13	2	3	2	300	33.3	6.05	8.79	2	0	68	42	77	103	40.6	146.8	271.5	61.5
P25007	Peptidyl-prolyl cis-trans isomerase OS=Drosophila melanogaster OX=7227 GN=Cyp1 PE=1 SV=2	36.316	24	6	23	5	227	24.7	9.22	59.2	6	0	2423.5	1014.4	2343.4	2627.4	977.7	1038	1331.9	2414.5
Q9W227	Peptidyl-prolyl cis-trans isomerase OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2852 PE=1 SV=1	20.615	29	5	15	5	205	22.2	8.75	41.38	5	0	326.9	169.4	1076.1	1182.9	153.1	215.2	1038.6	759.4
Q9VGK3	Peptidylprolyl isomerase OS=Drosophila melanogaster OX=7227 GN=BcDNA:RH50927 PE=1 SV=1	12.884	26	3	3	3	138	14.8	8.59	7.22	3	0	171.4	112.8	530.4	654.1	96.7	115.8	239.6	215.2
Q9V3V2	Peptidylprolyl isomerase OS=Drosophila melanogaster OX=7227 GN=Fkbp14 PE=1 SV=1	6.858	11	3	4	3	216	23.9	4.87	10.61	3	0	623.2	255	3135.8	2082.6	69.2	132.3	1399.7	846.3
Q7K3D4	Peptidylprolyl isomerase OS=Drosophila melanogaster OX=7227 GN=zda PE=1 SV=1	20.161	10	3	3	3	397	44.8	5.33	12.07	3	0	532.5	217.6	823.4	608.9	145.3	206.1	436.4	395.2
Q9VZZ4	Peroxidasin OS=Drosophila melanogaster OX=7227 GN=Pxn PE=1 SV=1	75.001	14	15	20	15	1527	170.4	6.28	59.54	15	0	1668	825.4	5750.8	3902.3	611.5	823	2466.1	1916.1
Q9VEJ0	Peroxiredoxin 3 OS=Drosophila melanogaster OX=7227 GN=Prx3 PE=1 SV=2	46.398	28	7	21	7	234	26.4	7.49	59.75	7	0	2391.1	1032.9	4091	3408.5	891.4	884.7	1700.4	4426.8
X2JFD6	Peroxisomal multifunctional enzyme type 2, isoform B OS=Drosophila melanogaster OX=7227 GN=Mfe2 PE=4	12.731	5	2	2	2	598	64	6.57	7.8	2	0	33.4	18.1	38.8	32.1	10.3	19.8	18.6	20.5
Q9VL96	Pescadillo homolog OS=Drosophila melanogaster OX=7227 GN=CG4364 PE=1 SV=1	8.81	4	3	3	3	627	73.8	7.08	8.7	3	0	1147.7	459.1	541.2	596.1	449.7	468.9	373.4	365.5
Q9VMC8	PHD finger-like domain-containing protein 5A OS=Drosophila melanogaster OX=7227 GN=Phf5a PE=3 SV=2	3.572	13	2	2	2	111	12.5	8.22	4.98	2	0	1587.6	758.7	963.3	943.3	574.5	736.6	602.9	490.8
Q9W3G0	Phosphatidylinositol glycan anchor biosynthesis class T OS=Drosophila melanogaster OX=7227 GN=PIG-T P	4.421	5	2	2	2	633	71.2	6.71	3.97	2	0	99.9	54	164.5	250.3	31.8	54.3	83.8	129.7
Q9VCE0	Phosphatidylserine decarboxylase proenzyme, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Pis	13.956	8	2	2	2	447	50.5	9.14	7.62	2	0	15.5	8.1	56.3	38.5	4	7.4	26.5	33.2
E2QD73	Phosphodiesterase OS=Drosophila melanogaster OX=7227 GN=dnc PE=1 SV=1	11.008	4	2	2	2	1070	115	5.55	7.72	2	0	83	47.2	81.6	80.5	48.5	41.3	36.8	47.8
Q8IP79	Phosphoethanolamine cytidylyltransferase, isoform C OS=Drosophila melanogaster OX=7227 GN=Pect PE=1	10.832	6	2	2	2	374	42	6.54	6.21	2	0	743.7	361.1	646.4	896.2	282.4	307.6	344.3	570
Q01604	Phosphoglycerate kinase OS=Drosophila melanogaster OX=7227 GN=Pgk PE=2 SV=2	15.984	12	5	7	5	415	43.8	7.42	19.64	5	0	2840	998.9	1537.1	1675.1	945.6	790.2	806.3	1080.9
Q9VPY2	Phospholipase A2 activator protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Plap PE=1 SV=1	7.293	3	2	2	2	787	85.7	5.83	4.11	2	0	65.1	28	59.5	65.3	27.2	32	39.2	45.6
P35421	Phosphoribosylformylglycinamidine synthase OS=Drosophila melanogaster OX=7227 GN=ade2 PE=2 SV=2	12.192	3	3	4	3	1354	148	5.68	10.51	3	0	301.9	262.4	278.3	433.4	136.6	342.4	186.5	213.7
A1Z757	Photorepair, isoform B OS=Drosophila melanogaster OX=7227 GN=phr PE=1 SV=1	20.091	12	5	7	5	535	61.3	8.87	21.72	5	0	1508.8	472.4	671.4	780.6	583	605.3	427.4	572.1
E1JHB4	Piezo-type mechanosensitive ion channel component OS=Drosophila melanogaster OX=7227 GN=Piezo PE=	8.657	1	2	3	2	2686	304.6	8.15	7.96	2	0	119.8	55.6	162.6	173.5	43.1	65.3	87.3	84.1
Q9VK58	Pih1D1, isoform D OS=Drosophila melanogaster OX=7227 GN=Pih1D1 PE=1 SV=5	16.954	4	4	4	3	1094	127.5	9.74	14.77	4	1	939.2	383.1	577.6	589.8	363.7	414.8	348.8	331
A8JQW3	Pinin, isoform B OS=Drosophila melanogaster OX=7227 GN=Pnn PE=1 SV=1	8.531	7	2	2	2	307	36.4	9.5	6.15	2	0	367.7	184	224.3	247.3	142.2	184.4	150.7	133.5
Q9VSS1	Pixie, isoform A OS=Drosophila melanogaster OX=7227 GN=pix PE=1 SV=1	24.217	10	5	5	5	611	69.3	8.13	15.99	5	0	392.9	162.1	336	372	158.1	205.2	224.1	213.7
O76902	Pleckstrin homology domain-containing family F member 1 homolog OS=Drosophila melanogaster OX=7227 (	18.686	16	3	3	3	316	34.2	7.78	11.23	3	0	166.9	74.8	239.4	236.7	59.5	73.1	100.9	217.3
Q9VU65	POC1 centriolar protein homolog OS=Drosophila melanogaster OX=7227 GN=Poc1 PE=2 SV=1	9.356	6	2	2	2	391	42.8	8.44	6.73	2	0	244.3	108.4	241.2	202.7	94.6	87.3	135.2	77.7
O46102	Poly(A) RNA polymerase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=MTPAP PE=2 SV=2	17.037	9	5	6	5	612	68.5	8.34	17.47	5	0	414.2	192.2	500.2	456.8	169.4	207.3	246.5	383.8
Q8T6B9	Poly(U)-binding-splicing factor half pint OS=Drosophila melanogaster OX=7227 GN=hfp PE=1 SV=2	11.696	5	3	3	3	637	67.9	5.96	8.82	3	0	196.4	119	204.2	169.7	91.7	103.7	88.3	102
P21187	Polyadenylate-binding protein OS=Drosophila melanogaster OX=7227 GN=pAbp PE=1 SV=3	38.568	10	5	17	5	634	69.9	9.31	64.7	5	0	1270	703.9	1626.4	1829.8	537.1	811.5	874.5	980.1
Q9VC36	Polybromo OS=Drosophila melanogaster OX=7227 GN=polybromo PE=1 SV=1	20.101	4	5	7	5	1654	189.6	6.71	19.44	5	0	582.7	252.7	442.6	464.9	214.2	231.2	220.4	438.4
P26017	Polycomb group protein Pc OS=Drosophila melanogaster OX=7227 GN=Pc PE=1 SV=1	7.803	6	2	2	2	390	44	7.58	6.37	2	0	407.3	130.6	191.2	235	150.7	149.9	114.3	150.8
Q8ST83	Polycomb protein PHO OS=Drosophila melanogaster OX=7227 GN=pho PE=1 SV=2	6.712	6	2	2	2	520	58.2	6.76	3.17	2	0	217.2	87.4	120.2	147	93.4	98.9	65.8	70.5
Q9VHA0	Polycomb protein Scm OS=Drosophila melanogaster OX=7227 GN=Scm PE=1 SV=2	22.613	9	3	4	3	877	93.5	8.6	16.81	3	0	413	149	211.1	230.7	160.1	178	126.9	170
A0A126GUZ1	Pre-mod(Mdg4)-V, isoform B OS=Drosophila melanogaster OX=7227 GN=pre-mod(mdg4)-V PE=4 SV=1	9.588	14	2	5	2	164	18.8	9.72	18.35	2	0	1078.5	402.2	551.9	522.5	386.2	547.5	286.9	421.9
A1Z8U0	Pre-mRNA processing factor 8 OS=Drosophila melanogaster OX=7227 GN=Prp8 PE=1 SV=1	44.25	6	10	14	10	2396	279.4	8.88	44.09	10	0	999.6	438.9	626.9	707.5	399.3	436.9	366.4	450.6
Q9VJ87	Pre-mRNA-splicing factor CWC22 homolog OS=Drosophila melanogaster OX=7227 GN=ncm PE=1 SV=3	11.777	2	3	3	3	1330	151.5	9.38	9.74	3	0	82.7	32.2	66	64.9	30	44.7	36.8	43.3
Q9V5Q4	Pre-mRNA-splicing factor Syf2 OS=Drosophila melanogaster OX=7227 GN=Syf2 PE=2 SV=1	8.724	12	2	2	2	226	26.5	9.57	6.48	2	0	88.1	108.5	64.1	144.4	52.1	49	57.7	65.5
Q9VP47	Pre-rRNA-processing protein TSR1 homolog OS=Drosophila melanogaster OX=7227 GN=CG7338 PE=1 SV=	15.098	6	4	4	4	814	93.7	6.87	12.1	4	0	666	278.7	376.2	501.3	283.2	289.2	194.7	335.1
A1Z8S6	Precocious dissociation of sisters 5, isoform A OS=Drosophila melanogaster OX=7227 GN=pds5 PE=1 SV=1	21.416	6	5	6	5	1218	138.8	7.64	17.6	5	0	519.8	174.5	310.7	337.5	207.8	205.6	156.5	380.5
E1JIT4	Prefoldin 5, isoform B OS=Drosophila melanogaster OX=7227 GN=Pfdn5 PE=1 SV=1	9.949	17	2	2	2	168	19.1	7.33	7.57	2	0	189.4	91.8	166.8	207	66.4	87.4	81.1	99.6
Q9VGP6	Prefoldin subunit 3 OS=Drosophila melanogaster OX=7227 GN=mgr PE=1 SV=3	9.59	14	3	4	3	194	22.3	5.11	10.55	3	0	192.4	125.9	274.2	311.7	79.7	110.1	148.3	154.6
O02194	Presenilin homolog OS=Drosophila melanogaster OX=7227 GN=Psn PE=1 SV=2	6.224	5	2	2	2	541	59.3	7.06	5.47	2	0	117.4	89.1	231.4	295.3	54.9	88.1	118.4	155.4
Q9VA02	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1 homolog, mitochondrial OS=Drosophila mel	47.878	11	9	14	9	919	103.6	6.54	40.67	9	0	1447	1164	3367	2117.6	459.5	913.1	1342.5	1177.2
Q9V6Y3	Probable 28S ribosomal protein S16, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpS16 PE	33.361	43	6	6	6	129	14.5	9.98	22.56	6	0	400.6	238.4	807.1	713.2	150.5	201.7	370.3	655
Q9VY28	Probable 28S ribosomal protein S25, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpS25 PE	8.974	12	2	2	2	167	19.1	9.11	6.84	2	0	278	148.5	633.5	496.8	109.9	147.1	293.6	320.2
Q9VVN2	Probable 28S ribosomal protein S26, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpS26 PE	15.133	20	4	8	4	225	26.2	8.41	19.79	4	0	492.8	347	1289.8	1040.2	150.5	277.9	587.1	479.9
Q9VMY1	Probable 39S ribosomal protein L24, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpL24 PE=	37.318	36	9	20	9	247	29.2	9.38	48.26	9	0	1197.4	645.1	2224.9	1838.3	642.2	606.4	934.9	1309.1
Q9VCX3	Probable 39S ribosomal protein L45, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mRpL45 PE=	19.585	19	8	9	8	361	41.6	9.23	22.96	8	0	636.6	330.4	1255.9	1016.1	235.3	306.7	679.6	1250.1
Q9VZ64	Probable 6-phosphogluconolactonase OS=Drosophila melanogaster OX=7227 GN=CG17333 PE=2 SV=1	10.391	13	2	2	2	243	26.7	8.21	6.93	2	0								
Q9VYH3	Probable alpha-aspartyl dipeptidase OS=Drosophila melanogaster OX=7227 GN=CG2200 PE=2 SV=1	18.773	22	4	8	4	240	26.6	7.03	23.35	4	0	826.3	342.3	770.6	826.4	303.2	337.2	358.1	493
Q9VXN4	Probable arginine--tRNA ligase, cytoplasmic OS=Drosophila melanogaster OX=7227 GN=ArgRS PE=2 SV=1	8.87	4	3	4	3	665	75.5	7.44	10.26	3	0	358.1	171.3	416.5	574.3	149.1	185.1	213	281.4
Q9VD51	Probable ATP-dependent RNA helicase pitchoune OS=Drosophila melanogaster OX=7227 GN=pit PE=2 SV=	12.498	6	3	3	3	680	76.9	7.97	6.42	3	0	470.7	164.4	249.6	315.7	181.9	184.2	126.7	211.2
Q9W401	Probable citrate synthase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=kdn PE=2 SV=1	79.301	18	7	125	7	464	51.5	8.81	332.76	7	0	2301.1	1533.8	4496.2	3844.8	1317.7	1475.4	2058.2	2533
Q9VKD3	Probable cysteine desulfurase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=CG12264 PE=2 S\	84.183	32	13	30	13	462	51	8.21	89.84	13	0	2196.9	1145.2	4450.2	3876.3	823.2	949.9	1874.9	2650
Q9VE01	Probable cytochrome P450 12a5, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Cyp12a5 PE=2	5.253	3	2	2	2	536	61.3	9.2	5.4	2	0	217.9	143.2	726.5	599.2	53.5	116.5	262.9	520.7
Q7KR10	Probable cytochrome P450 12d1 distal, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Cyp12d1-	65.218	32	14	23	1	521	60.2	9.1	65.98	14	0	45.3	21.4	67	36.3	10.2	19.6	35.4	22.4
Q9V773	Probable cytochrome P450 6a20 OS=Drosophila melanogaster OX=7227 GN=Cyp6a20 PE=2 SV=2	3.834	5	2	3	2	501	57.7	8.07	4.75	2	0	29.5	15.5	56.8	86	19.8	10.5	28.2	50.3
Q9VUM0	Probable DNA mismatch repair protein Msh6 OS=Drosophila melanogaster OX=7227 GN=Msh6 PE=1 SV=2	21.125	5	6	7	6	1190	133.1	7.28	19.31	6	0	2267.3	1251.1	1257.1	1473.6	1056.3	776.1	543	784.7
Q9Y105	Probable glutamine--tRNA ligase OS=Drosophila melanogaster OX=7227 GN=Aats-gln PE=2 SV=1	7.517	3	2	2	2	778	87.5	7.21	6.09	2	0	95.8	52.9	105.2	131.7	45.3	40.4	51	75.2
Q7KVQ0	Probable H/ACA ribonucleoprotein complex subunit 1 OS=Drosophila melanogaster OX=7227 GN=CG4038 F	8.587	11	3	6	3	237	22.7	11.19	15.47	3	0	2091.2	842.9	1179.4	1465.2	962.7	765.6	584.3	1447.2
Q24572	Probable histone-binding protein Caf1 OS=Drosophila melanogaster OX=7227 GN=Caf1 PE=1 SV=1	19.958	12	5	10	5	430	48.6	4.89	20.03	5	0	1907.4	700.2	969.6	907.9	720.3	477.6	393.5	623.2
Q8MT36	Probable histone-lysine N-methyltransferase Mes-4 OS=Drosophila melanogaster OX=7227 GN=Mes-4 PE=1	49.089	7	5	5	5	1427	158.9	7.65	25.07	5	0	941.6	313.6	323.6	440.1	353.1	361.4	230.8	280
Q9W265	Probable hydroxyacid-oxoacid transhydrogenase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=	50.588	17	6	11	6	464	50	7.31	40.14	6	0	1065.4	634.6	1783.1	1548.6	432	440.7	746	969.6

Q9VWH4	Probable isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Drosophila melanogaster OX=722	104.705	40	12	46	12	377	40.8	7.36	156.43	12	0	3125.9	1636.3	6707.3	4429.4	1103.5	1348.9	2408.8	5022.2
Q9VHD3	Probable maleylacetoacetate isomerase 1 OS=Drosophila melanogaster OX=7227 GN=GstZ1 PE=1 SV=1	9.149	10	2	5	2	246	27.9	8.9	16.88	2	0	274.1	121.7	356.6	382.9	127.8	126.7	160.3	342.2
Q8T3L6	Probable malonyl-CoA-acyl carrier protein transacylase, mitochondrial OS=Drosophila melanogaster OX=7227	18.437	12	4	7	4	379	42.1	9.16	22.91	4	0	410.7	239.4	837.1	638	153.9	216.4	403.7	442
Q9VSA3	Probable medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Drosophila melanogaster OX=72	86.569	32	12	36	12	419	45.8	7.94	99.91	12	0	3113	1523	5051.7	4403.4	1071.1	1230.5	2135.5	2796.6
Q9V9A7	Probable methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Drosophila melanogaster OX=7227	227.821	40	15	204	15	578	62.6	7.49	679.69	15	0	5979.6	3131.8	9291.3	9556.8	2793	3751.2	5062.6	8259.3
Q7KW39	Probable methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Drosophila melanogas	80.46	29	12	27	12	520	55.9	8.35	91.04	12	0	2505.3	1205.4	4795	3941.6	1008.4	1093.4	2002.3	5680.2
Q9VGY5	Probable methyltransferase-like protein 15 homolog OS=Drosophila melanogaster OX=7227 GN=CG14683 P	7.248	9	2	2	2	356	39.7	8.85	5.44	2	0	116.1	75	297.2	184.5	32.2	68	132.3	100.8
Q9VCI0	Probable oligoribonuclease OS=Drosophila melanogaster OX=7227 GN=CG10214 PE=2 SV=1	13.942	17	2	3	2	211	24.3	6.93	14.67	2	0	134.5	68.4	227.9	146	50	57.4	89.6	186.5
Q7KML2	Probable peroxisomal acyl-coenzyme A oxidase 1 OS=Drosophila melanogaster OX=7227 GN=CG5009 PE=	9.322	4	3	3	3	669	74.2	6.9	8.01	3	0	577.2	265.7	861.9	622.4	266.2	320.1	414	509.4
O16129	Probable phenylalanine--tRNA ligase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=PheRS-m P	3.43	5	2	3	2	453	52	7.17	4.05	2	0	59.7	34.4	85.4	104.1	36.2	33.4	48.1	67.8
Q9VTZ6	Probable phosphomannomutase OS=Drosophila melanogaster OX=7227 GN=CG10688 PE=2 SV=1	9.046	9	2	3	2	254	29.6	5.71	10.23	2	0	383.2	219.3	359.1	446.3	160.1	169.5	161.6	176.7
Q7K4Q5	Probable protein phosphatase CG10417 OS=Drosophila melanogaster OX=7227 GN=CG10417 PE=1 SV=1	9.651	5	3	4	3	662	72.3	4.58	10.72	3	0	950.2	342.2	367.2	366.5	330.8	246.9	217	293.3
Q9VGN9	Probable ribosome biogenesis protein RLP24 OS=Drosophila melanogaster OX=7227 GN=RpL24-like PE=1	6.407	14	3	4	3	191	22.4	9.54	7.17	3	0	630.9	262.5	305.2	353.7	317.6	267.2	203.4	212.9
Q9VXE0	Probable small nuclear ribonucleoprotein G OS=Drosophila melanogaster OX=7227 GN=SNRPG PE=1 SV=1	16.671	29	2	6	2	76	8.5	8.79	19.14	2	0	1782.8	632.1	833.8	1230.8	720.3	556.8	457.2	681
Q9VI10	Probable small nuclear ribonucleoprotein Sm D2 OS=Drosophila melanogaster OX=7227 GN=SmD2 PE=1 S	17.891	47	5	7	5	119	13.5	9.95	18.73	5	0	1398.5	599.8	949.4	1267.2	518.6	473.1	537.6	1588.7
Q9VK89	Probable tRNA (guanine(26)-N(2))-dimethyltransferase OS=Drosophila melanogaster OX=7227 GN=CG6388	21.578	11	5	5	5	578	64.9	7.21	15.78	5	0	765.9	231.4	398.6	507.2	273.2	234.5	176.1	494.7
M9NHD5	Probable tRNA N6-adenosine threonylcarbamoyltransferase, mitochondrial OS=Drosophila melanogaster OX=	16.517	8	2	4	2	409	45.3	8.41	17.15	2	0	143.5	74.5	171.7	170.3	66.2	67	76.2	123.1
Q9V4Q8	Probable U2 small nuclear ribonucleoprotein A' OS=Drosophila melanogaster OX=7227 GN=U2A PE=1 SV=1	6.1	12	2	2	2	265	29.7	8.51	5.28	2	0	162.8	86	106.1	136.9	63.9	71.6	42.4	58.8
Q9VTH0	Procollagen-lysine,2-oxoglutarate 5-dioxygenase OS=Drosophila melanogaster OX=7227 GN=Plod PE=1 SV	24.894	10	6	7	6	721	82.5	5.68	20.15	6	0	609.4	283.4	2458.1	2110.9	135	199.6	1011.6	842.4
P25843	Profilin OS=Drosophila melanogaster OX=7227 GN=chic PE=1 SV=1	46.881	52	4	16	4	126	13.7	5.41	64.49	4	0	2762.9	950.7	1518.1	1825.3	971.6	909.2	837.3	1258.7
A8DYI6	Prohibitin 2, isoform E OS=Drosophila melanogaster OX=7227 GN=Phb2 PE=1 SV=1	112.175	45	13	73	13	338	37.3	9.54	210.82	13	0	4438.6	2104.2	8404.4	6739.1	1490.4	1962.9	3769.3	7330.8
P17917	Proliferating cell nuclear antigen OS=Drosophila melanogaster OX=7227 GN=PCNA PE=1 SV=2	60.912	46	9	23	9	260	28.8	4.81	82.69	9	0	5497.7	3318.2	3311	3010.7	2376.7	969.2	748.8	907.7
Q9VA69	Prolyl 4-hydroxylase alpha-related protein PH4[alpha]EFB OS=Drosophila melanogaster OX=7227 GN=PH4a	60.752	21	12	24	12	550	63.1	5.48	67.44	12	0	854	477.8	3788.1	3644.6	281.4	337.5	1526.7	1762.6
Q7K2G1	Proteasomal ubiquitin receptor ADRM1 homolog OS=Drosophila melanogaster OX=7227 GN=Rpn13 PE=1 S	53.459	16	3	8	3	389	42	5.64	37.75	3	0	342.8	168.8	347.4	344.9	134.8	167.5	170.2	178.2
I0DHK3	Proteasome subunit alpha type OS=Drosophila melanogaster OX=7227 GN=Prosalpha6 PE=2 SV=1	31.905	22	3	5	3	279	31	6.55	24.78	3	0	1120.5	445.2	917.7	881.6	500.9	488.1	443	436.1
P40301	Proteasome subunit alpha type-2 OS=Drosophila melanogaster OX=7227 GN=Prosalpha2 PE=1 SV=1	19.497	14	3	7	3	234	25.9	6.68	25.21	3	0	930.8	421.8	635.1	545.9	321.6	379.9	338.4	313.6
P18053	Proteasome subunit alpha type-4 OS=Drosophila melanogaster OX=7227 GN=Prosalpha3 PE=1 SV=2	10.608	10	3	4	3	264	29.4	7.15	9.74	3	0	479.9	197	266.9	390.8	170.7	145.8	138.4	345.8
Q95083	Proteasome subunit alpha type-5 OS=Drosophila melanogaster OX=7227 GN=Prosalpha5 PE=2 SV=2	14.881	18	2	3	2	244	26.9	4.98	11.63	2	0	192.8	90.5	212.6	259.2	104.8	93.1	97.6	189
Q9XZJ4	Proteasome subunit alpha type-6 OS=Drosophila melanogaster OX=7227 GN=Prosalpha1 PE=1 SV=2	16.117	15	4	6	4	244	27.1	7.66	18.93	4	0	1277.3	558	858.4	768.7	403.7	464.7	447.9	384
P22769	Proteasome subunit alpha type-7-1 OS=Drosophila melanogaster OX=7227 GN=Prosalpha4 PE=1 SV=2	29.097	22	4	8	4	249	28	8.12	29.59	4	0	716.1	306.6	447.5	466.6	258.9	262.6	233.4	543.6
A0AQH0	Proteasome subunit beta OS=Drosophila melanogaster OX=7227 GN=Prosbeta1 PE=1 SV=1	13.416	17	2	9	2	224	24.2	5.25	24.4	2	0	147	80.9	135.8	146.2	63.3	70.4	63.9	79.2
Q9VUJ1	Proteasome subunit beta OS=Drosophila melanogaster OX=7227 GN=Prosbeta2 PE=1 SV=1	9.371	9	3	3	3	272	29.8	8.66	8.24	3	0	803.6	298	684.8	734.5	308.4	244.9	300.1	757.4
Q9VJJ0	Proteasome subunit beta OS=Drosophila melanogaster OX=7227 GN=Prosbeta4 PE=1 SV=1	11.343	21	4	5	4	201	22.5	6.39	9.99	4	0	265.5	135.1	267.1	312.9	149.5	128.5	163.2	384
P40304	Proteasome subunit beta type-1 OS=Drosophila melanogaster OX=7227 GN=Prosbeta6 PE=2 SV=2	30.92	13	2	8	2	235	25.8	6.54	31.69	2	0	722.2	310.9	533.8	513.2	244.1	246.2	259.7	271
Q9VNA5	Proteasome subunit beta type-4 OS=Drosophila melanogaster OX=7227 GN=Prosbeta7 PE=2 SV=1	51.406	24	5	10	5	268	30	6.58	43.77	5	0	685.1	310.9	528.7	642.4	266.3	319.7	289.6	291.1
Q9V8R9	Protein 4.1 homolog OS=Drosophila melanogaster OX=7227 GN=cora PE=1 SV=1	64.904	10	11	12	11	1698	184.1	8.7	43.95	11	0	1195.9	607.7	1429	1150.2	437.6	594.1	827	612.3
Q9VGR2	Protein arginine methyltransferase NDUFAF7 homolog, mitochondrial OS=Drosophila melanogaster OX=7227	7.318	13	4	4	4	437	49	6.93	4.56	4	0	53.2	29.6	119.9	109.6	41.6	46.8	53	73.7
Q9W1V1	Protein arginine N-methyltransferase 7 OS=Drosophila melanogaster OX=7227 GN=Art7 PE=2 SV=4	8.737	5	2	2	2	690	77.9	6.2	4.9	2	0	76.3	52.8	131.9	139.2	42.5	45.2	53.5	84.7
Q9VUQ5	Protein argonaute-2 OS=Drosophila melanogaster OX=7227 GN=AGO2 PE=1 SV=3	11.331	5	5	5	5	1214	136.8	9.61	5.57	5	0	426.5	173.1	504.4	538.5	172	208.4	251	386
Q9VEX5	Protein asunder OS=Drosophila melanogaster OX=7227 GN=Asun PE=1 SV=1	11.25	7	3	3	3	689	75.7	8.46	6.19	3	0	110.9	61.8	130.5	118.3	62.1	67.5	63.1	96.9
Q9VFR0	Protein BCCIP homolog OS=Drosophila melanogaster OX=7227 GN=CG9286 PE=2 SV=2	10.742	12	2	2	2	297	33.4	4.65	7.93	2	0	255.7	116.1	196.4	208.6	133.9	95.1	110	146.4
O46098	Protein bcn92 OS=Drosophila melanogaster OX=7227 GN=bcn92 PE=3 SV=1	40.225	38	7	15	7	92	11	10.14	42.96	7	0	1160.2	625.6	2118.2	2131.7	500.3	531	848.8	1418.6
A1ZAB5	Protein clueless OS=Drosophila melanogaster OX=7227 GN=clu PE=1 SV=1	24.222	4	6	6	6	1448	160.8	6.6	17.94	6	0	707.7	326.1	734.1	660.1	272.6	372.9	444	330.3
P17886	Protein crooked neck OS=Drosophila melanogaster OX=7227 GN=crn PE=2 SV=2	19.195	8	4	5	4	702	84.2	5.94	14.06	4	0	1051.6	458.4	534.9	683.8	345.8	383.7	305	495.3
Q3YMU0	Protein disulfide-isomerase (Fragment) OS=Drosophila melanogaster OX=7227 GN=ERp60 PE=1 SV=1	75.938	28	13	36	13	489	55.3	5.87	127.48	13	0	2860.8	1375.8	13243.7	11558.4	694.2	898.7	5879.7	5619.7
Q9V438	Protein disulfide-isomerase A6 homolog OS=Drosophila melanogaster OX=7227 GN=CaBP1 PE=1 SV=1	24.692	18	6	10	6	433	46.7	5.69	24.78	6	0	237.6	119.9	1002.6	872.4	69.9	101.2	397.3	927
P54399	Protein disulfide-isomerase OS=Drosophila melanogaster OX=7227 GN=Pdi PE=2 SV=1	74.553	29	12	35	12	496	55.7	4.82	115	12	0	1199.3	630.4	6225.5	4534.2	446.6	490	2715.9	2536.3
Q8SY33	Protein Gawky OS=Drosophila melanogaster OX=7227 GN=gw PE=1 SV=1	11.232	2	2	2	2	1384	142.9	6.74	6.97	2	0	240.8	122.8	267.9	263.5	120.7	142.5	157.2	140.1
O01367	Protein held out wings OS=Drosophila melanogaster OX=7227 GN=how PE=1 SV=1	8.112	6	3	3	3	405	44.3	7.93	7.62	3	0	390.1	158.7	256.5	298.8	148.7	155.5	146.9	345.1
Q24185	Protein hook OS=Drosophila melanogaster OX=7227 GN=hook PE=1 SV=2	7.06	3	2	2	2	679	76.6	5.35	5.25	2	0	215.4	96	248.5	215.5	81.6	127.3	129.6	130.8
Q7K1V5	Protein jagunal OS=Drosophila melanogaster OX=7227 GN=jagn PE=1 SV=1	17.027	15	2	4	2	197	23	6.77	12.59	2	0	167.5	111.7	254.3	257.5	68	134.3	113.4	113.5
A1Z9E2	Protein lin-54 homolog OS=Drosophila melanogaster OX=7227 GN=mip120 PE=1 SV=1	32.694	7	5	6	5	950	100	9.45	23.41	5	0	2632.3	813.1	1084.9	1347.7	928.6	1010.8	831.6	1185.1
P50535	Protein male-specific lethal-1 OS=Drosophila melanogaster OX=7227 GN=msl-1 PE=1 SV=2	7.677	3	3	3	3	1039	117.4	5.99	5.94	3	0	260.6	106.7	163.2	145.6	115.2	145.7	144.6	168.4
P50536	Protein male-specific lethal-3 OS=Drosophila melanogaster OX=7227 GN=msl-3 PE=1 SV=2	7.473	7	3	4	3	512	58.8	7.2	8.48	3	0	199.8	63.7	97.5	143.6	81.6	92.1	68	136.8
Q9VH39	Protein NDUFAF4 homolog OS=Drosophila melanogaster OX=7227 GN=CG11722 PE=2 SV=1	33.681	29	5	13	5	203	23.7	8.81	38.91	5	0	804.6	444.5	1739.9	1398.8	319.9	397.7	799.6	909
Q9VIP0	Protein nessun dorma OS=Drosophila melanogaster OX=7227 GN=nesd PE=1 SV=1	15.006	6	4	5	4	602	67.7	5.07	11.63	4	0	645.9	338.6	450.8	475.2	253.9	296.4	240	257.7
Q9VXK0	Protein NipSnap OS=Drosophila melanogaster OX=7227 GN=Nipsnap PE=2 SV=2	44.143	18	4	21	4	273	31.9	9.17	70.56	4	0	567.6	348.3	973.4	925.5	337	362.8	503.7	688.6
P40797	Protein peanut OS=Drosophila melanogaster OX=7227 GN=pnut PE=1 SV=2	12.109	6	3	4	3	539	60.1	8.75	12.67	3	0	410.5	183.7	432.3	427.1	150.6	221	258.7	268.7
O61345	Protein penguin OS=Drosophila melanogaster OX=7227 GN=peng PE=2 SV=1	15.93	6	5	6	5	737	81.3	8.94	14.86	5	0	1539.9	465.2	520.4	580.3	584	548.7	284	447.7
P36872	Protein phosphatase PP2A 55 kDa regulatory subunit OS=Drosophila melanogaster OX=7227 GN=tws PE=2	8.712	7	3	3	3	499	56.9	7.09	6.46	3	0	209.1	88.7	140.9	193.6	83.6	76.4	62.5	111.3
A1Z9A8	Protein PTCD3 homolog, mitochondrial OS=Drosophila melanogaster OX=7227 GN=CG4679 PE=2 SV=1	41.344	14	9	22	9	652	74.2	5.92	59.38	9	0	659.9	329	1071.3	772.7	269.7	349	518.9	1062.2
Q9VLT5	Protein purity of essence OS=Drosophila melanogaster OX=7227 GN=poe PE=1 SV=1	29.568	1	5	6	5	5322	590.3	6.38	21.91	5	0	297.9	130.1	317.5	378.9	130.1	171.7	188.1	185.5
Q07327	Protein ROP OS=Drosophila melanogaster OX=7227 GN=Rop PE=2 SV=2	12.61	5	2	2	2	597	67.8	6.7	7.67	2	0	169.8	115.8	192.4	261	85	118.3	115.4	148.6
Q7KKH3	Protein SDA1 homolog OS=Drosophila melanogaster OX=7227 GN=Mys45A PE=1 SV=1	5.106	2	2	2	2	712	81.9	6.76	4.91	2	0								
Q9V3J4	Protein SEC13 homolog OS=Drosophila melanogaster OX=7227 GN=Sec13 PE=1 SV=1	10.438	9	3	4	3	356	39.5	6.25	9.45	3	0	268.8	144.7	350.5	465.4	143.1	155.7	179.5	279
P53997	Protein SET OS=Drosophila melanogaster OX=7227 GN=Set PE=1 SV=2	18.349	26	3	4	3	269	31	4.36	14.1	3	0	629.6	190.5	210.9	210.9	198.1	177	114.8	183.4
Q8INM3	Protein slender lobes OS=Drosophila melanogaster OX=7227 GN=sle PE=1 SV=1	49.164	5	6	7	6	1420	158.6	5.24	30.53	6	0	1669.4	427.2	486.2	580.1	547.9	574.7	340.6	358.9
A8JUV0	Protein strawberry notch OS=Drosophila melanogaster OX=7227 GN=sno PE=1 SV=2	24.322	5	6	6	6	1653	180.3	8.41	21.93	6	0	742.9	319.4	438.7	544.5	296.5	329	247	330.6
P20193	Protein suppressor of variegation 3-7 OS=Drosophila melanogaster OX=7227 GN=Su(var)3-7 PE=1 SV=4	47.335	10	9	10	9	1250	139.9	6.43	37.67	9	0	2032.1	673.6	580.3	827.2	712.6	789.3	331.7	498
Q8INX3	Protein TIPIN homolog OS=Drosophila melanogaster OX=7227 GN=CG10336 PE=2 SV=2	11.877	14	3	5	3	307	34.1	5.11	14.34	3	0	547	326.3	491.4	480.5	236.2	256.4	211.8	264
A0A0B4K5Z8	Protein transport protein SEC23 OS=Drosophila melanogaster OX=7227 GN=Sec23 PE=1 SV=1	11.452	5	3	3	3	781	87.5	6.79	7	3	0	268.6	124.8	314	361.1	136.1	138.2	160.7	267.6
Q7JZN0	Protein transport protein Sec61 subunit beta OS=Drosophila melanogaster OX=7227 GN=Sec61beta PE=1 S	12.302	21	2	2	2	100	10.2	11.65	7.34	2	0	914.1	322.2	820.7	806.4	275.8	343.7	449.7	774.8
Q27237	Protein tumorous imaginal discs, mitochondrial OS=Drosophila melanogaster OX=7227 GN=l(2)tid PE=1 SV=2	148.95	34	14	38	1	520	56.1	9.1	159.03	14	0	117.6	73.7	290.4	170.7	49.7	70.6	138.7	76.7
Q9W517	Protein wings apart-like OS=Drosophila melanogaster OX=7227 GN=wapl PE=1 SV=1	36.534	5	4	4	4	1741	185	6.54	19.83	4	0	124.8	56.2	117.3	128.8	52.8	67.8	45.6	102.6
A0A0B4KGK0	Protein-L-isoaspartate O-methyltransferase OS=Drosophila melanogaster OX=7227 GN=Pcmt PE=1 SV=1	9.021	11	2	2	2	203	21.9	7.58	6.77	2	0	101.9	41.5	128.3	142	36.8	40	55.8	75.5
Q9VC52	Protoporphyrinogen oxidase OS=Drosophila melanogaster OX=7227 GN=Ppox PE=1 SV=1	26.716	9	5	7	5	475	53.2	9.45	24.52	5	0	718.4	416.9	2193.5	1648.8	190.4	347.7	993	731.2
Q9W141	Putative ATP synthase subunit f, mitochondrial OS=Drosophila melanogaster OX=7227 GN=CG4692 PE=3 S	16.484	32	3	3	3	107	12.5	10.1	9.94	3	0	305.9	166.6	880.2	517.6	65.4	92.3	375	1241.6
Q9VGK7	Putative elongator complex protein 1 OS=Drosophila melanogaster OX=7227 GN=Elp1 PE=1 SV=2	10.298	3	3	5	3	1252	142.7	6.43	13.44	3	0	226.5	104.9	243.6	241.9	97.9	119.9	149.1	145.6
P36951	Putative hydroxypyruvate isomerase OS=Drosophila melanogaster OX=7227 GN=Gip PE=2 SV=1	8.008	10	2	2	2	264	29.1	6.54	6.19	2	0	265.7	113.4	244.2	255.1	96.5	103.6	125.4	153.5
A0A126GUP4	Putative lipoyltransferase 2, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9804 PE=3 S	14.668	16	3	5	3	234	26	8.28	11.45	3	0	445	246.8	788.9	503.4	152.9	211.7	380.8	263.6
P83100	Putative mitogen-activated protein kinase 14C OS=Drosophila melanogaster OX=7227 GN=p38c PE=2 SV=1	4.497	5	2	3	2	356	41.9	7.27	6.29	2	0	472.3	288	450.3	480.3	216.9	325.7	322.3	290.1
Q9VCG3	Putative OPA3-like protein CG13603 OS=Drosophila melanogaster OX=7227 GN=CG13601 PE=2 SV=1	43.034	38	7	17	7	255	28.7	8.07	49.33	7	0	631.3	422.7	1975.7	1468.1	303.8	365.8	940.1	1122.2
P54353	Putative peptidyl-prolyl cis-trans isomerase dodo OS=Drosophila melanogaster OX=7227 GN=dod PE=2 SV=	13.109	17	3	3	2	166	18.4	7.44	9.93	3	1	1139	442.1	573.6	594.1	440.3	427.1	374.9	471
Q9VUV9	Putative U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Drosophila melanogaster OX=7227 GN=l(3	33.766	5	9	10	9	2142	244.4	6.04	26.4	9	0	2200.8	857.5	951.8	1113.6	767.2	805.9	647.3	751.6
Q8IN96	Pyrroline-5-carboxylate reductase-like 2, isoform B OS=Drosophila melanogaster OX=7227 GN=P5cr-2 PE=1	22.429	27	4	6	4	174	18	7.31	21.75	4	0	473	220.6	1074.6	795.9	154.8	181.2	454.5	1847
Q7KN97	Pyruvate carboxylase OS=Drosophila melanogaster OX=7227 GN=PCB PE=1 SV=1	398.227	36	36	428	36	1181	130.8	6.81	1505.78	36	0	12863.8	5744.8	16158.7	21297.5	6776.6	6941.9	7364.9	18325.8
Q7KVX1	Pyruvate dehydrogenase E1 component subunit alpha OS=Drosophila melanogaster OX=7227 GN=Pdha PE	118.422	33	13	50	13	443	48.8	8.13	169.95	13	0	3401.2	1692.6	5861.1	4785.5	1284.9	1494.1	2531.3	4307.8
Q7K5K3	Pyruvate dehydrogenase E1 component subunit beta OS=Drosophila melanogaster OX=7227 GN=Pdhb PE=	109.213	31	9	47	5	365	39.3	7.8	171.09	9	4	3009.8	1681.3	5772.7	4537	1232	1557	2326	4183.4
A0A0B4KFG2	Pyruvate dehydrogenase kinase, isoform D OS=Drosophila melanogaster OX=7227 GN=Pdk PE=1 SV=1	22.459	14	5	8	5	415	47.1	6.84	24.98	5	0	263.1	132	511.5	398.7	94	126.7	221.9	409.2
O62619	Pyruvate kinase OS=Drosophila melanogaster OX=7227 GN=PyK PE=2 SV=2	22.114	12	5	11	5	533	57.4	7.44	28.55	5	0	1271.8	527.4	951.3	1129.2	529.8	520.3	551	876.6
A0A0B4LG88	Quaking related 58E-1, isoform D OS=Drosophila melanogaster OX=7227 GN=qkr58E-1 PE=1 SV=1	9.397	11	2	2	2	379	43.5	9.1	6.5	2	0	148.6	79.9	144.7	143.9	91.8	87.9	151.4	87.8
Q9W2I2	Queuosine salvage protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9752 PE=1 SV=1	3.955	5	2	2	2	343	39.5	5.73	5.35	2	0	508.2	224.8	261.6	292.1	183.8	183.7	157	242.4
Q9VLB7	Rab GDP dissociation inhibitor OS=Drosophila melanogaster OX=7227 GN=Gdi PE=1 SV=1	12.928	6	2	3	2	443	49.9	5.72	9.46	2	0	178.7	84.3	192.2	204.4	79.4	109.4	87.7	309.8
Q9VWS3	Rab11 interacting protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Rip11 PE=1 SV=1	13.283	7	4	4	4	832	91.8	6.28	5.72	4	0	136.5	67.2	206.2	294	45.9	63.1	83.2	144.6
Q86BK8	Rab14, isoform B OS=Drosophila melanogaster OX=7227 GN=Rab14 PE=1 SV=1	16.103	13	3	5	2	239	27.1	7.01	17.1	3	0	459.6	296.6	1101.9	861.7	175.8	277.2	554.2	541.3
Q7KY04	Rab4 protein OS=Drosophila melanogaster OX=7227 GN=Rab4 PE=1 SV=1	8.216	12	2	3	1	213	23.6	6.79	8.01	2	0	79.8	38.2	108.9	136.3	33.3	33.9	53.4	126
X2J5T3	Rab6, isoform B OS=Drosophila melanogaster OX=7227 GN=Rab6 PE=1 SV=1	16.454	17	4	8	3	208	23.5	5.36	26.31	4	1	902.2	568.1	2449.2	2533.3	294.3	453.5	999.4	1664.3
Q9W543	Rabconnectin-3B, isoform A OS=Drosophila melanogaster OX=7227 GN=Rbcn-3B PE=1 SV=1	11.529	2	2	2	2	1525	168.4	7.49	6.64	2	0	263.6	131.2	327.1	328.8	85.6	113.7	153.6	134.6
Q8INB9	RAC serine/threonine-protein kinase OS=Drosophila melanogaster OX=7227 GN=Akt1 PE=1 SV=3	6.732	4	2	2	2	611	68.4	6.24	7.3	2	0	544	206.2	382.9	447.9	200.2	205.4	193.6	277.6
Q8IMB7	Rad23, isoform B OS=Drosophila melanogaster OX=7227 GN=Rad23 PE=1 SV=1	31.651	20	4	5	4	343	37.5	4.53	24.42	4	0	610.3	310.7	539.5	616.6	256.2	286	292.6	364.5
A0A0B4K7L0	Rad50, isoform E OS=Drosophila melanogaster OX=7227 GN=rad50 PE=1 SV=1	21.166	3	5	5	5	1318	152	7.65	13.71	5	0	1119.5	525	648.6	641.2	415.7	450.2	371.6	293.4
Q9VIW3	Ran GTPase-activating protein OS=Drosophila melanogaster OX=7227 GN=RanGAP PE=1 SV=1	5.981	4	2	2	2	596	66	4.65	6.47	2	0	140.1	47.9	108.8	80.3	50.7	49.2	58	49.2
P48148	Ras-like GTP-binding protein Rho1 OS=Drosophila melanogaster OX=7227 GN=Rho1 PE=1 SV=1	27.449	33	5	10	5	192	21.7	7.01	32.47	5	0	332.8	159.4	525.1	456.1	108.2	138.8	226.7	245.4
Q9VL60	RE01590p OS=Drosophila melanogaster OX=7227 GN=anon-WO0118547.208 PE=1 SV=1	33.537	12	7	8	7	463	53.7	8.69	24.65	7	0	591.2	345.2	1309.6	936.4	176.1	300.3	593.7	517
Q9VNF3	RE01652p OS=Drosophila melanogaster OX=7227 GN=anon-WO0118547.83 PE=1 SV=1	9.233	8	2	3	1	257	26.9	7.5	10.11	2	0	109.3	45	126.2	150.9	38.7	47.2	51.8	222.7
Q9W4R8	RE03721p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG14270 PE=1 SV=1	9.173	15	2	3	2	191	22.6	8.97	9.1	2	0	37.3	15.5	78.2	72.7	14.5	25	32.9	36.9
Q9VGC2	RE05302p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4860 PE=2 SV=1	60.601	31	11	20	11	415	44.9	8.38	66.2	11	0	1086.2	622.8	1818.9	1555.3	428.1	560.7	826.2	953.3
Q9W0E2	RE06653p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12091 PE=1 SV=1	11.884	11	2	2	2	321	34.4	6.87	8.99	2	0	60.2	39.7	91.5	95.1	32	37.6	53.4	97.6
Q9VKD8	RE11167p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6686 PE=1 SV=1	6.815	2	2	2	2	964	111.8	7.21	6.09	2	0	641.4	244.1	290.8	293.2	210.4	222.1	202.1	172.2
Q9VG01	RE12073p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG46280 PE=1 SV=1	18.395	12	4	6	4	532	58.8	6.15	15.89	4	0	387.6	219.4	776.9	438.3	97.1	176.7	365.3	341
Q7JXB5	RE12569p OS=Drosophila melanogaster OX=7227 GN=Pepck2 PE=1 SV=1	8.921	4	2	2	2	638	70.6	7.56	8.09	2	0	245.2	140.6	370.1	305.5	121.3	131.7	182.5	221.5
Q9VS57	RE14391p OS=Drosophila melanogaster OX=7227 GN=Sec63 PE=1 SV=1	20.934	5	4	5	4	753	85.8	5.99	14.49	4	0	986.7	387.3	1169.7	1307.8	330.5	361.6	614	766.4
Q9VM50	RE14786p OS=Drosophila melanogaster OX=7227 GN=Rab30 PE=2 SV=1	11.123	11	2	3	1	223	24.3	5.48	8.65	2	0								
Q8SXK0	RE18748p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG15390 PE=2 SV=1	12.742	12	3	4	3	275	31.8	6.9	9.8	3	0	240.4	125.9	412.9	386.8	101.1	131.4	197.4	345.2
Q9W5W8	RE22677p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9577 PE=1 SV=2	42.551	26	6	22	6	312	33.8	7.46	58.45	6	0	1314.8	690.5	2147.7	1689.1	464.1	649.3	986.9	1204.4
Q9VEC8	RE23139p1 OS=Drosophila melanogaster OX=7227 GN=CG32920 PE=1 SV=1	3.285	13	2	2	2	130	14.7	7.28	5.01	2	0	271	133.4	172.8	185.4	96.6	112.4	104.1	72.2
Q8SZ15	RE23670p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10914 PE=1 SV=1	21.504	6	2	5	2	624	70.5	9.11	20.09	2	0	198.9	127.4	423.8	309	66.4	109.2	229.6	193
Q9VJ19	RE25263p OS=Drosophila melanogaster OX=7227 GN=RpL30 PE=1 SV=1	18.347	25	2	3	2	111	12.2	9.58	12.19	2	0	675.6	275.2	567.1	619.4	281	318.4	401.7	303.7
Q7JRH5	RE28271p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5726 PE=1 SV=1	6.158	3	2	2	2	766	86.5	7.74	5.47	2	0	206.4	112.9	283.1	305.4	81.1	107.1	136.2	137.7
Q9VES8	RE28913p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10340 PE=1 SV=3	14.923	14	3	4	3	278	32	6.55	13.1	3	0	346.4	189	585.4	467.9	155	168.5	286.7	259.7

Q9VGG9	RE35509p OS=Drosophila melanogaster OX=7227 GN=CG14730 PE=1 SV=4	23.346	5	6	6	6	1483	171.9	6.1	17.17	6	0	588.9	237.3	389.2	427.2	264.9	234.3	203.9	283.3
Q8SXI2	RE36623p OS=Drosophila melanogaster OX=7227 GN=Yeti PE=1 SV=1	6.201	11	3	3	3	241	27.7	6.44	7.59	3	0	69.5	31.3	37	23.5	29.3	28.9	23.5	14.4
Q9VSR7	RE41093p OS=Drosophila melanogaster OX=7227 GN=ValRS-m PE=2 SV=1	9.134	3	3	3	3	994	113	6.7	8.03	3	0	86.9	58.4	170.8	160.6	86.4	53.8	74.9	152.1
Q8IPX7	RE44908p OS=Drosophila melanogaster OX=7227 GN=Rrp40 PE=1 SV=1	8.824	8	2	2	2	232	25	8.31	5.91	2	0	300.8	110.2	183	211	111.2	86.8	76.1	453.2
Q9VRJ7	RE45108p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4611 PE=1 SV=1	16.623	5	2	2	2	703	79.9	8.98	8.4	2	0	73.3	41.5	110.4	125.4	38.5	54.3	62	105.2
Q9VL16	RE45833p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5676 PE=2 SV=1	3.707	10	2	3	2	156	17.3	9.2	3.67	2	0	227.8	120.4	348.6	284.5	70.4	94.6	153.4	207.5
Q9VYD8	RE47308p OS=Drosophila melanogaster OX=7227 GN=Rbp1-like PE=2 SV=2	9.097	14	2	3	2	158	16.8	11.24	10.39	2	0	450.5	150.3	253.6	282.2	182.4	190.1	143.8	438.2
E8NH59	RE48478p OS=Drosophila melanogaster OX=7227 GN=WRNexo PE=2 SV=1	14.348	12	3	6	3	353	40.3	9.2	16.73	3	0	1907.9	657	583.4	724.6	702.9	795.9	419.8	533.3
Q9VQ27	RE49731p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG14352 PE=1 SV=1	2.98	5	2	2	2	251	29	7.33	4.06	2	0	518	207.6	281.4	337.8	218.4	244.6	152.1	262.6
Q9VND7	RE50009p OS=Drosophila melanogaster OX=7227 GN=cg2931 PE=1 SV=1	6.857	9	2	2	2	302	33.6	10.2	4.92	2	0	270.1	79.6	194.5	200.9	130.7	123.1	84.9	301.9
Q9VCC2	RE50040p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5510 PE=1 SV=1	5.339	9	2	2	2	329	37.6	6.87	6.75	2	0								
Q8INP9	RE51612p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11980 PE=1 SV=1	24.798	17	6	10	6	359	40.9	6.95	29.6	6	0	968.3	541.4	1113.6	1153.9	439.7	473.5	493.9	1010.9
Q9W1F5	RE54691p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3803 PE=2 SV=1	14.51	9	3	4	3	393	44.3	10.08	14.9	3	0	319.1	218.4	915.3	688.6	121.2	188.2	398.3	320
Q8SYJ9	RE55868p OS=Drosophila melanogaster OX=7227 GN=CG10438 PE=2 SV=1	13.106	16	3	3	3	248	27.6	8.37	9.88	3	0	135.1	79	203.9	216.2	60.1	68.6	90.7	150.8
Q86PD3	RE56416p OS=Drosophila melanogaster OX=7227 GN=CG30022;CG30023 PE=1 SV=1	10.877	8	2	2	2	279	31.4	6.93	6.76	2	0	200.6	109.5	338.7	324.1	95.1	80.6	139.9	476.8
Q9VC87	RE57978p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG18528 PE=1 SV=3	33.121	13	5	9	5	493	54.9	6.74	31.81	5	0	797.9	416.6	1577.3	1510.3	326.7	403.9	692.2	1166
Q494M1	RE58921p OS=Drosophila melanogaster OX=7227 GN=Top1 PE=1 SV=1	10.249	4	4	4	4	974	111.8	9.01	9.78	4	0	683.2	235.5	337.7	386.8	253.7	259.9	196.9	311.1
Q7JWH6	RE61424p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1888 PE=1 SV=1	7.645	8	2	3	2	372	42.2	6.05	9.9	2	0	58.4	22.7	37.9	52.9	25.6	28.9	35.8	45.9
Q7JZ37	RE62785p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12134 PE=1 SV=1	6.693	8	2	2	2	411	45.7	5.06	6.65	2	0	71	54.5	106.3	140	97.4	39.5	52.5	107.2
Q9VSL9	RE62833p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6638 PE=1 SV=1	32.183	15	6	9	6	420	46.2	8.18	28.5	6	0	461	256.4	896.5	877.4	187	188.3	374.8	1070.8
Q9VE24	RE63280p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG14291 PE=1 SV=1	6.161	4	2	2	2	524	59.9	7.08	4.91	2	0	120.8	65.3	394.4	509.9	32.1	28.7	172	147.5
Q9VNR9	RE67859p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG14450 PE=2 SV=1	18.892	16	5	6	5	372	41.8	9.33	18.86	5	0	383.6	200.4	707.4	599.4	145.7	191.8	285.3	281.7
Q9VRZ7	RE68357p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10075 PE=2 SV=1	13.285	15	2	2	2	259	29.4	8.84	9.13	2	0	17	7.5	33.1	22.9	7.3	9.7	12.6	12.2
Q9VZT2	RE68649p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG14966 PE=2 SV=1	11.411	16	2	3	2	140	14.7	9.85	6.21	2	0	194.6	101.1	238.1	195.2	75.9	86.9	115.2	149.8
Q9VZE4	RE70333p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1316 PE=1 SV=2	40.29	16	6	13	6	470	52.4	6.71	40.48	6	0	1103.5	504.8	662.7	666.4	448.2	459.5	380.9	424
Q7KVW1	RE73736p OS=Drosophila melanogaster OX=7227 GN=spoon PE=1 SV=1	21.99	12	5	8	5	607	67.3	6.79	22.78	5	0	888.6	327.7	643.5	426.3	264.3	367.6	340	486.5
Q9VD29	RE74312p OS=Drosophila melanogaster OX=7227 GN=Sar1 PE=1 SV=1	6.917	11	2	2	2	193	21.8	6.93	6.43	2	0	134.4	50.2	168.3	168.8	49.1	87.2	89	113
Q9VN39	RE74585p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9775 PE=1 SV=1	26.767	16	5	8	5	421	46.1	12.48	25.22	5	0	1891.3	777.4	876.7	844.4	707.4	829	545.5	514.5
P27864	Recombination repair protein 1 OS=Drosophila melanogaster OX=7227 GN=Rrp1 PE=1 SV=2	97.896	26	14	26	14	679	74.6	8.98	94.39	14	0	5746.4	1594.8	1685.8	1963.1	2182.7	2504.8	1194.3	1713.4
Q9VYR1	Regucalcin homologue OS=Drosophila melanogaster OX=7227 GN=regucalcin PE=1 SV=1	84.491	41	9	36	9	303	33.6	6.4	133.15	9	0	10093.2	5272	5241.9	5017.4	3401.2	5223.6	2783.2	2705.8
P25171	Regulator of chromosome condensation OS=Drosophila melanogaster OX=7227 GN=Rcc1 PE=1 SV=2	53.192	20	5	13	5	547	58.8	7.94	49.28	5	0	765	265.5	340.2	447.9	305.8	351	250.4	321.8
Q9VYS3	Regulator of nonsense transcripts 1 homolog OS=Drosophila melanogaster OX=7227 GN=Upf1 PE=1 SV=2	11.116	2	2	3	2	1180	129.8	7.33	9.7	2	0	64.5	31.4	76.3	82.3	33.9	38.9	43.2	65.3
M9PIG8	Regulatory particle non-ATPase 10, isoform B OS=Drosophila melanogaster OX=7227 GN=Rpn10 PE=4 SV=	12.543	14	2	3	2	396	42.6	4.83	9.39	2	0	943.3	454.9	750.2	809.3	362.6	375.2	363.7	363.5
M9PG62	Regulatory particle non-ATPase 3, isoform B OS=Drosophila melanogaster OX=7227 GN=Rpn3 PE=1 SV=1	32.135	19	10	10	10	494	56	9	28.09	10	0	1258.6	592.8	1133.8	1295.8	479.5	575.9	615.8	909.6
A0A0B4K7Z5	Regulatory particle non-ATPase 6, isoform C OS=Drosophila melanogaster OX=7227 GN=Rpn6 PE=1 SV=1	20.636	11	5	5	5	422	47.2	5.88	16.07	5	0	698.3	320.6	477.9	591.8	238	293.8	245.5	401.6
Q9W414	Regulatory particle triple-A ATPase 4 OS=Drosophila melanogaster OX=7227 GN=Rpt4 PE=1 SV=3	18.921	9	3	6	3	397	44.9	8.07	20.34	3	0	323.8	129	251.4	290	118.2	168.7	136	227.8
A0A0B4KER0	Relative of woc, isoform C OS=Drosophila melanogaster OX=7227 GN=row PE=1 SV=1	16.353	4	4	4	4	1301	146.1	8.06	10.98	4	0	496.4	166.4	276.5	286.4	223.5	169.1	141.3	503.1
Q9U9Q1	Replication factor C 38kD subunit, isoform A OS=Drosophila melanogaster OX=7227 GN=RfC38 PE=1 SV=1	19.131	18	5	6	5	356	40.8	8.4	14.86	5	0	625.4	303.3	411.4	454.9	320.8	211.3	167.1	241
P35600	Replication factor C subunit 1 OS=Drosophila melanogaster OX=7227 GN=Gnf1 PE=1 SV=2	50.675	12	9	14	9	986	108.5	9.31	50.11	9	0	2856.1	1389.5	1278.6	1122.9	1067.9	647.1	392.7	485.8
P53034	Replication factor C subunit 2 OS=Drosophila melanogaster OX=7227 GN=RfC4 PE=1 SV=1	18.707	11	5	8	5	331	37.2	7.72	20.16	5	0	2780.6	1584.6	1546.9	2066.6	1137.3	673.8	412.8	861
Q9VKW3	Replication factor C subunit 3 OS=Drosophila melanogaster OX=7227 GN=RfC3 PE=1 SV=2	10.614	9	3	3	3	332	37.4	7.2	9.44	3	0	664.1	294.3	540	648.6	289.4	211.4	210.3	497
Q24492	Replication protein A 70 kDa DNA-binding subunit OS=Drosophila melanogaster OX=7227 GN=RpA-70 PE=1	78.696	27	12	27	12	603	66.6	6.76	73.84	12	0	4360.2	2111.7	2332.2	2540	1715.3	1052	694.5	1289.7
Q9GQR5	RH02809p OS=Drosophila melanogaster OX=7227 GN=stai PE=1 SV=1	13.674	12	2	2	2	257	29.6	8.25	7.82	2	0	147.3	67.3	121.6	118.7	54.7	74.4	70.7	58
Q9W4U2	RH09070p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3603 PE=1 SV=2	13.73	13	3	3	3	249	26.2	7.8	9.91	3	0	447.2	243.4	738.8	756.4	177	217.1	294.6	360.8
Q9VU35	RH34413p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11267 PE=1 SV=1	20.49	43	6	20	6	103	11	9.09	47.45	6	0	1494.3	754.4	2354.7	1655.4	546.9	561.2	1009	1541.1
Q9VGS3	RH44771p OS=Drosophila melanogaster OX=7227 GN=SdhC PE=1 SV=2	5.436	9	2	4	2	171	18.5	9.31	10.14	2	0	703.1	268.1	1429.1	777.1	222.2	192.2	608.4	693.5
Q9VZ01	RH44935p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11752 PE=1 SV=1	11.648	19	2	4	2	109	10.9	9.61	10.96	2	0	164.2	74.4	248	251.4	64.9	71	133	274.7
A1Z9W2	RH47216p OS=Drosophila melanogaster OX=7227 GN=CG10220 PE=2 SV=1	14.082	12	3	6	3	320	36.4	9.38	18.93	3	0	232.8	146.6	1044.7	783.1	74.7	96.8	421.9	586.5
Q9VG81	RH49330p OS=Drosophila melanogaster OX=7227 GN=Sccpdh2 PE=1 SV=1	22.562	14	5	8	5	431	47.2	9.44	21.17	5	0	792.1	341.4	1700.3	1262.9	258.4	268.2	649.1	1744.2
Q9VJ74	RH55640p OS=Drosophila melanogaster OX=7227 GN=DmRH19 PE=1 SV=2	5.012	2	2	2	2	822	94.5	9.47	4.87	2	0	115.1	62.6	134.6	132.3	44.6	66.4	74.9	84
Q9W3N1	RH59310p OS=Drosophila melanogaster OX=7227 GN=spidey PE=1 SV=1	12.885	9	2	3	2	321	35.1	9.47	10.47	2	0	165.1	63.8	197.7	212.9	69.4	87	97.6	159.5
Q9VL22	RH68195p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4908 PE=2 SV=1	9.879	11	3	4	3	431	48.5	8.09	9.76	3	0	84.8	44.1	92.6	103.9	38.8	43.7	49	79.9
Q9VBI3	RH72336p OS=Drosophila melanogaster OX=7227 GN=Vps2 PE=1 SV=1	4.109	6	2	2	2	256	27.3	5.66	2.56	2	0	107.6	46.5	99.4	90.6	31.9	43.9	46.8	82.3
Q9VZ34	RH72958p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2076 PE=1 SV=1	8.519	9	3	3	3	341	35.8	9.96	8.63	3	0	64.5	65.2	327.3	181.6	17.5	38.2	118.6	173
Q9VL68	RH73277p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4598 PE=1 SV=2	24.602	21	6	10	6	281	31	9.23	27.69	6	0	858.2	422	1436.1	1184.2	330.5	355.8	615.5	1057.9
M9PHV3	Rho GTPase activating protein p190, isoform F OS=Drosophila melanogaster OX=7227 GN=RhoGAPp190 P	10.919	3	4	5	4	1621	185.1	5.5	11.08	4	0	523.6	259.8	727.9	803.3	272.6	350.2	371.6	515.6
Q9VDS5	Rho GTPase-activating protein 92B OS=Drosophila melanogaster OX=7227 GN=RhoGAP92B PE=1 SV=1	11.352	5	3	4	3	740	83	8.46	10.42	3	0	358.7	171.1	418.4	439.9	123.4	169.1	234.4	275.2
Q94915	Rhythmically expressed gene 2 protein OS=Drosophila melanogaster OX=7227 GN=Reg-2 PE=2 SV=1	13.318	16	4	5	4	260	30.1	7.78	11.76	4	0	73.3	58.9	114.6	124.7	96.5	127.5	61.5	86.4
Q9VPP5	Ribonuclease H2 subunit A OS=Drosophila melanogaster OX=7227 GN=CG13690 PE=2 SV=1	7.807	6	2	2	2	347	38.7	5.12	6.04	2	0	824.4	373.9	331.1	342.3	300.6	236.6	150.8	180.9
Q8MKW7	Ribonuclease Z, mitochondrial OS=Drosophila melanogaster OX=7227 GN=RNaseZ PE=2 SV=2	74.291	22	12	34	12	766	85.4	6.99	114.18	12	0	1629.8	885.8	2821	2505.6	675.8	810.5	1315.7	1530.1
P48592	Ribonucleoside-diphosphate reductase subunit M2 OS=Drosophila melanogaster OX=7227 GN=RnrS PE=1 S	19.722	11	3	8	3	393	45.1	5.63	17.27	3	0	583	236.1	405.8	310.8	222.2	196.3	246.3	155.4
Q9VLK2	Ribosomal L1 domain-containing protein CG13096 OS=Drosophila melanogaster OX=7227 GN=CG13096 PE	14.198	5	4	4	4	681	74.3	8.51	10.83	4	0	1440.3	384.9	502.5	586.8	470.9	546.2	290.2	635
M9PIM0	Ribosomal protein L10, isoform E OS=Drosophila melanogaster OX=7227 GN=RpL10 PE=4 SV=1	36.455	31	7	11	7	218	25.5	9.85	34.87	7	0	1241	415.7	1039.6	1019.9	386.1	465.3	780.5	648.3
Q9V9W2	Ribosomal protein L6, isoform A OS=Drosophila melanogaster OX=7227 GN=RpL6 PE=1 SV=1	12.849	15	4	6	4	243	27.7	10.68	14.18	4	0	956.6	266.9	857.5	693.2	320.9	389.1	624.3	802.4
X2J5G6	Ribosomal protein L7, isoform B OS=Drosophila melanogaster OX=7227 GN=RpL7 PE=4 SV=1	12.016	11	4	6	4	252	29.5	10.89	16.41	4	0	443.7	135.1	389.4	459.4	176.9	180.7	239.5	465
X2JDU0	Ribosomal protein L9, isoform C OS=Drosophila melanogaster OX=7227 GN=RpL9 PE=4 SV=1	9.016	9	2	7	2	190	21.4	9.69	18.1	2	0	1753.6	514	1311.6	1377.1	613.6	620.4	788.1	1373.4
Q7K1Q7	Ribosome assembly factor mrt4 OS=Drosophila melanogaster OX=7227 GN=RpLP0-like PE=1 SV=1	4.502	7	2	5	2	256	29.4	5.12	11.8	2	0	328.9	138.3	282.3	330.2	139.2	138	121.6	231.1
Q7K0Y1	Ribosome biogenesis protein BOP1 homolog OS=Drosophila melanogaster OX=7227 GN=CG5033 PE=2 SV	14.747	6	4	4	4	784	90.4	5.88	10.23	4	0	693.4	254.8	367.5	420.2	301.2	283.3	210.9	283.4
Q9VKQ3	Ribosome biogenesis protein WDR12 homolog OS=Drosophila melanogaster OX=7227 GN=CG6724 PE=2 S	21.261	12	4	4	4	420	47.2	5.38	14.46	4	0	986.2	364	545.6	565.6	413.4	392.7	287.9	300.4
Q8I937	Ribosome biogenesis regulatory protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG32409 PE=1 S	13.157	10	2	2	2	349	39.4	9.92	8.83	2	0	20.8	8.6	13.3	18.3	10.5	13.5	11.4	12.7
Q9VEB3	Ribosome production factor 2 homolog OS=Drosophila melanogaster OX=7227 GN=Non3 PE=2 SV=3	8.704	8	2	3	2	320	36.5	10.26	7.9	2	0	1330	489.8	575.1	521.1	532.5	579.2	352.3	349.1
Q9VCX4	Ribosome-releasing factor 2, mitochondrial OS=Drosophila melanogaster OX=7227 GN=EF-G2 PE=2 SV=3	46.207	14	7	9	7	740	81.9	6.02	31.89	7	0	451.6	264.3	883.8	699.1	150.2	225.5	362.5	368.8
Q9W3C1	RNA cytidine acetyltransferase OS=Drosophila melanogaster OX=7227 GN=l(1)G0020 PE=1 SV=2	36.441	9	7	8	7	1008	112.8	8.53	28.25	7	0	1633.9	518.5	571.5	731.7	607.2	662.6	417.6	483.7
Q9VX34	RNA helicase OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5800 PE=1 SV=2	8.278	3	2	2	2	826	92.8	6.83	6.02	2	0	234.2	82.7	124.4	160.9	86.9	111.3	105.1	142.2
Q9VLR5	RNA polymerase II transcriptional coactivator OS=Drosophila melanogaster OX=7227 GN=Ssb-c31a PE=2 S\	19.223	24	2	4	2	110	12.2	9.17	17.05	2	0	445.8	140.2	222.6	251.6	183.2	141.9	122.7	439.9
Q9W261	RNA polymerase-associated protein Rtf1 OS=Drosophila melanogaster OX=7227 GN=Rtf1 PE=1 SV=1	13.881	5	4	4	4	775	87.5	8.53	11.68	4	0	998.7	442.1	516.3	514.1	323.9	393.5	318.2	274.7
Q9W4D2	RNA-binding protein 4F OS=Drosophila melanogaster OX=7227 GN=Rnp4F PE=1 SV=1	14.32	4	3	3	3	941	106.7	5.11	8.99	3	0	1001.7	422.7	416.8	462.6	382.4	288.2	196.8	243
Q9V535	RNA-binding protein 8A OS=Drosophila melanogaster OX=7227 GN=tsu PE=1 SV=1	9.181	14	2	3	2	165	19	5.27	13.8	2	0	186.3	98.1	150.3	187.1	87.3	118.9	84.4	68.9
Q94901	RNA-binding protein lark OS=Drosophila melanogaster OX=7227 GN=lark PE=1 SV=1	15.693	12	6	7	6	352	39.9	9.07	15.44	6	0	1009.1	391	560.3	594.1	392.3	387.2	344.1	407.9
Q7KMJ6	RNA-binding protein spenito OS=Drosophila melanogaster OX=7227 GN=nito PE=1 SV=1	10.88	5	4	4	4	793	89	9.38	10.26	4	0	544.3	181.4	298.1	390.6	210.7	189.6	144.2	411.9
Q9W1V3	rRNA 2'-O-methyltransferase fibrillarin OS=Drosophila melanogaster OX=7227 GN=Fib PE=2 SV=1	28.48	12	3	10	3	344	34.6	10.29	35.57	3	0	1406	502.2	589.4	600.3	587.3	514.3	352.9	392.4
Q9VDT6	rRNA methyltransferase 2, mitochondrial OS=Drosophila melanogaster OX=7227 GN=CG11447 PE=2 SV=1	7.895	8	2	4	2	250	28.1	9.58	14.14	2	0	312	167.7	527.6	479.8	130	163.1	253.8	314
Q9VW14	rRNA methyltransferase 3, mitochondrial OS=Drosophila melanogaster OX=7227 GN=CG14100 PE=2 SV=1	29.575	14	4	9	4	407	45	8.56	28.64	4	0	306.4	173.8	577.9	479.4	127.3	172.6	254.4	328.1
Q9W1M9	Rrp4, isoform A OS=Drosophila melanogaster OX=7227 GN=Rrp4 PE=1 SV=1	36.498	24	5	7	5	298	33.6	6.19	30.77	5	0	391.6	197.2	272	340.3	170.3	154.5	130	175.5
Q9VFF3	Rrp6, isoform B OS=Drosophila melanogaster OX=7227 GN=Rrp6 PE=1 SV=3	5.97	3	2	2	2	900	102.9	9.25	5.43	2	0	57.1	26.8	68.3	74.7	32.3	42.3	40.9	81.4
Q7KVC2	RT07324p OS=Drosophila melanogaster OX=7227 GN=CG32318-PA PE=2 SV=1	7.987	12	2	2	1	164	18.7	8.69	5.71	2	0	291.9	132.6	165.6	261.9	119.6	58.5	52.3	133.8
Q9VH07	RuvB-like helicase 1 OS=Drosophila melanogaster OX=7227 GN=pont PE=1 SV=1	25.492	14	4	6	4	456	50.2	7.34	22.06	4	0	510.8	185.2	303.9	371.1	197	196.1	145.2	359.2
M9PFN1	RuvB-like helicase OS=Drosophila melanogaster OX=7227 GN=rept PE=3 SV=1	27.394	14	6	9	6	481	53.5	5.85	27.21	6	0	1524.8	607.2	823.1	1063.3	593.5	609.2	449.8	639.2
P40320	S-adenosylmethionine synthase OS=Drosophila melanogaster OX=7227 GN=Sam-S PE=2 SV=2	11.171	9	4	5	4	408	44.7	6.54	10.59	4	0	1433.2	519.8	685.4	708.9	499	495.5	383.9	612.1
Q7KSB5	S-formylglutathione hydrolase OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4390 PE=1 SV=1	10.902	9	2	2	2	330	36.3	6.58	6.71	2	0	131.8	57.4	98.2	87.5	54.2	54.3	54.9	42.6
M9MRM4	Sac1 phosphatase, isoform B OS=Drosophila melanogaster OX=7227 GN=Sac1 PE=4 SV=1	11.63	4	2	2	2	592	67.7	8.34	7.59	2	0	424.4	193.8	558.9	716.2	162.7	180.7	271.8	535.9
Q9V784	SAM50-like protein CG7639 OS=Drosophila melanogaster OX=7227 GN=CG7639 PE=2 SV=2	53.589	21	8	20	8	443	49	8.69	58.12	8	0	518.4	278.8	847.5	685.6	200	274.1	341.7	524.8
Q8IMV6	Scaffold attachment factor B, isoform B OS=Drosophila melanogaster OX=7227 GN=Saf-B PE=1 SV=2	19.73	7	7	10	7	928	102	7.47	27.57	7	0	3492.5	1557.9	1827.8	1620.5	1324.4	1688.1	1283.2	955
Q8T4G5	SD01613p OS=Drosophila melanogaster OX=7227 GN=DmCG6512 PE=1 SV=1	116.424	30	15	55	15	826	89.6	8.95	181.93	15	0	2152.4	1005.5	3467.6	3301.1	808.3	914.6	1549	3515.7
Q9VRJ4	SD02021p OS=Drosophila melanogaster OX=7227 GN=DHRS4 PE=1 SV=1	24.278	13	4	8	4	317	33.6	9.33	23.46	4	0	933.4	426.2	1425.6	1199	339.4	374	603.6	919.4
Q9W140	SD02086p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3548 PE=1 SV=1	24.421	11	5	7	5	453	50.4	6.43	20.04	5	0	1032.1	415.3	548.6	673.7	393.7	470.3	360.3	393.3
Q960D4	SD06560p OS=Drosophila melanogaster OX=7227 GN=EG:22E5.5 PE=1 SV=1	9.153	5	3	4	3	593	65	6.21	11.63	3	0	228.1	91.7	247.3	286.7	86.5	107.5	114.2	206.6
Q7K483	SD08549p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7943 PE=2 SV=1	8.772	8	2	4	2	332	37.3	9.69	12.54	2	0	49.5	28.1	117.8	114	17.8	30.3	58.5	101.3
Q9VAJ9	SD09259p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1907 PE=1 SV=1	26.536	19	6	11	6	317	34.6	9.79	32.75	6	0	635.1	321.2	2345.6	2108.6	231	206.6	931.8	1574.6
Q9VVI0	SD09427p OS=Drosophila melanogaster OX=7227 GN=U4-U6-60K PE=1 SV=1	12.256	9	4	4	4	553	61.5	6.21	11.93	4	0	367.2	170.1	305.8	438.8	171.6	177.1	151.1	263.9
Q7K1L4	SD10469p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8468 PE=1 SV=1	16.104	6	3	4	3	678	73.8	7.69	18.88	3	0	315.1	205.8	629.9	540.6	195	223.8	351.2	320.9
Q9VP50	SD17025p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7632 PE=1 SV=1	15.234	8	2	4	2	330	37.9	8.95	14.26	2	0	235.5	136	452.8	450	116.6	138.9	195.7	330
A1Z934	SD19268p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8778 PE=1 SV=1	31.681	21	6	14	6	299	31.9	8.22	35.63	6	0	813.8	389.8	1715.9	1520.9	216.9	249.3	631.2	1361
Q9VF85	SD21818p OS=Drosophila melanogaster OX=7227 GN=SerRS-m PE=1 SV=1	10.241	7	3	5	3	417	47.9	7.34	15.36	3	0	281.5	133.5	558.4	406.7	123.8	136.9	246.5	283
M9PDF2	Second mitotic wave missing, isoform C OS=Drosophila melanogaster OX=7227 GN=swm PE=1 SV=1	25.78	5	4	5	4	1063	115.8	9.26	20.31	4	0	806.5	311.8	392.1	441.8	300.7	268.3	219.4	221.4
A1Z7J7	Secretory 31, isoform A OS=Drosophila melanogaster OX=7227 GN=Sec31 PE=1 SV=1	11.808	3	3	3	3	1240	135.9	6.14	11.81	3	0	511.2	237.9	597.4	643.7	238.7	362.1	392.2	381.5
O18373	Selenide, water dikinase OS=Drosophila melanogaster OX=7227 GN=SelD PE=2 SV=1	21.618	15	5	8	5	398	43.4	6.93	23.8	5	0	1537.9	623.5	661.6	759.8	545.6	510.7	412.5	584.3
Q9VYB0	Selenoprotein BthD OS=Drosophila melanogaster OX=7227 GN=BthD PE=1 SV=5	19.249	24	4	5	4	249	27.8	9.74	13.41	4	0	1023.1	249.6	332.2	373.6	378.3	353.1	230.4	287.8
A0A0B4KHH2	Septin interacting protein 3, isoform B OS=Drosophila melanogaster OX=7227 GN=sip3 PE=1 SV=1	3.936	3	2	2	2	626	69.2	6.1	4.23	2	0	318	139.7	449.8	504.5	103.8	134.2	233.8	238.4
P42207	Septin-1 OS=Drosophila melanogaster OX=7227 GN=Sep1 PE=1 SV=1	20.001	19	4	5	4	361	41.1	6.55	18.38	4	0	234.3	112	240.5	291.8	92.5	129.1	126.5	210.2
X2J8R0	Septin-interacting protein 1 OS=Drosophila melanogaster OX=7227 GN=sip1 PE=3 SV=1	4.671	3	2	2	2	839	94.8	6.19	4.83	2	0	168.3	71.6	82.5	109.2	78.6	78.8	55	85.4
P07664	Serendipity locus protein delta OS=Drosophila melanogaster OX=7227 GN=Sry-delta PE=1 SV=2	6.482	4	2	2	2	433	50	5.06	5.4	2	0	53.9	25.2	53.1	68.4	28.7	38.6	33.3	49.6
Q9W457	Serine hydroxymethyltransferase OS=Drosophila melanogaster OX=7227 GN=Shmt PE=1 SV=1	46.446	16	10	16	10	537	58.8	9.04	45.91	10	0	1386.7	601.2	1804.5	1988.4	524.8	511.5	711.6	1878.1
Q9VFJ3	Serine protease HTRA2, mitochondrial OS=Drosophila melanogaster OX=7227 GN=HtrA2 PE=1 SV=1	24.84	19	5	6	5	422	46	9.48	22.32	5	0	668.3	244.2	963.2	723.7	239.3	260.6	398.8	674.8
Q95T19	Serine--tRNA synthetase-like protein Slimp OS=Drosophila melanogaster OX=7227 GN=Slimp PE=1 SV=1	6.555	4	2	2	2	464	52.9	7.75	5.47	2	0	76.5	35.1	117	134.8	36	40	54.4	427.8
P26686	Serine-arginine protein 55 OS=Drosophila melanogaster OX=7227 GN=B52 PE=1 SV=4	39.031	20	9	16	9	376	42.8	11.37	47.13	9	0	3349.6	1319.8	1732.6	1811.9	1267.2	1352.1	1142.2	1141.2
Q9VB23	Serine/threonine protein phosphatase 2A regulatory subunit OS=Drosophila melanogaster OX=7227 GN=wdl	7.293	4	2	2	2	524	59.7	7.49	6.14	2	0	119.6	49.2	108.9	134.7	49.1	32.3	52	91.9
P52304	Serine/threonine-protein kinase polo OS=Drosophila melanogaster OX=7227 GN=polo PE=1 SV=2	12.921	5	3	3	3	576	66.9	8.88	9.61	3	0	148.3	73.3	173	147.1	67.8	92.3	94.5	62.6
Q9W2U4	Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Drosophila melanogaster OX=7227 GN=PP	11.526	4	2	2	2	609	66.8	4.41	6.53	2	0	806	417.1	467.2	411.6	284.1	244.2	220.3	209.1
Q9VFS5	Serine/threonine-protein phosphatase 4 regulatory subunit 3 OS=Drosophila melanogaster OX=7227 GN=flfl	5.464	2	2	2	2	980	109.2	4.81	2.69	2	0	87.6	40.4	78.1	85.9	44.5	44.9	48.6	83.6

X2JDI1	Serine/threonine-protein phosphatase OS=Drosophila melanogaster OX=7227 GN=mts PE=3 SV=1	15.872	17	3	6	3	309	35.4	5.34	17.29	3	0	706.6	277.7	459.1	406.2	200.7	257.3	294.1	416.8
X2JG90	Serine/threonine-protein phosphatase OS=Drosophila melanogaster OX=7227 GN=Pp4-19C PE=3 SV=1	10.719	9	2	3	2	307	35.3	5.26	9.43	2	0	804.5	315.4	415.8	546	295.6	231.9	214	271.6
O46084	Serine/threonine-protein phosphatase Pgam5, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Pg	38.597	20	6	14	6	289	33.1	8.85	39.69	6	0	1107.8	630.2	2535.7	1616.2	290.5	530.8	1176.6	1016.4
Q94545	Set1/Ash2 histone methyltransferase complex subunit ASH2 OS=Drosophila melanogaster OX=7227 GN=ash	4.774	4	2	2	2	556	63.2	6.92	4.52	2	0	325	144.4	220.6	292.5	122.8	131.8	127.6	177.5
A4V3W1	Shaggy, isoform J OS=Drosophila melanogaster OX=7227 GN=sgg PE=1 SV=1	18.468	8	3	6	3	575	58.7	8.09	22.99	3	0	315.4	131.3	269.4	215.6	114.3	119.9	140.8	130.7
A4V4I8	Shibire, isoform F OS=Drosophila melanogaster OX=7227 GN=shi PE=1 SV=1	16.528	5	5	9	5	877	97.7	8.37	20.36	5	0	435.7	184.9	438.6	583.4	168.4	177.1	231.5	410.2
A1Z9J3	Short stop, isoform H OS=Drosophila melanogaster OX=7227 GN=shot PE=1 SV=1	40.012	1	11	12	11	8805	988.9	5.71	30.11	11	0	979.7	482.7	1004.2	987.8	386.6	500.5	567.2	461.4
Q9VN13	Sideroflexin OS=Drosophila melanogaster OX=7227 GN=Sfxn1-3 PE=1 SV=1	17.718	16	5	9	5	321	35.7	9.41	23.26	5	0	575.9	259.9	1188.9	974.8	199.1	241.2	530.4	695.5
Q9U5L1	Signal recognition particle receptor subunit alpha homolog OS=Drosophila melanogaster OX=7227 GN=Gtp-b	10.54	4	2	3	2	614	67.8	6.83	11.62	2	0	707.5	303.7	955.5	804.3	273.2	366.5	510.4	501.2
Q9VDK7	Signal recognition particle subunit SRP72 OS=Drosophila melanogaster OX=7227 GN=Srp72 PE=1 SV=1	13.688	7	3	4	3	650	72.8	9.06	10.08	3	0	253.6	108	282.2	287.3	112.3	165.1	161.6	162.1
A0A0B4KHS6	Signal transducer and activator of transcription OS=Drosophila melanogaster OX=7227 GN=Stat92E PE=3 S'	16.58	5	3	4	3	635	71.9	6.07	12.29	3	0	319.4	141.5	232.4	212.3	118.8	136	123.3	156.3
M9PET3	Simjang, isoform D OS=Drosophila melanogaster OX=7227 GN=simj PE=1 SV=1	13.178	4	3	3	3	924	96.6	9.77	8.9	3	0	978.8	415.4	654.2	789.9	336.1	364.2	358	493.2
A0A0B4LF93	Sin3A, isoform I OS=Drosophila melanogaster OX=7227 GN=Sin3A PE=1 SV=1	11.054	1	3	3	3	1747	186.3	7.23	9.66	3	0	1280.5	484.6	593.7	582.1	408	488.7	429.4	433.1
P54622	Single-stranded DNA-binding protein, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mtSSB PE=	47.085	40	6	73	6	146	16.4	9.85	186.56	6	0	3181.3	1670.8	6322.5	4351.1	1081.8	1387	2594.6	2256.5
Q05856	Small nuclear ribonucleoprotein-associated protein B OS=Drosophila melanogaster OX=7227 GN=SmB PE=1	19.178	14	2	7	2	199	21	11.22	32.18	2	0	726.6	222.6	433.2	569.9	265.4	226.5	200.2	506.6
M9PC89	Small ribonucleoprotein particle U1 subunit 70K, isoform C OS=Drosophila melanogaster OX=7227 GN=snRN	17.86	13	6	6	6	448	52.9	10.04	20.28	6	0	2789.4	1038.2	1270.5	1476.9	879.7	1064.6	796.3	997.5
O97102	Small ubiquitin-related modifier OS=Drosophila melanogaster OX=7227 GN=smt3 PE=1 SV=1	6.706	19	2	3	2	90	10.1	5.45	5.75	2	0	175.8	82.3	94	169.4	76.7	77.4	49	197.8
Q9VS62	Smallminded, isoform A OS=Drosophila melanogaster OX=7227 GN=smid PE=1 SV=1	18.397	7	4	4	4	944	104.3	5.44	13.33	4	0	443.3	206.7	223.8	281.9	209.3	213.2	184	189.5
P13607	Sodium/potassium-transporting ATPase subunit alpha OS=Drosophila melanogaster OX=7227 GN=Atpalpha	52.283	10	8	10	8	1041	115.5	5.69	34.67	8	0	410	306.9	694.5	682.2	273	278	394.5	479.1
Q9XZ21	Something that sticks like glue, isoform A OS=Drosophila melanogaster OX=7227 GN=snama PE=1 SV=1	5.953	2	2	2	2	1231	139	9.73	2.98	2	0	93.8	49	100.4	94.2	42.4	46.1	44.6	80.2
M9PF16	Spectrin beta chain OS=Drosophila melanogaster OX=7227 GN=beta-Spec PE=3 SV=1	29.912	3	7	7	7	2308	267.5	5.33	24.6	7	0	1291.1	577.9	1252.5	1371.2	480.9	582	744.8	749.8
M9ND86	Spellchecker1, isoform D OS=Drosophila melanogaster OX=7227 GN=spel1 PE=1 SV=1	16.222	6	6	6	6	917	103.2	5.92	12.45	6	0	1338.7	624.8	552.8	687.7	633.6	356.6	178.4	240.9
Q9V7Y2	Sphingosine-1-phosphate lyase OS=Drosophila melanogaster OX=7227 GN=Sply PE=1 SV=1	33.523	12	5	7	5	545	60.3	8.46	24.16	5	0	1084.6	655.3	2628.7	1548.8	387	568.4	1216.3	821.7
A0A0B4KGU8	Splicing factor 1, isoform C OS=Drosophila melanogaster OX=7227 GN=SF1 PE=1 SV=1	8.949	6	3	3	3	323	37.6	11.14	8.49	3	0	723.3	340	391.3	469.2	290.6	274.2	231.4	282.3
O46106	Splicing factor 3A subunit 3 OS=Drosophila melanogaster OX=7227 GN=noi PE=1 SV=1	12.683	8	2	3	2	503	58.4	5.62	10.79	2	0	125.2	68.1	117.2	109	62	65.7	47.8	59.3
Q9VPR5	Splicing factor 3b subunit 1, isoform A OS=Drosophila melanogaster OX=7227 GN=Sf3b1 PE=1 SV=2	6.85	2	2	2	2	1340	149.5	6.67	5.56	2	0	352.5	165.7	233.6	262.3	151	154.9	138.8	240.4
Q9W0M7	Splicing factor 3B subunit 3 OS=Drosophila melanogaster OX=7227 GN=Sf3b3 PE=1 SV=2	62.792	15	15	19	15	1227	136.5	5.47	54.78	15	0	1996.5	922.9	1386.7	1692.1	788.4	895.3	831.1	1067.7
Q9VRV7	Splicing factor 3B subunit 6 OS=Drosophila melanogaster OX=7227 GN=Sf3b6 PE=1 SV=1	4.914	18	2	2	2	121	14.2	9.32	4.83	2	0	126.8	41.2	124.1	125.1	57.3	64.9	77.6	79.9
A0A0B4K6U6	Squid, isoform E OS=Drosophila melanogaster OX=7227 GN=sqd PE=4 SV=1	14.37	13	3	10	3	308	33	6.96	28.06	3	0	2401.4	597.6	814.7	773.7	523.1	584.7	535.7	625.2
Q9V3H7	SR-Cl OS=Drosophila melanogaster OX=7227 GN=Sr-Cl PE=4 SV=1	14.391	6	3	6	3	629	69.9	7.36	20.26	3	0	865.8	611.4	1326.3	1309.7	468.3	635.6	713	593.4
M9PHZ3	Ssu72 CTD phosphatase, isoform B OS=Drosophila melanogaster OX=7227 GN=Ssu72 PE=1 SV=1	13.846	10	2	5	2	194	22.6	5.26	14.9	2	0	50.8	37.6	37.6	40	25.1	30.3	20	34
Q9W0S7	Staphylococcal nuclease domain-containing protein 1 OS=Drosophila melanogaster OX=7227 GN=Tudor-SN	78.488	19	13	15	13	926	103	8.05	53.1	13	0	1553.7	689.6	1899.8	1909.8	670.5	773.1	1035.8	1303.5
Q9W179	Sterile20-like kinase, isoform B OS=Drosophila melanogaster OX=7227 GN=Slik PE=1 SV=2	21.193	4	5	5	5	1703	192	6.62	16.35	5	0	673.8	322.6	832.4	876.6	232.6	318.5	449.2	403.4
P83094	Stromal interaction molecule homolog OS=Drosophila melanogaster OX=7227 GN=Stim PE=1 SV=1	9.634	6	3	4	3	570	64.8	6.43	8.96	3	0	244.8	113.7	294.8	236.3	120.2	115.1	150.6	150.8
Q9VCB8	Structural maintenance of chromosomes protein 6 OS=Drosophila melanogaster OX=7227 GN=jnj PE=1 SV=	9.378	2	2	2	2	1122	129.3	8.32	7.31	2	0	144	53.7	89.6	119.9	73.1	65.3	51.6	82.8
Q9V3A7	Structural maintenance of chromosomes protein OS=Drosophila melanogaster OX=7227 GN=glu PE=1 SV=1	73.79	10	11	17	11	1409	159.8	6.15	71.57	11	0	2020.5	824	1222.1	1329.7	866.5	871.8	737	775.2
Q9VCD8	Structural maintenance of chromosomes protein OS=Drosophila melanogaster OX=7227 GN=SMC1 PE=1 SV	40.625	9	9	11	9	1238	142.8	6.73	31.35	9	0	1719.7	687.2	718.1	959.1	661.7	934.8	515	530.5
Q7KK96	Structural maintenance of chromosomes protein OS=Drosophila melanogaster OX=7227 GN=SMC2 PE=1 SV	36.858	8	9	12	9	1179	134.3	8.18	37.32	9	0	3827	1460.1	1643.7	1583.8	1408.4	1480.9	1146.9	986.7
Q9VXE9	Structural maintenance of chromosomes protein OS=Drosophila melanogaster OX=7227 GN=SMC3 PE=1 SV	28.206	5	6	6	6	1200	139.9	8.1	19.54	6	0	852.8	340.6	397.2	422.7	379.7	437.9	252.2	258.9
A1Z9S6	Su(Var)2-HP2, isoform A OS=Drosophila melanogaster OX=7227 GN=Su(var)2-HP2 PE=1 SV=1	43.416	4	10	12	10	3257	355.8	6.14	39.41	10	0	3017.6	1342.7	1644.4	2262.7	1287.5	1311.7	828	1224
Q94523	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Drosophila melanogaster OX=	208.574	36	16	84	16	661	72.3	7.12	318.18	16	0	2994.2	1670.6	5937.8	5509.5	1454.7	1566.8	2613.8	4958.2
P21914	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Drosophila melanogaster OX=7	17.209	15	5	10	5	297	33.7	8.66	23.76	5	0	753.7	445.5	1859.2	1433.6	290.5	373.9	806.1	1183.2
Q8SZ16	Succinate dehydrogenase assembly factor 3, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Sdh	16.612	25	3	6	3	120	13.9	9.07	16.57	3	0	451.2	205.7	557.4	526	218	250.5	314.1	521.6
A0A0B4JCW4	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Drosophila melanogaster OX=7227 GN	111.217	34	12	63	12	451	49	6.83	213.44	12	0	4373.4	2179.6	7338	5990.9	1746.5	1858.1	3234.6	4806.9
Q94522	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Drosophila melanogaster OX=72	9.569	7	2	7	2	328	34.4	8.98	13.26	2	0	424.5	204.1	753.2	880.9	109.3	106.6	299.6	505.2
Q9V470	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Drosophila melanogaster OX=7227 GN	40.084	19	8	17	8	416	45	6.01	50.72	8	0	1752.6	1148.5	4056.9	2913	670.7	1046.3	1675.1	1628.4
Q9W058	Succinyl-CoA:3-ketoacid-coenzyme A transferase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=	77.486	32	10	25	10	516	54.9	8.37	82.74	10	0	1426.8	657.5	2232.6	1950	565.5	650.6	941.7	1887.7
Q9VG33	Sulfurtransferase OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12279 PE=1 SV=2	14.128	35	3	3	3	110	12.1	5.21	10.66	3	0	380	158.1	331.5	353.5	149.2	158.4	156.2	179.5
A1Z850	Superoxide dismutase [Cu-Zn] OS=Drosophila melanogaster OX=7227 GN=Ccs PE=1 SV=2	11.92	10	2	2	2	258	27.2	5.86	8.96	2	0	85	41.8	95	87.8	39.4	35.8	38.6	37.5
M9PF91	Superoxide dismutase [Cu-Zn] OS=Drosophila melanogaster OX=7227 GN=Sod1 PE=3 SV=1	8.963	11	2	3	2	167	17.4	6.6	9.91	2	0	764.8	354.8	499.7	481.6	304.7	317	263.6	323
A0A0B4LGQ1	Superoxide dismutase OS=Drosophila melanogaster OX=7227 GN=Sod2 PE=3 SV=1	10.225	14	2	4	2	217	24.6	7.93	14.41	2	0	212.1	91.3	304	247.7	82.5	64.3	121.7	643.8
A0A0B4K6W1	Suppressor of hairy wing, isoform C OS=Drosophila melanogaster OX=7227 GN=su(Hw) PE=4 SV=1	15.452	4	3	4	3	941	105.7	6.71	12.45	3	0	1017	311.9	333.7	427.9	378.7	374.9	221	339.1
A0A0B4JD33	Suppressor of variegation 2-10, isoform L OS=Drosophila melanogaster OX=7227 GN=Su(var)2-10 PE=1 SV	12.995	7	2	2	2	584	64.6	7.09	7.76	2	0	99.7	49.6	95.3	101.6	49.6	47.9	43.1	62
Q9U4F3	SURF1-like protein OS=Drosophila melanogaster OX=7227 GN=Surf1 PE=2 SV=1	19.371	16	2	2	2	300	34	9.99	9.7	2	0	108.8	68.9	285	195.7	53.5	61.3	111.3	95.6
O18405	Surfeit locus protein 4 homolog OS=Drosophila melanogaster OX=7227 GN=Surf4 PE=2 SV=1	10.532	4	2	3	2	270	30.5	8.97	10.37	2	0	470.5	293.8	591.9	505.5	162.9	329.7	349.2	371.1
Q9VL72	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H bo	13.941	4	3	3	3	844	95.4	8.16	10.23	3	0	1101	407.5	402.3	514.1	392.9	409.2	249.8	297.9
Q9VH76	Synaptosomal-associated protein OS=Drosophila melanogaster OX=7227 GN=Snap24 PE=1 SV=1	14.534	13	2	2	2	212	23.5	4.79	8.58	2	0	75.5	59.9	178.7	174.2	37.2	44.9	90.7	53.2
Q9VK69	T-complex protein 1 subunit delta OS=Drosophila melanogaster OX=7227 GN=CCT4 PE=1 SV=1	46.349	17	7	12	7	533	57.1	7.56	42.95	7	0	1133.7	526.9	1196.4	1563.5	388.9	518.7	627.6	833.6
A1Z8U4	T-complex protein 1 subunit epsilon OS=Drosophila melanogaster OX=7227 GN=CCT5 PE=1 SV=1	27.642	13	7	12	7	512	55.8	6.13	33.03	7	0	1959.6	705.1	1331.6	1318.2	612.8	776.9	785.4	1266.8
Q9VHL2	T-complex protein 1 subunit eta OS=Drosophila melanogaster OX=7227 GN=CCT7 PE=1 SV=2	7.54	3	2	4	2	544	59.3	6.34	12.11	2	0	987.7	385.9	807.9	1146.4	324.6	388.4	404	1336.1
A4V303	T-complex protein 1 subunit gamma OS=Drosophila melanogaster OX=7227 GN=CCT3 PE=1 SV=1	47.919	15	8	15	8	544	59.4	6.8	51.44	8	0	1164.6	482.2	1082.8	1193.2	372.1	499.2	594.2	861.8
Q9VM58	TA01441p OS=Drosophila melanogaster OX=7227 GN=Hmgcl PE=1 SV=2	32.402	24	6	10	6	323	34.2	8.4	28.94	6	0	801.5	426.8	1488.8	1093.8	294.3	370.5	621.2	919.4
Q9VH72	TA01656p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9471 PE=1 SV=1	12.213	13	2	3	2	204	22.7	7.49	11.62	2	0	108.3	58.1	120.1	144.4	72.9	72.9	59.6	177.8
Q9XZ34	Telomere-associated protein RIF1 OS=Drosophila melanogaster OX=7227 GN=Rif1 PE=1 SV=1	21.662	5	5	5	5	1416	156.7	6.65	18.83	5	0	880.5	361.6	441	595.4	425.9	289.9	192.6	300.3
Q9VI58	Terminal uridylyltransferase Tailor OS=Drosophila melanogaster OX=7227 GN=Tailor PE=1 SV=1	9.99	5	2	3	2	560	63.9	8.94	10.28	2	0	29.8	16.9	40.3	52.4	20.4	15	27.3	29.9
M9NDL5	Terribly reduced optic lobes, isoform AF OS=Drosophila melanogaster OX=7227 GN=trol PE=1 SV=2	49.132	3	12	14	12	4434	491.4	4.86	48.6	12	0	795.6	484	2854.8	3284	307.2	322.6	1206.5	1295.2
Q9VYV3	Thioredoxin domain-containing protein 5 homolog OS=Drosophila melanogaster OX=7227 GN=prtp PE=1 SV	19.905	13	5	5	5	416	46.6	5.27	16.23	5	0	418	222	1225.4	996.3	141	179.7	580.5	410
X2JF59	Thioredoxin peroxidase 1, isoform C OS=Drosophila melanogaster OX=7227 GN=Jafrac1 PE=1 SV=1	32.992	26	6	47	6	194	21.7	5.71	84.63	6	0	4211.9	1733.3	4309.1	5042	1682.1	1766.3	2130.7	2838.2
P91938	Thioredoxin reductase 1, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Trxr-1 PE=1 SV=2	76.977	15	9	21	9	596	64.3	7.91	73.95	9	0	1055.9	534.3	1305.4	1681.1	453	447.4	640.4	1341.9
Q9V429	Thioredoxin-2 OS=Drosophila melanogaster OX=7227 GN=Trx-2 PE=1 SV=3	9.478	18	2	3	2	106	11.7	4.88	8.93	2	0	650.7	176.2	271.1	247.3	228.3	170.1	145.1	218.4
Q7JW12	Thioredoxin-related transmembrane protein 2 homolog OS=Drosophila melanogaster OX=7227 GN=CG11007	7.031	7	2	2	2	271	31.3	8.95	6.17	2	0	126.3	70.2	186	180.2	62.3	89.3	73.2	71
Q9W1F4	THO complex subunit 5 OS=Drosophila melanogaster OX=7227 GN=thoc5 PE=1 SV=2	8.117	3	2	2	2	616	70.8	8.44	6.33	2	0	323.7	154.7	231.3	347.1	102.4	140.3	147.4	207.8
Q8IP94	Threonyl-tRNA synthetase, isoform B OS=Drosophila melanogaster OX=7227 GN=ThrRS PE=1 SV=1	38.124	9	6	10	6	690	79.3	6.9	35.57	6	0	1251.6	537	1475.7	1346.7	484.7	455.3	641.3	984.9
Q9VMD9	Tiggrin OS=Drosophila melanogaster OX=7227 GN=Tig PE=1 SV=2	8.207	1	3	3	3	2188	257.3	5.96	7.46	3	0	386.7	193.6	1045.7	1291.9	143	194.8	478	427.2
Q8INH7	Timeout OS=Drosophila melanogaster OX=7227 GN=timeout PE=1 SV=2	45.614	10	10	10	10	1384	159.3	5.16	33.45	10	0	1409.4	778.5	1006.9	1068	516.9	463.1	348.4	466.9
Q8IRT7	Tousled-like kinase, isoform C OS=Drosophila melanogaster OX=7227 GN=Tlk PE=1 SV=4	12.673	3	4	5	4	1254	135.4	8.94	14.53	4	0	868.6	452.1	651.1	797.3	328.3	207.7	212	335
A0A0B4KFE3	Toutatis, isoform F OS=Drosophila melanogaster OX=7227 GN=tou PE=1 SV=1	12.123	1	3	3	3	3058	328	6.51	10.93	3	0	317.7	156.9	246.9	299.3	152.4	154.7	131.5	169.9
M9PFF9	Trailer hitch, isoform D OS=Drosophila melanogaster OX=7227 GN=tral PE=1 SV=1	43.715	14	7	12	7	646	68.7	9.54	47.92	7	0	637.3	528.7	934	1000.6	287.7	372.4	517.5	412
Q9V460	Transcription elongation factor SPT5 OS=Drosophila melanogaster OX=7227 GN=Spt5 PE=1 SV=1	32.279	7	6	13	6	1078	119.4	6.25	50.08	6	0	1416.3	561.2	863.2	1002.2	559.2	617.8	473.8	679.4
N0D8I3	Transcription elongation factor spt6 OS=Drosophila melanogaster OX=7227 GN=Spt6 PE=1 SV=1	30.514	4	6	6	6	1831	208.5	5.31	23.03	6	0	966.3	373.3	492.3	580.9	362.5	384.3	292.1	340.2
Q7KM15	Transcription factor BTF3 OS=Drosophila melanogaster OX=7227 GN=bic PE=1 SV=1	26.899	25	2	3	2	169	17.7	7.49	13.63	2	0	55.1	20.7	48	35.1	20.3	21.2	37.2	20.9
Q24318	Transcription factor Dp OS=Drosophila melanogaster OX=7227 GN=Dp PE=1 SV=2	12.038	8	2	2	2	445	49.7	6.76	6.98	2	0	228.6	107.2	134.6	171.1	91.7	126	85.5	96.6
O77051	Transcription factor E2F2 OS=Drosophila melanogaster OX=7227 GN=E2f2 PE=1 SV=1	5.934	5	2	2	2	370	41.4	5.21	4.63	2	0	148.8	49.6	55	65.5	60.7	67.3	39.2	36.3
P52654	Transcription initiation factor IIA subunit 1 OS=Drosophila melanogaster OX=7227 GN=TfIIA-L PE=1 SV=2	16.478	9	2	2	2	366	39.2	4.73	9.06	2	0	287.2	130.3	207	302.1	109.9	115.2	121.8	211.6
P29052	Transcription initiation factor IIB OS=Drosophila melanogaster OX=7227 GN=TfIIB PE=2 SV=1	6.777	6	2	3	2	315	34.3	8.29	7.21	2	0	320.9	174.9	253.6	252.3	174.9	193.2	148.5	189.6
Q24325	Transcription initiation factor TFIID subunit 2 OS=Drosophila melanogaster OX=7227 GN=Taf2 PE=1 SV=2	12.269	4	3	3	3	1221	139.4	7.23	8.49	3	0	104.6	45.8	98	107	44.9	50.6	59.6	84.3
Q9VWY6	Transcription initiation factor TFIID subunit 8 OS=Drosophila melanogaster OX=7227 GN=Taf8 PE=1 SV=1	5.924	7	2	2	2	328	36.6	5.57	6.79	2	0	134.8	61.8	75	96.5	59.9	63.6	51	48
Q9VPD5	Transcription termination factor 3, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mTerf3 PE=2 S\	11.852	10	4	4	4	354	41.2	9.19	9.85	4	0	336.8	175.6	532.2	531.8	225.4	204.8	300.3	354.1
Q9VEB4	Transcription termination factor 5, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mTerf5 PE=1 S\	57.473	16	11	17	11	560	64.8	9.03	62.54	11	0	1060.2	596.4	2245.7	1881.7	489.5	600.3	965	1680.4
Q9V3F3	Transcription termination factor, mitochondrial OS=Drosophila melanogaster OX=7227 GN=mTTF PE=2 SV=1	49.523	21	9	17	9	410	48.3	9.58	55.18	9	0	884.5	449.5	1512	1233.5	389.2	460.8	667.4	1227.8
Q9GQN5	Transcriptional regulator ATRX homolog OS=Drosophila melanogaster OX=7227 GN=XNP PE=1 SV=2	12.258	1	3	3	3	1311	148.1	8.44	10.13	3	0	861.6	379.5	383.8	441.9	346.6	362.8	212.1	251.9
A0A0B4JD97	Transforming acidic coiled-coil protein, isoform K OS=Drosophila melanogaster OX=7227 GN=tacc PE=1 SV=	8.479	1	2	2	2	1322	147.1	4.98	5.92	2	0	243.6	114.9	303.7	270.4	80.4	128.4	183.3	128.6
Q9VZI1	Transgelin OS=Drosophila melanogaster OX=7227 GN=Chd64 PE=1 SV=2	39.521	44	6	11	6	188	20.6	8.43	36.28	6	0	1494.3	518.7	913	1019.8	491.8	479.3	503.1	1154.9
Q7KN62	Transitional endoplasmic reticulum ATPase TER94 OS=Drosophila melanogaster OX=7227 GN=TER94 PE=1	61.118	14	12	24	12	801	88.8	5.35	83.73	12	0	5032.3	2422.8	3630.2	3626.2	1809.8	1629.4	1650.9	2269.1
Q9VRH6	Translation factor waclaw, mitochondrial OS=Drosophila melanogaster OX=7227 GN=waw PE=3 SV=2	83.694	24	16	22	16	696	77.9	9.31	72.42	16	0	1090.8	611	2331.9	2045.9	441.4	604.3	1036.6	1833.5
Q9VGS2	Translationally-controlled tumor protein homolog OS=Drosophila melanogaster OX=7227 GN=Tctp PE=1 SV=	28.001	38	4	8	4	172	19.6	4.81	31.48	4	0	551.8	182.6	286.1	277	193.2	189.9	138.8	437.5
Q7PLT4	Translocase of the inner mitochondrial membrane 17b, isoform A OS=Drosophila melanogaster OX=7227 GN	19.505	27	3	9	3	173	18.2	8.18	38.31	3	0	302.5	165.1	570.7	458.3	157.5	183.3	233.6	334.4
Q9VUZ0	Translocon-associated protein subunit beta OS=Drosophila melanogaster OX=7227 GN=SsRbeta PE=1 SV=	25.033	32	3	4	3	190	21.2	8.72	21.52	3	0	251.7	118.6	386	390	86.2	132.1	191.3	202.6
Q9V3N6	Transmembrane 9 superfamily member OS=Drosophila melanogaster OX=7227 GN=TM9SF4 PE=1 SV=1	8.023	4	2	3	2	630	72.5	8.73	10.67	2	0	136.9	116.6	262.9	275.7	72.8	88.6	131.7	127.2
Q8SXY6	Transmembrane emp24 domain-containing protein bai OS=Drosophila melanogaster OX=7227 GN=bai PE=2	7.852	10	2	2	2	206	23.7	8.22	5.05	2	0	41.4	22.1	51.9	68.9	12.8	36.8	27.4	34.9
Q7YU24	Transmembrane GTPase Marf OS=Drosophila melanogaster OX=7227 GN=Marf PE=1 SV=1	25.838	12	8	8	8	810	91.3	6.71	20.91	8	0	697	400.8	957.7	824.4	210.9	357.9	453.6	505.2
Q95SS8	Transmembrane protein 70 homolog, mitochondrial OS=Drosophila melanogaster OX=7227 GN=CG7506 PE	8.107	5	2	2	2	236	26.6	9.33	6.32	2	0	279.3	187.5	1135.4	563.9	71.3	129.1	538.6	163.5
Q9VMA7	Transport and Golgi organization protein 1 OS=Drosophila melanogaster OX=7227 GN=Tango1 PE=1 SV=2	4.348	1	2	2	2	1430	159	4.73	3.35	2	0	240.1	97.9	226.1	236.9	116.8	133.5	152.9	129.7
X2J516	Trifunctional purine biosynthetic protein adenosine-3 OS=Drosophila melanogaster OX=7227 GN=Gart PE=1	7.924	1	2	2	2	1353	144.4	7.21	5.98	2	0	396	205.2	382.7	454	194.7	234.8	236.1	240.5
P29613	Triosephosphate isomerase OS=Drosophila melanogaster OX=7227 GN=Tpi PE=1 SV=3	9.784	11	2	3	2	247	26.6	6	10.7	2	0	258	94.6	422.4	452.5	116.8	127.5	218.5	411.9
A0A0B4LGC0	Tripeptidyl-peptidase II, isoform F OS=Drosophila melanogaster OX=7227 GN=TppII PE=4 SV=1	29.523	6	8	9	8	1354	148.8	6.99	22.37	8	0	850.9	419.1	1169.2	970	309.9	348.4	576.7	473
Q8MS69	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 OS=Drosophila melanogaster OX=722	16.346	7	3	5	3	444	49.9	6.64	15.88	3	0	713.1	341	541.3	690.3	299.6	274.4	243	352.8
Q9W4M9	tRNA (cytosine(34)-C(5))-methyltransferase OS=Drosophila melanogaster OX=7227 GN=Nsun2 PE=2 SV=1	14.299	6	4	4	4	746	84.1	6.83	10.77	4	0	473.1	216	277	378.1	222.6	190.5	168.3	259.7
O77263	tRNA (guanine-N(7)-)-methyltransferase OS=Drosophila melanogaster OX=7227 GN=CG4045 PE=2 SV=1	16.794	9	2	3	2	256	29.4	7.91	9.92	2	0	1303.7	527.8	599.1	531.7	480	507.7	379	263.9
Q8IRE4	tRNA (guanine(37)-N1)-methyltransferase OS=Drosophila melanogaster OX=7227 GN=CG32281 PE=2 SV=2	16.67	10	4	4	4	457	53	8.43	13.08	4	0	598	319.3	762.8	665.6	225	289.1	367.9	390.3
E1JIR1	tRNA pseudouridine synthase OS=Drosophila melanogaster OX=7227 GN=Pus1 PE=3 SV=1	14.212	7	3	4	3	442	51	8.02	14.28	3	0	687.8	364.4	867.2	625.1	279.8	345.3	449.8	379.5
A0A0B4K661	Tropomyosin 1, isoform Q OS=Drosophila melanogaster OX=7227 GN=Tm1 PE=1 SV=1	40.009	24	9	14	6	250	29.2	4.87	40.76	9	3	1476.2	702.2	1485.1	1783.2	591.4	713.4	769.5	959.4
Q9W0Y1	Troponin C-akin-1 protein OS=Drosophila melanogaster OX=7227 GN=Tina-1 PE=2 SV=1	19.387	15	2	7	2	167	19	7.44	21.51	2	0	134.2	71.7	184.7	171.2	53.7	73.4	80.6	98.8
P06605	Tubulin alpha-3 chain OS=Drosophila melanogaster OX=7227 GN=alphaTub84D PE=2 SV=1	71.975	26	9	34	9	450	49.9	5.14	112.42	9	0	1894.9	865.8	2002.9	1966.6	723.3	910.4	1104.8	1210.6
A0A0B4LGH1	Tubulin beta chain OS=Drosophila melanogaster OX=7227 GN=betaTub60D PE=1 SV=1	27.723	14	5	10	1	453	50.7	4.88	25.51	5	3	297.3	178.1	412.5	512.4	128.4	169.1	264	225.7
Q9VAX7	Tubulin beta chain OS=Drosophila melanogaster OX=7227 GN=betaTub97EF PE=1 SV=3	16.788	8	3	7	2	457	51.3	4.83	24.71	3	0	373.2	181.8	427.7	522.4	166	191.4	238	352.2
Q24560	Tubulin beta-1 chain OS=Drosophila melanogaster OX=7227 GN=betaTub56D PE=1 SV=2	54.698	22	7	23	5	447	50.1	4.86	75.7	7	2	1265.2	584	1589	1798.2	484.7	660.1	817.9	1412.7
P08841	Tubulin beta-3 chain OS=Drosophila melanogaster OX=7227 GN=betaTub60D PE=2 SV=2	30.539	14	5	11	1	454	50.8	4.88	28.18	5	0	147.2	92.2	260.2	286.7	66.1	97.4	115.6	143.6
P23257	Tubulin gamma-1 chain OS=Drosophila melanogaster OX=7227 GN=gammaTub23C PE=1 SV=2	29.048	8	3	6	3	475	53.3	5.94	22.71	3	0	707	314.5	778.5	818	315.7	533.2	669.9	830.9
Q9VQ91	Tudor and KH domain-containing protein homolog OS=Drosophila melanogaster OX=7227 GN=papi PE=1 S\	33.96	22	8	9	8	576	63.8	6.3	26.46	8	0	148.8	85.6	217.1	215.2	59.9	87.8	100	185.8

Q9VVA7	Tumor suppressor protein 101 OS=Drosophila melanogaster OX=7227 GN=TSG101 PE=1 SV=2	13.796	9	2	2	2	408	45.2	6.37	6.73	2	0	192.5	73.1	98.6	137.6	85.1	78.9	53.5	89.7
Q9W0G1	Tyrosine-protein phosphatase non-receptor type 61F OS=Drosophila melanogaster OX=7227 GN=Ptp61F PE	14.36	5	2	4	2	548	62.1	5.55	13.58	2	0	653.2	312.9	556.5	684.8	253	310.6	279.2	347.2
M9PDU3	U-shaped, isoform D OS=Drosophila melanogaster OX=7227 GN=ush PE=1 SV=1	7.754	2	2	3	2	1175	122.8	6.52	9.06	2	0	872	395.8	483.7	654.7	359.5	351.9	297	427.9
P43332	U1 small nuclear ribonucleoprotein A OS=Drosophila melanogaster OX=7227 GN=snf PE=1 SV=1	7.207	8	2	3	2	216	24.5	9.64	7.98	2	0	903.8	244.6	425.8	441.2	259.8	242.2	219.1	616.4
M9PBM1	U2 small nuclear riboprotein auxiliary factor 38, isoform B OS=Drosophila melanogaster OX=7227 GN=U2af38	18.272	7	2	2	2	264	29.9	8.91	9.77	2	0	1264.1	502.4	474.1	484.8	566.5	373.6	260.8	277.8
Q9VMQ5	Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial OS=Drosophila melanogaster OX=7227 GN=	17.901	8	3	4	3	477	52	7.33	13.07	3	0	345.9	165.6	613.7	462.7	94.7	121.5	284.8	288.6
Q8MKN0	Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Coq9 PE=	11.044	6	2	2	2	326	36.3	7.91	7.75	2	0	184	102.3	491.1	339.2	64	58.6	194.5	195.6
Q9W462	Ubiquitin carboxyl-terminal hydrolase 30 homolog OS=Drosophila melanogaster OX=7227 GN=Usp30 PE=2 S	28.076	9	4	9	4	558	60.8	7.34	25.09	4	0	139.1	110.2	282.3	222.2	46.8	113.3	129	103
Q9VYQ8	Ubiquitin carboxyl-terminal hydrolase 7 OS=Drosophila melanogaster OX=7227 GN=Usp7 PE=1 SV=1	10.944	5	4	4	4	1129	130.4	6.04	9.34	4	0	622.7	278.5	475.8	525.3	290.5	288.5	346.4	445.2
Q9VWN5	Ubiquitin carboxyl-terminal hydrolase MINDY-3 homolog OS=Drosophila melanogaster OX=7227 GN=mindy3 I	12.183	4	2	3	2	560	61.7	5.92	10.44	2	0	499.8	220.2	317.3	290.2	184.3	204.5	178.8	146.6
Q9VZU7	Ubiquitin carboxyl-terminal hydrolase OS=Drosophila melanogaster OX=7227 GN=Usp5 PE=1 SV=1	25.332	9	5	6	5	827	92	5.49	19.2	5	0	278.6	171.9	190.8	210.4	142.1	166.8	97.5	177.1
M9PBW0	Ubiquitin conjugating enzyme E2M, isoform B OS=Drosophila melanogaster OX=7227 GN=UbcE2M PE=3 SV	7.828	6	2	2	2	181	20.7	7.15	6.12	2	0	384.3	162.6	218.9	249.9	155	148.4	108.5	173.9
P15357	Ubiquitin-40S ribosomal protein S27a OS=Drosophila melanogaster OX=7227 GN=RpS27A PE=1 SV=2	47.464	44	7	37	7	156	17.9	9.77	96.27	7	0	14055.5	4347.6	4439.2	6955.4	5210	6857.4	3620.3	6919.9
P35128	Ubiquitin-conjugating enzyme E2 N OS=Drosophila melanogaster OX=7227 GN=ben PE=1 SV=1	6.923	18	2	2	2	151	17.2	5.6	6.06	2	0	239.3	107.7	184.4	222.4	105	108.3	93.8	117.4
M9ND19	UDP-galactose 4'-epimerase, isoform B OS=Drosophila melanogaster OX=7227 GN=Gale PE=1 SV=1	37.377	22	8	13	8	350	38.7	7.46	35.31	8	0	1845.9	656.4	1171	1700.8	629.6	615.6	573.3	1948.6
O02373	UDP-glucose 6-dehydrogenase OS=Drosophila melanogaster OX=7227 GN=sgl PE=1 SV=1	16.105	14	4	4	4	476	52.8	6.18	11.07	4	0	139.5	74.4	137.3	147.7	48.4	59.3	65.1	81
Q09332	UDP-glucose:glycoprotein glucosyltransferase OS=Drosophila melanogaster OX=7227 GN=Ugt PE=1 SV=2	48.801	11	13	17	13	1548	174.2	6.15	43.93	13	0	726.4	414.2	1985	2053.3	259.7	277.3	934.7	941
M9PGS2	Ultraspiracle, isoform B OS=Drosophila melanogaster OX=7227 GN=usp PE=3 SV=1	4.092	4	3	3	3	508	55.2	8	4.18	3	0	664.3	230	363.6	488.2	251.5	188.9	199.6	393.6
Q9VBI2	UMP-CMP kinase OS=Drosophila melanogaster OX=7227 GN=Dak1 PE=1 SV=1	46.234	29	8	20	8	253	27.8	8	50.95	8	0	1842.4	691.6	1704.6	1317.1	647.6	617.7	873.3	935.4
Q9W3R8	Uncharacterized protein CG2059 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2059 PE=1 SV=1	15.214	9	3	5	3	308	35.4	8.27	13.45	3	0	185.8	106.8	414.3	440.1	72.6	68.4	166.8	246.4
A1Z729	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=BcDNA:SD07613 PE=1 SV=1	13.258	10	3	5	3	330	36.6	8.66	16.37	3	0	388.2	187.9	667.3	697.4	132.8	164.9	340.6	404.9
Q9VJG2	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=cg12288 PE=1 SV=1	14.813	6	3	5	3	435	47.9	10.04	15.11	3	0	3227.8	713	718.5	699.5	1139.1	1269.3	636.6	621.4
B7Z0I8	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=CG14896 PE=1 SV=1	123.879	9	24	28	24	3441	378.4	4.93	102.94	24	0	4312.4	1691.3	2205.4	2373.1	1651.5	1670.9	1265.9	1481.9
Q8IPP8	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=CG2907 PE=1 SV=1	38.842	36	6	21	5	256	27.1	8.72	79.79	6	1	936.7	442.3	1621.4	1714.9	346.5	383.6	661.4	2198.5
Q9VVV7	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=cg3808 PE=1 SV=3	3.437	3	2	2	2	615	68.6	6.23	4.3	2	0	291.3	123.5	222.5	255	130.5	126.7	97.7	290.9
Q8I725	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1236 PE=1 SV=2	33.129	24	7	14	7	347	38.4	8.27	42.91	7	0	778.3	391.2	1424.5	1262.1	325	372.2	578.6	950.5
Q9VLN0	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG13390 PE=4 SV=1	15.643	13	4	7	4	381	41.4	9.39	20.96	4	0	394.8	253.5	822.5	754.3	117.4	195	355.5	514.5
A1Z843	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1371 PE=1 SV=1	21.35	6	5	8	5	1199	130.8	7.23	22.22	5	0	1166	444.7	1271.6	1240.2	397.1	490.7	655.1	561.9
Q9VPR3	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2794 PE=1 SV=1	31.018	9	6	10	6	700	76.4	8.12	36.61	6	0	814.2	512.2	1585.6	1331.4	378.9	434	720.4	1220.5
A1Z9M5	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG30069 PE=1 SV=1	6.394	1	2	2	2	4012	460.7	8.35	2.17	2	0	37.4	23.1	54.5	67.1	20.7	22.7	26.5	26.2
Q9VPU0	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3862 PE=4 SV=1	8.908	4	3	3	3	454	49.7	7.31	7.76	3	0	388.9	185.8	673.3	382.5	110.7	149.1	331.1	275
Q8IP30	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4793 PE=4 SV=2	4.247	2	2	2	2	910	97.5	7.27	3	2	0	231.4	122.4	518.4	473.3	121.4	129.8	231.8	233.7
Q9VL11	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4957 PE=4 SV=2	16.589	15	2	8	2	246	27.6	6.04	25.69	2	0	57.2	28.9	91	65.6	24.1	28.4	42.7	41.7
Q9VST4	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5144 PE=3 SV=1	3.179	4	2	2	1	388	43.6	8.06	1.66	2	0								
Q9VBK9	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5913 PE=1 SV=1	12.475	6	3	3	3	454	49.9	9.7	9.12	3	0	431.6	182.4	249.7	270	164.1	200.7	151.9	146
A1Z6H6	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7791 PE=1 SV=1	32.626	11	7	13	7	699	80.2	6.87	38.76	7	0	575.8	381.2	1042	1346.7	317.1	407.5	451.5	776.6
Q9W2M4	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=FAMeT PE=1 SV=1	5.743	6	2	3	2	296	31.5	4.77	6.73	2	0	93.3	26.2	72.4	81.5	42.8	30.3	32.3	200.5
Q9VIW9	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Alp12 PE=1 SV=1	9.558	5	2	2	2	596	65.4	5.49	6.39	2	0	47.9	20.9	39.1	54.8	16.2	16.4	25.4	45.7
Q9VTY2	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=anon-WO0172774.89 PE=1	15.294	8	2	3	2	317	35.8	6.11	10.89	2	0	632.2	323.4	444.7	493.1	256.2	276.1	230.4	306.8
Q9VP68	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10512 PE=1 SV=1	8.844	5	4	6	4	446	47	8.25	13.63	4	0	602.4	289.1	750.8	846.2	211.7	205.5	299.9	429.3
Q9VRP2	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10576 PE=1 SV=1	18.975	17	6	10	6	391	42.7	7.11	23.49	6	0	2600.1	1053.7	1810.1	1645.9	905.6	1100.2	1209.7	1061.8
Q9VYA4	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11164 PE=1 SV=1	28.892	18	5	6	5	340	37.6	8.95	22.35	5	0	1943.2	1005	928.6	944.7	770.4	700.4	392.3	419.2
A1Z830	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12128 PE=1 SV=1	8.62	6	3	3	3	485	53.8	7.27	8.05	3	0	415.5	199.9	213.7	280.9	277.2	219.7	148.5	296.4
Q9VRD4	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1532 PE=1 SV=1	22.943	20	3	4	3	288	31.6	5.39	18.48	3	0	290.2	142.9	297.3	331.4	114.5	126.5	130.4	163
Q9VZ60	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2186 PE=1 SV=1	8.243	2	2	2	2	1128	122.6	9.6	6.42	2	0	130.9	58.6	76.9	84.1	58.5	52.2	47.2	54.3
Q9VX51	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5613 PE=4 SV=1	15.67	7	4	5	4	655	75.7	6.28	12.95	4	0	883.1	409.7	569.2	676.4	654.2	442	389.4	439.6
Q9VMU2	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5828 PE=1 SV=1	9.758	8	3	4	3	361	40.4	5.53	8.55	3	0	379.3	353.8	553.5	578.6	158.4	196.4	278.2	347.4
Q0KHZ6	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7834 PE=1 SV=1	93.275	51	11	49	11	253	27.2	8.05	171.19	11	0	4065.8	2237.9	7866.5	5843.2	1286.7	1744.7	3427.2	3467
Q9VRY5	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8549 PE=1 SV=1	9.782	13	4	5	4	252	28.6	8.56	13.55	4	0	1317.7	524.1	932.5	1281.5	461.8	553.5	483.5	660.6
Q9W039	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9018 PE=1 SV=1	14.983	11	3	3	3	375	41.9	7.46	10.96	3	0	112.4	41.7	74.5	101.7	47.6	39.8	40.2	192.7
Q9VMI0	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9147 PE=1 SV=2	12.015	9	3	6	3	391	43.7	6.1	17.69	3	0	245	111.5	323.4	396.6	99.6	118.2	134.1	300
Q9VMD3	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=HemK1 PE=1 SV=1	8.606	10	3	3	3	323	36.6	7.33	8.48	3	0	384.7	213	869.5	696.1	105.5	155.4	323.2	432.9
Q9W4W8	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Spg7 PE=1 SV=1	134.474	26	18	42	18	819	90	8.46	136.17	18	0	2907.2	1401.7	6173.6	4872.5	1195.9	1360.7	2804.2	3587.8
Q9VID9	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=BEST:LD19244 PE=1 SV=3	26.602	4	7	7	7	2663	292.4	5.27	19.08	7	0	564.2	271.9	443.6	472.8	245.8	247.2	227.6	282.5
X2JFW6	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=CC4 PE=1 SV=1	30.44	13	5	9	5	335	37.2	9.7	31.46	5	0	3343.8	1168	975.8	1243.9	1298.1	2032.4	980.7	668.5
Q8IQI5	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=CG10982 PE=4 SV=2	4.965	4	2	3	2	510	58.1	7.08	8.38	2	0	109.4	47.6	155.3	137.1	42.9	57.3	144.9	193.6
A0A0B4LGA9	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=CG3884 PE=4 SV=1	6.946	7	3	4	3	450	48.3	6.32	9.78	3	0	623.9	357.8	650.3	719.2	397.3	380.5	391.5	535.1
M9PGG8	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=CG40016 PE=1 SV=1	11.087	18	2	3	2	182	20.7	5.05	10.51	2	0	477.6	239.2	371.2	378.9	205.4	240.5	190.8	172.5
A1ZBJ2	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=cg7461 PE=1 SV=2	126.055	28	13	60	13	627	68.3	7.77	217.14	13	0	2041.9	1026.3	4449	3601.4	819.2	1283.8	2347.4	3780.4
X2J9A5	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=CG9332 PE=1 SV=1	47.151	21	4	25	4	325	35.6	7.96	71.54	4	0	921.2	491.4	1623.3	1532.4	366.7	449.9	667.2	949.8
M9NF33	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Cpsf6 PE=4 SV=1	10.886	4	2	2	2	605	66.1	9.5	7.24	2	0	478.4	151.2	205.7	195.2	148.9	167.2	156.2	434
B7YZX6	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10600 PE=1 SV=1	8.351	2	2	2	2	1406	153.6	8.95	6.47	2	0	225	103.7	231	211.4	85.7	95.1	108.8	127.8
E2QCZ9	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1129 PE=1 SV=1	6.728	5	2	2	2	369	40.4	6.33	5.97	2	0	501.7	239.1	485.2	523.8	178	226.3	241.8	366
A0A0B4KFV4	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG15107 PE=4 SV=1	5.795	8	2	3	2	243	28.5	4.92	5.31	2	0	633.6	227.1	224.2	248	309.4	386	271.2	307.7
Q7KVQ8	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1628 PE=3 SV=1	10.892	5	2	4	2	459	50.1	5.31	7.81	2	0	325.3	188.9	483	503.2	179.7	217.6	226.3	582.5
Q86BQ4	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2862 PE=1 SV=1	21.552	29	4	11	4	126	13.8	7.24	20.6	4	0	1041	567	1773.1	958.4	325.2	374.7	740.2	683.2
Q9VY24	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5321 PE=4 SV=2	9.609	8	3	3	3	413	48	6.37	5.59	3	0								
A1Z9K0	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6701 PE=1 SV=2	13.577	3	3	3	3	1333	151	9	10.38	3	0	278.8	144	378.2	417.3	106	156.9	180.4	273.7
M9PGB6	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7519 PE=1 SV=1	9.589	15	2	2	2	151	17.6	5.27	6.71	2	0	166.6	92.6	156.2	184.2	76.4	95.6	82.1	129.1
A0A0B4K6X7	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7741 PE=1 SV=1	4.475	3	2	2	2	524	59.8	6.49	2.12	2	0	117.1	65.6	85.9	95.5	46.3	61.2	54.1	39
X2JGV8	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9231 PE=4 SV=1	29.907	26	2	9	2	125	14.1	10.07	32.37	2	0	579.4	307.6	1578.8	909.5	296.9	279.3	682.9	538.4
Q8IPZ5	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9641 PE=1 SV=1	10.293	6	2	2	2	443	50	4.82	8.51	2	0	593.4	263.4	376.5	332.7	234.4	260.5	249.6	213.6
A8JV07	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG9915 PE=1 SV=1	13.102	4	2	2	2	820	90.5	11.93	8.56	2	0	519.6	184.8	192.7	203.3	159.4	147.1	108.5	139.7
Q9VDE2	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=FBgn0038858 PE=1 SV=3	3.988	10	2	2	2	220	23.6	5.99	2.03	2	0	5.1	6.4	20	16.6	5.2	1.1	8.6	6.9
X2JCB6	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=28575006 PE=1 SV=1	18.882	13	4	5	4	435	49.7	5.95	14.23	4	0	159.8	91.6	184.2	175.6	267.4	196.1	444.5	117.8
B7YZY0	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=38D.30 PE=1 SV=1	6.625	2	2	2	2	1252	137.3	5.47	5.56	2	0	302.6	154.9	507.6	535.5	116.8	154.2	252.8	297.6
A0A0B4KFB8	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=CG33097 PE=1 SV=1	22.575	4	4	6	4	1123	129.7	8.27	20.72	4	0	1330.5	637.2	815.2	1073.9	569.4	625.6	495.5	692.8
Q0E8G6	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Cpsf5 PE=1 SV=1	5.666	7	2	3	2	237	26.9	8.85	8.81	2	0	634.5	195.4	277.7	397.8	216.7	198.4	158.8	274
Q8IP91	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=d3635 PE=1 SV=2	9.132	6	3	3	3	564	64.1	5.8	5.66	3	0	102.8	55.9	168.8	164.6	29.7	46.7	74.1	96.9
A0A140SRF8	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11857 PE=1 SV=1	9.3	12	2	2	2	265	29.7	8.94	7.9	2	0	86.9	53.1	118.2	111.4	48.4	58.1	69.3	56.3
A0A0B4KFJ0	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Dmel\CG12945 PE=4 SV=1	8.156	7	2	2	2	440	49.6	5.74	6.95	2	0	13	8.7	16.6	19.4	11.4	10.5	19.2	8.4
E1JJ73	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1307 PE=1 SV=1	14.972	19	4	4	4	186	19.9	8.9	12.63	4	0	456	271.9	895.4	610.3	112.6	246.1	473.5	377.4
A0A0B4LEQ0	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Dmel\CG17337 PE=1 SV=1	17.891	9	2	4	2	431	47.9	5.63	14.38	2	0	55.4	21.2	31.2	35	29.6	23.6	12	19.7
Q7PLE6	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Dmel\CG17691 PE=1 SV=3	24.732	12	3	7	3	364	40.2	7.42	22.94	3	0	243.5	150.3	553.8	403.9	101.3	145	258.5	266.8
A0A0B4K6E6	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Dmel\CG17734 PE=1 SV=1	19.33	16	2	4	2	106	11.8	6.51	15.02	2	0	237.4	129.1	804.1	424	91.4	119	370.8	231.4
M9PDA6	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2614 PE=4 SV=1	11.63	6	3	4	3	669	75.5	6.29	8.21	3	0	406.2	175.1	276.5	346.3	221.3	260.3	168.4	218.7
E1JGL8	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Dmel\CG30122 PE=1 SV=1	68.944	13	11	16	11	1272	140.5	5.01	51.06	11	0	2200.8	882.7	1228.5	1366.3	832.8	923.7	747.5	764.5
A0A0B4LID7	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4538 PE=1 SV=1	98.829	26	14	34	14	679	71.6	7.46	100.22	14	0	1440.8	860.8	3022.1	2508.5	561.5	766.1	1278.1	1593.6
X2JDP6	Uncharacterized protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Ndf PE=4 SV=1	105.733	23	11	30	11	602	65.2	6.1	103.08	11	0	6724.6	2148.5	2837.2	3542.1	2505.5	2419.9	1947.1	2505.3
M9PAY6	Uncharacterized protein, isoform D OS=Drosophila melanogaster OX=7227 GN=Dmel\CG17078 PE=1 SV=1	12.451	6	3	3	3	605	67	7.49	9.92	3	0	281.8	86.6	155.9	198.6	111.7	104.7	86.5	383.1
A0A0B4LES3	Uncharacterized protein, isoform D OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3107 PE=4 SV=1	74.67	19	14	34	14	1034	119.2	6.81	116.73	14	0	1269.9	652.3	2107.2	1900.4	576.2	589.6	880.4	1963.6
Q9V9M8	Uncharacterized protein, isoform D OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3262 PE=1 SV=3	7.047	8	2	2	2	293	32	9	5.95	2	0	150.4	84.9	316.8	258.8	52.9	74	141.2	227.8
M9NEX3	Uncharacterized protein, isoform D OS=Drosophila melanogaster OX=7227 GN=Dmel\CG3566 PE=1 SV=1	22	50	5	8	5	106	11.6	6.3	21.07	5	0	360.5	183.4	924.8	668.1	128.4	176.6	394.9	394.1
A8JRC1	Uncharacterized protein, isoform D OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5028 PE=1 SV=1	41.857	21	6	13	6	393	43.4	6.76	51.85	6	0	772.6	375.6	1258.4	1047.2	284.3	350.8	531	1199.6
Q7KSU6	Uncharacterized protein, isoform D OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8036 PE=1 SV=1	40.98	15	7	12	7	580	63	6.8	39.72	7	0	1462.3	744.3	1086.9	1221.1	592	667	597.6	1008
A0A0B4KGH7	Uncharacterized protein, isoform E OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4662 PE=1 SV=1	12.982	7	2	2	2	494	56.9	8.75	8.56	2	0	53	25.3	129.8	102.1	21.9	25.5	49.9	56.3
X2JKH9	Uncharacterized protein, isoform F OS=Drosophila melanogaster OX=7227 GN=huwe1 PE=1 SV=1	20.12	1	3	3	3	5127	554.9	5.48	12.01	3	0	195.5	91.7	161.9	159.7	82.4	91	95.5	86.8
M9PC31	Uncharacterized protein, isoform G OS=Drosophila melanogaster OX=7227 GN=Naprt PE=4 SV=1	20.545	12	5	7	5	550	61.5	6.71	19.91	5	0	1281.6	480.8	855	1295.5	485.7	353.8	411.4	1150.5
M9NFF0	Uncharacterized protein, isoform H OS=Drosophila melanogaster OX=7227 GN=Dmel\CG17715 PE=1 SV=1	15.396	11	3	4	3	268	30	8.91	13.03	3	0	160.6	99.3	279.8	349.5	104.2	156.3	125	368.8
M9PGK3	Uncharacterized protein, isoform I OS=Drosophila melanogaster OX=7227 GN=CG4564 PE=1 SV=1	6.372	2	2	2	2	1367	143.2	9.2	5.25	2	0	344.1	124.3	203.6	212.4	135.8	164	108.5	166.1
E1JIJ7	Uncharacterized protein, isoform I OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7518 PE=1 SV=2	11.778	1	2	2	2	2310	252.9	8.51	6.75	2	0	98.3	37.4	88.4	57.7	36.3	44.6	58.2	49.1
A0A0B4J401	Uncharacterized protein, isoform V OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10737 PE=1 SV=1	31.467	9	4	5	4	852	92.7	6.79	22.21	4	0	186.2	103.3	269.5	303.4	106.8	105.4	157.1	152.5
Q9V595	Uroporphyrinogen decarboxylase OS=Drosophila melanogaster OX=7227 GN=Updo PE=3 SV=1	8.817	9	2	2	2	356	40	6.54	6.44	2	0	82.8	41.3	130	114.9	36.7	43.5	64.6	98.2
Q9VLM7	UT01133p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG13392 PE=1 SV=1	10.445	13	3	3	3	223	25.5	9.39	10.69	3	0	107.4	83.6	298	253.8	28	16	101.2	446.6
Q8IML4	V-type proton ATPase subunit a OS=Drosophila melanogaster OX=7227 GN=Vha100-1 PE=1 SV=1	9.712	3	2	3	2	850	96.5	6.65	8.61	2	0	215.2	161.4	336.4	392.4	120.4	215.1	187	246.4
Q9VE75	V-type proton ATPase subunit a OS=Drosophila melanogaster OX=7227 GN=Vha100-2 PE=1 SV=2	6.433	2	2	2	2	834	94.8	6.68	5.13	2	0	34.9	21	27.8	36.6	20.6	22.1	23.8	23.2
Q9V7D2	V-type proton ATPase subunit D 1 OS=Drosophila melanogaster OX=7227 GN=Vha36-1 PE=2 SV=1	12.513	23	3	3	3	246	27.6	9.54	8.33	3	0	29.6	20.3	46.9	51.9	21.4	27.3	26.6	32
Q9W4P5	V-type proton ATPase subunit d 1 OS=Drosophila melanogaster OX=7227 GN=VhaAC39-1 PE=2 SV=1	8.606	8	3	4	3	350	39.8	4.91	6.66	3	0	140.9	100.7	236.3	192.5	50.8	68.3	106.7	115.4
P54611	V-type proton ATPase subunit E OS=Drosophila melanogaster OX=7227 GN=Vha26 PE=2 SV=1	17.544	23	4	8	4	226	26.1	6.15	16.49	4	0	817	578.4	1093.1	1308.3	320.7	401.7	585.1	646
Q9XZH6	V-type proton ATPase subunit G OS=Drosophila melanogaster OX=7227 GN=Vha13 PE=3 SV=1	10.916	9	2	3	2	117	13.6	9.58	10.37	2	0	581.2	382.7	642.9	527.1	208.1	314.2	342.4	278.3
Q9V3J1	V-type proton ATPase subunit H OS=Drosophila melanogaster OX=7227 GN=VhaSFD PE=2 SV=2	15.826	9	3	4	3	468	53.7	6.61	13.79	3	0	104.4	62.3	112.5	128.9	48.2	58.4	70.4	91.9
M9PD18	Vacuolar H[+] ATPase 68kD subunit 1, isoform B OS=Drosophila melanogaster OX=7227 GN=Vha68-1 PE=1	31.834	10	5	8	2	614	68.3	5.29	24.08	5	0	108.6	51.1	120.7	133.7	47.5	47	61.9	76
E1JIJ5	Vacuolar H[+]-ATPase 55kD subunit, isoform C OS=Drosophila melanogaster OX=7227 GN=Vha55 PE=1 SV	52.041	24	8	14	8	490	54.5	5.4	40.26	8	0	1269	667.6	1320.8	1449.6	467.3	558.7	657	1418.7
A1Z713	Vacuolar protein sorting-associated protein 13 OS=Drosophila melanogaster OX=7227 GN=Vps13 PE=1 SV=	4.25	1	2	3	2	3321	374.3	5.85	7.05	2	0	304.9	188.4	448	381.7	115.6	166.5	260.8	163.3
Q9VPX5	Vacuolar protein sorting-associated protein 29 OS=Drosophila melanogaster OX=7227 GN=Vps29 PE=1 SV=	11.394	16	3	4	3	182	20.5	7.01	13.62	3	0	603	287.6	612	723.3	282	285.5	291.6	377.4
Q0E993	Valyl-tRNA synthetase, isoform A OS=Drosophila melanogaster OX=7227 GN=ValRS PE=1 SV=1	5.604	2	2	2	2	1049	118.2	6.65	4.89	2	0	225.1	117.2	305.5	364.5	102.9	110.2	152.6	268.5
P54351	Vesicle-fusing ATPase 2 OS=Drosophila melanogaster OX=7227 GN=Nsf2 PE=2 SV=2	8.086	4	3	3	3	752	83.4	6.74	5.19	3	0	252.7	118.3	278.2	354.5	102.6	149.6	159.2	184.5
Q9VBX3	Vig2, isoform B OS=Drosophila melanogaster OX=7227 GN=vig2 PE=1 SV=2	37.013	19	7	12	7	443	48.7	9.38	28.82	7	0	1037.2	454.8	1092.3	918.1	412.3	489.1	662.3	524.4
Q9VMV5	Viking, isoform A OS=Drosophila melanogaster OX=7227 GN=vkg PE=1 SV=1	263.937	22	37	76	37	1940	193.7	6.43	274.7	37	0	3942.2	1892.3	20129.5	15819.5	1308.3	1689.4	8387.9	5250.9
X2JAB9	Vinculin, isoform B OS=Drosophila melanogaster OX=7227 GN=Vinc PE=1 SV=1	26.091	7	5	5	5	961	106.2	6.7	19.02	5	0	598.6	311.9	702.1	903.8	253.1	337.5	428.1	440.3

Q94920	Voltage-dependent anion-selective channel OS=Drosophila melanogaster OX=7227 GN=porin PE=1 SV=3	38.676	34	7	39	7	282	30.5	6.96	50.31	7	0	734.1	885.3	1972.4	1767.6	420.1	659.6	785	1754.2
Q7KN94	Walrus, isoform A OS=Drosophila melanogaster OX=7227 GN=wal PE=1 SV=1	74.63	33	8	35	8	330	34.2	8.32	147.3	8	0	1868.1	980.1	3737.2	2716.9	635.6	779.7	1627.2	2293
A8JRE3	Without children, isoform B OS=Drosophila melanogaster OX=7227 GN=woc PE=1 SV=1	51.848	8	12	16	12	1703	188.6	4.75	46.94	12	0	3016.4	1356.2	1625.5	1972.4	1300.2	1301.8	1153.5	1390.9
Q9VJG0	Xaa-Pro aminopeptidase ApepP OS=Drosophila melanogaster OX=7227 GN=ApepP PE=1 SV=1	4.452	3	2	2	2	613	68.5	5.95	5.16	2	0	363.8	166.9	380.1	353.5	147	141.9	171.5	277.6
Q7KVP9	Xeroderma pigmentosum D OS=Drosophila melanogaster OX=7227 GN=Xpd PE=1 SV=1	9.753	2	2	2	2	769	88	6.77	6.07	2	0	387.5	142.6	200.6	235	135.1	156.6	107.2	162.8
A0A0B4KFY4	YME1 like ATPase, isoform D OS=Drosophila melanogaster OX=7227 GN=YME1L PE=1 SV=1	73.83	17	11	16	11	739	80.9	8.57	57.31	11	0	980	519.7	1720.3	1226.4	342.1	489.4	804.8	936.2
X2JEX8	Yolk protein 3, isoform B OS=Drosophila melanogaster OX=7227 GN=Yp3 PE=1 SV=1	7.81	8	2	2	2	420	46.1	8.5	6.59	2	0	206.6	210.8	199.2	425.5	139.8	188.4	115	324.8
Q9VBZ5	YTH domain-containing family protein OS=Drosophila melanogaster OX=7227 GN=Ythdf PE=2 SV=1	7.957	3	2	2	2	700	78.9	8.95	6.93	2	0	694.4	125.4	333.3	364.7	133.9	142.7	180.9	271.4
Q7JWR9	Zinc finger CCCH domain-containing protein 15 homolog OS=Drosophila melanogaster OX=7227 GN=CG863	14.376	9	3	5	3	404	45.3	5.55	13.5	3	0	833.2	424.5	1081.6	967.2	359.5	534.7	662.5	572.7
P28166	Zinc finger protein 1 OS=Drosophila melanogaster OX=7227 GN=zfh1 PE=1 SV=2	9.545	2	2	2	2	1054	116.5	7.15	6.24	2	0	63.5	22.4	27	26.7	20.6	25.8	15.7	22
Q9W3Y0	Zinc finger protein 593 homolog OS=Drosophila melanogaster OX=7227 GN=CG3224 PE=2 SV=1	12.886	17	2	2	2	162	18.9	9.67	7.75	2	0	436.5	172.1	167.2	227	146.6	161.6	95.1	109.5
Q8IRH5	Zinc finger protein CG2199 OS=Drosophila melanogaster OX=7227 GN=CG2199 PE=1 SV=1	24.181	9	5	9	5	733	81.9	8.56	28.27	5	0	2618.7	553.1	693.4	715.3	776.2	887.9	517.5	637.7
Q9VXG1	Zinc finger protein hangover OS=Drosophila melanogaster OX=7227 GN=hang PE=1 SV=4	24.183	2	4	6	4	1959	213.7	5.38	16.58	4	0	1096.6	490	650.5	882.1	438.3	383.5	338.8	434.9
P41073	Zinc finger protein on ecdysone puffs OS=Drosophila melanogaster OX=7227 GN=Pep PE=1 SV=1	70.698	11	9	23	9	716	78	5.58	82.83	9	0	2507.4	946.3	1213.3	1356.7	924.3	965.1	727.5	1003.1
Q86BI3	Zinc-finger protein at 72D, isoform B OS=Drosophila melanogaster OX=7227 GN=Zn72D PE=1 SV=1	18.936	6	5	5	5	884	96	8.44	13.38	5	0	850.9	355.8	507.5	531.1	336.5	367.3	277	414.5
A0A0B4JD57	Zipper, isoform F OS=Drosophila melanogaster OX=7227 GN=zip PE=1 SV=1	234.717	20	30	54	30	1979	227.7	5.47	204.67	30	0	2771.2	1429.9	3767.9	3943.3	1137	1636.9	2119.8	2316.6

Supplemental Table 3-4: Normalized TMT Intensities for iPOND S2 Cell Replicates

Accession	Description	EdU Pulse R1	EdU Pulse R2	EdU Pulse R3	EdU Pulse R4	Thy Chase R1	Thy Chase R2	Thy Chase R3	Thy Chase R4	Pulse Average	Thy Average	Pulse - Chase	Fold Change	p-value	q-value
P92177	14-3-3 protein epsilon OS=Drosophila melanogaster OX=7227 GN=14-3-3epsilon PE=1 SV=2	10.55635254	10.27324234	9.856975013	10.11562687	9.839360297	9.469929095	9.089968238	9.72995894	10.20054919	9.532304142	0.668245049	1.5891387	0.038857	0.039786
P29310	14-3-3 protein zeta OS=Drosophila melanogaster OX=7227 GN=14-3-3zeta PE=1 SV=1	10.62249748	10.66610344	10.06211389	10.21058404	9.993078911	9.701898266	9.452727569	9.563227749	10.39032471	9.677733124	0.712591591	1.638745241	0.027617	0.023713
Q9V3P6	26S proteasome non-ATPase regulatory subunit 1 OS=Drosophila melanogaster OX=7227 GN=Rpn2 PE=	10.12124792	10.28705957	9.580692951	9.769719357	9.237209039	9.210030701	8.91413145	8.834563563	9.93967995	9.048983688	0.890696262	1.854070704	0.005911	0.015093
Q9VW54	26S proteasome non-ATPase regulatory subunit 2 OS=Drosophila melanogaster OX=7227 GN=Rpn1 PE=	7.092847669	7.112590107	7.167251148	7.475877519	6.529820295	6.303573464	6.499522967	7.103243047	7.212141611	6.609039943	0.603101667	1.518978729	0.062261	0.037058
Q9V436	26S proteasome regulatory complex subunit p30 OS=Drosophila melanogaster OX=7227 GN=Rpn12 PE=	7.017141899	7.103527955	6.639749116	6.779604468	6.251718468	6.211003113	6.17959397	5.868933944	6.885005859	6.127812374	0.757193485	1.690199433	0.019261	0.011489
Q7KMQ0	26S proteasome regulatory complex subunit p48B OS=Drosophila melanogaster OX=7227 GN=Rpt1 PE=1	8.639903329	9.269834018	8.469204815	9.136454667	8.333154518	7.988351635	7.840067896	8.104420566	8.878849207	8.066498654	0.812350554	1.756070243	0.012046	0.023912
Q0E9B6	40S ribosomal protein S11 OS=Drosophila melanogaster OX=7227 GN=RpS11 PE=1 SV=1	9.680958132	9.459749119	9.446766637	9.61867052	8.800251928	8.879535017	9.004125966	9.21916965	9.551536102	8.97577064	0.575765462	1.490468062	0.075082	0.012055
Q06559	40S ribosomal protein S3 OS=Drosophila melanogaster OX=7227 GN=RpS3 PE=1 SV=1	10.32025328	9.983013861	10.02999315	10.03309506	9.431078732	9.443520368	9.41170194	9.990132429	10.09158884	9.569108367	0.522480469	1.436422811	0.106246	0.032847
Q9V3G1	60S ribosomal protein L8 OS=Drosophila melanogaster OX=7227 GN=RpL8 PE=1 SV=1	8.576982803	8.148682621	8.432712816	8.727974578	7.689997204	7.854552631	7.97248837	8.233465128	8.471588205	7.937625833	0.533962371	1.447900407	0.098783	0.03524
A0A0B4KH51	Abelson interacting protein, isoform C OS=Drosophila melanogaster OX=7227 GN=Abi PE=1 SV=1	4.747081761	4.243627326	5.012278268	5.145862916	4.017921507	4.13800075	4.278065393	3.811204929	4.787212568	4.061298145	0.725914423	1.653948626	0.024843	0.032847
P02572	Actin-42A OS=Drosophila melanogaster OX=7227 GN=Act42A PE=1 SV=3	12.61519947	13.01316491	12.40860234	12.45426601	12.09654925	12.1146957	11.72549979	11.7017684	12.62280818	11.90962828	0.713179899	1.639413632	0.027489	0.020368
P10987	Actin-5C OS=Drosophila melanogaster OX=7227 GN=Act5C PE=1 SV=4	7.681873852	7.508670537	7.501741898	7.869021573	6.892390338	6.775000154	6.64734485	6.408258633	7.640326965	6.680748494	0.959578472	1.944741595	0.003024	0.008347
Q9VF28	Actin-related protein 2/3 complex subunit 3 OS=Drosophila melanogaster OX=7227 GN=Arpc3A PE=1 SV=	6.406644126	5.772233243	6.234243821	6.516643232	5.501438596	5.907057191	5.550127907	5.591631255	6.232441105	5.637563737	0.594877368	1.510344198	0.065913	0.035316
O97182	Actin-related protein 2/3 complex subunit OS=Drosophila melanogaster OX=7227 GN=Arpc1 PE=1 SV=1	7.604642873	7.03221793	7.6074108	8.056158071	6.459430974	6.569562945	6.844196906	7.114552247	7.575107418	6.746935768	0.82817165	1.775433901	0.010478	0.033613
P32392	Actin-related protein 3 OS=Drosophila melanogaster OX=7227 GN=Arp3 PE=2 SV=3	8.513462571	8.574994317	8.867394577	9.272626876	7.917072872	7.881410417	8.129281841	7.920239034	8.807119585	7.962001041	0.845118544	1.796412348	0.009002	0.015163
Q7KSM5	Activator of SUMO 1 OS=Drosophila melanogaster OX=7227 GN=Aos1 PE=1 SV=1	8.237902287	8.33429261	7.5963914	7.695697787	7.546122005	7.406339447	6.658883709	6.548392376	7.966071021	7.039934384	0.926136636	1.900180722	0.004209	0.041625
Q9VB05	ALG-2 interacting protein X OS=Drosophila melanogaster OX=7227 GN=ALiX PE=1 SV=1	7.572271529	7.246624597	7.511511576	7.427695162	6.722465353	6.472239726	6.703077712	6.277172927	7.439525716	6.543738929	0.895786786	1.860624316	0.005633	0.008347
Q9VAK1	Alphabet, isoform A OS=Drosophila melanogaster OX=7227 GN=alph PE=1 SV=1	9.95720411	10.11008921	9.606060749	9.757000576	9.19918063	9.068558334	8.826794385	8.505087923	9.857588661	8.899905318	0.957683343	1.942188653	0.003082	0.012367
Q9V4P1	Anillin OS=Drosophila melanogaster OX=7227 GN=scra PE=1 SV=3	7.450269979	6.894534766	6.985555328	6.851692241	6.545349991	6.361557985	6.353480787	6.097551456	7.045513078	6.339485055	0.706028023	1.631306673	0.029079	0.017813
P25439	ATP-dependent helicase brm OS=Drosophila melanogaster OX=7227 GN=brm PE=1 SV=2	9.906943206	9.847790414	9.169005676	9.153376902	9.195002109	8.744090765	8.539063476	8.258093352	9.51927905	8.684062426	0.835216624	1.78412491	0.00984	0.041955
Q9VHP0	ATP-dependent RNA helicase bel OS=Drosophila melanogaster OX=7227 GN=bel PE=1 SV=1	9.982692214	10.11479772	10.13142857	10.02168829	9.348727221	9.438178654	9.65536433	8.885753207	10.0626517	9.332005853	0.730645845	1.659381773	0.023917	0.016463
Q9VNV3	ATP-dependent RNA helicase Ddx1 OS=Drosophila melanogaster OX=7227 GN=Ddx1 PE=2 SV=1	9.016374599	8.96495143	8.531923032	8.733985023	8.217229896	8.197343215	7.824579334	8.056858348	8.811808521	8.074002698	0.737805823	1.66763762	0.022574	0.012367
A1Z9L3	ATP-dependent RNA helicase DHX8 OS=Drosophila melanogaster OX=7227 GN=pea PE=1 SV=1	7.326902434	7.105042028	7.113271862	7.343354159	6.899658338	6.59190036	6.511210787	6.653478856	7.222142621	6.664062085	0.558080536	1.472309049	0.084471	0.012055
P19109	ATP-dependent RNA helicase p62 OS=Drosophila melanogaster OX=7227 GN=Rm62 PE=1 SV=3	11.75385779	12.1607094	11.58338821	11.70697748	11.29416009	11.18337949	10.81497198	10.84672119	11.80123322	11.03480819	0.76642503	1.70104939	0.017838	0.016463
Q9V3Y5	BcDNA.LD23634 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4119 PE=1 SV=1	9.522740503	9.69109563	9.157874211	9.194408377	8.923920785	8.761506958	8.551406856	8.392192102	9.39152968	8.657256675	0.734273005	1.663558967	0.023228	0.017884
Q9V3H9	BcDNA.LD27873 OS=Drosophila melanogaster OX=7227 GN=Nab2 PE=1 SV=1	8.921248897	9.038979143	8.438391675	8.642658202	8.303323298	8.288518554	7.968488666	7.663176286	8.760319479	8.055876701	0.704442778	1.629515164	0.029442	0.029326
Q9VHH8	Beag OS=Drosophila melanogaster OX=7227 GN=beag PE=1 SV=1	8.712457928	8.549773745	8.029233295	8.079883205	7.942513712	7.947640065	7.540676709	7.438057198	8.342837043	7.717221921	0.625615122	1.542868518	0.053114	0.042632
Q9Y118	BG:DS07295.3 OS=Drosophila melanogaster OX=7227 GN=Pol32 PE=1 SV=1	10.03708043	10.41827775	9.247142317	9.11371208	9.200162055	8.274384625	7.60122049	7.433213691	9.704053146	8.127245215	1.576807931	2.983090881	0.000001	0.037436
Q9W384	Brahma associated protein 111kD OS=Drosophila melanogaster OX=7227 GN=Bap111 PE=1 SV=1	7.442095433	7.405166294	6.814720501	7.042290659	6.757556014	6.568237877	6.475843037	6.145711912	7.176068222	6.48683721	0.689231012	1.612423832	0.033128	0.028829
A1Z6M0	Brahma associated protein 170kD OS=Drosophila melanogaster OX=7227 GN=Bap170 PE=1 SV=1	8.030852446	8.040573233	7.585766137	7.861931536	7.246027257	6.92881909	6.761479626	6.521187942	7.879780838	6.864378479	1.015402359	2.02146659	0.001704	0.011489
Q9VYG2	Brahma-associated protein of 60 kDa OS=Drosophila melanogaster OX=7227 GN=Bap60 PE=1 SV=1	7.935667356	7.891062373	7.307220192	7.706377737	7.432123531	6.923678944	6.727136402	7.222046091	7.710081915	7.076246242	0.633835673	1.551684957	0.050067	0.040218
Q9VC96	BRWD3 OS=Drosophila melanogaster OX=7227 GN=BRWD3 PE=1 SV=2	10.00664441	10.41757592	9.388343102	9.913832528	9.516093013	8.844180075	8.331785322	8.808196253	9.93159899	8.875063666	1.056535324	2.079930503	0.001097	0.032725
Q9VAJ2	Bub3, isoform A OS=Drosophila melanogaster OX=7227 GN=Bub3 PE=1 SV=1	7.916567727	7.590268846	7.096647366	7.437470407	6.956520669	6.929844871	6.335070336	6.824487951	7.510238586	6.761480957	0.748757629	1.680345185	0.020646	0.030794
Q9VIE7	Burgundy, isoform B OS=Drosophila melanogaster OX=7227 GN=bur PE=1 SV=3	8.946069707	8.948613773	8.508652639	8.413054251	8.155323415	8.096721805	7.511328557	7.525595021	8.704097593	7.822242199	0.881855393	1.842743658	0.006423	0.021109
A0A0B4LF57	Calmodulin, isoform C OS=Drosophila melanogaster OX=7227 GN=Cam PE=1 SV=1	10.22896842	10.3723404	9.42600487	9.53685452	9.321927164	9.320486696	8.743522235	8.803105636	9.891042053	9.047260433	0.84378162	1.794748411	0.009112	0.041625
Q0KIA8	Carnitine O-Acetyl-Transferase, isoform B OS=Drosophila melanogaster OX=7227 GN=CRAT PE=1 SV=1	8.335854006	8.618017286	9.421292179	9.12242123	7.541483111	7.589760126	8.274410254	8.145717672	8.874396175	7.887842791	0.986553384	1.981445635	0.0023	0.03463
M9NFF8	Cdc42, isoform C OS=Drosophila melanogaster OX=7227 GN=Cdc42 PE=4 SV=1	7.054068836	7.072929123	7.908865562	7.301514597	4.781359236	5.89855031	7.011392429	6.091404601	7.334344529	5.945676644	1.388667885	2.618368017	0.000018	0.047006
Q9VIH1	CG9273 protein OS=Drosophila melanogaster OX=7227 GN=RPA2 PE=1 SV=2	10.31583263	10.69157176	9.321264351	9.164391247	9.506802489	8.390955327	7.598072337	7.70288825	9.873264997	8.299679601	1.573585396	2.976435016	0.000001	0.048727
A1Z898	Chromatin assembly factor 1, p105 subunit OS=Drosophila melanogaster OX=7227 GN=Caf1-105 PE=1 S'	9.425621817	9.999916443	8.797602623	9.154891047	9.024584737	7.251164854	6.93248975	6.983793161	9.344507983	7.548008126	1.796499857	3.473764273	<0.000001	0.034087
Q9W3D1	Chromatin assembly factor 1, p180 subunit OS=Drosophila melanogaster OX=7227 GN=Caf1-180 PE=1 S'	10.7341911	11.60280513	10.18901391	10.57213011	10.3348309	8.82802927	8.358239449	8.544675801	10.77453506	9.016443854	1.758091208	3.382502987	<0.000001	0.032914
Q494K2	Chromosome transmission fidelity 4 OS=Drosophila melanogaster OX=7227 GN=Ctf4 PE=1 SV=1	7.805982993	7.881959087	7.385955127	7.533024127	7.091699126	6.710595035	5.985444299	6.444491443	7.651730333	6.558057476	1.093672858	2.134166682	0.000727	0.017884
Q8IRB5	Claspin OS=Drosophila melanogaster OX=7227 GN=Claspin PE=1 SV=1	9.984024843	10.53495086	9.286704785	9.175316316	9.249112529	8.380747937	7.495565573	7.342338447	9.745249201	8.116941122	1.628308079	3.0915023	<0.000001	0.040218
Q9V9V0	Cleavage stimulation factor 50 kD subunit OS=Drosophila melanogaster OX=7227 GN=CstF50 PE=1 SV=1	8.196954757	7.794612687	7.471473013	7.471663708	7.245076552	7.208071438	6.672396084	6.732006899	7.733676041	6.964387743	0.769288298	1.704428757	0.017416	0.030794
Q9VKJ9	Coiled-coil and C2 domain-containing protein 1-like OS=Drosophila melanogaster OX=7227 GN=l(2)gd1 PE	7.308321356	6.739464566	6.914062128	7.007755703	6.234577337	6.581432768	6.182557741	6.456659684	6.992400938	6.363806883	0.628594056	1.546057585	0.051993	0.018812
Q9VP13	CR6-interacting factor OS=Drosophila melanogaster OX=7227 GN=CRIF PE=1 SV=1	8.465128114	8.870468467	9.25840465	8.917559172	7.527476255	8.032611919	8.418043853	7.88169604	8.8778901	7.964957017	0.912933084	1.882869594	0.004783	0.023912
Q7K0X3	Ctr9, isoform A OS=Drosophila melanogaster OX=7227 GN=Ctr9 PE=1 SV=1	7.296196469	6.972358711	6.610079117	6.943739768	6.316507188	6.353860402	5.93137824	5.921905106	6.955593517	6.130912734	0.824680783	1.771143104	0.010808	0.015913
Q9V9R2	Cullin 2, isoform A OS=Drosophila melanogaster OX=7227 GN=Cul2 PE=1 SV=3	8.346249486	8.130148507	7.823827808	7.769162269	7.463523628	7.301666556	7.259421506	7.14570681	8.017347017	7.292579625	0.724767393	1.652634159	0.025072	0.014278
Q8IQ05	Cutlet OS=Drosophila melanogaster OX=7227 GN=cutlet PE=1 SV=2	9.069835082	9.577498034	8.525177232	8.81406943	8.475732585	7.360272623	6.794980724	6.647052253	8.996644945	7.319509546	1.677135398	3.197923436	<0.000001	0.027408
A1ZAW0	Dicer-2, isoform A OS=Drosophila melanogaster OX=7227 GN=Dcr-2 PE=1 SV=1	7.408333012	7.308837892	7.967107962	7.910796024	6.834154299	6.95020509	6.902231998	7.286294455	7.648768723	6.993221461	0.655547262	1.575213371	0.042717	0.031289
Q9VC93	Dis3, isoform A OS=Drosophila melanogaster OX=7227 GN=Dis3 PE=1 SV=1	8.970971447	9.00988204	8.447377203	8.610182708	8.252191516	7.995104092	7.59964732	7.562072227	8.759603349	7.852253789	0.907349561	1.875596589	0.005046	0.017884
Q9XYZ5	DNA damage-binding protein 1 OS=Drosophila melanogaster OX=7227 GN=pic PE=1 SV=1	10.91876169	11.22757384	10.18950585	10.47131285	10.38952275	9.935251002	9.344615146	9.538992883	10.70178856	9.802095446	0.899693112	1.865669079	0.005428	0.047888
X2JAI4	DNA helicase OS=Drosophila melanogaster OX=7227 GN=Mcm3 PE=1 SV=1	10.94058637	11.10868757	10.14100437	10.4334018	10.2976031	9.794683326	9.146427009	9.636126102	10.65592003	9.718709885	0.937210141	1.914821806	0.003776	0.043135
Q9W1H4	DNA ligase 1 OS=Drosophila melanogaster OX=7227 GN=DNAlig1 PE=1 SV=2	9.517106206	9.814121235	9.047763247	9.457992859	9.07868364	8.702206839	8.062139149	8.163997216	9.459245887	8.501756711	0.957489176	1.941927279	0.003088	0.030794
M9NEY8	DNA N6-methyl adenine demethylase OS=Drosophila melanogaster OX=7227 GN=Tet PE=1 SV=1	8.987611326	9.022978717	8.402367562	8.633777315	8.319219672	8.080060254	7.852769585	7.599501847	8.76168373	7.96288784	0.79879589	1.739648566	0.013552	0.023854
P26019	DNA polymerase alpha catalytic subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-alpha180 PE	9.090479242	9.15255437	8.430641831	8.545166715	8.350938348	7.57621957	7.213565987	7.797019961	8.804710539	7.734435966	1.070274573	2.099832968	0.000944	0.027408
P54358	DNA polymerase delta catalytic subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-delta PE=2 S'	9.816458674	10.28725061	9.092258426	8.879675531	9.20579233	7.988835029	7.125155121	7.258353189	9.51891081	7.894533917	1.624376892	3.08308976	<0.000001	0.045813
Q9W088	DNA polymerase delta small subunit OS=Drosophila melanogaster OX=7227 GN=CG12018 PE=2 SV=1	9.593146566	9.866739885	8.820106527	8.976180074	8.922434849	7.866728434	7.020241018	7.42657983	9.314043263	7.808996033	1.50504723	2.838339632	0.000003	0.036019
Q9VCN1	DNA polymerase epsilon catalytic subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-epsilon255	9.677515519	10.07386929	8.97433674	9.555869514	9.157093338	8.183100881	7.652144313	8.368910269	9.570397765	8.3403122	1.230085564	2.345809021	0.000145	0.034799
Q9VRQ7	DNA polymerase epsilon subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-epsilon58 PE=3 SV=	7.333434756	7.336423726	6.839407407	6.884710224	6.45614839	6.076646511	5.494940688	5.534389112	7.098494028	5.890531175	1.207962853	2.310112087	0.00019	0.015913
Q9VJV8	DNA polymerase gamma 35kD OS=Drosophila melanogaster OX=7227 GN=DNApol-gamma35 PE=2 SV=2	7.114616688	7.127576001	7.680767915	7.528985497	6.592456379	6.531981335	6.933344487	6.957391596	7.362986525	6.753793449	0.609193076	1.525405785	0.059666	0.030794
Q9VPH2	DNA primase large subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-alpha60 PE=1 SV=2	9.9211465	10.23380104	9.176922091	9.285462066	9.415952042	8.450692725	7.676663774	7.902188376	9.654332925	8.361374229	1.292958695	2.45030051	0.000065	0.046507
Q24317	DNA primase small subunit OS=Drosophila melanogaster OX=7227 GN=DNApol-alpha50 PE=2 SV=2	8.129004703	8.202981016	7.711592365	8.039990743	7.204570425	6.222912782	5.909861294	7.469753259	8.020892207	6.70177444	1.319117767	2.495134812	0.000046	0.030794
Q24595	DNA repair protein complementing XP-C cells homolog OS=Drosophila melanogaster OX=7227 GN=Xpc PE	8.098082638	8.07155336	8.165519483	8.455667655	7.494254838	7.446690999	7.320623981	7.069298808	8.197705784	7.332717157	0.864988628	1.82132531	0.007511	0.008347
P49735	DNA replication licensing factor Mcm2 OS=Drosophila melanogaster OX=7227 GN=Mcm2 PE=1 SV=1	9.577827362	9.784738913	9.275123655	9.41638758	9.013740492	8.703952872	8.256035794	8.609893953	9.513519378	8.645905778	0.8676136	1.824642214	0.007331	0.015603
Q9VGW6	DNA replication licensing factor Mcm5 OS=Drosophila melanogaster OX=7227 GN=Mcm5 PE=1 SV=1	10.86854357	11.1660471	10.18097693	10.44867123	10.33113985	9.862831678	9.246991759	9.520383143	10.66605971	9.740336608	0.925723101	1.89963613	0.004226	0.042632
Q9V461	DNA replication licensing factor Mcm6 OS=Drosophila melanogaster OX=7227 GN=Mcm6 PE=1 SV=1	10.54787936	10.6827353	9.741860568	10.13280427	9.817622277	9.195952759	8.701777086	9.172602408	10.27631987	9.221988632	1.054331241	2.076755306	0.001123	0.030794
Q9XYU0	DNA replication licensing factor Mcm7 OS=Drosophila melanogaster OX=7227 GN=Mcm7 PE=1 SV=1	10.0250205	10.0900242	9.320193485	9.716412864	9.298978073	8.827762954	8.320067959	9.388549316	9.787912762	8.958839575	0.829073187	1.776543712	0.010395	0.048306
Q9NG98	DNA topoisomerase 3-alpha OS=Drosophila melanogaster OX=7227 GN=Top3alpha PE=2 SV=2	9.418175039	9.330806562	9.902681688	9.538563236	8.166915436	8.14901	8.821011785	9.000145159	9.547556631	8.534270595	1.013286036	2.018503427	0.001742	0.020439
O96651	DNA topoisomerase 3-beta OS=Drosophila melanogaster OX=7227 GN=Top3beta PE=2 SV=2	8.346249486	8.188837478	8.492417978	8.572250276	7.417007846	7.650668087	7.791698321	7.504045475	8.399838805	7.590854932	0.809083872	1.752098487	0.012395	0.008347
P20028	DNA-directed RNA polymerase I subunit RPA2 OS=Drosophila melanogaster OX=7227 GN=Rpl135 PE=1 :	7.948126762	7.619785284	7.177135958	7.302711128	7.096977928	6.880806513	6.482990208	7.002329959	7.511939783	6.865776152	0.646163631	1.565001057	0.045773	0.041625
Q7KN75	Dodeca-satellite-binding protein 1, isoform A OS=Drosophila melanogaster OX=7227 GN=Dp1 PE=1 SV=1	9.909760658	10.0198209	9.851659061	9.939271645	9.162138613	9.403220072	9.208587252	8.874826221	9.930128066	9.162193039	0.767935027	1.702830725	0.017615	0.008347
Q8MLW2	Domino, isoform D OS=Drosophila melanogaster OX=7227 GN=dom PE=1 SV=1	7.924622491	7.898306394	7.98885545	7.773807992	7.368069141	7.319661435	7.270815765	6.684363575	7.896398082	7.160727479	0.735670603	1.665171305	0.022968	0.016463
P13496	Dynactin subunit 1 OS=Drosophila melanogaster OX=7227 GN=DCTN1-p150 PE=1 SV=2	7.27409356	7.369905833	7.573100064	7.67770764	6.542257397	6.734357364	6.870394493	6.491591932	7.473701774	6.659650296	0.814051478	1.758141854	0.011868	0.008638
Q9VZ20	Dynein light intermediate chain, isoform A OS=Drosophila melanogaster OX=7227 GN=Dlic PE=1 SV=2	7.865206983	7.776140589	7.873299508	7.902390776	7.095923712	7.139085951	7.289378077	7.038035707	7.854259464	7.140605862	0.713653603	1.639952015	0.027386	0.00171
A0A0B4K7J2	E3 SUMO-protein ligase RanBP2 OS=Drosophila melanogaster OX=7227 GN=Nup358 PE=1 SV=1	8.949297196	8.400863206	8.517183241	8.358981446	7.656066509	7.97670011	7.97607812	7.249751386	8.556581272	7.714649031	0.841932241	1.792449211	0.009265	0.021891
O76876	EG:132E8.1 protein OS=Drosophila melanogaster OX=7227 GN=ssx PE=1 SV=1	8.101441763	8.057770937	7.375227909	7.512708871	7.375907527	7.173138773	6.595820839	6.632475735	7.76178737	6.944335719	0.817451651	1.762290366	0.011519	0.039598
Q9NJH0	Elongation factor 1-gamma OS=Drosophila melanogaster OX=7227 GN=eEF1gamma PE=2 SV=2	9.573885673	9.586262417	9.614913973	9.309962439	8.762215041	8.798971955	9.032730852	8.711064444	9.521256126	8.826245573	0.695010552	1.618896274	0.031684	0.008347
Q9VIH0	Endonuclease III homolog OS=Drosophila melanogaster OX=7227 GN=NTH1 PE=3 SV=2	6.071891015	5.999441381	6.511568944	6.625685518	5.388877801	5.745466514	5.339512176	5.689076485	6.302146715	5.540733244	0.761413471	1.695150624	0.018599	0.019716
Q9VDL1	Esterase CG5412 OS=Drosophila melanogaster OX=7227 GN=CG5412 PE=2 SV=1	7.998295183	8.271101872	7.849986836	8.038952173	7.187846192	7.230611429	7.062867283	6.591110519	8.039584016	7.018108856	1.02147516	2.029993574	0.001598	0.010442
C9QP42	Eukaryotic translation initiation factor 4A, isoform E OS=Drosophila melanogaster OX=7227 GN=eIF4A PE-	11.41927379	11.49790256	10.95607195	11.31582928	10.71938775	10.66113777	10.26909128	10.80803472	11.2972694	10.61441288	0.682856518	1.605315115	0.034787	0.019997
Q9TVM2	Exportin-1 OS=Drosophila melanogaster OX=7227 GN=emb PE=1 SV=1	8.725836594	8.4086614	8.066740968	8.230103886	7.840462451	7.948137639	7.488753937	7.572819664	8.357835712	7.712543423	0.645292289	1.564056131	0.046066	0.025841
Q9N6D7	FI03258p OS=Drosophila melanogaster OX=7227 GN=hrg PE=1 SV=1	9.543892887	9.651172081	8.844910861	8.96350742	8.886305376	8.685510623	7.924942505	7.869118144	9.250870813	8.341469162	0.90940165	1.878266336	0.004948	0.047874
Q9Y095	FI04011p OS=Drosophila melanogaster OX=7227 GN=XRCC1 PE=1 SV=1	8.582163331	8.561555723	7.732192268	8.057183473	7.836680811	7.652510467	6.912681745	7.168594581	8.233273699	7.392616901	0.840656798	1.790865261	0.009372	0.045193
Q9VGZ2	FI06805p OS=Drosophila melanogaster OX=7227 GN=Rrp46 PE=1 SV=3	8.609615703	8.595795634	8.492912821	8.905049225	7.914683315	7.67140853	7.61218225	8.257389388	8.650843346	7.863915871	0.786927475	1.72539595	0.015004	0.015163
Q9VN44	FI07923p OS=Drosophila melanogaster OX=7227 GN=Karybeta3 PE=1 SV=1	6.745179919	6.642407895	6.457797326	6.747489048	5.646738135	5.973322814	5.612190788	6.050093305	6.648218547	5.82058626	0.827632287	1.774770265	0.010528	0.008881
A1Z9G2	FI18620p1 OS=Drosophila melanogaster OX=7227 GN=fand PE=1 SV=1	8.485478077	8.562142459	7.797979806	7.95647895	7.701825489	7.734175764	7.076016018	6.529144542	8.200519823	7.260290453	0.940229369	1.918833283	0.003666	0.048727
A1Z7V9	FI20020p1 OS=Drosophila melanogaster OX=7227 GN=45551045 PE=1 SV=1	8.645072847	8.572082858	9.299275746	8.936020048	7.509378399	7.716107033	8.510270184	8.341689888	8.863112875	8.019361376	0.843751499	1.79471094	0.009114	0.042734
Q24113	FI21126p1 OS=Drosophila melanogaster OX=7227 GN=nonA-l PE=1 SV=2	5.663067104	5.343056938	5.867442272	5.918240265	5.12101489	4.645362659	5.077173627	4.83142769	5.697951645	4.918744717	0.779206928	1.716187199	0.016021	0.015603
Q9W0D6	FI22004p1 OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7879 PE=1 SV=1	8.875312935	8.952259396	8.829389451	8.829376638	8.090111612	8.131649921	8.018821297	7.957677238	8.871584605	8.049565017	0.822019588	1.767879065	0.011065	0.000257
Q7K7A9	Flap endonuclease 1 OS=Drosophila melanogaster OX=7227 GN=Fen1 PE=2 SV=1	9.837777152	9.87625254	9.227060451	9.289987267	9.02762869	8.776226074	8.129281841	8.712887479	9.557769353	8.661506021	0.896263332	1.861239012	0.005608	0.028852
A0A0B4KG97	Fruitless, isoform O OS=Drosophila melanogaster OX=7227 GN=fru PE=1 SV=1	8.482698071	8.459662447	7.972941685	8.281986291	8.018477595	7.841197526	7.268811906	7.596001521	8.299322124	7.681122137	0.618199986	1.534958857	0.055994	0.037814
Q05913	General transcription factor IIF subunit 1 OS=Drosophila melanogaster OX=7227 GN=TfIIFalpha PE=1 SV-	6.805181244	6.577681762	6.322477042	6.599744536	5.791813493	5.928102196	5.317385413	5.629030255	6.576271146	5.666582839	0.909688307	1.878639576	0.004934	0.011489
Q8T9H0	GEO06673p1 OS=Drosophila melanogaster OX=7227 GN=38E.22 PE=1 SV=1	7.254138209	7.246624597	6.737825272	6.866650503	6.371558226	6.343012586	6.007495518	5.678976916	7.026309645	6.100260811	0.926048834	1.90006508	0.004212	0.016463
Q9W256	GEO12186p1 OS=Drosophila melanogaster OX=7227 GN=Mes4 PE=1 SV=1	6.986855804	7.103527955	6.37586828	6.548409629	6.102237585	5.757307497	5.434873971	5.567931154	6.753665417	5.715587551	1.038077865	2.05348992	0.001339	0.015163
Q7KRS9	GH01331p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG1815 PE=1 SV=1	7.91733692	7.685493089	7.232450932	7.347409714	7.136477806	7.16100923	6.598006916	6.591110519	7.545672664	6.871651118	0.674021546	1.595514308	0.037202	0.039786
Q7K3Z3	GH01724p OS=Drosophila melanogaster OX=7227 GN=p47 PE=1 SV=1	9.178981838	9.367027032	8.59277151	8.599257488	8.511751804	8.47963704	7.831681612	7.583086136	8.934509467	8.101539148	0.832970319	1.781349152	0.01004	0.04948
Q9VZJ3	GH01794p OS=Drosophila melanogaster OX=7227 GN=Rcd5 PE=1 SV=1	8.217121827	8.005589761	7.597833832	8.015546441	7.576672536	7.541455222	7.056635583	7.270900878	7.959022965	7.361416055	0.59760691	1.513204436	0.064682	0.030794
Q9VNH5	GH04919p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2091 PE=1 SV=1	3.778296974	3.686861325	3.090228034	3.77043241	3.217230395	3.227624335	2.492877638	2.699745203	3.581454686	2.909369393	0.672085293	1.593374391	0.03775	0.049676
Q95U54	GH06271p OS=Drosophila melanogaster OX=7227 GN=Mms19 PE=1 SV=1	6.16226301	5.818345182	5.91012958	5.84619837	5.224965843	5.132372699	5.012504875	5.135767888	5.934234036	5.126402826	0.807831209	1.750577835	0.012531	0.004099
Q24090	GH08712p OS=Drosophila melanogaster OX=7227 GN=Snr1 PE=1 SV=2	8.933444535	9.086422176	8.34893891	8.501405647	8.413203949	8.231111004	7.674678597	7.548815233	8.717552817	7.966952196	0.750600621	1.682493138	0.020336	0.048029
Q9VE08	GH10002p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6013 PE=1 SV=1	7.677748164	7.684455262	7.835964317	7.971854307	6.794415188	7.113219748	7.291352021	7.290237717	7.792505513	7.122306168	0.670199344	1.591292829	0.03829	0.013746
O96880	GH11150p OS=Drosophila melanogaster OX=7227 GN=TfIIEalpha PE=1 SV=1	6.769681086	6.551876279	6.270747667	6.313499801	6.277984121	6.005321568	5.519209493	5.643000488	6.476451208	5.861378917	0.615072291	1.531634743	0.057247	0.041541
Q9V3Z4	GH11341p OS=Drosophila melanogaster OX=7227 GN=Rpn5 PE=1 SV=1	8.797641428	8.660419496	8.229573134	8.593990937	7.984132797	7.794263694	7.356823622	8.126919335	8.570406249	7.815534862	0.754871386	1.68748115	0.019634	0.025133
Q9VNC0	GH11824p OS=Drosophila melanogaster OX=7227 GN=POLDIP2 PE=1 SV=1	10.18972499	10.57380484	10.94997053	10.75556194	9.53818798	9.551732487	9.865080754	10.11604763	10.61726558	9.767762211	0.849503365	1.801880537	0.008652	0.020439
A1Z6H7	Glycoprotein 210 kDa, isoform A OS=Drosophila melanogaster OX=7227 GN=Gp210 PE=1 SV=1	10.24546376	9.512495696	9.309707714	9.513978148	8.841091662	8.912770704	8.538007809	8.271397076	9.64541133	8.640816813	1.004594518	2.006379507	0.001908	0.020727
Q9VSC5	GM09977p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8209 PE=1 SV=1	7.122950102	6.712353576	6.546610251	6.540011522	6.203592095	5.928102196	5.738730681	5.700761458	6.730481363	5.892796607	0.837684755	1.787179764	0.009625	0.014925
Q7JVK6	GM27569p OS=Drosophila melanogaster OX=7227 GN=trsn PE=1 SV=1	6.763371483	6.545356663	6.557051454	6.794508138	5.894817175	5.735921497	5.810552645	6.280375718	6.665071934	5.930416759	0.734655175	1.663999702	0.023157	0.012055
A0A0B4JD02	Groucho, isoform F OS=Drosophila melanogaster OX=7227 GN=gro PE=1 SV=1	7.996120721	7.925171503	7.31257512	7.482696989	7.160879147	7.115018962	6.463847369	6.109759063	7.679141083	6.712376135	0.966764948	1.954453076	0.002813	0.035316
O18640	Guanine nucleotide-binding protein subunit beta-like protein OS=Drosophila melanogaster OX=7227 GN=F	9.953547698	9.861961396	9.995872026	9.931469066	9.243411109	9.246700088	9.252323966	9.280000716	9.935712547	9.25560897	0.680103577	1.602254783	0.035524	0.00009
P11147	Heat shock 70 kDa protein cognate 4 OS=Drosophila melanogaster OX=7227 GN=Hsc70-4 PE=1 SV=3	12.5586451	13.02804887	12.34702446	12.45878668	11.87870117	11.88368454	11.63887901	11.15338999	12.59812628	11.63866367	0.959462606	1.944585416	0.003027	0.017884
M9PBL3	Heat shock protein 83, isoform B OS=Drosophila melanogaster OX=7227 GN=Hsp83 PE=3 SV=1	11.73895545	11.76507721	11.2700516	11.41915153	10.94975268	10.85955239	10.62018235	11.08629761	11.54830895	10.87894626	0.669362692	1.590370269	0.038532	0.017813
E1JGN7	Heterogeneous nuclear ribonucleoprotein K, isoform E OS=Drosophila melanogaster OX=7227 GN=HnRNF	9.901202102	10.08828588	9.615021581	9.673844323	9.268190154	9.303492175	9.016644611	9.583624217	9.819588472	9.292987789	0.526600683	1.440530976	0.103518	0.031919
Q9W1A9	Histone acetyltransferase OS=Drosophila melanogaster OX=7227 GN=enok PE=1 SV=2	7.791289883	7.29686218	7.155292891	7.388991756	7.103287099	6.726086092	6.413533459	6.666237975	7.408109177	6.727286156	0.680823021	1.603053996	0.03533	0.029331
Q9VYF3	Histone deacetylase OS=Drosophila melanogaster OX=7227 GN=HDAC4 PE=1 SV=3	8.052593206	8.095577921	8.224752556	8.479854773	7.095923712	7.428819668	7.527465025	7.324722156	8.213194614	7.34423264	0.868961974	1.826348361	0.00724	0.008347
Q32KD2	Histone-lysine N-methyltransferase eggless OS=Drosophila melanogaster OX=7227 GN=egg PE=1 SV=1	5.500657551	5.208840608	4.969060305	5.470711644	4.548436171	4.576152129	4.600728799	3.951648474	5.287317527	4.419241393	0.868076134	1.825227296	0.0073	0.017156
Q9VUC1	Hsc70Cb, isoform A OS=Drosophila melanogaster OX=7227 GN=Hsc70Cb PE=1 SV=1	10.53653532	10.76147527	9.9320871	10.27069561	9.709427532	9.573697797	9.278523705	9.647673993	10.37519833	9.552330757	0.822867569	1.768918486	0.010982	0.019716
A0A126GUQ3	Humpty dumpty, isoform B OS=Drosophila melanogaster OX=7227 GN=hd PE=4 SV=1	8.70539681	9.282003128	8.593001203	8.607459694	8.218199123	7.026910509	7.377351132	7.026041092	8.796965209	7.412125464	1.384839745	2.611429479	0.000019	0.017813
A0A0B4LGZ6	Hyperplastic discs, isoform B OS=Drosophila melanogaster OX=7227 GN=hyd PE=1 SV=1	8.176482006	8.129371382	7.314355379	7.324657485	7.200652717	7.060951016	6.370356888	6.340801049	7.736216563	6.743190417	0.993026145	1.990355514	0.002151	0.039786
Q9VHI1	Hyrax OS=Drosophila melanogaster OX=7227 GN=hyx PE=2 SV=1	7.23515846	7.190401126	6.934654047	6.890406123	6.467604904	6.6518737	6.365186408	5.695766407	7.062654939	6.295107855	0.767547084	1.702372893	0.017672	0.030137
P52295	Importin subunit alpha OS=Drosophila melanogaster OX=7227 GN=Pen PE=1 SV=2	8.023053088	7.467383883	7.601193516	7.847638588	7.185865828	6.962281372	6.623970601	7.262381579	7.734817269	7.008624845	0.726192424	1.654267365	0.024788	0.022071
O77460	Inorganic pyrophosphatase OS=Drosophila melanogaster OX=7227 GN=Nurf-38 PE=1 SV=3	9.780065854	10.01617959	9.738919151	9.791315007	9.197461528	8.96639683	8.711112946	8.735381908	9.831619902	8.902588303	0.929031599	1.903997519	0.004092	0.008347
A0AVU6	IP06021p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10375 PE=2 SV=1	8.006958194	7.893782882	7.664858663	7.947613639	7.344295175	7.138201879	6.808154496	6.901606765	7.878303345	7.048064579	0.830238766	1.777979594	0.010287	0.010713
Q4QQ70	IP09819p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG15602 PE=1 SV=1	5.465693479	5.10683717	5.578314797	5.56075458	4.678071438	5.11014248	4.624084886	4.709517101	5.427900006	4.780453976	0.64744603	1.566392791	0.045345	0.018812
Q4V3Z5	IP10727p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11788 PE=2 SV=1	8.832649534	9.058217355	8.054125663	7.897783907	7.950117636	6.952225011	6.399713318	6.547535781	8.460694115	6.712397936	1.748296178	3.359615614	<0.000001	0.039786
Q9VZF5	Kinesin-like protein OS=Drosophila melanogaster OX=7227 GN=pav PE=1 SV=1	9.208865872	9.026886065	8.665651558	8.686634023	8.487437266	8.221311303	7.85015132	8.052746905	8.897009379	8.152911698	0.744097681	1.674926376	0.021448	0.021109
A1Z6Q1	Klaroid, isoform B OS=Drosophila melanogaster OX=7227 GN=koi PE=1 SV=2	8.568225037	7.596877196	7.671699919	7.596529768	7.149746406	7.247896403	6.834126995	6.904254925	7.85833298	7.034006182	0.824326798	1.770708583	0.010842	0.034349
Q9Y134	L.2.35Df OS=Drosophila melanogaster OX=7227 GN=Mtr4 PE=1 SV=1	8.578633309	8.315813154	7.581881545	8.006707775	7.529039304	7.377538286	6.83871343	7.071628197	8.120758946	7.204229804	0.916529142	1.887568684	0.00462	0.029078
Q8IPN8	L82C OS=Drosophila melanogaster OX=7227 GN=mtd PE=1 SV=1	5.920504917	5.479614734	5.923508871	5.997694046	5.031218228	4.650548244	4.951928952	5.151045307	5.830330642	4.946185183	0.884145459	1.845671065	0.006286	0.011489
Q8MLV1	Lamin-B receptor OS=Drosophila melanogaster OX=7227 GN=LBR PE=1 SV=1	10.05054019	9.851091766	9.624564458	9.798562513	8.922137479	9.243928271	8.853460894	8.593302428	9.831189731	8.903207268	0.927982464	1.902613426	0.004134	0.010713
Q7K180	LD02709p OS=Drosophila melanogaster OX=7227 GN=Map60 PE=1 SV=1	8.015208432	7.932256956	7.480939749	7.569328147	7.499047849	7.376045301	6.80252414	6.664649884	7.749433321	7.085566794	0.663866527	1.58432304	0.040153	0.049676
Q9VVU6	LD04472p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6841 PE=1 SV=2	7.822994071	7.565792285	6.858670182	7.182708286	6.768183649	6.873354554	6.200206612	6.087702555	7.357541206	6.482361843	0.875179363	1.834236114	0.006835	0.039786
Q9VYT5	LD06533p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10347 PE=1 SV=1	6.856741062	6.760435687	6.421486645	6.667521677	6.0639337	5.997389803	5.390670187	6.066523765	6.676546268	5.879629364	0.796916904	1.737384298	0.013773	0.017884
Q9V9M6	LD10456p OS=Drosophila melanogaster OX=7227 GN=Tif-IA PE=2 SV=3	7.202920575	6.845159953	6.830096552	7.150291167	6.383703655	6.384401395	6.061923748	6.644634102	7.007117062	6.368665725	0.638451337	1.556657266	0.048422	0.018812
Q9W3Y3	LD13807p OS=Drosophila melanogaster OX=7227 GN=Q9W3Y3 PE=1 SV=1	8.018066309	7.607828387	7.221059716	7.258952459	6.976133776	6.693719504	6.700040369	6.504229806	7.526476717	6.718530864	0.807945854	1.750716951	0.012518	0.02172
Q9VIL2	LD19544p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG2608 PE=1 SV=1	7.277185122	6.786719072	6.484402516	6.740247168	6.346956256	6.246434074	6.019223468	6.238114072	6.82213847	6.212681967	0.609456502	1.525684339	0.059556	0.030137
Q9VT75	LD19812p OS=Drosophila melanogaster OX=7227 GN=vnc PE=1 SV=1	7.037207735	7.043285108	7.0455071	7.097720481	6.643855526	6.627935936	6.430922938	5.988904633	7.055930106	6.422904758	0.633025348	1.55081366	0.050361	0.018812
Q8T092	LD21421p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4282 PE=2 SV=1	6.346496021	6.098671977	6.071507471	6.090478999	5.392316884	5.384150604	5.210112913	5.312745857	6.151788617	5.324831565	0.826957053	1.773939801	0.010592	0.002251
Q9W1G7	LD21576p OS=Drosophila melanogaster OX=7227 GN=Nap1 PE=1 SV=1	8.452251913	8.459035263	8.689379931	8.67544992	7.900262255	7.874088564	7.571016051	7.630968927	8.569029257	7.744083949	0.824945308	1.771467881	0.010782	0.006473
Q9W5X0	LD21953p OS=Drosophila melanogaster OX=7227 GN=Rab35 PE=1 SV=1	6.270593848	6.392047286	7.062770336	7.158967896	5.799604843	5.735921497	6.14199397	5.804546367	6.721094841	5.870516669	0.850578172	1.803223437	0.008568	0.029078
Q9VLX2	LD22651p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7154 PE=1 SV=1	5.427373086	5.015357965	5.466294181	5.416075953	4.542257596	4.769595286	4.610119199	5.250915701	5.331275296	4.793221946	0.53805335	1.452011974	0.096227	0.045901
Q9VYQ9	LD24662p OS=Drosophila melanogaster OX=7227 GN=Tango4 PE=1 SV=1	8.017709405	7.50634093	7.34078091	7.376594671	7.128251441	6.78980215	6.692926865	6.387795483	7.560356479	6.749693984	0.810662494	1.754016713	0.012225	0.023912
Q9VAX8	LD28793p OS=Drosophila melanogaster OX=7227 GN=Snu114 PE=1 SV=1	9.855380644	10.02504021	9.509761529	9.478740212	9.2863258	9.199638858	8.880028056	8.622378252	9.71723065	8.997092742	0.720137908	1.647339497	0.026014	0.027408
Q9VL71	LD29830p OS=Drosophila melanogaster OX=7227 GN=Srp54 PE=1 SV=1	8.199141119	8.154046585	7.753766873	7.87372763	7.536052148	7.616456706	7.055073207	7.229801137	7.995170552	7.359345799	0.635824752	1.553825779	0.049352	0.023749
Q9W3M7	LD32873p OS=Drosophila melanogaster OX=7227 GN=mahe PE=1 SV=1	8.256873573	8.266842754	8.192991444	8.281697075	7.746177608	7.809716914	7.60122049	7.235972193	8.249601211	7.598271801	0.65132941	1.570614815	0.044069	0.012931
Q9VWQ3	LD35981p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG6961 PE=2 SV=1	8.165328324	8.088409886	8.07013034	8.193239819	7.372429056	7.419436142	7.248609993	7.547603353	8.129277092	7.397019636	0.732257456	1.661236477	0.023609	0.002251
Q9VQ76	LD36155p OS=Drosophila melanogaster OX=7227 GN=tho2 PE=1 SV=2	9.084983314	9.380866375	8.837459896	9.140896334	8.493053994	8.472799316	8.072200571	7.937743884	9.11105148	8.243949441	0.867102039	1.823995334	0.007366	0.014278
Q9W379	LD37736p OS=Drosophila melanogaster OX=7227 GN=Zpr1 PE=1 SV=1	7.959354617	8.068321534	7.813220379	8.195091743	7.561478137	7.389425508	7.254701992	7.165349351	8.008997068	7.342738747	0.666258321	1.586951812	0.039441	0.011489
Q9VXL4	LD38104p OS=Drosophila melanogaster OX=7227 GN=Rrp47 PE=1 SV=1	7.638148924	7.401426834	7.0455071	7.401275858	7.004500693	6.560261172	6.320428914	6.49068453	7.371589679	6.593968828	0.777620851	1.714301486	0.016237	0.019523
Q9VXW2	LD41277p OS=Drosophila melanogaster OX=7227 GN=Prp5 PE=1 SV=1	7.647571377	7.265826959	6.907662341	7.216915658	6.877743563	6.568237877	5.950808787	6.674149594	7.259494084	6.517734955	0.741759128	1.672213585	0.021861	0.041541
Q9W2K4	LD44216p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG4266 PE=1 SV=2	7.149005084	6.933939077	6.752300069	6.973839947	6.253610528	6.578803664	6.224825256	5.848316987	6.952271044	6.226389109	0.725881936	1.653911382	0.024849	0.017813
Q960M4	LD45324p OS=Drosophila melanogaster OX=7227 GN=Prx5 PE=1 SV=1	9.197140557	9.406145328	8.890632285	9.620600061	8.653919009	8.525933342	8.917335432	9.011921787	9.528629558	8.777277392	0.751352165	1.683369829	0.020211	0.020093
Q95RB1	LD46870p OS=Drosophila melanogaster OX=7227 GN=cg14641 PE=1 SV=1	9.009883285	9.041558189	8.538156904	8.825517798	8.393175076	8.312532574	7.930307826	7.747338057	8.853779044	8.095838383	0.757940661	1.691075018	0.019142	0.021109
A0A0B4K7U5	Lingerer, isoform H OS=Drosophila melanogaster OX=7227 GN=lig PE=1 SV=1	9.706450671	9.840144747	9.799661408	9.694282801	9.264207072	9.075053001	9.225452366	8.540902823	9.760134907	9.026403815	0.733731091	1.662934208	0.02333	0.017765
M9NEV0	Little imaginal discs, isoform C OS=Drosophila melanogaster OX=7227 GN=lid PE=4 SV=1	8.685731797	8.555086811	8.299886467	8.40198862	8.094868625	8.0832276	7.609580273	7.71574329	8.485673424	7.875854947	0.609818477	1.526067184	0.059405	0.020055
P82890	Low molecular weight phosphotyrosine protein phosphatase 1 OS=Drosophila melanogaster OX=7227 GN	8.249978391	8.465920252	8.623880361	8.543976733	7.489445851	7.390165138	7.700750957	7.189494297	8.470938934	7.442464061	1.028474874	2.039866693	0.001483	0.006473
Q9VKZ8	LP08774p OS=Drosophila melanogaster OX=7227 GN=Usp14 PE=1 SV=1	6.969904371	6.540994842	6.766621081	7.217552808	5.842978248	5.954998678	5.875084256	6.273962263	6.873768276	5.986755861	0.887012414	1.84934247	0.00612	0.012367
E2QCZ3	LP22035p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG7705 PE=2 SV=1	7.362155499	7.947205996	7.942029052	7.626959657	6.274261035	7.299302349	7.212173227	6.506025276	7.719587551	6.822940472	0.896647079	1.861734155	0.005588	0.037814
A0A0B4K8A5	Mahjong, isoform B OS=Drosophila melanogaster OX=7227 GN=mahj PE=4 SV=1	8.156982697	8.116099815	7.980198513	8.200939438	7.451210368	7.334355228	7.0989154	6.900943885	8.113555116	7.19635622	0.917198896	1.888445169	0.00459	0.008347
O02193	Males-absent on the first protein OS=Drosophila melanogaster OX=7227 GN=mof PE=1 SV=1	7.432770744	7.278045889	7.408263497	7.328769601	6.757556014	6.683064646	6.528557162	6.949749228	7.361962433	6.718481762	0.64348067	1.56209335	0.04668	0.008347
A0A0B4KFE9	Megator, isoform B OS=Drosophila melanogaster OX=7227 GN=Mtor PE=1 SV=1	9.621967942	9.507745799	9.087810782	9.398697306	8.708393318	8.675159571	8.285253944	8.549001297	9.404055457	8.554452033	0.849603425	1.802005513	0.008644	0.011489
Q0E8J0	MEP-1, isoform A OS=Drosophila melanogaster OX=7227 GN=MEP-1 PE=1 SV=1	7.631988891	7.480479546	7.733931001	7.905070863	6.928369631	6.873354554	7.013005532	7.20639649	7.687867575	7.005281552	0.682586023	1.605014157	0.034859	0.010589
Q9VNF7	Metastasis associated 1-like, isoform B OS=Drosophila melanogaster OX=7227 GN=MTA1-like PE=1 SV=2	8.573675728	8.744997522	8.13747596	8.331388021	7.947782233	7.86038898	7.382896429	7.163723707	8.446884308	7.588697837	0.85818647	1.812758163	0.007994	0.023912
Q7JUX9	Mitochondrial ribonuclease P protein 1 homolog OS=Drosophila melanogaster OX=7227 GN=trmt10c PE=1	7.837348119	7.994598222	8.572870046	8.235502659	6.980710132	7.263354407	7.657687111	7.398343741	8.160079762	7.325023848	0.835055914	1.783926176	0.009854	0.021109
E1JHD6	Mitogen-activated protein kinase OS=Drosophila melanogaster OX=7227 GN=bsk PE=1 SV=1	7.128477284	7.222980359	7.393245922	7.265730443	6.449560731	6.233041492	6.627181643	6.53266531	7.252608502	6.460612294	0.791996208	1.73146858	0.014368	0.006473
Q86B87	Modifier of mdg4 OS=Drosophila melanogaster OX=7227 GN=mod(mdg4) PE=1 SV=1	8.263733734	7.921616494	7.642730354	7.674988288	7.398315425	7.513960531	6.925632532	7.014543272	7.875767218	7.21311294	0.662654278	1.582992343	0.040519	0.032847
M9PHG2	Moesin, isoform M OS=Drosophila melanogaster OX=7227 GN=Moe PE=1 SV=1	10.52704576	10.74468526	10.53697379	10.52071506	9.754552532	9.906208791	9.871064986	9.451856044	10.58235497	9.745920588	0.83643438	1.785631497	0.009734	0.008347
A0A0B4JDA0	Moira, isoform B OS=Drosophila melanogaster OX=7227 GN=mor PE=1 SV=1	8.387592335	8.378551086	7.829100384	7.810818605	7.649614695	7.438141067	7.171152925	6.903593388	8.101515602	7.290625519	0.810890084	1.754293436	0.012201	0.027649
A0A0B4KHR8	Multiple ankyrin repeats single KH domain, isoform E OS=Drosophila melanogaster OX=7227 GN=mask PE	8.153436273	8.39367995	7.749049999	8.036525724	7.750203735	7.545434173	7.000047068	6.83359534	8.083172986	7.282320079	0.800852907	1.742130753	0.013313	0.036301
M9MRJ4	Muscle-specific protein 300 kDa, isoform G OS=Drosophila melanogaster OX=7227 GN=Msp300 PE=1 SV-	9.285560813	9.583245856	9.377606462	9.218440796	8.399170255	8.821891199	8.61948727	8.206168509	9.366213482	8.511679308	0.854534174	1.808174826	0.008265	0.011489
Q9VY97	Mutagen-sensitive 101 OS=Drosophila melanogaster OX=7227 GN=mus101 PE=1 SV=1	6.598282695	6.338178889	6.270747667	6.258839464	5.812497645	5.672249779	5.331256576	5.942782552	6.366512179	5.689696638	0.676815541	1.598607254	0.036423	0.016463
A0A0B4LIF3	Negative elongation factor A, isoform C OS=Drosophila melanogaster OX=7227 GN=Nelf-A PE=4 SV=1	8.989524874	8.951804166	8.544123946	8.426629879	8.268658129	8.243668826	7.829022583	7.574800263	8.728020716	7.97903745	0.748983266	1.68060801	0.020608	0.030137
Q9W321	Nejire, isoform B OS=Drosophila melanogaster OX=7227 GN=nej PE=1 SV=2	8.200077049	8.200756457	7.405495058	7.624606904	7.342518457	7.3134284	6.985320363	6.304672982	7.857733867	6.98648505	0.871248817	1.829245636	0.007089	0.047627
A0A0B4KF23	Nipped-B protein OS=Drosophila melanogaster OX=7227 GN=Nipped-B PE=1 SV=1	8.06850029	7.929603736	7.655222195	7.753845153	7.195740575	7.416536276	7.008969199	6.956756437	7.851792843	7.144500622	0.707292222	1.632736774	0.028792	0.012367
Q9VFK4	NK7.1, isoform A OS=Drosophila melanogaster OX=7227 GN=NK7.1 PE=4 SV=2	7.264152736	7.200389824	6.558091139	6.831486116	6.346956256	6.231358426	5.924243509	5.928901397	6.963529954	6.107864897	0.855665057	1.809592753	0.008181	0.017156
Q9V466	Nuclear pore complex protein Nup107 OS=Drosophila melanogaster OX=7227 GN=Nup107 PE=1 SV=1	8.129990498	7.990349696	8.119321443	8.23789519	7.212374067	7.465740593	7.358076532	7.073953439	8.119389207	7.277536158	0.841853049	1.792350823	0.009271	0.005239
Q9VCW3	Nuclear pore complex protein Nup133 OS=Drosophila melanogaster OX=7227 GN=Nup133 PE=2 SV=2	6.23899701	6.823504094	5.599643605	5.867177654	5.177917275	5.193516504	4.647048414	4.975178698	6.132330591	4.998415223	1.133915368	2.194535135	0.00046	0.02172
Q9VXE6	Nuclear pore complex protein Nup153 OS=Drosophila melanogaster OX=7227 GN=Nup153 PE=1 SV=4	8.566561755	8.259003596	8.231676727	8.363888825	7.426264013	7.625244244	7.682108185	7.204821168	8.355282726	7.484609403	0.870673323	1.828516092	0.007127	0.008347
Q8IQV9	Nuclear pore complex protein Nup205 OS=Drosophila melanogaster OX=7227 GN=Nup205 PE=2 SV=1	6.696702273	6.439432873	6.857006043	7.032095859	5.904483508	6.192081961	6.123571699	6.124259168	6.756309262	6.086099084	0.670210178	1.591304779	0.038287	0.014278
Q7K0D8	Nuclear pore complex protein Nup50 OS=Drosophila melanogaster OX=7227 GN=Nup50 PE=2 SV=1	9.615859114	9.379832734	8.960768384	9.210477505	8.749533394	8.594529965	8.339744955	8.179784626	9.291734434	8.465898235	0.825836199	1.772562134	0.010698	0.016463
A1YK02	Nuclear pore complex protein Nup75 OS=Drosophila melanogaster OX=7227 GN=Nup75 PE=2 SV=1	6.419524792	5.556082787	5.959631563	6.102187144	5.221103204	5.476357619	5.582660343	5.470564803	6.009356571	5.437671493	0.571685079	1.486258519	0.077169	0.041625
Q9XZ06	Nuclear pore complex protein Nup93-1 OS=Drosophila melanogaster OX=7227 GN=Nup93-1 PE=1 SV=1	8.883423026	8.546221474	8.196078124	8.663082859	7.881419121	7.78144185	7.480191358	7.613794334	8.572201371	7.689211666	0.882989705	1.844193076	0.006355	0.012138
Q9VCH5	Nuclear pore complex protein Nup98-Nup96 OS=Drosophila melanogaster OX=7227 GN=Nup98-96 PE=1	8.420838794	8.12703765	8.305299366	8.443409366	7.422064025	7.648823694	7.686054174	7.13022241	8.324146294	7.471790976	0.852355318	1.805446059	0.008431	0.010713
Q9VBP9	Nuclear protein localization protein 4 homolog OS=Drosophila melanogaster OX=7227 GN=Npl4 PE=1 SV-	9.037677908	9.417285752	9.338679829	9.364160327	8.488240995	8.516329952	8.539327266	8.273948937	9.289450954	8.454461788	0.834989167	1.783843644	0.00986	0.006473
Q9U1H9	Nuclear RNA export factor 1 OS=Drosophila melanogaster OX=7227 GN=sbr PE=1 SV=2	8.259562135	8.299894294	7.898909049	7.998167778	7.5576544	7.555990058	7.166117865	6.942061882	8.114133314	7.305456051	0.808677262	1.751604744	0.012439	0.016278
Q24169	Origin recognition complex subunit 5 OS=Drosophila melanogaster OX=7227 GN=Orc5 PE=1 SV=1	3.896509682	3.555617092	3.925710457	4.044645457	2.459431373	3.337029616	3.132285137	3.143962259	3.855620672	3.018177096	0.837443576	1.786881021	0.009646	0.022075
A1ZAW9	Oxpecker OS=Drosophila melanogaster OX=7227 GN=Oxp PE=4 SV=1	9.409286295	9.110427335	8.898327995	8.865494922	8.744496633	8.362704969	8.125002126	8.075066423	9.070884137	8.326817538	0.744066599	1.674890291	0.021454	0.023308
A0A0B4LI06	Pasilla, isoform T OS=Drosophila melanogaster OX=7227 GN=ps PE=1 SV=1	7.950379812	7.892876581	7.765275154	7.681776409	7.215289585	7.019232865	6.901357567	6.660671189	7.822576989	6.949137802	0.873439187	1.832024995	0.006946	0.008347

P25007	Peptidyl-prolyl cis-trans isomerase OS=Drosophila melanogaster OX=7227 GN=Cyp1 PE=1 SV=2	10.52598724	10.64293685	10.45924647	10.61296266	9.933247051	9.777830305	9.829640481	10.17434926	10.5602833	9.928766774	0.631516529	1.549192615	0.050912	0.008347
E2QD73	Phosphodiesterase OS=Drosophila melanogaster OX=7227 GN=dnc PE=1 SV=1	5.968542345	5.92628708	5.933456905	5.914895619	5.599912283	5.238544941	4.926183683	5.051125853	5.935795487	5.20394169	0.731853797	1.660771737	0.023686	0.013324
Q9VPY2	Phospholipase A2 activator protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Plap PE=1 SV=	5.640434837	5.123399706	5.507702122	5.632828854	4.765534271	4.879356138	5.012504875	4.989580215	5.47609138	4.911743875	0.564347505	1.47871857	0.08104	0.017884
Q8T6B9	Poly(U)-binding-splicing factor half pint OS=Drosophila melanogaster OX=7227 GN=hfp PE=1 SV=2	7.131920322	7.348096381	7.169894193	6.920119566	6.518849178	6.53469926	6.122025238	6.041159776	7.142507616	6.304183363	0.838324253	1.787972135	0.00957	0.012055
P21187	Polyadenylate-binding protein OS=Drosophila melanogaster OX=7227 GN=pAbp PE=1 SV=3	9.653168369	10.08109448	9.966928532	10.12531148	9.069046006	9.431256037	9.254826057	8.996684661	9.956625714	9.18795319	0.768672524	1.703701425	0.017506	0.012055
Q9VC36	Polybromo OS=Drosophila melanogaster OX=7227 GN=polybromo PE=1 SV=1	8.60083587	8.505986716	8.212625146	8.278511595	7.742813897	7.663514397	7.371783237	7.945813357	8.399489832	7.680981222	0.71850861	1.645480135	0.026353	0.014278
A1Z8U0	Pre-mRNA processing factor 8 OS=Drosophila melanogaster OX=7227 GN=Prp8 PE=1 SV=1	9.329787077	9.354814573	8.681875205	8.844511961	8.641328399	8.55952199	8.066247195	7.981666437	9.052747204	8.312191005	0.740556199	1.670819862	0.022076	0.037511
Q9VJ87	Pre-mRNA-splicing factor CWC22 homolog OS=Drosophila melanogaster OX=7227 GN=ncm PE=1 SV=3	5.963651441	5.338289366	5.647455724	5.624546851	4.906890106	5.3499241	4.926183683	4.921977501	5.643485845	5.026243847	0.617241998	1.533939942	0.056376	0.024339
Q9VD51	Probable ATP-dependent RNA helicase pitchoune OS=Drosophila melanogaster OX=7227 GN=pit PE=2 S	8.312526201	7.844997196	7.440508781	7.756837144	7.507000983	7.343557121	6.615370744	6.991858092	7.838717331	7.114446735	0.724270596	1.652065167	0.025171	0.049676
Q9VKD3	Probable cysteine desulfurase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=CG12264 PE=2	10.39339478	10.82941283	11.32375067	11.13713933	9.685098205	9.6529589	10.29684441	10.29591432	10.9209244	9.982703959	0.938220441	1.916163201	0.003739	0.029331
Q9V4Q8	Probable U2 small nuclear ribonucleoprotein A' OS=Drosophila melanogaster OX=7227 GN=U2A PE=1 SV	6.8784866	6.848739794	6.287365595	6.630617437	5.997743427	6.013208898	5.119720469	5.321661962	6.661302356	5.613083689	1.048218667	2.067974889	0.0012	0.021109
Q7K2G1	Proteasomal ubiquitin receptor ADRM1 homolog OS=Drosophila melanogaster OX=7227 GN=Rpn13 PE=1	7.884253643	7.885606872	7.886165097	7.876074511	7.07467598	7.209753498	7.01863644	6.769935225	7.883025031	7.018250286	0.864774745	1.821055314	0.007525	0.003575
I0DHK3	Proteasome subunit alpha type OS=Drosophila melanogaster OX=7227 GN=Prosalpha6 PE=2 SV=1	9.484003747	9.376727636	9.195557677	9.141049234	8.968377906	8.715538081	8.325630817	7.938942512	9.299334574	8.487122329	0.812212245	1.755901899	0.012061	0.030137
P18053	Proteasome subunit alpha type-4 OS=Drosophila melanogaster OX=7227 GN=Prosalpha3 PE=1 SV=2	8.338671494	8.123140206	7.530841038	8.044481993	7.415318508	7.014412988	6.736050301	7.635888724	8.009283683	7.20041763	0.808866053	1.751833973	0.012418	0.038338
Q95083	Proteasome subunit alpha type-5 OS=Drosophila melanogaster OX=7227 GN=Prosalpha5 PE=2 SV=2	7.106932294	6.927158291	7.224233611	7.491043095	6.711494237	6.382889978	6.258842726	6.846792944	7.187341823	6.550004971	0.637336852	1.555455209	0.048815	0.028127
Q9XZJ4	Proteasome subunit alpha type-6 OS=Drosophila melanogaster OX=7227 GN=Prosalpha1 PE=1 SV=2	9.660910026	9.723958644	9.105513978	8.956337301	8.657138912	8.646371152	8.340660397	7.772755405	9.361679987	8.354231467	1.007448521	2.010352544	0.001852	0.027408
P22769	Proteasome subunit alpha type-7-1 OS=Drosophila melanogaster OX=7227 GN=Prosalpha4 PE=1 SV=2	8.879279761	8.803256279	8.227466252	8.283431441	8.016250355	7.842806844	7.450085274	8.226754339	8.548358433	7.883974203	0.66438423	1.584891667	0.039998	0.045901
P40304	Proteasome subunit beta type-1 OS=Drosophila melanogaster OX=7227 GN=Prosbeta6 PE=2 SV=2	8.890736813	8.824670145	8.465170536	8.411741668	7.931327693	7.752015538	7.595969531	7.317512177	8.648079791	7.649206235	0.998873556	1.998439027	0.002025	0.011489
Q9VEX5	Protein asunder OS=Drosophila melanogaster OX=7227 GN=Asun PE=1 SV=1	6.359960324	6.340668834	6.566379882	6.433788901	5.956520769	5.930189497	5.662922764	5.97416025	6.425199485	5.88094832	0.544251165	1.458263232	0.092457	0.010442
Q9VFR0	Protein BCCIP homolog OS=Drosophila melanogaster OX=7227 GN=CG9286 PE=2 SV=2	7.488305381	7.310162787	7.117396147	7.19830605	7.065011445	6.412814263	6.422255864	6.513182579	7.278542591	6.603316038	0.675226554	1.596847514	0.036864	0.02172
P17886	Protein crooked neck OS=Drosophila melanogaster OX=7227 GN=crn PE=2 SV=2	9.398285147	9.421652337	8.4679454	8.798586388	8.433793217	8.376717556	7.815649251	8.105211965	9.021617318	8.182842997	0.838774321	1.788530004	0.009532	0.038338
Q8SY33	Protein Gawky OS=Drosophila melanogaster OX=7227 GN=gw PE=1 SV=1	7.407211632	7.396426698	7.535882003	7.513220502	6.915281175	6.982181132	6.910076791	6.455727679	7.463185209	6.815816694	0.647368514	1.566308631	0.045371	0.012367
Q24185	Protein hook OS=Drosophila melanogaster OX=7227 GN=hook PE=1 SV=2	7.25664881	7.017870635	7.434555156	7.242169638	6.350496613	6.823378095	6.646291014	6.3660084	7.23781106	6.54654353	0.69126753	1.614701547	0.032613	0.014278
P36872	Protein phosphatase PP2A 55 kDa regulatory subunit OS=Drosophila melanogaster OX=7227 GN=tws PE	7.216554321	6.89626916	6.669737098	7.097720481	6.3854304	6.10456318	5.649868865	6.155134527	6.970070265	6.073749243	0.896321022	1.86131344	0.005605	0.015163
Q9VLT5	Protein purity of essence OS=Drosophila melanogaster OX=7227 GN=poe PE=1 SV=1	7.694629323	7.485214085	7.764850669	8.002800325	7.023476451	7.244620347	7.155265562	6.822377198	7.736873601	7.061434889	0.675438711	1.597082358	0.036805	0.014278
Q9V3J4	Protein SEC13 homolog OS=Drosophila melanogaster OX=7227 GN=Sec13 PE=1 SV=1	7.555790198	7.648745747	7.898140108	8.279960474	7.160879147	7.106904331	7.091324837	7.355513531	7.845659132	7.178655461	0.66700367	1.587771901	0.039221	0.02172
A8JUV0	Protein strawberry notch OS=Drosophila melanogaster OX=7227 GN=sno PE=1 SV=2	8.928906792	8.866142103	8.200694931	8.491539972	8.211887475	8.160180336	7.527465025	7.577173024	8.62182095	7.869176465	0.752644485	1.684878413	0.019997	0.039786
Q8INX3	Protein TIPIN homolog OS=Drosophila melanogaster OX=7227 GN=CG10336 PE=2 SV=2	8.515439451	8.899003909	8.353610241	8.322998627	7.883864367	7.809167924	7.317402339	7.283329177	8.522763057	7.573440952	0.949322105	1.930965121	0.00335	0.015163
Q9W517	Protein wings apart-like OS=Drosophila melanogaster OX=7227 GN=wapl PE=1 SV=1	6.519456174	6.194623069	6.422636285	6.548409629	5.722465453	5.936432898	5.219131413	6.048820821	6.421281289	5.731712646	0.689568643	1.612801228	0.033042	0.029333
Q8INB9	RAC serine/threonine-protein kinase OS=Drosophila melanogaster OX=7227 GN=Akt1 PE=1 SV=3	8.508011184	8.19331793	8.017316841	8.22829948	7.645297401	7.496928088	7.194642863	7.3489426	8.236736358	7.421452738	0.81528362	1.759644047	0.011741	0.010713
Q9VGG9	RE35509p OS=Drosophila melanogaster OX=7227 GN=CG14730 PE=1 SV=4	8.615131599	8.409309468	8.039314741	8.164520335	8.04930323	7.682266305	7.265465595	7.375491437	8.307069036	7.593131642	0.713937394	1.640274641	0.027325	0.032645
Q8INP9	RE51612p OS=Drosophila melanogaster OX=7227 GN=Dmel\CG11980 PE=1 SV=1	9.286816827	9.677524018	9.456363239	9.503853639	8.780374846	8.672782893	8.474233868	9.037100838	9.481139431	8.741123111	0.74001632	1.670194732	0.022173	0.01223
M9PIG8	Regulatory particle non-ATPase 10, isoform B OS=Drosophila melanogaster OX=7227 GN=Rpn10 PE=4 S	9.251485684	9.409867779	8.923903856	9.025711807	8.502234266	8.345178435	8.056141673	7.701092779	9.152742282	8.151161788	1.001580493	2.002192229	0.001969	0.014278
Q9U9Q1	Replication factor C 38kD subunit, isoform A OS=Drosophila melanogaster OX=7227 GN=RfC38 PE=1 SV=	8.696356213	8.786617703	8.114089209	8.249202074	8.3255295	7.536798854	6.993521455	7.164265813	8.4615663	7.505028906	0.956537394	1.940646564	0.003118	0.045652
P53034	Replication factor C subunit 2 OS=Drosophila melanogaster OX=7227 GN=RfC4 PE=1 SV=1	10.71164674	11.32873332	9.899374468	10.2893473	10.15139613	9.169458412	8.229161237	8.827452686	10.55727546	9.094367117	1.46290834	2.75663516	0.000006	0.042632
Q9VKW3	Replication factor C subunit 3 OS=Drosophila melanogaster OX=7227 GN=RfC3 PE=1 SV=2	8.777454186	8.740302738	8.480736561	8.727351276	8.176920295	7.537464993	7.307691582	8.109687526	8.68146119	7.782941099	0.898520091	1.864152764	0.005489	0.020368
Q7K1Q7	Ribosome assembly factor mrt4 OS=Drosophila melanogaster OX=7227 GN=RpLP0-like PE=1 SV=1	7.828343398	7.579191416	7.606456159	7.817365754	7.12101469	6.937004489	6.559236239	7.109475221	7.707839182	6.931682659	0.776156522	1.71256236	0.016439	0.012055
Q9V535	RNA-binding protein 8A OS=Drosophila melanogaster OX=7227 GN=tsu PE=1 SV=1	7.060609785	7.051141746	6.756791751	7.051688709	6.447909105	6.727270682	6.060305871	5.528714066	6.980057998	6.191049931	0.789008067	1.727886036	0.01474	0.041955
Q9W1M9	Rrp4, isoform A OS=Drosophila melanogaster OX=7227 GN=Rrp4 PE=1 SV=1	8.064023767	8.124700369	7.556355097	7.857976452	7.411933885	7.096011552	6.650501488	6.749992786	7.900763921	6.977109928	0.923653994	1.896913633	0.004312	0.017813
Q9VVI0	SD09427p OS=Drosophila melanogaster OX=7227 GN=U4-U6-60K PE=1 SV=1	7.977127285	7.897402756	7.714239736	8.200632297	7.422905002	7.288216587	6.85600281	7.282834309	7.947350518	7.212489677	0.734860841	1.664236934	0.023118	0.015163
Q9W457	Serine hydroxymethyltransferase OS=Drosophila melanogaster OX=7227 GN=Shmt PE=1 SV=1	9.771908588	9.83861104	10.10700043	10.23735312	9.035623008	8.78146549	8.973182436	9.846189442	9.988718295	9.159115094	0.829603201	1.777196494	0.010346	0.034719
Q9VB23	Serine/threonine protein phosphatase 2A regulatory subunit OS=Drosophila melanogaster OX=7227 GN=v	6.461970764	5.990094601	6.322477042	6.608780716	5.617650559	4.89249357	5.3985755	5.904959515	6.345830781	5.453419786	0.892410995	1.856275693	0.005816	0.027408
P52304	Serine/threonine-protein kinase polo OS=Drosophila melanogaster OX=7227 GN=polo PE=1 SV=2	6.752485972	6.603061275	6.94639246	6.727479492	6.083212761	6.370739874	6.214741832	5.403460952	6.7573548	6.018038855	0.739315945	1.669384111	0.022299	0.032558
Q9W2U4	Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Drosophila melanogaster OX=7227 GN=	9.039019222	9.276483651	8.285537252	8.11437838	8.150254208	7.740531913	7.371163179	6.978805263	8.678854626	7.56018864	1.118665986	2.171460916	0.000548	0.041541
Q9VFS5	Serine/threonine-protein phosphatase 4 regulatory subunit 3 OS=Drosophila melanogaster OX=7227 GN=	6.041399805	5.687100949	5.874363738	6.002409707	5.475732884	5.35620931	5.306186188	5.781317461	5.90131855	5.479861461	0.421457089	1.339279514	0.192553	0.035316
X2JDI1	Serine/threonine-protein phosphatase OS=Drosophila melanogaster OX=7227 GN=mts PE=3 SV=1	8.861241002	8.651035805	8.261962398	8.096577643	7.648896043	7.814101144	7.765927037	7.87981706	8.467704212	7.777185321	0.690518891	1.613863869	0.032802	0.022698
X2JG90	Serine/threonine-protein phosphatase OS=Drosophila melanogaster OX=7227 GN=Pp4-19C PE=3 SV=1	9.036503165	8.846765153	8.128429265	8.495248068	8.20750164	7.667770583	7.331521089	7.320400946	8.626736413	7.631798564	0.994937848	1.992994665	0.002109	0.029331
Q94545	Set1/Ash2 histone methyltransferase complex subunit ASH2 OS=Drosophila melanogaster OX=7227 GN=a	7.812231438	7.645554724	7.274025146	7.653955629	6.940166058	6.872286762	6.625041787	6.764794127	7.596441734	6.800572183	0.795869551	1.736123467	0.013898	0.010442
A4V3W1	Shaggy, isoform J OS=Drosophila melanogaster OX=7227 GN=sgg PE=1 SV=1	7.771732617	7.499330854	7.543408279	7.242794964	6.836680911	6.739062079	6.759540239	6.36500939	7.514316679	6.675073155	0.839243524	1.789111776	0.009492	0.011489
A0A0B4KHS6	Signal transducer and activator of transcription OS=Drosophila melanogaster OX=7227 GN=Stat92E PE=3	7.788754937	7.614361855	7.344265494	7.222004448	6.892390338	6.916451064	6.578205153	6.598653587	7.492346684	6.746425035	0.745921648	1.677045287	0.021131	0.014439
M9PET3	Simjang, isoform D OS=Drosophila melanogaster OX=7227 GN=simj PE=1 SV=1	9.301384668	9.270204198	8.739333134	8.993007476	8.392745894	8.303285351	8.034559134	8.099662074	9.075982369	8.207563113	0.868419256	1.825661448	0.007277	0.011489
Q05856	Small nuclear ribonucleoprotein-associated protein B OS=Drosophila melanogaster OX=7227 GN=SmB PE	8.898941	8.310985708	8.183688767	8.552994353	8.052023757	7.634598993	7.240444843	8.134677451	8.486652457	7.765436261	0.721216196	1.648571199	0.025792	0.047006
Q9XZ21	Something that sticks like glue, isoform A OS=Drosophila melanogaster OX=7227 GN=snama PE=1 SV=1	6.133766104	5.983831698	6.212931874	6.126734325	5.40599182	5.393342484	5.188835321	5.727083848	6.114316	5.428813368	0.685502632	1.608262199	0.03409	0.011489
A0A0B4KGU8	Splicing factor 1, isoform C OS=Drosophila melanogaster OX=7227 GN=SF1 PE=1 SV=1	8.892792537	8.962240515	8.046568315	8.290921349	8.182890076	7.903663789	7.438327045	7.370872605	8.548130679	7.723938378	0.8241923	1.770543513	0.010854	0.047006
Q9VPR5	Splicing factor 3b subunit 1, isoform A OS=Drosophila melanogaster OX=7227 GN=Sf3b1 PE=1 SV=2	7.921942904	7.857107546	7.351207754	7.507068075	7.238404017	7.09965185	6.739993443	7.161009798	7.65933157	7.059764777	0.599566793	1.515261501	0.06381	0.030137
Q9W0M7	Splicing factor 3B subunit 3 OS=Drosophila melanogaster OX=7227 GN=Sf3b3 PE=1 SV=2	10.26419781	10.49759053	9.752008069	10.0198574	9.622783005	9.569615149	9.185278535	9.108505519	10.13341345	9.371545552	0.7618679	1.695684657	0.018528	0.024455
M9PHZ3	Ssu72 CTD phosphatase, isoform B OS=Drosophila melanogaster OX=7227 GN=Ssu72 PE=1 SV=1	5.305422349	5.576665967	4.889029298	4.972210152	4.649614995	4.802502267	4.093062339	4.606147586	5.185831942	4.537831797	0.648000145	1.566994531	0.045161	0.041625
Q9W0S7	Staphylococcal nuclease domain-containing protein 1 OS=Drosophila melanogaster OX=7227 GN=Tudor-S	9.92550024	10.0495371	10.1763729	10.18299026	9.389092584	9.363007451	9.486108927	9.369153578	10.08360013	9.401840635	0.681759492	1.604094896	0.035079	0.002645
A0A0B4JD33	Suppressor of variegation 2-10, isoform L OS=Drosophila melanogaster OX=7227 GN=Su(var)2-10 PE=1 S	6.216160111	6.00254439	6.142659878	6.228666418	5.632267653	5.44726806	5.142093096	5.390881037	6.147507699	5.403127462	0.744380238	1.675254448	0.021399	0.008347
Q9W1F4	THO complex subunit 5 OS=Drosophila melanogaster OX=7227 GN=thoc5 PE=1 SV=2	7.806817791	7.751492088	7.337870193	7.88464495	6.678071238	6.960275838	6.822129706	6.970659083	7.695206255	6.857783966	0.837422289	1.786854656	0.009648	0.010442
Q8INH7	Timeout OS=Drosophila melanogaster OX=7227 GN=timeout PE=1 SV=2	9.793840305	10.23597508	9.32059516	9.399581045	9.013740492	8.641515326	7.997420781	8.028082506	9.687497898	8.420189776	1.267308122	2.407120095	0.000091	0.021109
Q8IRT7	Tousled-like kinase, isoform C OS=Drosophila melanogaster OX=7227 GN=Tlk PE=1 SV=4	9.140050444	9.400374664	8.732930528	9.005576115	8.358870105	7.512605493	7.318691907	7.594442804	9.069732938	7.696152577	1.37358036	2.591128134	0.000022	0.012367
A0A0B4KFE3	Toutatis, isoform F OS=Drosophila melanogaster OX=7227 GN=tou PE=1 SV=1	7.781546647	7.773203548	7.425848126	7.684932537	7.251718369	7.097832878	6.666176204	6.707633865	7.666382715	6.930840329	0.735542386	1.665023322	0.022991	0.016463
M9PFF9	Trailer hitch, isoform D OS=Drosophila melanogaster OX=7227 GN=tral PE=1 SV=1	8.721815696	9.641027088	9.219289592	9.311714786	8.168420595	8.334632434	8.538007809	7.86468711	9.22346179	8.226436987	0.997024804	1.995879752	0.002064	0.017947
Q9V460	Transcription elongation factor SPT5 OS=Drosophila melanogaster OX=7227 GN=Spt5 PE=1 SV=1	9.800436809	9.732750894	9.113030461	9.313868398	9.127219639	9.047298308	8.417467235	8.51803318	9.490021641	8.77750459	0.71251705	1.638660573	0.027633	0.04227
P52654	Transcription initiation factor IIA subunit 1 OS=Drosophila melanogaster OX=7227 GN=TfIIA-L PE=1 SV=2	7.645221919	7.487575899	7.188251807	7.697483665	6.780046899	6.682763148	6.561481593	6.994329624	7.504633323	6.754655316	0.749978007	1.681767192	0.02044	0.012367
Q24325	Transcription initiation factor TFIID subunit 2 OS=Drosophila melanogaster OX=7227 GN=Taf2 PE=1 SV=2	6.280963982	5.879992038	6.180318528	6.298467396	5.488642992	5.52447092	5.584954715	5.792209043	6.159935486	5.597569417	0.562366068	1.476689052	0.082113	0.014278
A0A0B4JD97	Transforming acidic coiled-coil protein, isoform K OS=Drosophila melanogaster OX=7227 GN=tacc PE=1 S	7.422826872	7.294188196	7.7049511	7.548062123	6.329122964	6.835491373	7.119947337	6.343851741	7.492507073	6.657103354	0.835403719	1.784356297	0.009824	0.021109
Q8MS69	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 OS=Drosophila melanogaster OX=7	8.873609294	8.966756056	8.483977732	8.811338534	8.226892992	7.904690318	7.505157627	7.66206604	8.783920404	7.824701744	0.95921866	1.944256632	0.003035	0.012367
Q9W4M9	tRNA (cytosine(34)-C(5))-methyltransferase OS=Drosophila melanogaster OX=7227 GN=Nsun2 PE=2 SV=1	8.319395654	8.264708763	7.580908645	7.999951411	7.798309004	7.390904379	7.003298225	7.261878709	8.041241118	7.363597579	0.677643539	1.599524998	0.036195	0.043424
E1JIR1	tRNA pseudouridine synthase OS=Drosophila melanogaster OX=7227 GN=Pus1 PE=3 SV=1	8.824817078	9.068802146	9.119262338	8.677607928	8.128251341	8.228259797	8.346443999	7.757357925	8.922622372	8.115078266	0.807544107	1.750229498	0.012562	0.013746
M9PDU3	U-shaped, isoform D OS=Drosophila melanogaster OX=7227 GN=ush PE=1 SV=1	9.145327241	9.195890435	8.332321245	8.739968785	8.489847113	8.254915895	7.779333551	7.914148073	8.853376927	8.109561158	0.743815769	1.674599116	0.021498	0.042923
Q9W462	Ubiquitin carboxyl-terminal hydrolase 30 homolog OS=Drosophila melanogaster OX=7227 GN=Usp30 PE=2	6.66598133	7.22997237	7.606456159	7.283437995	5.548436071	6.659349211	6.639950874	6.053903335	7.196461964	6.225409873	0.971052091	1.960269609	0.002694	0.041625
Q9VYQ8	Ubiquitin carboxyl-terminal hydrolase 7 OS=Drosophila melanogaster OX=7227 GN=Usp7 PE=1 SV=1	8.690512283	8.655458794	8.31012413	8.443152796	8.182393536	7.975236866	7.989554911	7.965918303	8.524812001	8.028275904	0.496536097	1.410822116	0.124755	0.014278
M9PBW0	Ubiquitin conjugating enzyme E2M, isoform B OS=Drosophila melanogaster OX=7227 GN=UbcE2M PE=3	8.038607026	7.828069973	7.263597247	7.441792308	7.276123679	7.039298068	6.403496332	6.738029754	7.643016639	6.864236958	0.77877968	1.715679033	0.016079	0.039786
P35128	Ubiquitin-conjugating enzyme E2 N OS=Drosophila melanogaster OX=7227 GN=ben PE=1 SV=1	7.398771467	7.194689945	7.032413017	7.284650674	6.714244847	6.595805729	6.204583438	6.224830523	7.227631276	6.434866134	0.792765142	1.732391672	0.014274	0.012055
O02373	UDP-glucose 6-dehydrogenase OS=Drosophila melanogaster OX=7227 GN=sgl PE=1 SV=1	6.669859878	6.625963454	6.634849247	6.732966169	5.596934584	5.747842691	5.705556419	5.740048762	6.665909687	5.697595614	0.968314073	1.95655284	0.002769	0.00009
M9PGS2	Ultraspiracle, isoform B OS=Drosophila melanogaster OX=7227 GN=usp PE=3 SV=1	8.777860901	8.361267698	7.947601415	8.344427315	7.974413794	7.379029689	7.236343896	7.805009003	8.357789332	7.598699096	0.759090237	1.692423046	0.018961	0.036495
Q9VBI2	UMP-CMP kinase OS=Drosophila melanogaster OX=7227 GN=Dak1 PE=1 SV=1	10.15570044	10.05398987	10.0302304	9.682159283	9.338958243	9.047070403	9.252949918	8.935710567	9.980519999	9.143672283	0.836847717	1.786143159	0.009698	0.010442
A1Z9M5	Uncharacterized protein OS=Drosophila melanogaster OX=7227 GN=Dmel\CG30069 PE=1 SV=1	4.89180237	4.827620112	5.389384765	5.669480736	4.371558426	4.395929433	4.477555556	4.265749268	5.194571996	4.377698171	0.816873825	1.761584677	0.011578	0.020981
Q9VRP2	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10576 PE=1 SV=	10.62099182	10.7013795	10.11117712	9.982543693	9.822729167	9.859763833	9.698156046	9.101267551	10.35402303	9.620479149	0.733543885	1.662718438	0.023366	0.04227
Q9VMU2	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG5828 PE=1 SV=1	8.020918151	9.023413357	8.51402103	8.573415567	7.307427796	7.43384655	7.689988799	7.641918529	8.532942026	7.518295419	1.014646608	2.020407928	0.001717	0.015625
Q9VRY5	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=Dmel\CG8549 PE=1 SV=1	9.702970003	9.627591047	9.217123046	9.645225589	8.851123479	8.892567529	8.445156657	8.48137907	9.548227421	8.667556684	0.880670738	1.841231127	0.006494	0.011898
Q9VMD3	Uncharacterized protein, isoform A OS=Drosophila melanogaster OX=7227 GN=HemK1 PE=1 SV=1	8.04001218	8.243204348	9.122832664	8.822616401	6.721098518	7.104189027	7.894839255	7.929322551	8.557166398	7.412362338	1.144804061	2.211160978	0.000405	0.041625
Q9VID9	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=BEST:LD19244 PE=1 SV=	8.557257218	8.61858287	8.215667243	8.301223756	7.941340313	7.757722415	7.415703732	7.371797679	8.423182772	7.621641035	0.801541737	1.74296275	0.013234	0.014278
M9PGG8	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=CG40016 PE=1 SV=1	8.332182464	8.421571137	7.975486022	8.002800325	7.682291604	7.719037075	7.174738069	6.727471462	8.183009987	7.325884553	0.857125434	1.811425452	0.008072	0.032645
B7YZX6	Uncharacterized protein, isoform B OS=Drosophila melanogaster OX=7227 GN=Dmel\CG10600 PE=1 SV=	7.315544385	7.136497925	7.336120741	7.216278206	6.421222658	6.412814263	6.407268901	6.335700674	7.251110314	6.394251624	0.85685869	1.811090564	0.008092	0.000257
X2JKH9	Uncharacterized protein, isoform F OS=Drosophila melanogaster OX=7227 GN=huwe1 PE=1 SV=1	7.12571652	6.947411589	6.857006043	6.838255203	6.364571797	6.350769545	6.229124047	5.830382549	6.942097339	6.193711984	0.748385354	1.679911643	0.020709	0.012055
Q9VBX3	Vig2, isoform B OS=Drosophila melanogaster OX=7227 GN=vig2 PE=1 SV=2	9.379661598	9.409529746	9.430330979	9.195730343	8.687549784	8.718419549	8.875085903	8.179784626	9.353813167	8.615209965	0.738603201	1.668559579	0.022429	0.015163
Q7KVP9	Xeroderma pigmentosum D OS=Drosophila melanogaster OX=7227 GN=Xpd PE=1 SV=1	8.049807532	7.626268248	7.145918121	7.358930227	7.077883158	7.115018962	6.387027082	6.651875167	7.545231032	6.807951092	0.73727994	1.667029853	0.02267	0.045813
Q9VXG1	Zinc finger protein hangover OS=Drosophila melanogaster OX=7227 GN=hang PE=1 SV=4	9.454881869	9.524149752	8.731687793	9.141813475	8.775773992	8.375983518	7.959244669	7.935343324	9.213133223	8.261586376	0.951546847	1.933945108	0.003277	0.027611

Supplemental Table 4: TMT intensities for each protein was log2 transformed and normalized based on median TMT intensity per channel. Log2-transformed, median normalized TMT intensities were further normalized to the level of Histone H4. Only proteins that were statistically enriched are shown (unpaired t-test with a Benjamini, Krieger and Yekutieli multiple test correction and false discovery rate of 5%).

Supplemental Table 3-5: Primers used in iPOND study

dsRNAs Primers:	
GFP-dsRNA-RP	TAATACGACTCACTATAGGGGTGAGTTATAGTTGTATTC
GFP-dsRNA-FP	TAATACGACTCACTATAGGGGGAGAAGAACTTTTCACTGG
BRWD3-dsRNA1-FP	TAATACGACTCACTATAGGGAAACGACTACCCAGGACATT
BRWD3-dsRNA1-RP	TAATACGACTCACTATAGGGCCCACGGAGCTGTTCTTT
BRWD3-dsRNA2-FP	TAA TAC GAC TCA CTA TAG GAT GGA AAC TAG ACAACC CAG TTC
BRWD3-dsRNA2-RP	TAA TAC GAC TCA CTA TAG GAT GTC TGT AAT CTC GGA TGA GG
Hd-dsRNA-FP	TAATACGACTCACTATAGGGGTCGCAGCTCACGCTC
Hd-dsRNA-RP	TAATACGACTCACTATAGGGGGTTCAACCAATGCAATTACTA
Cul4-dsRNA-FP	TAATACGACTCACTATAGGGATCTGTGGTTCCCTTGTTGC
Cul4-dsRNA-RP	TAATACGACTCACTATAGGGGCCGAACACCTAACGTCAAT
RTEL-dsRNA-FP	TAATACGACTCACTATAGGGAGACGCGAAGTAGGGACAGA
RTEL-dsRNA-RP	TAATACGACTCACTATAGGGCAGATTTTTCGGGTCTTGGA
ELG1-dsRNA-FP	TAATACGACTCACTATAGGGCTTGGCAGCGGTTCTACTTC
ELG1-dsRNA-RP	TAATACGACTCACTATAGGGCCTAATCGAGGATGCGGATA
Polybromo-dsRNA-FP	TAATACGACTCACTATAGGGGATTTTCCATTCTGCTCCCA
Polybromo-dsRNA-RP	TAATACGACTCACTATAGGGGGAAGTGTTCAAGAGCAGCC
Pont -dsRNA-FP	TAATACGACTCACTATAGGGTCAGTTTTCTTCGGCTTCA
Pont -dsRNA-RP	TAATACGACTCACTATAGGGGTATTCAGCAATGAGATCAAGA
Flfl-dsRNA-RP	TAATACGACTCACTATAGGGGTATCTGAAGCAGTTAGCCA
Flfl-dsRNA-FP	TAATACGACTCACTATAGGGGCCGATTGGCCTGGTTG
Hyd -dsRNA-FP	TAATACGACTCACTATAGGGCTTGTGCAGCGTTTGGAATA
Hyd -dsRNA-RP	TAATACGACTCACTATAGGGAGGGTTCGCAATGTTAGCAC
Mei41 (ATR)-dsRNA-RP	TAATACGACTCACTATAGGGGTGCGACATGGACACAAAAC
Mei41 (ATR)-dsRNA-FP	TAATACGACTCACTATAGGGTTTGGGTAAGCACTTGGACC
DNApol-alpha180-dsRNA-RP	TAATACGACTCACTATAGGGTCCTTGCTGATATTTTGGGC
DNApol-alpha180-dsRNA-FP	TAATACGACTCACTATAGGGGAAACCTTCTCGGTCTGCTG
DEK-dsRNA-FP	TAATACGACTCACTATAGGGGACTCGTCCGGTTCCATTAG
DEK-dsRNA-RP	TAATACGACTCACTATAGGGATGGCCTGGACAAGAACAAC

qPCR Primers:	
BRWD3-qPCR-FP	CAGTGCGCTATTTGAGTCGC
BRWD3-qPCR-RP	TCGCTCCTTTTTGACTCGCT
DEK-qPCR-FP	ACAAATGTTTAACTGCTGTTCCCA
DEK-qPCR-RP	GCAGGAGTTGGGATGCGATA
Hyd-qPCR-FP	TGTGAGGTATCCGAGGCTCT
Hyd-qPCR-RP	TCGTCAGAGTTATCCAGATTCGAC
DNApolalpha180-qPCR-FP	CACAGCAGACCGAGAAGGTT
DNApolalpha180-qPCR-RP	TTTCGGCGACTTTGCTTTGG
Hd-qPCR-FP	CGTTTCTTCTGTCCCACGGA
Hd-qPCR-RP	CGTTGCGTCCGAGATATCCA
Cul4-qPCR-FP	CGCCAGCTAATAGTGTAGCGA
Cul4-qPCR-RP	TTTCAAAGGACTCGGCTTGT
RTEL-qPCR-FP	CCCAGGCGGATATCACCTTC
RTEL-qPCR-RP	ATGTTGTGGGCCTCATCCAG
ELG1-qPCR-FP	ATGCTCGGAATCGCTCTCTG
ELG1-qPCR-RP	TGCCTCACTGCCGATTTCTT
Polybromo-qPCR-FP	CATGCGCAAGTTCCAACACA
Polybromo-qPCR-RP	GAGCTCAGCGAGGGTGTATC
Pont-qPCR-FP	GCTGTGTTATTCGTGGCACC
Pont-qPCR-RP	GAGCTGGTTCCAATCTCGCT
mei41(ATR)-qPCR-FP	GATCGCATCTTCCGGCAAAC
mei41(ATR)-qPCR-RP	CTGACTCCTGGAAGCCACTG
flfl-qPCR-RP2	CGTGAGGATGTCGATGGAGG
flfl-qPCR-FP2	CGCGACACAGTTCTCTTCCT
alphatub84b qPCR Fwd	CACACCACCCTGGAGCATTC
alphatub84b qPCR Rev	CCAATCAGACGGTTCAGGTTG

Chapter IV: R-loop mapping and characterization during Drosophila embryogenesis reveals developmental plasticity in R-loop signatures

Abstract

R-loops are involved in transcriptional regulation, DNA and histone post-translational modifications, genome replication and genome stability. To what extent R-loop abundance and genome-wide localization is actively regulated during metazoan embryogenesis is unknown. Drosophila embryogenesis provides a powerful system to address these questions due to its well-characterized developmental program, the sudden onset of zygotic transcription and available genome-wide data sets. Here, we measure the overall abundance and genome localization of R-loops in early and late-stage embryos relative to Drosophila cultured cells. We demonstrate that absolute R-loop levels change during embryogenesis and that RNaseH1 catalytic activity is critical for embryonic development. R-loop mapping by strand-specific DRIP-seq reveals that R-loop localization is plastic across development, both in the genes which form R-loops and where they localize relative to gene bodies. Importantly, these changes are not driven by changes in the transcriptional program. Negative GC skew and absolute changes in AT skew are associated with R-loop formation in Drosophila. Furthermore, we demonstrate that while some chromatin binding proteins and histone modifications such as H3K27me3 are associated with R-loops throughout development, other chromatin factors associated with R-loops in a developmental specific manner. Our findings highlight the importance and developmental plasticity of R-loops during Drosophila embryogenesis.

* This chapter is in press as Munden, A., Benton, M. L., Capra, J. A. & Nordman, J. R-loop mapping and characterization during Drosophila embryogenesis reveals developmental plasticity in R-loop signatures. *Journal of Molecular Biology.* (2021). doi: 10.1016/j.jmb.2022.167645.

Introduction

R-loops are a three-stranded nucleic acid structure canonically formed when nascent RNA from transcription reanneals to the template DNA strand, resulting in a displaced single strand of DNA (Aguilera and García-Muse 2012). R-loops were initially identified at the highly transcribed *18S* and *28S* sequences within the rDNA locus of *Drosophila melanogaster* (White and Hogness 1977; Glover and Hogness 1977). More recent studies have demonstrated that R-loops are critical for a diverse set of biological processes (Chédin 2016; Skourtie-Stathaki and Proudfoot 2014). In fact, genome-wide R-loop mapping studies have revealed that R-loops are abundant in eukaryotes and can occupy 10% or more of the genome (Dumelie and Jaffrey 2018; Wahba and Koshland et al. 2016; Fang and Zhang et al. 2019; Xu and Sun et al. 2017; Yan and Liu et al. 2020; Zeller and Gasser et al. 2016; Chen and Fu et al. 2017; Chen and Fazzio et al. 2015; Crossley and Cimprich et al. 2020; Ginno and Chédin et al. 2012; Tan-Wong and Proudfoot et al. 2019; Chan and Hieter et al. 2014; Liu and Han et al. 2021). While R-loops were identified over 40 years ago, their physiological relevance remained elusive for many years.

R-loops are found in all domains of life and their formation is often conserved across cell types and even species (Sanz and Chédin et al. 2016). Deciphering the function of R-loops, however, has been challenging due to their diverse and sometimes contradictory roles in genome function. R-loops are essential for initiation of replication in

plasmids and promote mitochondrial genome stability (Dasgupta and Tomizawa et al. 1987; Silva and Aguilera et al. 2018). In contrast, R-loops can block replication fork progression and promote genome instability in an orientation-specific manner (Hamperl and Cimprich et al. 2017; Lang and Merrikh et al. 2017). While potentially causing double-strand breaks at head-on replication-transcription conflicts, R-loops can promote recombination and double strand break repair pair (Stork and Cimprich et al. 2016; Ouyang and Zou et al. 2021). R-loops also have diverse roles in transcription and chromatin function. In mammalian cells, R-loops have been shown to regulate both histone and DNA methylation at promoter regions (Ginno and Chédin et al. 2012; Chen and Fazzio et al. 2015). While R-loops are often associated with histone modifications correlated with active transcription, recent work has shown that R-loops can help recruit the Polycomb complex to target loci to promote transcriptional silencing (Skourti-Stathaki and Pombo et al. 2019; Alecki and Francis et al. 2020). Genome-wide R-loop mapping studies in yeast, plants and mammalian cultured cells have identified factors such as DNA sequence, DNA topology and histone modifications associated with R-loop formation (Ginno and Chédin et al. 2012; Stolz and Chédin et al. 2019; Hage and Tollervey et al. 2010). R-loop mapping studies in plants and mammalian cells have further revealed that R-loop formation can be dynamic as a function of development (Fang and Zhang et al. 2019; Xu and Sun et al. 2020; Yan and Liu et al. 2020). The extent of R-loop plasticity in other metazoans has yet to be defined. Studying R-loops in the context of development could provide insight into the functional roles R-loops play in establishing developmental-specific changes in chromatin structure, function and transcriptional programs.

Drosophila provide a well-established developmental system to interrogate R-loop plasticity during development. At the earliest stages of Drosophila embryogenesis, rapid cell proliferation is driven by maternally stockpiled proteins and RNA (Tadros and Lipshitz 2009). Approximately two hours after fertilization, zygotic genome activation is triggered and the transcription of over 3000 genes necessary for growth and differentiation are induced in a process known as the maternal-to-zygotic transition (MZT) (Hamm and Harrison 2018; Harrison and Eisen et al. 2011). Prior to the MZT, cells are largely undifferentiated and have abbreviated cell cycles (Foe and Alberts 1983). After the MZT, however, the cell cycle slows and cells become differentiated as morphogenesis proceeds (Farrell and O'Farrell 2014). The changes in cell cycle programs, the onset of zygotic gene activation and cell differentiation during embryogenesis provide a unique system to interrogate whether R-loop formation or resolution impacts embryogenesis and the extent to which, if any, R-loop position and properties change as a function of development.

In this study, we measured R-loop abundance and position in Drosophila embryos and cultured cells. We show that absolute R-loop levels change during embryogenesis and resolution of R-loops is essential for embryogenesis. We mapped R-loops at near base-pair resolution in 2-3 hour embryos (immediately after the MZT), late-stage embryos (14-16 hours after fertilization) and cultured S2 cells, which are derived from late-stage embryos. We show that, while some sites of R-loop formation are constant during development, there is extensive R-loop plasticity during Drosophila development. Furthermore, we were able to demonstrate changes in the localization of R-loops across gene bodies and the role AT and GC skew play in Drosophila R-loop formation. By

leveraging data available through modENCODE and other publicly available datasets, we were able to identify specific histone modifications and chromatin binding proteins associated with R-loop formation in Drosophila and the role active transcription has on R-loop formation. Importantly, developmental-specific R-loops are not driven by transcriptional changes, emphasizing the role that chromatin and R-loop binding proteins play in regulating R-loop formation. Our work establishes Drosophila as a powerful developmental model system to study R-loop biology.

Results

R-loop abundance is developmentally regulated and R-loop homeostasis is necessary for development

To determine if R-loop abundance and genomic location are regulated throughout development, we turned to the powerful Drosophila embryogenesis system. For our analysis, we chose embryos at two distinct time points: 2-3 hours after egg laying (AEL) and 14-16 hours AEL (Figure 4-1A). The 2-3 hour time point corresponds with the onset of the maternal-to-zygotic transition (MZT) occurring during nuclear cleavage cycle 14 (Blythe and Wieschaus 2015). This time point represents the onset of zygotic transcription and allows us to draw upon the wealth of scientific literature that has previously been published, including time-matched modENCODE datasets. The wide-scale activation of zygotic transcription at this time point should provide the first opportunity for R-loop formation during development. To complement this developmental stage, we chose 14-16 hour AEL embryos to understand how R-loop formation might differ in differentiated cells with a more mature chromatin environment and a transcription program

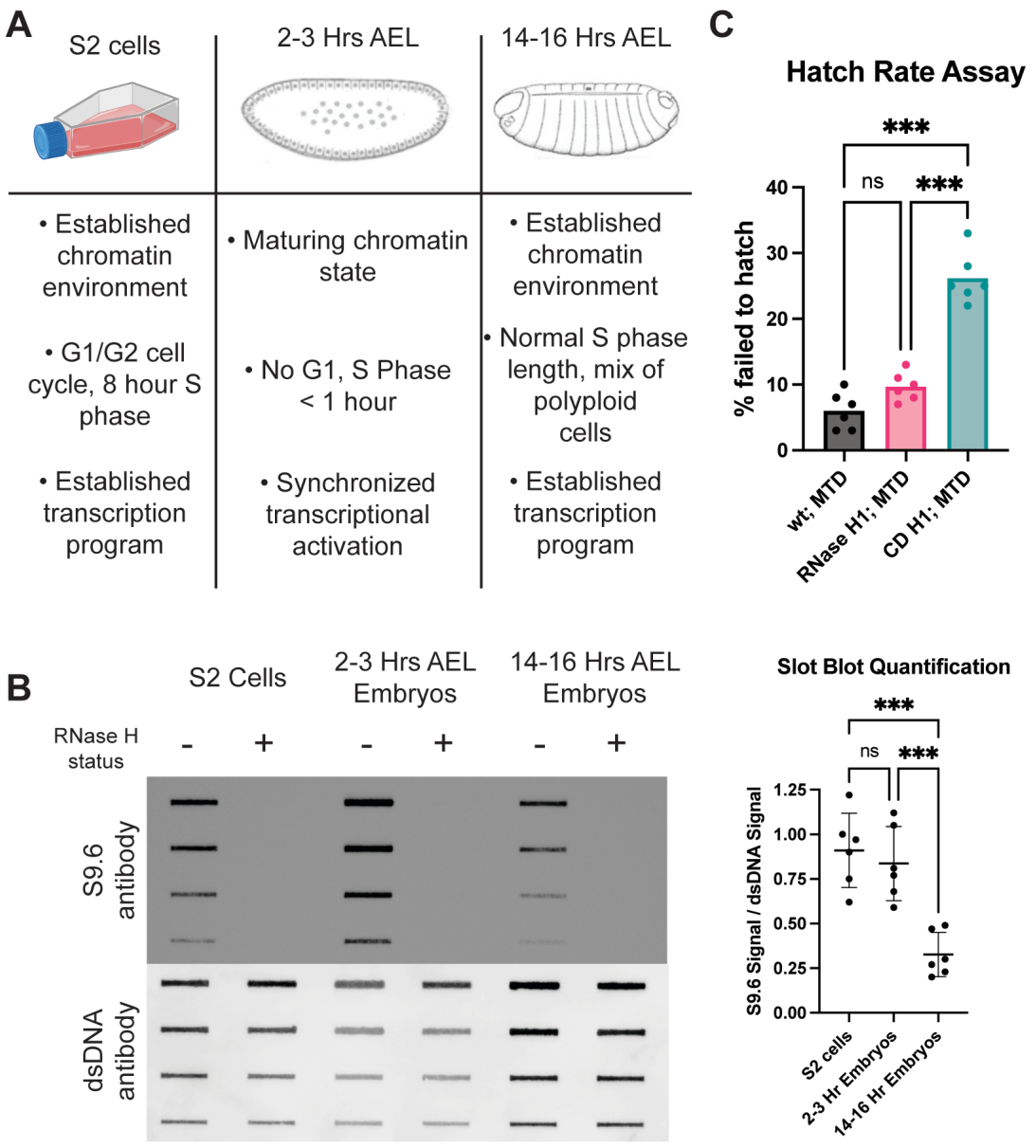


Figure 4-1. **R-loop abundance is developmentally regulated and R-loop homeostasis is necessary for development. (A)** Schematic summarizing how the chromatin environment, developmental stage, and replication program vary among the developmental samples used. **(B)** Representative slot blot of RNA:DNA hybrid levels, measured by S9.6 antibody intensity, across samples. RNase H treatment verifies specificity of antibody, and antibody specific for double-stranded DNA is used as a loading control. Quantification of signal for six biological replicates is to the right. *** < 0.05, one-way ANOVA with Tukey's multiple comparisons test. **(C)** Hatch rate among embryos that overexpress RNase H1 (H1) or a catalytic dead RNase H1 (CD). 6 biological replicates from 2 independent crosses, counting 100 embryos in each replicate. *** < 0.05, one-way ANOVA with Tukey's multiple comparisons test. Contributions: Experiment, analysis, visualization.

characterized by cell-type-specific maintenance (Bonnet and Müller et al. 2019; Bowman and Bender 2014; Smith and Orr-Weaver 1991). S2 cells, an established Drosophila cell

culture line derived from late-stage embryos (Schneider 1972), were used to determine how R-loops might differ between embryos and cultured cells, where the majority of R-loop research has been conducted.

To begin, we asked whether the absolute levels of R-loops are influenced by development. To this end, genomic DNA was extracted from each sample and spotted onto a nitrocellulose membrane and probed with the S9.6 antibody, which recognizes RNA:DNA hybrids (Boguslawski and Carrico 1986). S2 cells and 2-3h embryos showed similar amounts of S9.6 signal, while DNA from 14-16h embryos showed a significant decrease in S9.6 signal (Figure 4-1B). To ensure that the S9.6 signal stems from R-loops, we pretreated control samples with RNase H, which degrades the RNA moiety of a RNA:DNA hybrid. The S9.6 antibody has some specificity to double-stranded RNA and Drosophila embryos are known to contain dsRNA (Hartono and Vanoosthuyse et al. 2018). In fact, in the RNase H treated control samples we initially detected some signal with the S9.6 antibody, which was completely eliminated by pretreatment with RNase III. Therefore, for all R-loop assays we pretreat our samples with RNase III to ensure S9.6 signal isn't due to dsRNA.

Next, we asked whether perturbing R-loop homeostasis affects embryogenesis. *rnh1* mutants survive into larval development, which suggests that *rnh1* and R-loop processing may be dispensable during embryogenesis (Filippov et al 2001). More likely, however, *rnh1* mutant embryos survive from maternal stockpiles of RNase H1. To circumvent this, we generated flies that overexpress a GFP-tagged, nuclear localized version of Drosophila RNase H1 or a catalytically dead version of the same protein (RNase H1^{CD}). To ensure that the RNase H1 proteins were maternally deposited and

present at the earliest stages of embryogenesis, we used the pUASz expression system coupled with the maternal triple driver (DeLuca and Spradling 2018; Rørth 1998). After confirming that the GFP was observable by Western blot (Supplemental Figure 4-1A), we performed a hatch rate assay to determine if perturbing RNaseH1 catalytic activity affects embryogenesis. We observed a consistent but statistically insignificant hatching defect in the RNase H1 overexpression embryos (Figure 4-1C). The RNase $H1^{CD}$ expressing embryos, however, had a ~25% failure to hatch rate, which was significantly different from the wild-type and the RNase H1 overexpression controls. To determine the effect overexpression of RNase H1 or RNase $H1^{CD}$ constructs have on absolute R-loop levels, we measured bulk R loop levels from 2-6h embryos expressing these constructs. While there wasn't a significant reduction in R-loop levels upon RNaseH1 overexpression, R-loop levels increased upon overexpression of the $RNaseH1^{CD}$ mutant, suggesting the catalytic dead mutant blocks the processing of R-loops even in the presence of endogenous RNaseH1 (Supplemental Figure 4-1B). Overall, we conclude that the absolute abundance of R-loops changes during development and that RNase H1 catalytic activity is important for R-loop resolution and embryonic development.

R-loop position and properties are influenced during development

While the absolute abundance of R-loops changes during development, we wanted to determine how R-loop position throughout the genome changes during Drosophila development. Genome-wide R-loop mapping during Drosophila development would allow us to ask if R-loop formation is hardwired into the genome and driven only by cell-type-specific transcription, or, more interestingly, is R-loop formation plastic during

development changing independent of sequence composition and transcription status. To address this question, we performed DNA:RNA immunoprecipitation on sonicated nucleic acids followed by strand-specific sequencing of the DNA strand (ssDRIP-seq) in S2 cells, 2-3h and 14-16h embryos (Figure 4-2A) (Xu and Sun 2017). We initially tried DNA-RNA immunoprecipitation followed by cDNA conversion coupled to high-throughput sequencing (DRIPc-seq) (Sanz and Chédin et al. 2016). When conducted in Drosophila, however, we found high levels of RNA contamination in the final sequencing results (data not shown). Even with the ssDRIP-seq method, it was necessary to pre-treat genomic DNA preps with RNase A and RNase III as Drosophila embryos are stockpiled with RNA. ssDRIP-seq of embryos and S2 cells revealed strand-specific signal that was sensitive to RNase H pretreatment, and showed cell-type specific R-loop formation (Figure 4-2B and 4-2C). Providing validity to our data sets, biological replicates were highly correlated (Supplemental Figure 4-2A) and our ssDRIP data sets correlated with recently published ssDRIP-seq data sets in Drosophila S2 cells and embryos as expected based on the similar but different time points (Supplemental Figure 4-2B) (2-3h and 14-16h vs. 2-6h and 10-14h embryos) and known differences in R-loop mapping between different labs (Alecki et al 2020, Chédin et al 2021). Furthermore, our S2 data sets were highly correlated with two R-loop mapping studies performed in cultured cells, but not correlated with an R-loop data set generated for a spike-in control and not used in mapping studies (Supplemental Figure 4-2C, D) (Crossley et al 2020, Bayona-Feliu et al 2017). We validated several sites using DRIP-qPCR to confirm our sequencing results (Supplemental Figure 4-2F-G). Taken together, these data indicate that our ssDRIP

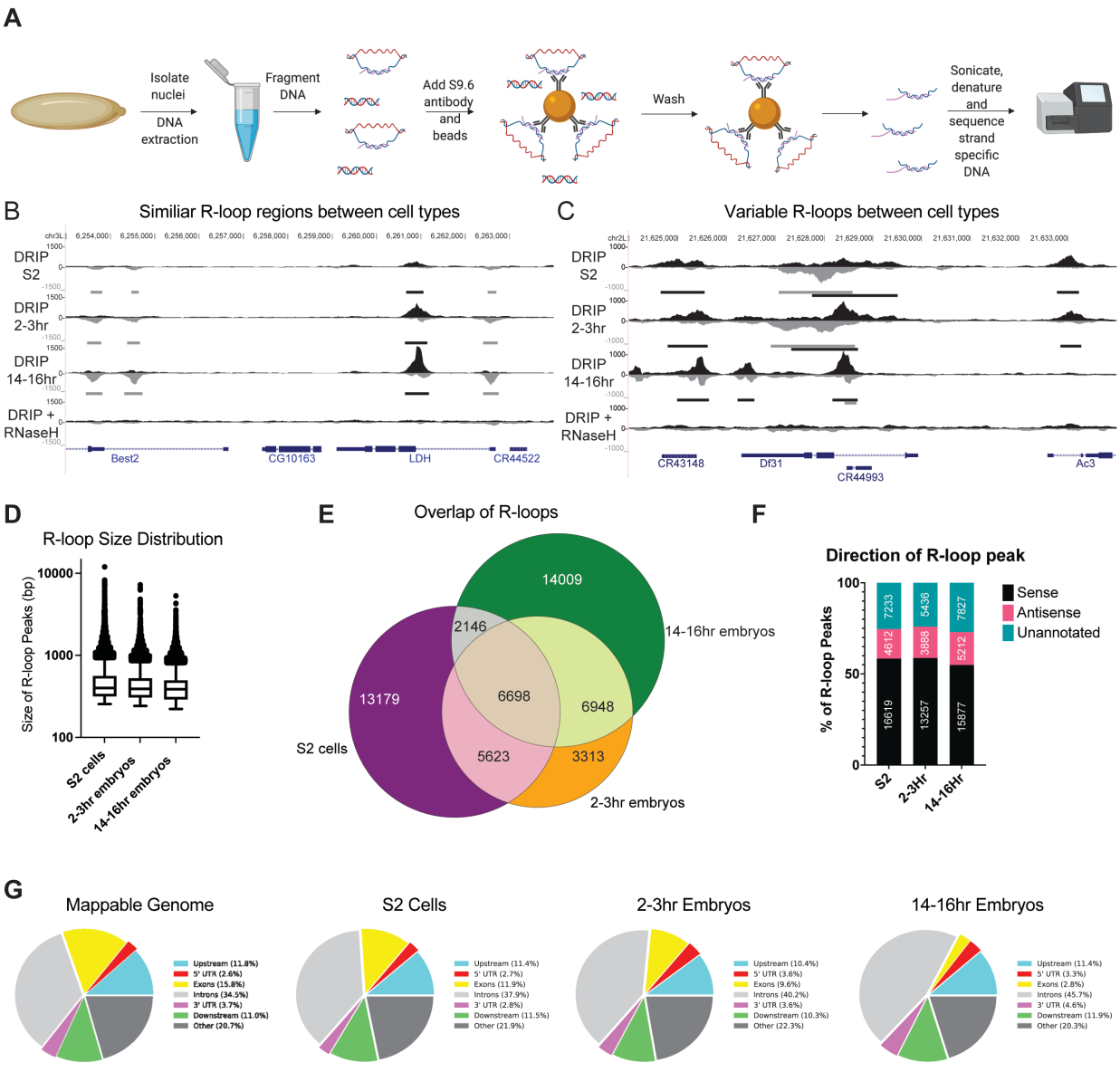


Figure 4-2: **The R-loop landscape changes as a function of development. (A)** Diagram of the ssDRIP-seq mapping strategy. **(B)** ssDRIP-seq snapshot of a 10kb region on chromosome *3L* where R-loop distribution is similar between samples. Black and grey bars below each track represent peak calls for forward and reverse strands, respectively **(C)** ssDRIP-seq snapshot of a 10kb region on chromosome *2L* where R-loop distribution varies between samples. Note the reverse strand coming from a lncRNA in the middle of the Df31 gene. **(D)** The distribution of R-loop sizes for each developmental sample. **(E)** Overlap of R-loops between developmental samples. **(F)** Quantification of the percent of R-loops mapping to sense, antisense and untranscribed regions of the genome. Numbers represent absolute R-loop peaks in each category **(G)** R-loop enrichment relative to the expected distribution for common genomic features. Contributions: Experiment, analysis, visualization.

signal reflects high quality and robust RNA:DNA hybrid mapping throughout the genome and that ssDRIP is a robust method to map sites of R-loop formation in Drosophila.

To map the precise location of R-loops throughout the genome and allow us to compare both quantitative and qualitative properties of R-loops, we used MACS to define R-loop peaks. Peaks were called separately against the input samples and RNase H treated controls, and only overlapping peaks were kept for analysis. Using this criterion, we identified 27,646, 22,581 and 29,801 peaks in S2 cells, 2-3h and 14-16h, respectively, which occupied between 8.3 and 12.5% of the genome. The overlap of sense and antisense R-loops had similar ratios (Supplemental Figure 4-2E). R-loop peak size was similar between sample types with a median of approximately 500 bp, but R-loops could occupy zones up to 10kb in size (Figure 4-2D). Out of the 51,916 total unique R-loop peaks identified between all samples, 12.9% were common to all sample types, 28.3% were present in at least two samples and 58.8% were specific to an individual sample (Figure 4-2E).

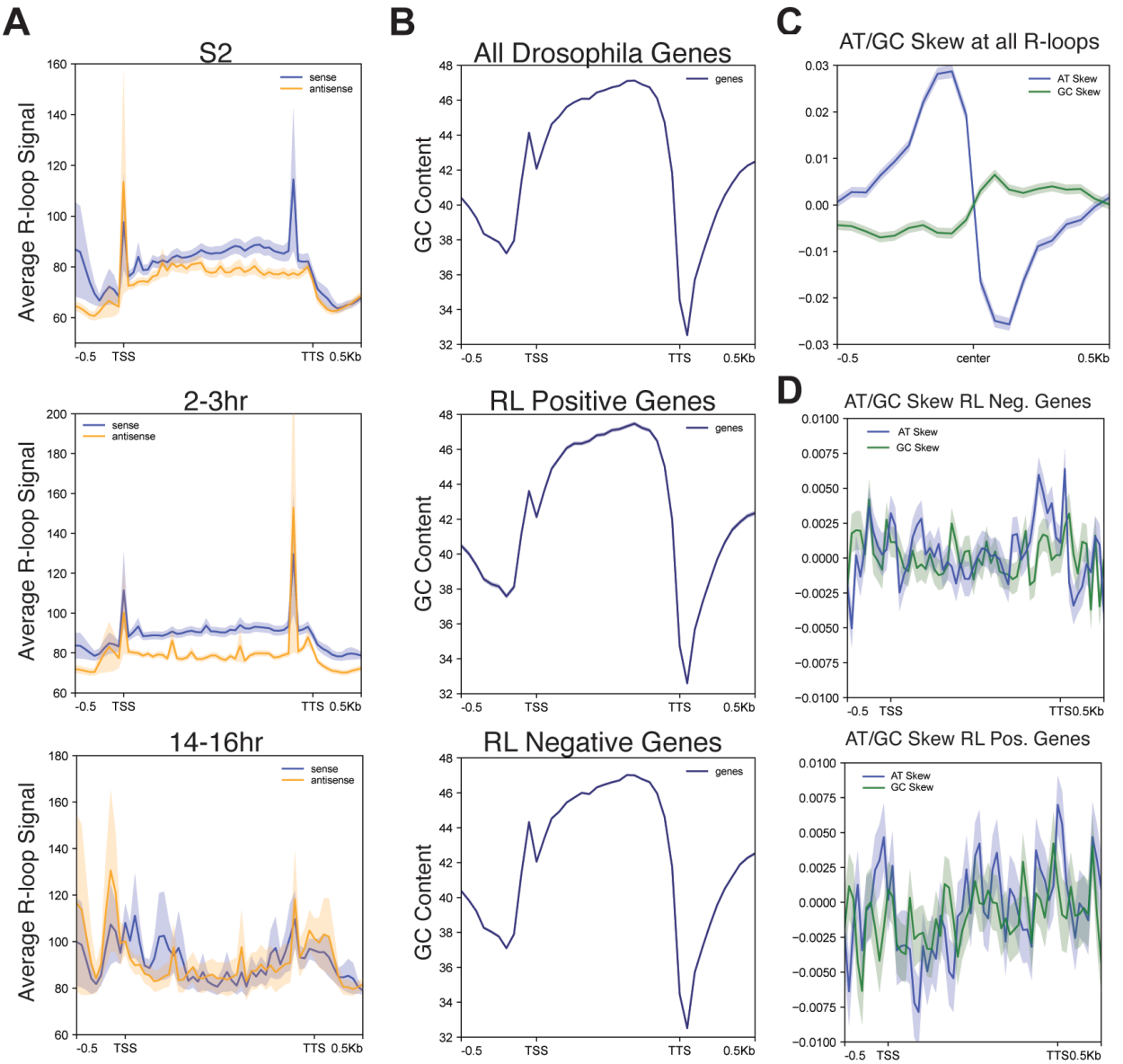
Since ssDRIP allows for strand-specific annotation, we characterized R-loops relative to strand-specific genomic features. Relative to transcription units,
55-60% of R-loops occur in sense to transcription in S2 cells and 2-3h embryos, whereas ~15% of R-loops are antisense (Figure 4-2F). In all samples, 25-30% of the R-loops form in unannotated regions of the genome. Next, we used Pavis to annotate R-loop signal relative to genomic features. In all samples, we found that ~50% of R-loops mapped to introns or exons (Figure 4-2G). This is expected given that a significant fraction of R-loops should be produced from coding regions. GO term analysis of R-loop forming genes revealed that R-loops preferentially form in genes associated with RNA Pol II-dependent transcription and sample-specific R-loops form in genes associated with sample-specific

development (Supplemental Table 4-2). Taken together, these results demonstrate that R-loop signal across Drosophila development is dynamic.

R-loop enrichment at transcription units changes during development

In mammals, R-loops are known to preferentially form at transcription start sites (TSS), gene bodies and transcription termination sites (TTS) (Sanz and Chédin et al. 2016; Skourti-Stathaki and Proudfoot et al. 2014). To ask if this pattern of R-loop formation is similar in Drosophila, and whether it changes during development, we measured R-loop abundance across gene bodies in our developmental samples. We then generated metaplots using strand-specific data for all time points. S2 cells and 2-3h embryos display a very similar pattern of R-loop formation, with a strong peak at the TSS and continued signal over the gene body (Figure 4-3A), which is similar to R-loop positions in other metazoans (Sanz and Chédin et al. 2016). In 2-3h embryos and S2 cells, there was a greater signal for sense R-loop over the gene body, as would be expected given that the majority of R-loops are generated during transcription. Antisense R-loop signal was prevalent at the TSS and close to the TTS in 2-3h embryos (Figure 4-3A). Interestingly, there is a depletion of R-loops immediately after the TTS in 2-3h embryos and S2 cells (Figure 4-3A). The 14-16h embryos, however, have a significantly different pattern altogether. In 14-16h embryos, we observed the most abundant signal within and around the TSS and TTS regions with a relative reduced signal within the gene body (Figure 4-3A), The enrichment of R-loops at the TTS in 14-16h embryos was not driven by differences in R-loop forming genes between the samples as R-loop forming

genes are similar between 2-3h and 14-16h embryos (Supplemental Figure 4-3B). In the 14-16h



E

Rank	Motif	P-value	log P-pvalue
1	AAAAAAAAAAAA	1e-1413	-3.254e+03
2	AGGAGGAGGA	1e-1352	-3.114e+03

Figure 4-3. **R-loop signal as a function of transcription unit and sequence composition. (A)** Metaplots of ssDRIP-seq signal for all samples relative to the gene body. Each plot represents the signal derived from sense R-loops in blue and antisense R-loops in orange. Shaded region represents the standard error of the mean (SEM). **(B)** The GC composition of all Drosophila genes, genes that have an R-loop in one of the developmental samples and genes that lack any R-loop signal. Shaded region represents the SEM. **(C)**

Metaplot of GC and AT skew across all identified R-loops. Shaded region represents the SEM. **(D)** Metaplot of GC and AT skew across the gene body of genes that lack R-loops (top) and genes that form an R-loop. Shaded region represents the SEM. **(E)** DNA sequence motifs in the peaks of all R-loops identified by HOMER. Motif analysis was not strand specific. Contribution: Experiment, partial analysis, and visualization.

embryos, however, both sense and antisense R-loops have similar levels throughout the transcription unit (Figure 4-3A). Taken together, we conclude that R-loop enrichment at transcription units is not hardwired into the genome, but can be dynamic as a function of development.

Given that the absolute levels and relative position of R-loops can change between developmental states in Drosophila, we wanted to assess the contribution DNA sequence composition has on R-loop formation in Drosophila. Unlike in mouse and human cells, Drosophila lack high GC content at the TSS. In fact, GC content decreases relative to the gene body in Drosophila (Figure 4-3B). We asked if R-loop forming genes differ in their GC content relative to genes that lack R-loops. We found that genes with and without R-loops have a near-identical GC content along the gene body (Figure 4-3B). While overall GC content is not different in R-loop positive or negative genes, GC and AT skew has been shown to be a contributing factor to R-loop formation (Ginno and Chédin et al. 2012). To test if GC or AT skew is associated with R-loop formation in Drosophila, we measured the AT/GC skew directly over all identified R-loops. This analysis revealed a striking transition from positive to negative AT skew at the center of our combined R-loop signal. This is mirrored by a less dramatic transition from negative to positive GC skew centered at the combined R-loop signal (Figure 4-3C). Interestingly, developmental-specific R-loops had AT/GC skew profiles that were distinct from all R-loops combined (Figure 4-3C; Supplemental Figure 4-3A).

We also calculated GC and AT skew for R-loop forming and deficient genes in all samples. Stronger negative GC skew at the TSS was observed in R-loop forming genes relative to genes that fail to form R-loops (Figure 4-3D). Specifically, AT skew at the TSS transitioned from positive skew in R-loop deficient genes to negatively skew in R-loop forming genes. At the TTS, there is a strong positive AT skew around the TTS in both R-loop positive and negative genes (Figure 4-3D). Negative GC skew is stronger at the TSS in R-loop forming genes. This analysis reveals a correlation between altered AT skew and negative GC skew in R-loop forming genes, suggesting that AT/GC skew could contribute to R-loop formation in Drosophila. Due to the strong presence of R-loops at promoters and TSS in this and other R-loop mapping studies, we examined whether the AT and GC skew specifically at the promoter or TSS regions to determine if they were driving the overall skew. AT and GC skew was calculated for R-loops at promoter and TSS regions versus every other R-loop peak for each cell type (Supplemental Figure 4-3B). AT and GC skew at promoter and TSS regions was similar to overall skew, though this varied in S2 cells. Together, we conclude that while AT and GC skew could facilitate R-loop formation, developmental-specific R-loop formation is not likely driven by changes in AT or GC skew. This suggests that transcription, chromatin environment or other factors could contribute to cell type specific R-loop formation.

To test whether any specific DNA sequence motifs are associated with R-loop formation, we searched for motifs enriched in the set of all Drosophila R-loops. Two motifs stood out as an order of magnitude more significantly enriched that any others: a polyadenine tract and a polypurine tract (Figure 4-3D, Supplemental Figure 4-3B for the entire table). This indicates that polypurine tracts are conducive to R-loop formation,

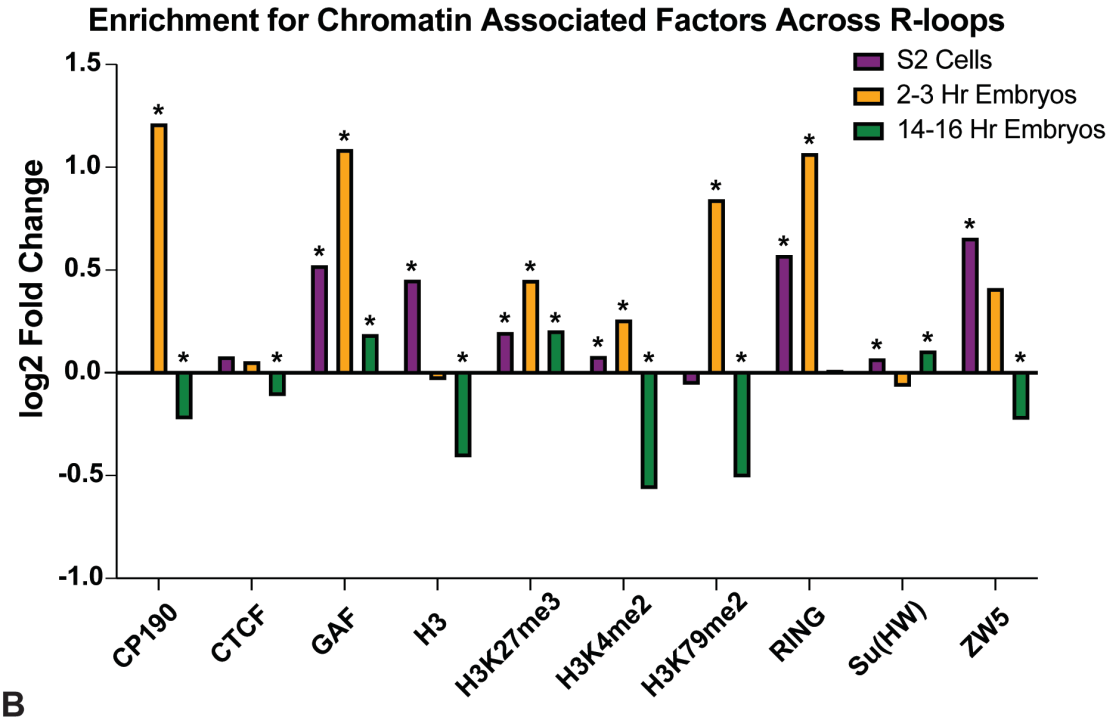
which is consistent with the known thermodynamic stability of RNA:DNA hybrid formation in purine-rich template sequences (Huppert 2008).

Common and cell-type specific chromatin features associated with R-loops

R-loops are associated with activating chromatin marks such as H3K4me1/2/3 and H3K9ac and, to a lesser extent, with repressive chromatin marks such as H3K27me3 (Sanz and Chédin et al. 2016). Chromatin marks associated with R-loops, however, vary depending on species. One possibility is that there are marks that are universally associated with R-loop formation whereas some chromatin marks could associate with R-loops in a developmental-specific manner. To answer this question, we leveraged time-matched ChIP-seq modENCODE datasets for S2 cells, 2-4h embryos (ChIP-chip and ChIP-seq) and 14-16h embryos.

To quantitatively determine if chromatin marks were positively or negatively associated with R-loops, we evaluated the probability of R-loops overlapping a variety of histone modifications and chromatin-associated proteins by chance using a peak shuffling bootstrap procedure (see Materials and Methods). The available chromatin proteins vary for each sample, but there are 10 chromatin or histone markers common in all three developmental samples (Figure 4-4A). Several factors that are associated with transcriptional activation, and have been previously shown to be associated with R-loops, are enriched at R-loops in S2 cells and 2-3 hour embryos (Figure 4-4A, Supplemental Figure 4-4). Additionally, repressive chromatin marks such as Polycomb complex subunits and H3K27me3 are enriched in all samples, which is consistent with recent work

A


Enrichment for Chromatin Associated Factors Across R-loops
S2 Cells
2-3 Hr Embryos
14-16 Hr Embryos
log2 Fold Change
1.5
1.0
0.5
0.0
-0.5
-1.0
CP190
CTCF
GAF
H3
H3K27me3
H3K4me2
H3K79me2
RING
Su(HW)
ZW5

B

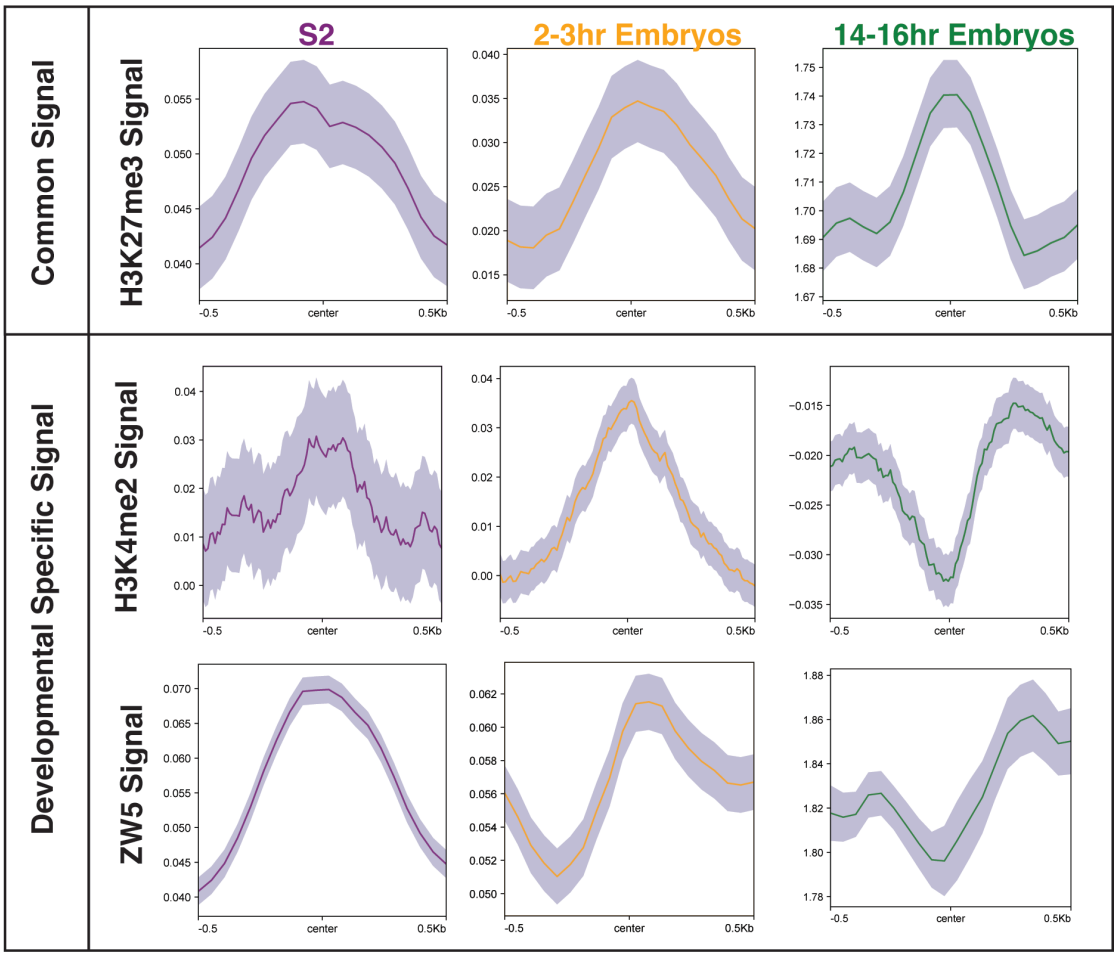

Common Signal
Developmental Specific Signal
S2
2-3hr Embryos
14-16hr Embryos
H3K27me3 Signal
H3K4me2 Signal
ZW5 Signal
-0.5
center
0.5Kb

Figure 4-4. **Common chromatin features associated with R-loops. (A)** Log2 fold enrichments of chromatin-associated factors within R-loop regions in common for S2 cells, 2-3 hour embryos and 14-16 hour embryos. * < 0.05 with Bonferroni correction for multiple testing. **(B)** Metaplots of H3K27me3, H3K4me2, and ZW5 ChIP-chip (S2 and 2-4 hour embryos) and ChIP-seq (14-16 hour embryos) confirming common and developmental-specific enrichment of chromatin factors at R-loops. Shaded region represents the standard error of the mean (SEM). Contribution: Analysis for B, visualization.

linking R-loops to transcriptional repression (Figure 4-4A, Supplemental Figure 4-4) (Skourti-Stathaki and Pombo et al. 2019; Alecki and Francis et al. 2020).

We asked which marks are consistently associated with R-loops (positively or negatively) across development and which factors are developmental specific. We found that the repressive mark H3K27me3 was positively associated with R-loops in all developmental samples, highlighting the link between R-loops and transcriptional repression (Figure 4-4B). Interestingly, we identified factors (H3K4me2 and ZW5) that were enriched in one developmental sample but not in others (Figure 4-4B). These results suggest while some factors are associated with R-loops regardless of development state, other factors are associated with R-loops in a developmentally-specific manner.

R-loop formation as a function of transcription

In this study, we have noted distinctive changes in R-loop formation across development. One possibility is that these changes are driven by developmental-specific changes in the transcription program. As embryos are stockpiled with maternally deposited RNA and RNA-seq is an indirect readout of active transcription, we turned to previously published and time-matched GRO-seq datasets in S2 cells and 2-2.5h embryos, respectively (Core and Lis et al. 2012; Saunders and Ashe et al. 2013). Unfortunately, time-matched GRO or PRO-seq datasets do not exist for 14-16h embryos. We converted GRO-seq signal to FPKM for each annotated transcript in the Drosophila

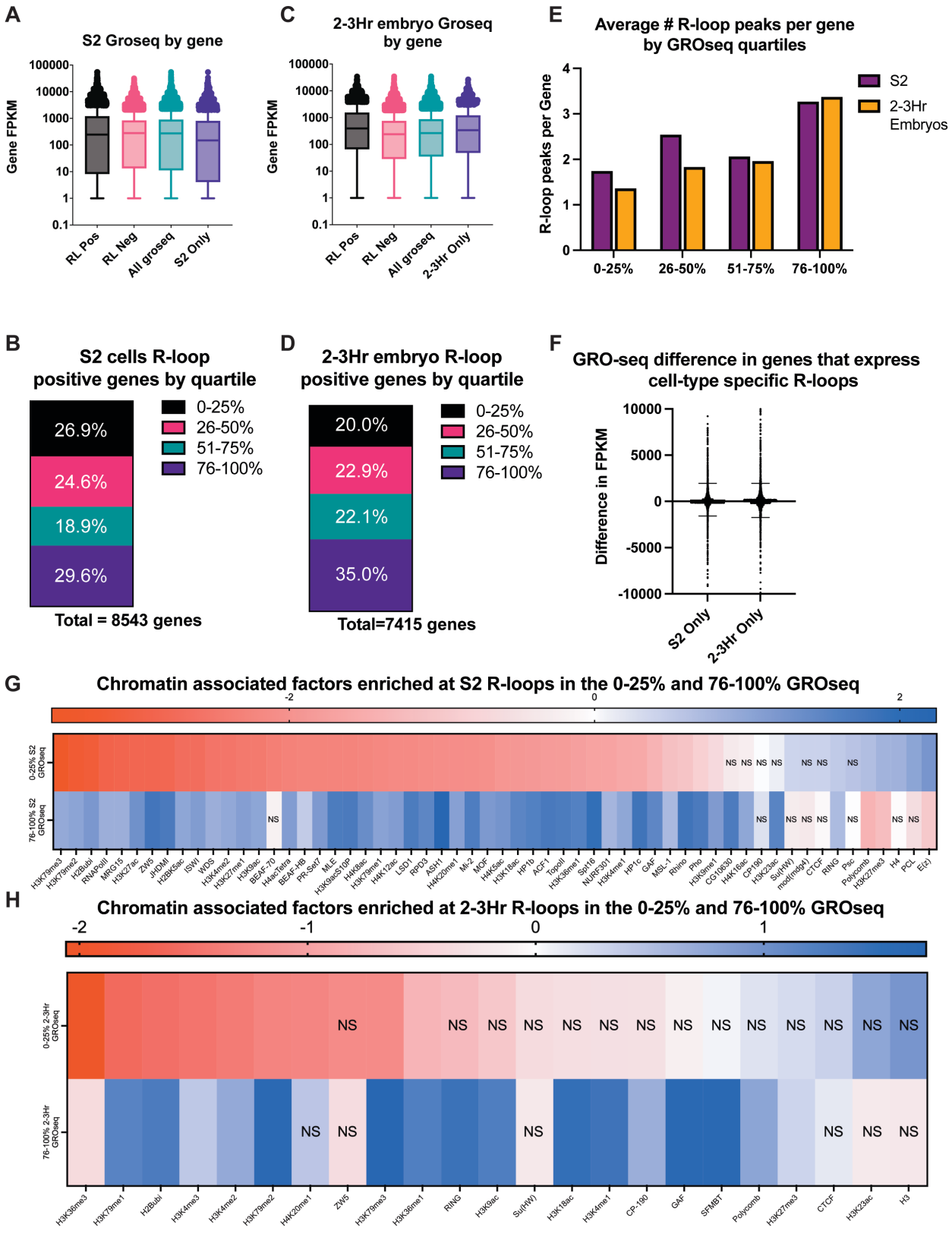


Figure 4-5. **R-loop formation as a function of transcription. (A)** GRO-seq values for genes that contain strand-specific R-loops (RL Pos), genes that do not contain strand-specific R-loops (RL Neg) in S2 cells,

every transcript in S2 cells, and transcripts that only form R-loops in S2 cells. **(B)** Transcripts were sorted into quartiles based upon GRO-seq expression, and R-loop forming genes were assigned to their respective quartile. **(C)** Same as A, except for 2-3h embryos. **(D)** Same as B, except for 2-3h embryos. **(E)** The average number of R-loops peaks detected for each gene in each of the expression quartiles is graphed for S2 cells and 2-3h embryos. **(F)** The difference in GRO-seq values between S2 cell and 2-3h embryos were queried for genes that showed developmental-specific R-loop formation. **(G)** Log2 fold enrichments of chromatin-associated factors within R-loop regions in the highest or lowest expression quartiles in S2 cells. ns > 0.05 with Bonferroni correction for multiple testing. **(H)** Log2 fold enrichments of chromatin-associated factors within R-loop regions in the highest or lowest expression quartiles in 2-3h embryos. ns > 0.05 with Bonferroni correction for multiple testing. Contributions: Analysis, visualization.

transcriptome. Then, we compared the GRO-seq value of all R-loop-containing genes to genes devoid of R-loops. In S2 cells, R-loop positive and negative genes had a similar median FPKM value by GRO-seq (Figure 4-5A). R-loop-containing genes in 2-3h embryos, however, revealed a different paradigm. R-loop positive genes had a significantly higher expression level than R-loop negative genes (Figure 4-5C).

To ask if R-loop-containing genes were over or underrepresented with genes that have high or low expression levels, we binned GRO-seq FPKM values into quartiles and asked what fraction of R-loop containing genes fell within each expression quartile (Figure 4-5B, D). In S2 cells, R-loop containing genes were slightly overrepresented in the highest expression quartile and, to a lesser extent, in the lowest expression quartile (Figure 4-5B). In 2-3h embryos, however, R-loops were significantly overrepresented in the highest expression quartile and underrepresented from the lowest expression quartile (Figure 4-5D). While analyzing this data, we also found the number of R-loops forming sites per gene was correlated with transcriptional activity (Figure 4-5E). We observe a consistent increase in the average number of R-loops per gene as transcriptional activity increases (Figure 4-5E). The increase in the average number of R-loops per gene could represent multiple R-loops within a given gene or larger R-loop zones allowing R-loops to form over a larger target region.

One explanation for developmental-specific R-loop formation is that specificity is driven by developmental-specific transcription status. To test this, we compared expression level of genes that exhibit R-loops only in S2 cell or only in 2-3h embryos (Figure 4-5F). If active transcription drives the changes in R-loop formation, we would expect R-loop positive genes that are unique to 2-3h embryos would have significantly higher expression level in 2-3h embryos relative to S2 cells, and vice-versa. The median difference of GRO-seq values in developmental-specific R-loop-containing genes, however, is approximately zero with a normal distribution (Figure 4-5F). Therefore, we conclude that active transcription is not a driver of developmental-specific R-loop formation and that factors such as chromatin state or R-loop-specific proteins drive these differences.

We asked if the chromatin signature of R-loops in highly expressed genes differs from the signature of R-loops in transcriptionally repressed genes. To this end, we selected R-loops in the highest expression quartile and lowest expression quartile from S2 cells (Figure 4-5B). Next, we used the random shuffling method to identify chromatin-associated factors enriched at R-loops derived from highly and lowly expressed genes. This analysis revealed that the chromatin signature of R-loops in highly and lowly expressed genes are distinct (Figure 4-5G). For example, R-loops in highly expressed genes are enriched for active chromatin marks (e.g. H3K27ac and H3K36me1; Figure 4-5G). In contrast, repressive chromatin marks such as H3K27me3 are enriched at R-loops derived from lowly expressed genes. We repeated the same analysis with the 2-3h embryo time point and noticed a striking difference; both active chromatin marks and repressive chromatin marks were associated with highly expressed genes (Figure 4-5H).

Given the differentiation state of cells in the early embryo, this would suggest that R-loops can be associated with poised or bivalent genes (Lesch and Page, 2014).

R-loops have the potential to trigger ATR activation at the MZT

The onset of zygotic transcription at the MZT is associated with RPA accumulation at the 5' end of genes and activation of the ATR-mediated DNA damage checkpoint response (Blythe and Wieschaus, 2015). Delaying the onset of zygotic transcription delays the activation of ATR (Mei41 in Drosophila), indicating that replication-transcription conflicts drive the activation of the DNA damage response at the MZT (Blythe and Wieschaus, 2015; Sibon and Theurkauf et al. 1999). It is unknown, however, what aspect of the replication-transcription conflict triggers ATR activation at the MZT. If genome - instability at the MZT was at least partially due to R-loops, we would predict to see an enrichment of RPA at R-loop forming sequences in 2-3h embryos. Qualitatively, we see overlap between RPA and R-loops in 2-3h embryos (Figure 4-6A). We tested the significance of this overlap by using the random shuffling method previously described. Quantitatively, we observe a significant enrichment of RPA at R-loop forming sequences in the 2-3h embryo. Importantly, there was an even more substantial enrichment of RPA at R-loop peaks that are unique to 2-3h embryos (Figure 4-6B). Further supporting the hypothesis that R-loops could be partially responsible for the transcription-induced genome instability at the MZT, only R-loops from the 2-3h sample were enriched at RPA binding sites (Figure 4-6B). This data suggests that R-loops could contribute to the transcription-induced DNA damage that occurs in the absence of ATR at the MZT. We do note, however, that the RPA ChIP-seq data comes from a time point

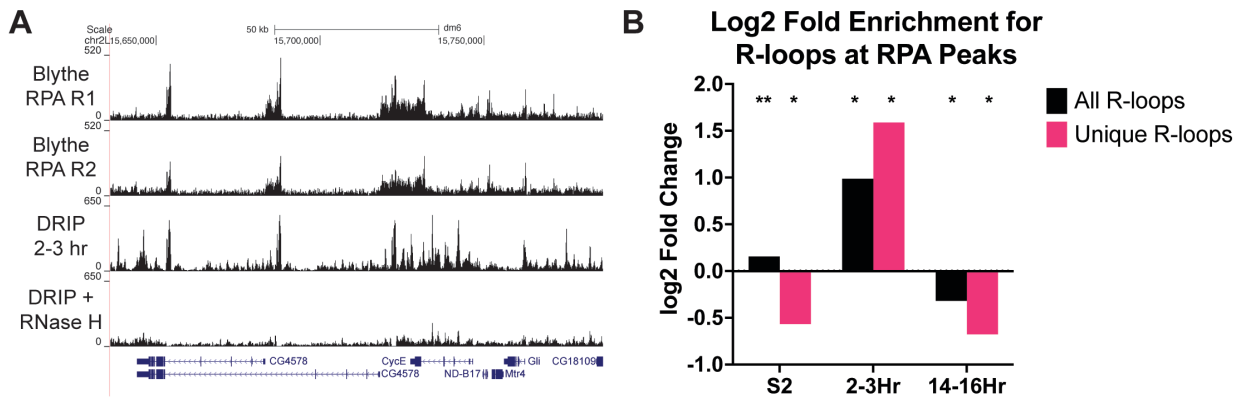


Figure 4-6. **R-loops have the potential to trigger ATR activation at the MZT. (A)** Overlap of RPA ChIP-seq profiles from cycle 13 embryos (Blythe and Wieschaus et al. 2015) and ssDRIP-seq profiles from 2-3h embryos. **(B)** Log2-fold enrichment of RPA at R-loop peaks for all samples. Each sample was separated into total R-loops or R-loops unique to that sample type. P values were generated with Bonferroni correction for multiple testing. * is P value < 0.01 and ** = P value < 0.001. Contributions: Visualization.

~20 minutes earlier in development than the time point we chose for R-loop mapping (Blythe and Wieschaus, 2015). Given this caveat, we think it is even more notable that significant overlap of RPA and R-loops is observed in this analysis.

Discussion

By mapping R-loops in a developing organism, we have been able to provide new insight into the role that DNA sequence, active transcription and chromatin associated factors has on R-loop formation. While previous R-loop mapping and genome-wide analysis of R-loop metabolism across development has been performed in plants and mammalian cultured cells (Yan and Liu et al. 2020; Xiu and Sun et al. 2020; Shafiq and Sun et al. 2017), we present a functional characterization of R-loops during Drosophila embryogenesis. The benefit of a developmental approach to studying R-loop formation is that it allows the distinction between factors that are stably linked to R-loop formation from those that are developmental specific. This has the potential to

identify key molecules and processes that could drive R-loop formation and resolution during development and disease.

One surprising finding is that the absolute level of R-loops changes during embryogenesis. This is unlikely due to changes in transcription during development as the stages of embryogenesis used in this study are similarly active. This suggests that there is an active mechanism which prevents R-loop formation or resolves active R-loops during later stages of Drosophila embryogenesis. The importance of R-loop processing during development is further highlighted by the observation that RNase H1 catalytic activity is necessary to prevent hatching defects in Drosophila embryos. Interestingly, overexpression of catalytically active and inactive RNaseH1 do not have the same effect. One possible explanation for this is that maternally deposited RNaseH1 is highly active in the embryo. Therefore, additional RNaseH1 has no further effect on R-loop levels. Overexpression of catalytic inactive RNaseH1, however, could bind to RNA:DNA hybrids and block RNaseH1-mediated processing of R-loops.

Consistent with R-loops as a driving force of genome instability during embryogenesis, we have found and enrichment of R-loops at potential sites of replication fork stalling in the early embryo. Given that we see an enrichment of R-loops and RPA specifically in the 2-3h embryo sample, our data suggests that R-loops could contribute to ATR activation at the MZT. It is interesting to note, however, that we do not observe RPA accumulation at all sites of R-loop formation. Therefore, there must be something unique about the R-loops associated with RPA accumulation at this time point. Perhaps these R-loops represent sites of head-on conflicts. Alternatively, hyper stable R-loops could drive chromatin or transcriptional changes that negatively impact embryogenesis

(Lima and Crooke et al. 2016). Further work will be required to distinguish between these and other possibilities.

Specific DNA sequence biases are associated with R-loop formation (Ginno and Chédin et al. 2012; Stolz and Chédin et al. 2019). While we found that overall GC content is the same for R-loop positive and negative genes, AT and GC skew were associated with R-loop forming sequences. Interestingly, this skew varied as a function of the transcription unit (Ginno and Chédin et al. 2012; Lee and Myong et al. 2020). G4 quadraplex forming regions with high GC skew on the non-template strand are associated with R-loop formation (Ginno and Chédin et al. 2012; Lee and Myong et al. 2020). Additionally, R-loops can modulate DNA methylation at CpG islands in promoter regions (Ginno and Chédin et al. 2012). Unlike in plants and mammals, however, Drosophila lack wide-scale DNA methylation (Capuano and Ralser et al. 2014). Therefore, Drosophila allows the uncoupling between R-loop formation and DNA methylation, which could explain why R-loops are associated with a higher AT skew than GC skew in Drosophila. Similar to mammalian cells, we see a transition to positive GC skew at the center of R-loops peaks. What's unique to Drosophila, however, is the drastic transition from positive to negative AT skew at the center of R-loop peaks. These biases in AT and GC skew could create a thermodynamically stable environment for R-loop formation and resolution. Similar to other organisms, we have found several polypurine motifs associated with R-loops. Again, this likely reflects the thermodynamic stability associated with RNA:DNA hybrids at purine-rich sequences (Huppert 2008). One interesting observation in Drosophila is that the R-loop signal relative to the transcription unit can vary as a function of development. The most significant difference is in 14-16h embryos where R-loops are

broadly enriched at the TSS and the TTS but not the gene body in comparison to 2-3h embryos or S2 cells. This difference does not appear to be driven by AT or GC skew. We propose that a combination of factors such as transcription status, chromatin marks and R-loop binding proteins drive these changes in R-loop formation during development.

We have found that R-loops are positively and negatively associated with specific histone modifications and chromatin associated factors. Many of the factors we analyzed in Drosophila have been shown to be enriched or depleted in other systems, including mammalian cells (Sanz and Chédin et al. 2016; Pinter and Rathert et al. 2021; Herrera-Moyano and Aguilera et al. 2014). More importantly, however, factors associated with R-loops can change as a function of development. For example, R-loops in 14-16h embryos lose their association with common activating histone marks such as H3K4me3 and H3K36me2/3. In contrast, H3K27me3 is enriched at R-loops in all developmental states. Therefore, it is critical to assay multiple cell types or developmental states before concluding that a chromatin factor is correlated with R-loop formation.

The link between R-loops, transcription state, histone marks and chromatin associated factors has been seen in other organisms (Sanz and Chédin et al. 2016). In Drosophila, we see a consistent relationship between active and repressive chromatin marks, signified by enrichment in both H3K27ac and H3K27me3, and R-loop formation. This is supported by the association of R-loops with both highly active and silent genes in both embryos and cultured cells. Our work, and that of others, identify R-loops associated with transcriptionally active and inactive genes[25]. This suggests that, at least in Drosophila, there may exist at least two classes of R-loops. R-loops that form as a byproduct of active transcription and R-loops that function in a repressive capacity to

prevent transcription within repressive chromatin domains. This would be consistent with recent work demonstrating that R-loops facilitate silencing by the Polycomb complex (Skourti-Stathaki and Pombo et al. 2019). Understanding how different categories of R-loops maintain their identity will be an exciting challenge. For example, how do cells know which R-loops should function in a repressive manner versus those that function as activators? The question of whether R-loops help establish a chromatin state or are a function of it remains an outstanding question in R-loop biology.

Mapping of R-loops has been performed in a variety of organisms ranging from yeast, worms, plants, and mammalian cultured cells. While there are factors and processes that are consistently associated with R-loops across organisms, there are also key differences. For example, in plants there are low levels of R-loops at gene terminators compared to other organisms and high accumulation of antisense R-loops that regulate specific loci (Xu et al. 2020; Sun et al. 2013). In contrast, mammalian cells exhibit R-loops at promoters and TTS and the number of antisense R-loops are much more limited (Sanz and Chédin et al. 2016). The fact that Drosophila exhibit changes in antisense R-loop signal across the gene body depending on developmental state highlights the importance of examining R-loops in a developmental context. Drosophila provides a powerful model to understand key properties of R-loop biology in the context of unperturbed metazoan development. Here, we demonstrate that R-loop formation within the same genomic sequence can vary as a function of development. Our work suggests that a combination of transcription, chromatin-associated factors and sequence elements drive differential R-loop formation during development. Therefore, Drosophila provides a powerful model to

understand, mechanistically, the factors responsible for R-loop formation and resolution to execute specific developmental programs.

Materials and Methods

S9.6 antibody

A hybridoma cell line producing the S9.6 antibody was purchased through ATCC (product #HB-8730). The cell line was grown under recommended conditions. The S9.6 antibody was purified on a protein G column using the GE aKTA system and run over a desalting column for buffer exchange into PBS to obtain a final concentration of 1 mg/mL. The antibody was aliquoted and stored at -80^{o}C. A fresh aliquot was used for every ssDRIP-seq experiment.

RNase H1 overexpression

Drosophila RNase H1 was cloned from RNA derived from Oregon R embryos. RNA was converted into cDNA, PCR amplified, and cloned into the pUASz vector with a C-terminal GFP tag (DeLuca and Spradling 2018). The A isoform was chosen as the isoform B isn't detected in Drosophila tissues (Cózar de and Jõers et al. 2019). The mitochondrial localization start site was converted to AAA to ensure RNase H1-GFP would only be present in the nucleus. The catalytically dead version of RNase H1 (D201N) was made by site-directed mutagenesis (Agilent QuickChange Lightning). Plasmids were injected into an *attP2* containing stock (BestGene) for site-specific integration.

Hatch rate assay

For the overexpression experiments, homozygous RNase H1 males were crossed with unmated female homozygous for the maternal triple driver (MTD, Bloomington Stock 31777) to drive expression early in embryogenesis. Male Oregon R flies were crossed with MTD females as a control. Progeny were transferred to bottles with a grape juice agar plate with wet yeast for embryo collection. 100 unhatched embryos were carefully moved to a fresh grape juice plate and incubated overnight at 25□C. After 36 hours, unhatched embryos were counted. This was repeated three times each from two separate crosses.

Cell culture

S2 cells were obtained directly from the Drosophila Genomic Resource Center (DGRC). Cells were confirmed negative for mycoplasma contamination via PCR. Cells were grown at 25□C in Schneider's Drosophila Medium with 10% heat-inactivated FBS (Gemini Bio Products) and 100 U/mL of Penicillin/Streptomycin (Fisher Scientific).

Embryo collection and staging

Oregon R flies were expanded into population cages containing grape juice plates supplemented with wet yeast. Population cages were kept at 25□C in a humidified room and plates were changed daily. Before embryo collections, flies were precleared for at least one hour to minimize the number of late-stage embryos. Embryos were collected and aged at 25□C to obtain embryos that were 2-3 or 14-16 hours old. After aging and collection, embryos were dechorionated in 50% bleach for 2 minutes and thoroughly

rinsed in water. Embryos were flash frozen in liquid nitrogen and kept at -80□C until ready to use. An aliquot of embryos was taken from each batch before freezing to verify staging. For this, embryos were fixed in heptane and 2% paraformaldehyde for 20 minutes with shaking, devitellinized in methanol, washed with methanol and rehydrated in PBS + 0.1% Triton X-100 overnight. Embryos were stained with DAPI and mounted in Vectashield medium (Vector Labs). Images were acquired on a Nikon Ti-E inverted microscope with a Zyla sCMOS digital camera.

Genomic DNA purification and RNase treatment

Genomic DNA purification is based on Alecki et al., 2019. For genomic DNA isolation from S2 cells, cells were collected at 70-80% confluency, washed once in PBS, resuspended in TE with 0.5% SDS and 100 µg/mL proteinase K and incubated at 37C overnight. Embryos were devitellinized in heptane and methanol, rinsed thoroughly in PBS and incubated in 50 mM Tris-HCl pH 8.0, 100 mM EDTA, 100 mM NaCl, 0.5% SDS, and 5 mg/ml proteinase K for 3 hours at 50C. At this point, cells and embryos were processed the same. Extracts were purified with phenol:chloroform, and DNA was precipitated with sodium acetate and ethanol. DNA was spooled using a glass pipette and transferred to 70% ethanol. After several washes in ethanol, the DNA was air dried and resuspended in TE. To degrade free RNA, samples were incubated with 100 µg of RNase A with 500mM NaCl for 1 hour at 37C. RNase A was degraded by spiking in 100 µg/mL proteinase K and incubated for an additional 45 minutes. Samples were cleaned with phenol:chloroform, precipitated with sodium acetate and ethanol, and resuspended in TE. Samples were diluted to 100 ng/µL and sonicated in a Bioruptor Plus for 8 cycles (30”

on/90” off) on low power. 10 µg of nucleic acid was digested with 5 µL RNase H (NEB) at 37C for 16 hours and 10 µg was mock digested without RNase H. Both samples had 1 µL of RNase III added (Thermo Fisher). After phenol:chloroform purification and precipitation, samples were immediately used for DRIP or slot blot experiments.

Slot blot

Hybond Nylon membrane (Amersham) was pre-soaked in TE and a slot blot apparatus was assembled according to manufacturer’s instructions (Bio-Rad). Samples with matching RNase H-digested controls were added to the blot in decreasing amounts, and nucleic acids were crosslinked to the membrane with a Strategene UV Stratalinker 1800 using the auto crosslink setting. Blots were blocked in milk, incubated with S9.6 (1:2,000) followed by mouse-HRP and imaged in a Bio-Rad Chemidoc MP. After imaging the R-loops, blots were stripped and re-probed using a dsDNA-specific antibody (Abcam ab27156) at 1:20,000. Intensities were measured with ImageJ (Schneider and Eliceiri et al. 2012), and normalized intensity was obtained by dividing the S9.6 signal by the dsDNA signal (Ramirez and Grunseich et al. 2021). A standard plot was made for each sample and antibody, and samples were chosen for analysis when their intensity was linear.

DRIP-qPCR and ssDRIP-seq

DRIP was carried out as described in Ginno and Chédin et al. 2012. Briefly, 4.4 µg of DNA was resuspended in 500 µL of TE. 10% was taken for the input sample. DRIP binding buffer was added to each sample (10mM sodium phosphate, 140mM NaCl, 0.05% Triton X-100 final concentration) and 20 µL of 1 mg/mL S9.6 was added to each

DRIP reaction. After overnight incubation at 4C, 50 µL of pre-washed protein G Dynabeads (Life Technologies) were added to the extract. After 2 hours at 4C, beads with captured nucleic acid were washed in 1x DRIP binding buffer 5 times and eluted in 50mM Tris, 10mM EDTA, 0.5% SDS with proteinase K at 50□C for 45 minutes. Nucleic acid in the eluate was purified with phenol:chloroform, precipitated and resuspended in 10mM Tris. For DRIP-qPCR, 1µL of nucleic acid was diluted 1:10 in water and mixed with 10µL SSoAdvanced Universal Sybr (Bio-Rad). Primers were added to a final concentration of 250 nM each. A list of primers used in this study can be found in Supplemental Table 4-1. qPCR was carried out on a Bio-Rad CFX96 Touch instrument using the following protocol: 98^{o}C heat denaturation for 60" followed by 40 cycles of 98^{o}C for 15" and 60^{o}C for 30". A heat denaturation was included to monitor the purity of the reaction products. For ssDRIP, nucleic acid was sonicated in a Bioruptor Plus for 8 cycles at high power (30" on/30" off) to 250 bp. Libraries were constructed with the Accel-NGS 1S Plus DNA Library Kit according to the manufacturer's instruction (Swift Biosciences 10024). Barcoded libraries were sequenced using an Illumina Novaseq for 150bp PE reads.

Bioinformatics

Alignment and peak calling

Fastq files were initially trimmed of adapters using Trimmomatic v0.3.8 (Bolger and Usadel et al. 2014). Each paired read was trimmed 10 base-pairs at the 3' end to eliminate the additional low complexity from the library preparation kit. Reads for sequencing were mapped to the Drosophila genome (dm6) using bowtie2 version 2.3.4.1 using the –very-sensitive-local setting (Li and Durbin et al. 2009). Duplicates were marked using picard

MarkDuplicates v2.17.10, and stranded bam files were created using samtools as described in Xu and Sun et al. 2017. Stranded bam files were used to generate ssDRIP peaks with callpeaks from MAC2 v2.1.2 (Zhang and Liu et al. 2008). The RNase H pretreated DRIP file was used as control, peak calling was done on the 2 replicates in paired-end mode, with –keep-dup=auto and effective genome size for Drosophila dm6. A small number of peaks mapped to both strands as determined with bedtools. These were discarded for downstream analysis. Bam files were combined and 50 million reads were randomly selected for visualization. Stranded reads were visualized using deeptools bamCoverage using --binSize 50bp, --ignoreForNormalization chrY chrM, and --normalizeUsing RPKM (Ramírez and Manke et al. 2014). Pearson correlation plots were created using deeptools multiBamCoverage and plotCorrelation with default settings, 1kb windows and the mitochondrial genome excluded.

ssDRIP-seq analysis

Peak annotation was performed using Pavis to the dm6 genome with up- and downstream regions set to 5kb (Huang et al. 2013). Overall sense and antisense R-loops were determined via bedtools intersect with strandedness against the Refseq Drosophila transcriptome, downloaded from UCSC genome browser. Metagene plots were made with the Deeptools software package, using computeMatrix and plotProfile. For computeMatrix, scale-regions or reference-point as appropriate, with a 1kb region size and 500bp up- and down-stream of the start and end site, respectively. For options -binSize was 50 and the mean was plotted. For plotProfile, ‘add standard error’ was added

to Plot type. –yMin and –yMax were chosen to be the same for both sense and antisense to aid in visualization.

Gene Ontology enrichment analysis of R-loop containing genes was performed with PANTHER, with Fisher's exact test and using the Bonferroni correction for multiple testing (Ashburger et al 2000; Consortium et al 2020; Mi et al 2019).

GRO-seq FPKM counts were determined with HOMER analyzeRepeats.pl using S2 datasets from Core and Lis et al. 2012 and GRO-seq data on 2-2.5 embryos from Saunders and Ashe et al. 2013. R-loops peaks were split into 2 files containing their + and – peaks and annotation of R-loop peaks was done with HOMER software package using annotatePeaks.pl against dm6 and requiring the appropriate strandedness. R-loops mapping to transcripts were extracted from the HOMER annotation, and GROseq values for these transcripts was determined using custom R scripts. Plots summarizing these data were created in Prism 9.

Functional genomic data from modENCODE

We downloaded histone modification peaks and transcription factor binding sites identified by ChIP-chip or ChIP-seq in Drosophila from ModENCODE (Table 4-1) (Contrino and Hu et al. 2012). We considered samples assayed in S2 cells and at two developmental timepoints (2-4hr, 14-16hr). These were chosen to match the ssDRIP timepoints.

Table 4-1 List of available ChIP-chip and ChIP-seq from modENCODE.

Assay	Time	Mark

	2-4 hr	BEAF-32, CP-190, CTCF, RING, SFMBT, GAF, H2Av, H2Bubi, H3, H3K18ac, H3K23ac H3K27ac, H3K27me3, H3K36me1, H3K36me3, H3K4me1, H3K4me2, H3K4me3, H3K79me1, H3K79me2, H3K79me3, H3K9ac, H3K9me2, H3K9me3, H4, H4K20me1, HP1a, HP1c, HP2, Polycomb, POF, Su(HW), ZW5
ChIP-chip	S2 cells	ACF1, ASH1, BEAF-70, BEAF-HB, CG10630, Chriz-WR, CP190, CTCF, Mi-2, TopoII, RING, SFMBT, E(z), GAF, H1, H2Av, H2BK5ac, H2Bubi, H3, H3K18ac, H3K23ac, H3K27ac, H3K27me1, H3K27me2, H3K27me3, H3K36me1, H3K36me3, H3K4me1, H3K4me2, H3K4me3, H3K79me1, H3K79me2, H3K79me3, H3K9ac, H3K9acS10P, H3K9me1, H3K9me2, H3K9me3, H4, H4acTetra, H4K12ac, H4K16ac, H4K20me1, H4K5ac, H4K8ac, HP1a, HP1b, HP1c, HP2, HP4, ISWI, JHDMI, JIL-2, JMJD2A, LSD1, MBD-R2, MLE, mod(mdg4), MOF, MRG15, MSL-1, NURF301, ORC2, Polycomb, PCL, Pho, Pof, PR-Set7, Psc, Rhino, RNAPolII, RPD3, Smc3, Spt16, Su(HW), Su(var)3-7, Su(var)3-9, WDS, ZW5
ChIP-seq	14-16 hr	Beaf-HB, Chriz, CP190, CTCF, Mi-2, RING, GAF, H1, H2Av, H2B-ubi, H3, H3K18ac, H3K23ac, H3K27ac, H3K27me2, H3K27me3, H3K36me1, H3K36me2, H3K36me3, H3K4me1, H3K4me3, H3K79me1, H3K79me2, H3K79me3, H3K9acS10P, H3K9me1, H3K9me2, H3K9me3, H4, H4K16ac, H4K20me1, HP1a, HP1b,

	HP1c, HP2, HP4, JHDMI, LSD1, MBD-R2, MOF, NURF301, POF, Psc, RNAPolII, RPD3, Su(HW), Su(var)3-7, ZW5

Chromatin associated factor enrichment in R-loops

For each ChIP-chip or ChIP-seq marker with a matching DRIP timepoint, we calculated the number of overlapping base-pairs (bp) between the marker and the R-loop peaks. We used permutation-based approach to determine whether the observed amount of overlap was more or less than expected by chance. Briefly, we calculated an empirical *p* value for the observed amount of overlap by comparing the number of overlapping bp to a null distribution. We obtained the null distribution by randomly shuffling length-matched regions throughout the genome and calculating the amount of overlap in each permutation. The *p*-values are adjusted for multiple testing using the Bonferroni method.

When permuting, we matched the length distribution of the shuffled peaks to the original set of peaks, and excluded all gap and blacklisted regions from consideration (dm3; version 1) (Amemiya and Boyle et al. 2019). Peaks called from DRIP were lifted over to dm3 for this analysis. For peaks obtained from ChIP-chip data, we required that the shuffled peaks maintained both the overall length distribution and the probe density of the original peak. We reshuffled any peaks that fell more than 2 standard deviations (approx. 0.03) away from the original probe density until at least 99% of the original peaks were appropriately matched. We performed 1000 permutations for each marker and R-loop pair.

For the general analyses, we maintained the location of the R-loop peaks and shuffled the locations of the histone modification or transcription factor binding peaks. For a secondary analysis, we examined a subset of R-loops quantified specifically in the TTS and 3' UTR. For this set of R-loops, we maintained the R-loop location within the TTS/3' UTR and shuffled the chromatin markers.

Calculation of AT- and GC-skew in R-loops

We calculated GC and AT skew over the entire Drosophila genome (dm6). GC skew was calculated for 50 bp windows tiled across the annotation regions as $S_i = \frac{(G_i - C_i)}{G_i + C_i}$ (McLean and Devine et al. 1998).

In the equation, G_i represents the frequency of guanine nucleotides and C_i represents the frequency of cytosine nucleotides in the window i. The range of GC skew for a window (S_i) spans from -1 to 1. AT Skew was calculated in the same way. The resulting GC and AT skew was converted to a bigwig file, and the value across each set of genomic regions was calculated using the computeMatrix function from deeptools and visualized using plotProfile (For computeMatrix, scale-regions or reference-point as appropriate, with 500bp up- and down-stream of the start and end site, respectively. For options -binSize was 50 and the mean was plotted. For plotProfile, 'add standard error' was added to Plot type. –yMin and –yMax were chosen to be the same for AT and GC skew to aid in visualization).

Accession Numbers

Data sets generated in this study can be found under the GEO accession number: GSE185403.

Acknowledgment

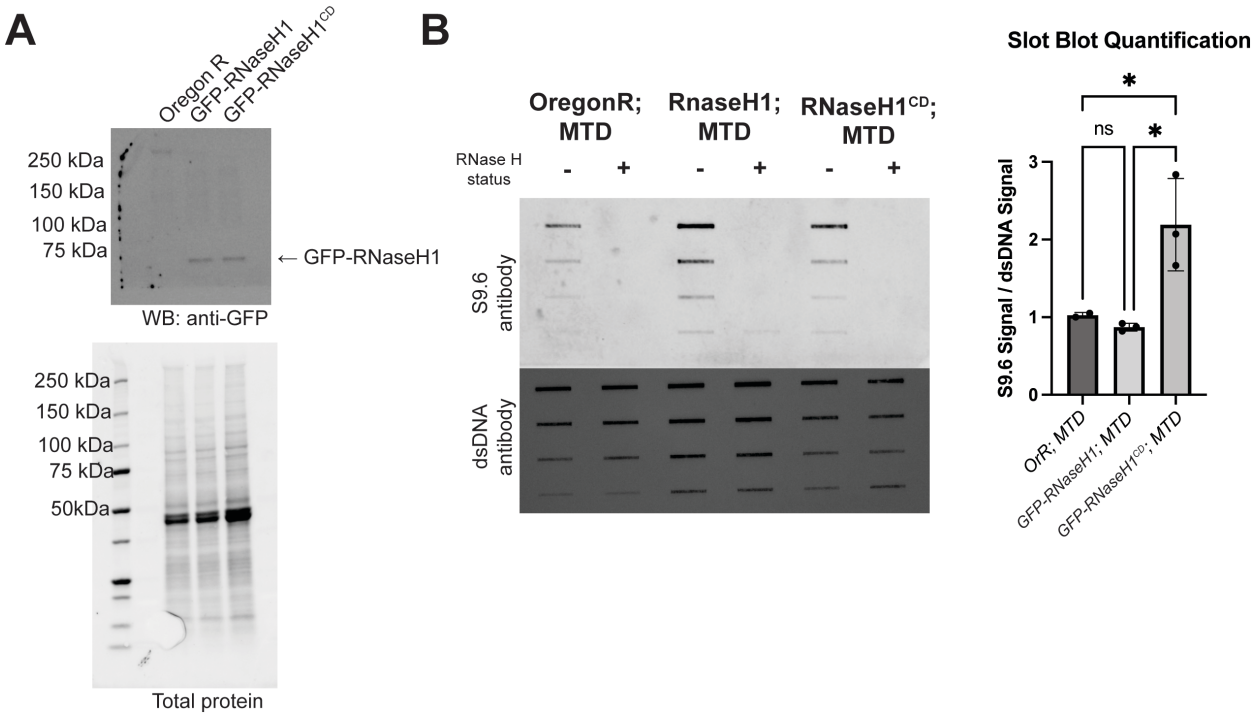
We thank the Vanderbilt VANTAGE core for Illumina sequencing and the Vanderbilt Antibody and Protein Resource core for purifying the S9.6 antibody. The Vanderbilt Antibody and Protein Resource core is supported by the Vanderbilt Institute of Chemical Biology and the Vanderbilt Ingram Cancer Center (P30 CA68485). Figures 4-1 and 4-2 partially created with BioRender.com. We thank Martina Brienza-Ramos for cloning of the RNase H1 plasmids used for fly injections. We thank Emily Hodges, Robin Armstrong and Frederic Chédin for providing critical feedback on the manuscript. We thank Lionel Sanz, Célia Alecki and Nicole Francis for technical advice.

Funding

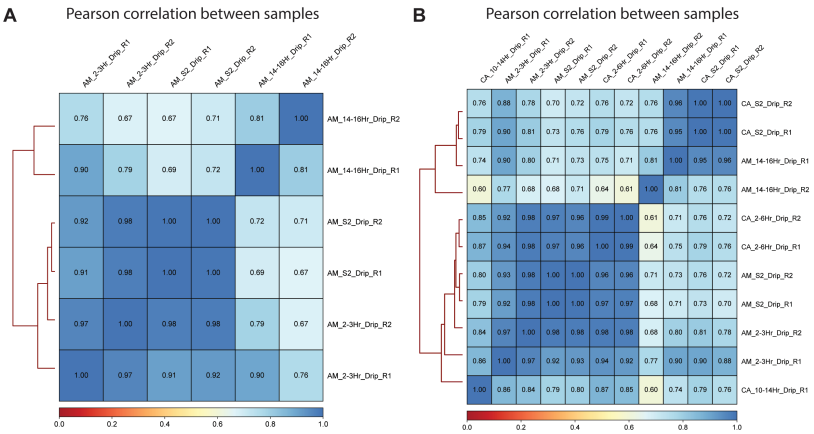
This work was supported by National Institutes of Health (NIH) General Medical Sciences awards [R35GM127087 to JAC] and [R35GM128650 to JTN].

Conflict of Interest

The authors declare no conflicts of interests

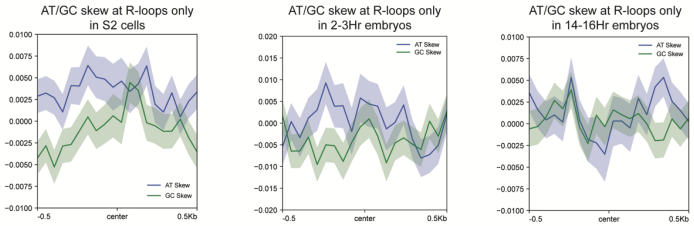


Supplemental Figure 4-1: Expression of RNaseH1 constructs in early embryos. (A) Western blot (anti-GFP) showing maternally deposited GFP-RNaseH1 and GFP-RNaseH1^{CD} in 0-6 hour embryos. Expected size of GFP + RNaseH1 = 65.1 kDa. (B) Representative slot blot of RNA:DNA hybrid levels, measured by S9.6 antibody intensity, from 2-6h embryos upon *RNaseH1* and *RNaseH1^{CD}* overexpression. RNase H treatment verifies specificity of antibody, and antibody specific for double-stranded DNA is used as a loading control. Oregon R is a wildtype control. Quantification of signal for 2 (Oregon R) or 3 (RNaseH and RNaseH^{CD}) biological replicates is to the right. * < 0.05, one-way ANOVA with Tukey's multiple comparisons test. Contributions: Experiment, analysis, and visualization.


A
Pearson correlation between samples
AM_2-3Hr_Drip_R1
AM_2-3Hr_Drip_R2
AM_S2_Drip_R1
AM_S2_Drip_R2
AM_14-16Hr_Drip_R1
AM_14-16Hr_Drip_R2
0.76 0.67 0.67 0.71 0.81 1.00 AM_14-16Hr_Drip_R2
0.90 0.79 0.69 0.72 1.00 0.81 AM_14-16Hr_Drip_R1
0.92 0.98 1.00 1.00 0.72 0.71 AM_S2_Drip_R2
0.91 0.98 1.00 1.00 0.69 0.67 AM_S2_Drip_R1
0.97 1.00 0.98 0.98 0.79 0.67 AM_2-3Hr_Drip_R2
1.00 0.97 0.91 0.92 0.90 0.76 AM_2-3Hr_Drip_R1
0.0 0.2 0.4 0.6 0.8 1.0
B
Pearson correlation between samples
CA_10-14Hr_Drip_R1
AM_2-3Hr_Drip_R1
AM_2-3Hr_Drip_R2
AM_S2_Drip_R1
AM_S2_Drip_R2
CA_2-6Hr_Drip_R1
CA_2-6Hr_Drip_R2
AM_14-16Hr_Drip_R2
AM_14-16Hr_Drip_R1
CA_S2_Drip_R1
CA_S2_Drip_R2
0.76 0.88 0.78 0.70 0.72 0.76 0.72 0.76 0.96 1.00 1.00 CA_S2_Drip_R2
0.79 0.90 0.81 0.73 0.76 0.79 0.76 0.76 0.95 1.00 1.00 CA_S2_Drip_R1
0.74 0.90 0.80 0.71 0.73 0.75 0.71 0.81 1.00 0.95 0.96 AM_14-16Hr_Drip_R1
0.60 0.77 0.68 0.68 0.71 0.64 0.61 1.00 0.81 0.76 0.76 AM_14-16Hr_Drip_R2
0.85 0.92 0.98 0.97 0.96 0.99 1.00 0.61 0.71 0.76 0.72 CA_2-6Hr_Drip_R2
0.87 0.94 0.98 0.97 0.96 1.00 0.99 0.64 0.75 0.79 0.76 CA_2-6Hr_Drip_R1
0.80 0.93 0.98 1.00 1.00 0.96 0.96 0.71 0.73 0.76 0.72 AM_S2_Drip_R2
0.79 0.92 0.98 1.00 1.00 0.97 0.97 0.68 0.71 0.73 0.70 AM_S2_Drip_R1
0.84 0.97 1.00 0.98 0.96 0.98 0.98 0.68 0.80 0.81 0.78 AM_2-3Hr_Drip_R2
0.86 1.00 0.97 0.92 0.93 0.94 0.92 0.77 0.90 0.90 0.88 AM_2-3Hr_Drip_R1
1.00 0.86 0.84 0.79 0.80 0.87 0.85 0.60 0.74 0.79 0.76 CA_10-14Hr_Drip_R1
0.0 0.2 0.4 0.6 0.8 1.0
C
MC_S2_Drip_R2
MC_S2_Drip_R1
CA_S2_Drip_R1
CA_S2_Drip_R2
ABF_S2_Drip_R2
ABF_S2_Drip_R1
AM_S2_Drip_R1
AM_S2_Drip_R2
0.52 0.51 0.78 0.74 0.91 0.91 1.00 1.00 AM_S2_Drip_R2
0.51 0.50 0.75 0.72 0.90 0.90 1.00 1.00 AM_S2_Drip_R1
0.57 0.57 0.78 0.74 1.00 1.00 0.90 0.91 ABF_S2_Drip_R1
0.58 0.57 0.78 0.74 1.00 1.00 0.90 0.91 ABF_S2_Drip_R2
0.45 0.45 1.00 1.00 0.74 0.74 0.72 0.74 CA_S2_Drip_R2
0.47 0.47 1.00 1.00 0.78 0.78 0.75 0.78 CA_S2_Drip_R1
1.00 1.00 0.47 0.45 0.57 0.57 0.50 0.51 MC_S2_Drip_R1
1.00 1.00 0.47 0.45 0.58 0.57 0.51 0.52 MC_S2_Drip_R2
0.0 0.2 0.4 0.6 0.8 1.0
E
Overlap of sense R-loops
2746
2-3hr embryos
3087
2788
4636
14-16hr embryos
4310
1224
4609
S2 cells
Overlap of antisense R-loops
701
2-3hr embryos
1197
837
1153
14-16hr embryos
2523
2283
339
S2 cells
D
AM_S2
CA_S2
ABF_S2
MC_S2
F
S2 DRIP-qPCR
DRIP
DRIP+RNaseH
% Input
2.5
2.0
1.5
1.0
0.5
0.0
* * ns * * * ns ns
Act5C
dF31
Psq263
RpL18
Zld162
Zld221
chr2RHet
Untran
Positive Sites
Neg. Sites
G
Act5C Melting Curve (MC)
dF31 MC
Psq263 MC
RpL18 MC
Zld162 MC
Zld221 MC
chr2RHet MC
Untran MC
Temperature, Celsius

Supplemental Figure 4-2: **Properties of R-loops in Drosophila (A)** Pearson's correlation between ssDRIP-seq replicates at 1kb resolution. AM- Alex Munden, this study. **(B)** Correlation between ssDRIP-seq replicates at 1kb resolution between this study (AM - Alex Munden) or data obtained from Alecki et al. 2020 (CA) **(C)** Correlation at 1kb resolution between ssDRIP-seq replicates specifically from S2 cells. AM – this study; CA – Alecki et al. 2020; ABF – Bayona-Feliu et al., 2017; and MC – Crossley et al., 2020) **(D)** Screen shot of unstranded ssDRIP-seq or DRIP-seq data for the same data sets as in C. **(E)** Venn diagrams of overlap of stranded R-loops between S2 cells, 2-3 hour embryos, and 14-16 hour embryos. Sense R-loops on top, antisense R-loops on bottom. **(F)** DRIP-qPCR validation of several R-loop positive and negative loci in S2 cells. **(G)** Melting curves for the qPCR products from the reactions in F. Contributions: Experiment, analysis, and visualization.

A



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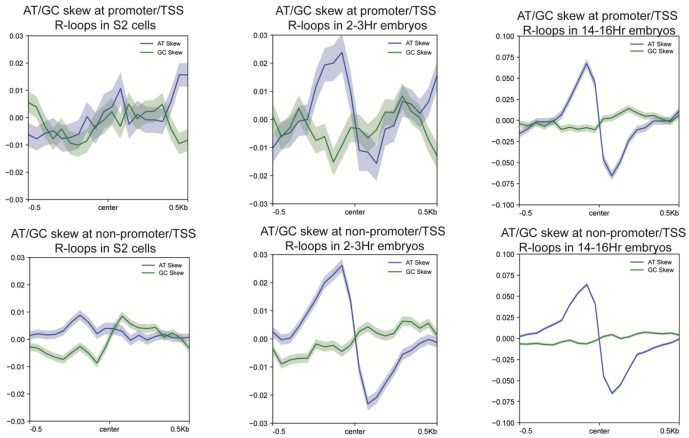
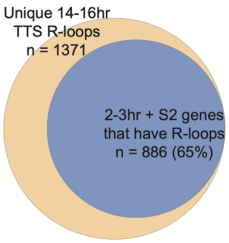


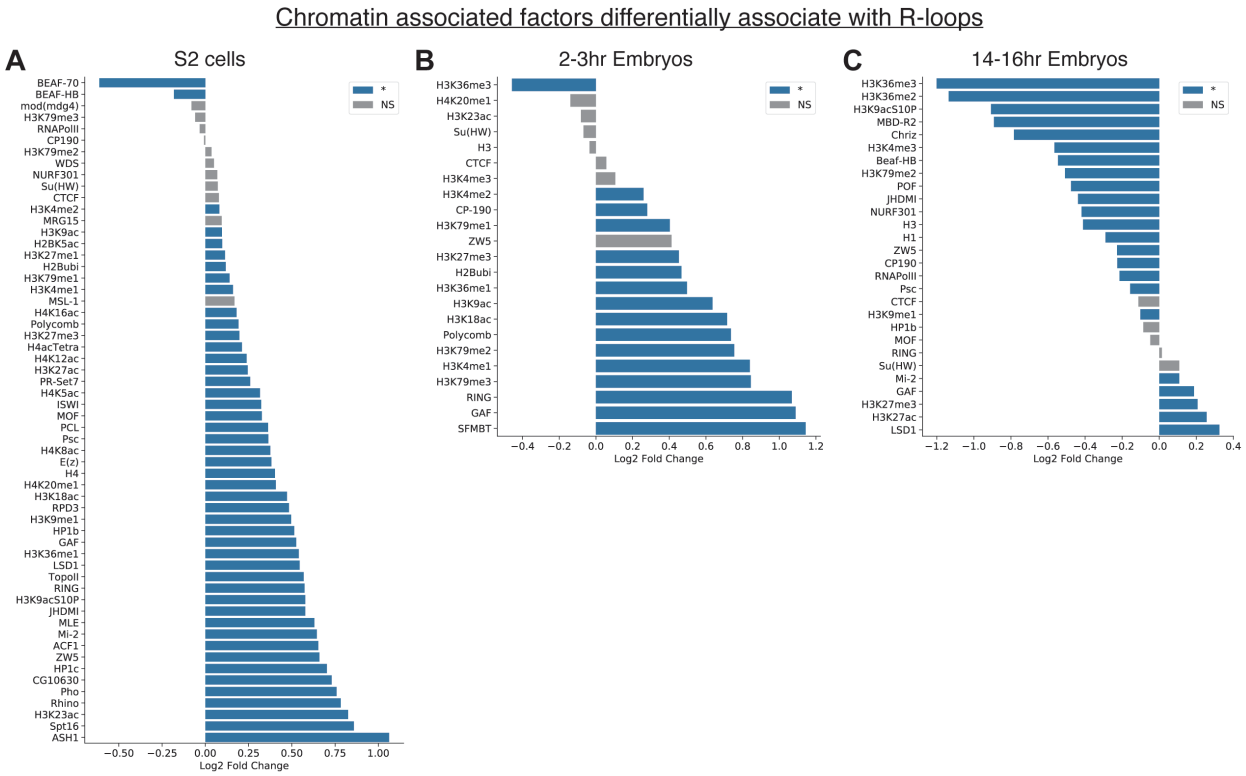
C



D

Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background	STD(Bg STD)	Best Match/Details
1		1e-1413	-3.254e+03	21.44%	8.73%	48.4bp (78.7bp)	hb/dmmpmm(Noyes)/fly(0.794) More Information | Similar Motifs Found
2		1e-1352	-3.114e+03	31.82%	18.65%	51.4bp (70.0bp)	Trl/dmmpmm(Down)/fly(0.559) More Information | Similar Motifs Found
3		1e-149	-3.432e+02	42.12%	36.14%	56.1bp (64.8bp)	Trl(Zf)/S2-GAGAfactor -ChIP-Seq(GSE40646)/Homer(0.647) More Information | Similar Motifs Found
4		1e-127	-2.947e+02	27.92%	23.00%	55.2bp (68.4bp)	Kr/dmmpmm(Noyes)/fly(0.718) More Information | Similar Motifs Found
5		1e-106	-2.457e+02	14.88%	11.43%	56.1bp (66.6bp)	Aef1/dmmpmm(Pollard)/fly(0.864) More Information | Similar Motifs Found
6		1e-104	-2.398e+02	40.18%	35.22%	56.3bp (67.1bp)	Trl/MA0205.2/Jaspar(0.781) More Information | Similar Motifs Found
7		1e-53	-1.239e+02	7.78%	5.96%	56.7bp (57.1bp)	ttk/MA0460.1/Jaspar(0.615) More Information | Similar Motifs Found
8		1e-52	-1.201e+02	0.13%	0.01%	58.2bp (42.2bp)	Btn/dmmpmm(Noyes_hdf)/fly(0.690) More Information | Similar Motifs Found
9		1e-38	-8.804e+01	0.08%	0.00%	53.6bp (31.1bp)	POL013.1_MED-1/Jaspar(0.622) More Information | Similar Motifs Found
10		1e-37	-8.600e+01	0.12%	0.01%	55.1bp (27.4bp)	ct/MA0218.1/Jaspar(0.627) More Information | Similar Motifs Found
11		1e-36	-8.456e+01	0.07%	0.00%	51.8bp (18.8bp)	dl-B/dmmpmm(Bergman)/fly(0.559) More Information | Similar Motifs Found
12		1e-36	-8.456e+01	0.07%	0.00%	53.5bp (38.4bp)	ara/dmmpmm(Noyes_hdf)/fly(0.712) More Information | Similar Motifs Found
13		1e-34	-7.985e+01	0.09%	0.01%	52.3bp (18.5bp)	Hr46/dmmpmm(Pollard)/fly(0.574) More Information | Similar Motifs Found
14		1e-34	-7.935e+01	2.89%	2.02%	56.0bp (60.3bp)	h/dmmpmm(Noyes)/fly(0.670) More Information | Similar Motifs Found
15		1e-33	-7.768e+01	0.07%	0.00%	56.8bp (15.9bp)	eyg/dmmpmm(Bergman)/fly(0.689) More Information | Similar Motifs Found
16		1e-30	-7.018e+01	0.09%	0.01%	55.7bp (14.8bp)	POL010.1_DCE_S_III/Jaspar(0.589) More Information | Similar Motifs Found

Supplemental Figure 4-3: **Sequence properties of R-loops in Drosophila (A)** Metaplots of AT and GC skew at developmental-specific sites of R-loop formation (note the difference in scale for each window). Shaded regions represent the standard error of the mean. **(B)** Metaplots of AT and GC skew at promoter TSS sites and all other R-loops for each cell type. **(C)** Measurement of the R-loops found only at the TTS/3' UTR in the 14-16hr embryos and whether those genes have R-loops elsewhere in the gene in S2 and 2-3hr embryos. **(D)** The top 16 results from the HOMER motif analysis. Only P-values less than 1e-100 should be considered as potential motifs. Contributions: Analysis for C and D, visualization.



Supplemental Figure 4-4: **Expanded chromatin associated factors associated with R-loops for every cell type. (A)** Markers positively and negatively associated with R-loops in S2 cells. * < 0.05 with Bonferroni correction for multiple testing. **(B)** Same as A, except for 2-3 hour embryos. **(C)** Same as A, except for 14-16 hour embryos. Contributions: None.

Supplemental Table 4-1: Primers used in R-loop study

Primer Name	Sequence
Act5C_Fwd	CCACGAGACCACCTACAACT
Act5C_Rev	TGATCTTCATGGTCGACGGT
Df31_Fwd	CTCAGACGCCTTTTCACCAT
Df31_Rev	TCGCAGCTGAGGAAGTTGAT
Psq263_Fwd	GTCTGTCCAATTGCTGCGG
Psq263_Rev	TGGCCACCCTCATCTACC
RpL18_Fwd	CTTGCCGAAGTGCTTGCA
RpL18_Rev	TGACCTTCGATCAACTGGCT
Zld162_Fwd	CAACGGAATAGGGTGGGAAT
Zld162_Rev	ACCCCGAATGTGATTAGCCA
Zld221_Fwd	CCACTGGGTTCTGGGTTTTG
Zld221_Rev	CAGTTGCCCGCCGATAATC
chr2RHet_Fwd	TTAAGCGCGGAAAGAAGATCA
chr2RHet_Rev	CAGTTTTGGCGTAGCTAGGGATA
Untranscribed_Fwd	TCAAGCCGAACCCTCTAAAAT
Untranscribed_Rev	AACGCCAACAAACAGAAAATG

Supplemental Table 4-2: GO analysis of R-loop forming genes

S2 cell (total)

PANTHER GO-Slim Biological Process	#	#	expected	Fold Enrichment	+/-	P value
regulation of transcription by RNA polymerase II	603	243	101.05	2.4	+	1.21E-25
transcription by RNA polymerase II	645	250	108.08	2.31	+	2.25E-24
cell surface receptor signaling pathway	133	56	22.29	2.51	+	0.0000676
negative regulation of cellular process	233	79	39.04	2.02	+	0.000396
chemical synaptic transmission	78	38	13.07	2.91	+	0.000538
actin cytoskeleton organization	88	40	14.75	2.71	+	0.00111
regulation of biological quality	253	81	42.4	1.91	+	0.00156
axonogenesis	36	23	6.03	3.81	+	0.00367
cell-cell adhesion	52	28	8.71	3.21	+	0.00397
animal organ development	29	20	4.86	4.12	+	0.00709
cAMP-mediated signaling	43	24	7.21	3.33	+	0.0126
regulation of adenylate cyclase activity	43	24	7.21	3.33	+	0.0126
protein phosphorylation	142	51	23.8	2.14	+	0.0137
adenylate cyclase-modulating G protein-coupled receptor signaling pathway	42	23	7.04	3.27	+	0.0242
regulation of cAMP-mediated signaling	42	23	7.04	3.27	+	0.0242
positive regulation of biological process	296	85	49.6	1.71	+	0.0295
negative regulation of nitrogen compound metabolic process	121	44	20.28	2.17	+	0.0378

S2 cell (unique)

GO biological process complete	#	#	expected	Fold Enrichm	+/-	P value
cellular process	7322	914	764.46	1.2	+	1.64E-10
biological regulation	4402	564	459.6	1.23	+	0.000134
regulation of biological process	3964	513	413.87	1.24	+	0.000299
regulation of cellular process	3661	474	382.23	1.24	+	0.00133
localization	2243	306	234.18	1.31	+	0.00999
transport	1717	241	179.27	1.34	+	0.0267

2-3h embryo (total)

PANTHER GO-Slim Biological Process	#	#	expected	Fold Enrichment	+/-	P value
regulation of transcription by RNA polymerase II	603	223	92.89	2.4	+	1.37E-23
transcription by RNA polymerase II	645	228	99.36	2.29	+	3.71E-22
animal organ development	29	22	4.47	4.92	+	0.000215
protein phosphorylation	142	53	21.87	2.42	+	0.000293
G protein-coupled receptor signaling pathway	93	41	14.33	2.86	+	0.000321
axonogenesis	36	24	5.55	4.33	+	0.000333
cell-cell adhesion	52	28	8.01	3.5	+	0.000914
regulation of intracellular signal transduction	98	40	15.1	2.65	+	0.00213
chemical synaptic transmission	78	34	12.02	2.83	+	0.00286
regulation of cellular component size	26	17	4.01	4.24	+	0.0223
actin filament organization	60	27	9.24	2.92	+	0.0239
cAMP-mediated signaling	43	22	6.62	3.32	+	0.0257
regulation of adenylate cyclase activity	43	22	6.62	3.32	+	0.0257
negative regulation of RNA metabolic process	61	27	9.4	2.87	+	0.0282
enzyme linked receptor protein signaling pathway	62	27	9.55	2.83	+	0.0338
chemotaxis	31	18	4.78	3.77	+	0.0414
positive regulation of cellular metabolic process	214	62	32.96	1.88	+	0.0435

2-3h embryo (unique)

GO biological process complete	#	#	expected	Fold Enrichm	+/-	P value
biological regulation	4402	405	290.15	1.4	+	6.31E-11
regulation of biological process	3964	367	261.28	1.4	+	1.55E-09
regulation of cellular process	3661	344	241.31	1.43	+	2.39E-09
cellular process	7322	591	482.62	1.22	+	7.62E-09
multicellular organism development	2280	233	150.28	1.55	+	8.36E-08
system development	1643	178	108.3	1.64	+	6.03E-07
anatomical structure development	2635	253	173.68	1.46	+	0.00000279
developmental process	2765	260	182.25	1.43	+	0.0000094
animal organ development	1148	129	75.67	1.7	+	0.0000601
multicellular organismal process	3487	305	229.84	1.33	+	0.000271
tube development	689	85	45.41	1.87	+	0.000714
epithelium development	925	105	60.97	1.72	+	0.000966
animal organ morphogenesis	709	86	46.73	1.84	+	0.00105
regulation of macromolecule metabolic process	1989	190	131.1	1.45	+	0.00133
tissue development	1000	110	65.91	1.67	+	0.00182
post-embryonic development	611	76	40.27	1.89	+	0.00207
imaginal disc development	538	69	35.46	1.95	+	0.00256
anatomical structure morphogenesis	1456	146	95.97	1.52	+	0.00325
regulation of metabolic process	2150	199	141.72	1.4	+	0.00487
regulation of nitrogen compound metabolic process	1769	169	116.6	1.45	+	0.00647
regulation of cellular metabolic process	1930	181	127.21	1.42	+	0.00899
regulation of primary metabolic process	1797	170	118.45	1.44	+	0.012
instar larval or pupal development	536	66	35.33	1.87	+	0.0194
post-embryonic animal morphogenesis	444	57	29.27	1.95	+	0.0255
tube morphogenesis	496	61	32.69	1.87	+	0.047
tissue morphogenesis	589	69	38.82	1.78	+	0.0498

14-16h embryo (total)

PANTHER GO-Slim Biological Process	#	#	expected	Fold Enrichment	+/-	P value
regulation of transcription by RNA polymerase II	603	185	82.24	2.25	+	3.59E-17
transcription by RNA polymerase II	645	189	87.97	2.15	+	7.51E-16
chemical synaptic transmission	78	39	10.64	3.67	+	0.00000146
cell-cell adhesion	52	30	7.09	4.23	+	0.0000103
positive regulation of cellular process	285	76	38.87	1.96	+	0.000924
protein phosphorylation	142	47	19.37	2.43	+	0.00104
negative regulation of cellular process	233	66	31.78	2.08	+	0.00111
axon guidance	29	19	3.96	4.8	+	0.00141
cAMP-mediated signaling	43	23	5.86	3.92	+	0.00153
regulation of adenylate cyclase activity	43	23	5.86	3.92	+	0.00153
adenylate cyclase-modulating G protein-coupled receptor signaling pathway	42	22	5.73	3.84	+	0.00339
regulation of cAMP-mediated signaling	42	22	5.73	3.84	+	0.00339
positive regulation of catalytic activity	76	30	10.37	2.89	+	0.00751
synapse organization	35	19	4.77	3.98	+	0.011
regulation of membrane potential	43	21	5.86	3.58	+	0.0131
transmembrane receptor protein tyrosine kinase signaling pathway	32	18	4.36	4.12	+	0.0131
animal organ development	29	17	3.96	4.3	+	0.0154
actin filament organization	60	25	8.18	3.06	+	0.0173
ion transport	346	82	47.19	1.74	+	0.0197
regulation of phosphorylation	62	25	8.46	2.96	+	0.027
ncRNA metabolic process	220	8	30.01	0.27	-	0.0106

14-16h embryo (unique)

GO biological process complete	#	#	expected	Fold Enrichm	+/-	P value
cellular process	7322	144	98.01	1.47	+	1.9E-08
anatomical structure development	2635	71	35.27	2.01	+	0.00000498
multicellular organismal process	3487	85	46.67	1.82	+	0.00000507
multicellular organism development	2280	63	30.52	2.06	+	0.0000255
signaling	1199	42	16.05	2.62	+	0.0000316
developmental process	2765	71	37.01	1.92	+	0.0000369
cell communication	1269	43	16.99	2.53	+	0.000052
response to stimulus	2513	66	33.64	1.96	+	0.0000917
biological regulation	4402	96	58.92	1.63	+	0.0000989
signal transduction	994	35	13.31	2.63	+	0.00063
behavior	515	24	6.89	3.48	+	0.000632
system development	1643	47	21.99	2.14	+	0.00188
regulation of cellular process	3661	81	49	1.65	+	0.002
anatomical structure morphogenesis	1456	43	19.49	2.21	+	0.00294
cellular component organization	2598	63	34.78	1.81	+	0.00366
regulation of biological process	3964	84	53.06	1.58	+	0.00607
cellular response to stimulus	1476	42	19.76	2.13	+	0.0123
cell differentiation	1593	44	21.32	2.06	+	0.0151
cellular component organization or biogenesis	2757	64	36.9	1.73	+	0.016
cellular developmental process	1605	44	21.48	2.05	+	0.0164
positive regulation of multicellular organismal proce	203	13	2.72	4.78	+	0.0206
positive regulation of biological process	1717	45	22.98	1.96	+	0.0341

Chapter V: Summary and Discussion

DNA is the foundation of genetic information in every eukaryote. Efficiently copying and maintaining DNA is vital for the preservation of the genome. A multitude of studies using yeast, mammalian cell cultures, *in vitro* reconstitution systems, Xenopus, Drosophila, and other species have laid the groundwork for a greater understanding of the fundamentals of DNA replication. The chromatin environment in which DNA resides is exquisitely regulated in order to safeguard epigenetic information, organize chromatin, and allow for transcription of RNA. However, the confines of development pose a unique obstacle due to the transition from maternal-to-zygotic transcription, establishing the proper cascade of chromatin markers as cells differentiate and divide, constrained cell cycles, and the alternative DNA replication programs needed in certain tissues. By combining next-generation sequencing technologies, mass spectrometry, and other techniques, my work in Drosophila has (1) helped define a new role for Rif1 as a regulator of replication fork progression (chapter II); (2) made available new widescale tools to study replication fork composition during development (chapter III); and (3) highlighted the dynamic role of R-loop biology during embryogenesis (chapter IV). However, many questions remain. The rest of this thesis will describe specific experiments that would give new insight to the biology of DNA replication and discuss larger questions that remain in the field.

Rif1 at replication forks

Previous research demonstrated that SuUR acts as a novel regulator of fork progression to control underreplication and gene amplifications programs during

development (Nordman et al. 2014, Kolesnikova et al. 2013). However, due to its likely catalytically dead ATP binding motif and a lack of known functional protein domains, it was unclear how SuUR functioned to control the underreplication and gene amplification program (Yurlova et al. 2009). Our lab's work demonstrated that it controls these programs via an interaction with Rif1. However, SuUR and Rif1 act at only at only a subset of replication forks during gene amplification and underreplication. How both proteins are targeted to specific replication forks remains unknown. Based on how these proteins function to halt replication fork progression and the need for complete replication throughout the remainder of the genome, it is unlikely they are at all replication forks. Previous ChIP-seq and polytene chromosome immunofluorescence demonstrated that they are found only at replication forks in a subset of the genome (Nordman et al. 2014, Kolesnikova et al. 2013). Our own unpublished iPOND mass spectrometry experiments detect SuUR and Rif1 at levels below that of essential proteins present at every replication fork. Therefore, the question remains how SuUR is ultimately targeted to replication forks.

Our immunopurified SuUR mass spectrometry data does not include any obvious candidates for what directs SuUR to replication forks. One possibility is that SuUR is post-translationally modified during S phase to control its localization to the replisome like other dynamic replication fork components are (Sirbu et al. 2011). This could work well during the constrained environment of gene amplification but how it might be targeted to replication forks during a more normal S phase is not clear. Underreplicated regions are normally replicated late in S phase (Belyaeva et al. 2012). Therefore, SuUR might be modified at some point as a byproduct of the replication timing program and is only recruited to replication forks during late S phase. More detailed mass spectrometry

examining changes in posttranslational modifications in early versus late S phase could reveal both the type of modification and where it is modified. These could reveal new insights into what regulates the recruitment of SuUR and Rif1 to replication forks.

Alternatively, recent work has shown that heterochromatin protein 1 (HP1) can exist in a liquid-liquid phase separated compartment (Keenen et al. 2021). SuUR has previously been shown to interact with a variety of chromatin associated factors involved with repressed chromatin including HP1 (Pindyurin et al. 2008). Perhaps SuUR and its interacting partner Rif1 exist in a phase separated environment around potential sites of underreplication, where they can interact with the replication fork machinery only when it enters the compartment and can subsequently be modified (Frattini et al. 2021). This would elegantly allow these complexes to be targeted to the genomic hubs where they are needed. However, some sites of underreplication exist in euchromatin. Specifically testing whether SuUR and Rif1 could form phase separated condensates with other heterochromatin components would be the first step in testing such this hypothesis.

The loss of SuUR or Rif1 lacks obvious phenotypes, such as organismal death or transcriptional derepression of genes within underreplicated regions, therefore it remains unclear why organisms utilize underreplication (Sher et al. 2011). There are several hypotheses as to why underreplication exists. It could be a way to divert developmental resources away from duplicating DNA that is ultimately “useless” as it will no longer be transcriptionally active in a terminally differentiated tissue (Nordman and Orr-Weaver, 2015). The rarity of underreplication in this scenario then is due to the relative rarity of polyploid tissue. Underreplication would normally cause double-strand breaks in a diploid

chromosome, but the polyploid nature of the salivary glands and other tissues that undergo underreplication allow this possibility.

Another hypothesis is that underreplication is involved with or a byproduct of avoiding some cell cycle checkpoints that may need to be suppressed during endoreplication (Hassel et al. 2014). Indeed, loss of function Cdc14 mutants in yeast can result in underreplicated regions (Dulev et al. 2009). Underreplicated regions in these mutants are generally late replicating, which supports the idea that there is some stress response or lack of metabolites available which results in genomic underreplication. Perhaps if Rif1 or SuUR mutant flies were grown under nutrient starved these mutants would be more likely to die. In the trophoblast giant cells of the mammalian placenta where underreplication occurs, a redirection of resources by avoiding cytokinesis and unnecessary DNA replication program in order to better divert resources to the embryo has been hypothesized (Hannibal and Baker, 2016). Experiments with Rif1 and SuUR mutant flies may prove a way to test the theory that the resources saved by underreplication could be significant.

Alternatively, underreplication might occur to resolve probable DNA damage. The dampened DNA damage checkpoints during gene amplification and endoreplication may make it untenable to repair DNA as normal (Mehrotra et al. 2008). Certain cancers with defective DNA damage checkpoints also undergo underreplication (Bertolin et al. 2020). The large size of metazoan genomes increases the probability that, by chance, some replication forks will stall and be unable to replicate some regions of the genome (Bertolin et al. 2020). Therefore, the underreplication program in dispensable regions of the genome may allow the polyploid cell to survive otherwise lethal DNA damage that would

occur without normal DNA damage control. Previous research indicates that underreplicated regions have a mutational signature of DNA damage (Yarosh and Spradling, 2014). Testing SuUR and Rif1 null mutant flies to see if they are more vulnerable to DNA damaging agents could help answer this question.

Replication fork remodeling during embryogenesis

Our work establishing iPOND coupled to quantitative mass spectrometry as a tool to study Drosophila embryogenesis likely undercounted the number of proteins at replication forks in embryo. Compared to earlier label-free attempts that we made, significantly fewer proteins at replication forks were found. However, the label-free approach makes it difficult to directly compare proteomics data from multiple different cell types, as absence of a protein does not guarantee it was missing in the alternative sample. It could instead be due to variance in the mass spectrometry run itself. Therefore, we opted for the safer approach of labeling with isobaric reagents that let us definitively ask whether a protein was present or absent in one sample versus the other. The use of stable-isotope labeling by amino acids in cell culture (SILAC) flies in the future could be a valuable improvement upon our method (Beati et al. 2019). This method utilizes flies fed on yeast containing a ‘heavy’ version of Lysine and Arginine which is incorporated into the fly proteome. The slight mass difference between flies fed on heavy and normal yeast can be detected on modern mass spectrometry machines and obviates the need to label the peptides with a tag. It still retains the simplified and accurate quantitative comparison of isobaric labeling. The post-experiment isobaric labeling has several drawbacks, including loss of sensitivity, which may account for the

decline in identified proteins we observed (Bąchor et al. 2019). This method has other drawbacks, such as the inability to label arginine. This limits the spectrum of peptides that can ultimately be identified.

Nonetheless, this research will be a valuable resource to the community of scientists studying DNA replication during development. It can serve as the jumping off point for a variety of projects examining when precisely during development certain replication fork components are required and demonstrated a novel role of the BRWD3 protein at replication forks in Drosophila. Several proteins identified had no known function at the replication fork in Drosophila. Comparison of these datasets to those generated in human cells may highlight proteins uniquely required for proper DNA replication in mammalian or Drosophila species, respectively (Wessel et al. 2019).

R-loop formation during embryogenesis is dynamic

R-loops have multiple functions such as repair of DNA double strand breaks, promoting transcription termination, preventing DNA methylation, and more (Aguilera and García-Muse, 2012). In contrast, R-loops can be a source of DNA damage. R-loop mapping studies across development have been performed in plants and in induced pluripotent stem cells (Xu et al. 2020, Yan et al. 2020). I showed that bulk R-loop levels vary as a function of development, and that impeding normal R-loop metabolism through overexpression of a catalytically dead RNase H1 causes elevated R-loop levels and embryonic death. This demonstrates the requirement for proper R-loop resolution during development.

I mapped R-loop formation across the Drosophila genome at multiple timepoints during embryogenesis and in the S2 cell culture line. Though a core set of sites always form R-loops, many loci vary across development. The overlap of R-loops with many chromatin associated factors changes with development, though a subset of markers associated with both active and repressed chromatin remain consistent. Importantly, I demonstrated that changes in transcription cannot account for the plastic formation of R-loops by examining deposited GRO-seq data. This implies that R-loop formation is actively regulated across cell type and not just a byproduct of changing transcription. By comparing R-loop formation at 2-3 hour embryos with RPA ChIP-seq data from a similar timepoint, I suggest that R-loops may play an important role in activating the ATR checkpoint during the maternal-to-zygotic transition. The groundwork in establishing this system grants us the ability to ask more scintillating questions in the future.

The role of R-loops in establishing the chromatin environment remains a ‘chicken or the egg question’, and it is unclear whether R-loops modify the chromatin environment around them or if instead their formation is a byproduct of the surrounding genomic landscape (Chédin 2016). There is compelling biochemical evidence that at minimum R-loops play a role in establishing repressive H3K27me3 chromatin domains through its interaction with Polycomb complex members in Drosophila and mammals (Alecki et al. 2020, Skourti-Stathaki et al. 2019). In addition, genetic screens in yeast show that R-loops can promote H3S10 phosphorylation (Castellano-Pozo et al. 2013). Proteomics screens for R-loop interacting factors show a wide variety of proteins that can potentially bind R-loops and may play a role in modifying the nearby chromatin either directly or indirectly (Cristini et al. 2018, Mosler et al. 2021).

In early embryogenesis chromatin exists in a naïve state without established histone modification and heterochromatin domains (Eckersley-Maslin et al. 2018). This makes it uniquely suited to interrogate the interplay between R-loops and chromatin and directly ask to what extent R-loops establish the surrounding chromatin environment. By overexpressing RNase H1 using the flies we engineered, R-loops could be degraded prematurely before they have time to modify the surrounding chromatin. My data shows that overexpression does not cause embryonic lethality. Therefore, one could perform ChIP-seq for a variety of different histone markers and chromatin associated proteins in a wild-type and RNase H1 overexpression background and interrogate how disrupting R-loop formation impacts establishment of normal histone modifications and chromatin associated factors. Delay or altered chromatin domain formation, combined with careful RNA-seq controls to ensure that the results aren't due to altered transcription, would conclusively demonstrate the extent to which R-loops determine the chromatin environment.

The RNase H1 overexpression experiment could also be used to address the question to what extent R-loops may play in activating ATR, an essential DNA damage checkpoint regulator, at the maternal-to-zygotic transition (Hamm and Harrison, 2018). Data from previous work combining mutants of ATR and Zelda, a ubiquitous transcription factor necessary for much of the transcription at the maternal-to-zygotic transition, shows that loss of Zelda bypasses the requirement for ATR at the MZT (Blythe and Wieschaus 2015). This demonstrated that the activation of ATR is due to some sort of DNA damage caused by transcription. At cycle 14, the cell cycle is still abbreviated and is concluded within an hour (Farrell and O'Farrell, 2014). One explanation for the activation of ATR is

due to collisions between the replication and transcription machinery occurring within the shortened cell cycle (Hamperl et al. 2017). If the lethality of ATR mutants at this timepoint is bypassed by overexpressing RNase H1 and eliminating R-loops, that would conclusively demonstrate that R-loops drive the requirement for ATR. This would illustrate a new role for R-loops in embryogenesis and DNA damage signaling.

My work and others have shown that R-loops form across the histone locus in Drosophila and mice (Wulfridge and Sarma, 2021). The Drosophila histone locus body undergoes a precise and well-characterized formation during embryogenesis and has been used as an important model for research in nuclear body formation (Duronio and Marzluff, 2017). Mass spectrometry screens revealed that many putative R-loop interacting factors have intrinsically disordered domains (IDR), which often play a role in formation of nuclear bodies via liquid-liquid phase separation (LLPS) (Protter et al. 2018, Dettori et al. 2021). Formation of the histone locus body occurs through a hierarchal process and is nucleated by the onset of transcription (White et al. 2011, Koreski et al. 2020). It is possible that this process may involve recruitment of IDR-containing proteins via their interaction with R-loops. I performed initial experiments testing whether overexpression of RNase H1 delayed or impacted formation of the histone locus body using immunofluorescence. These preliminary results failed to show a clear delay in histone locus body, though more careful analysis using time-lapse microscopy may yet reveal a role for R-loops in the formation of this nuclear body. Alternatively, initially investigating this question in a tractable cell culture system may be better simpler than the very fast embryonic system.

Finally, R-loops may function in organizing chromatin. Due to the abundance of RNA binding proteins, RNA can make an ideal scaffold for chromatin organization and it is essential for the formation of some nuclear bodies (Chujo and Hirose, 2017). Exciting experiments have been done examining the function of RNA in genome organization by analyzing untreated and RNase A treated with next-generation sequencing approaches. Treatment with RNase A seems to alter genome organization (Barutcu et al. 2019, Thakur et al. 2019). Both facultative and constitutive heterochromatin were impacted in these experiments. However, RNase A is known have off-target R-loop degradation activity in common buffer conditions (Smolka et al. 2021). Indeed, disrupting active transcription where R-loops might form via treatment with actinomycin D had a much greater impact on chromatin organization than treatment with RNase A (Barucu et al. 2019). As R-loops often form as a byproduct of transcription, they may function to regulate chromatin organization and establishment of topologically associating domains. The embryo RNase H1 overexpression system could be utilized to separate the function of active transcription and R-loops in regulating chromatin organization. This line of inquiry is bolstered by recent research demonstrating that R-loop formation at the *HOTTIP* lncRNA loci is required for proper chromatin domain formation in a mouse model of leukemia and disruption of this process promotes tumorigenesis (Luo et al. 2022). The relative infancy of R-loop biology as a field lends itself to reveal key mechanistic insights into a suite of fundamental genome organization and stability. The system I developed mapping and modulating R-loop abundance in Drosophila embryogenesis is well-position to answer important questions in R-loop biology in the context of development.

Improvements in R-loop science

The field of R-loop biology is at a crossroads. The last decade has been marked by an explosion of R-loop mapping studies in a multitude of different organisms and an increased appreciation for the variety of roles that R-loops can play in the cell. Due to the newness of the topic and lack of understanding, some research that may be flawed has also come out. For example, several studies have used immunofluorescence with the S9.6 antibody to test whether modulation of a specific protein impacts R-loops levels. In my own hands, this was an ineffective way to measure R-loop levels because there is abundant cytoplasmic S9.6 staining. Recently, other research has demonstrated the shortcomings of the S9.6 antibody and the challenge in properly interpreting R-loop phenotypes. The Chédin lab showed that spike-in fluorescent labeled dsRNA overlaps with the S9.6 antibody and that what S9.6 is binding to is not a bona fide R-loop (Smolka et al. 2021). The Stirling lab examined R-loop dependent genome instability in an RNA processing factor mutant. Instead, they found the supposed R-loop phenotype was driven by changed gene expression of an important cytoskeletal component (Tam et al. 2019). Finally, several studies used the DRIPc method that maps the RNA strand of an R-loop to allow for greater resolution and strand-specificity. A meta-analysis of these studies showed that there was large contamination by RNA not from R-loops (Chédin et al. 2021). Indeed, this is another obstacle I encountered in my own hands mapping R-loops. I mention these studies not to criticize the work done, but to highlight the challenges of developing a new field of biology. What does the field look like going forward? I see several key challenges: (1) develop new mapping strategies and assays for detecting R-

loops; (2) more careful analysis of R-loop phenotypes; and (3) an increased need for precise language to describe R-loops.

Improved R-loop detection. My early attempts at mapping R-loops by sequencing of the RNA strand of the R-loop failed due to contamination of RNA, and this has since been shown to be a wider problem in the field (Chédin et al. 2021). In addition, I was only able to obtain consistent, RNase H1-degradable results through careful reduction of the contaminating RNA in the extract. Many of the studies analyzing R-loops have used the S9.6 antibody. Other alternative approaches relied on expressing tagged, catalytically dead RNase H1 in live cells and purifying the protein:nucleic acid complex (Chen et al. 2017). The dramatic embryonic death I observed when overexpressing catalytically dead RNase H1 demonstrates how this could alter the R-loop environment. If overexpression of this protein perturbs the cell's environment so intensely that embryos die, then it is unlikely to accurately map native R-loop formation.

New methods utilizing *in vitro* purified RNase H1 combined with 'CUT&RUN' purification of R-loops may ultimately be a more consistent and robust method to map R-loop formation genome wide (Yan and Sarma, 2020). RNase H1 recognizes an R-loop over dsRNA with 25-fold greater affinity (Nowotny et al. 2008). In comparison, the S9.6 antibody recognizes R-loops with only 4.5 fold greater affinity than dsRNA (Phillips et al. 2013). The minimum required R-loop size is similar between the RNase H1 and S9.6 antibody (4 basepairs versus 6) (Phillips et al. 2013). The nucleic acid sequence can also have large impacts on the S9.6 antibody's binding affinity to both dsRNA and R-loops, while the sequence preferences for RNase H1 are less clear (Konig et al. 2017).

Therefore, using purified RNase H1 may give more accurate results compared to the S9.6 antibody.

Despite the advantages of RNase H1 over the S9.6 antibody, the affinity of RNase H1 for R-loops is in the order of 10^{-7} M (Nowotny et al. 2008). In comparison, the K_d of commercial antibodies for common epitope tags is in the order of 10^{-9}-10^{-10} M (Ranawakage et al. 2019). RNase H1 is an essential, well-studied enzyme and is only composed of one subunit. These traits have led it to be the workhorse and first alternative for R-loop mapping. Several proteomic screens have been performed to identify proteins which interact with R-loops (Wu et al. 2021; Mosler et al. 2021; Wang et al. 2018; Cristini et al. 2018). One of these may ultimately prove to be much more robust and reliable way to measure R-loops localization across the genome going forward. Alternatively, directed evolution of RNase H1 may result in a more suitable tool to evaluate R-loop formation (Zeymer and Hilvert 2018).

Proper evaluation of R-loop phenotypes. Due to the excitement in the field around R-loops, there has been a rush to publish and link previously observed mutants and phenotypes to R-loop biology. However, R-loops are involved with double-strand break repair, regulation of chromatin, transcription termination, DNA methylation, modulation of transcription, and mitochondria replication (Santos-Pereira and Aguilera, 2015). These disparate functions and the infancy of the field means that it can be difficult to properly link R-loops to the correct biology. Work by multiple labs emphasized this when they demonstrated that mutants previously thought to cause genome stability in *cis* due to increased R-loops was instead due to altered transcript levels in cohesion proteins (Tam

et al. 2019, Darman et al. 2015). Going forward, careful controls must be done to ensure the veracity of claims made.

The gold standard to specifically test for R-loop driven phenotypes has long been overexpression of RNase H1, used in one of the first papers that showed R-loop driven genome instability (Li and Manley, 2005). This theoretically degrades abundant R-loops. RNase H1 overexpression has been consistently used across the field and despite the potential drawbacks of overexpression mentioned earlier, should still be widely used. Many labs are examining the potential role of RNA processing factors and spliceosome components, as these proteins can impact R-loop formation and resolution. Ensuring that any result is due to impaired R-loop processing and not altered transcription can be done with RNA-seq experiments and should be required in the field.

One of the most exciting research avenues is how R-loops cause DNA damage. While the exposed single-strand of DNA is subject to deamination, this is unlikely to cause damage beyond point mutations. Exceptions can theoretically occur at transcriptionally active loci where high levels of transcription and single strand break from TOP1 cleave complexes can act with nucleases at an R-loop to generate two independent single strand breaks (Cristini et al. 2019, Sollier et al. 2014). The primary source of R-loop driven genome instability occurs during S phase and seems to be driven by collisions with the replication fork machinery (Gan et al. 2011). Careful cell cycle analysis can be used to show that genome instability due to R-loops only occurs during S phase, such as done in some previous work (Stork et al. 2016).

Precise language. While R-loops were originally defined as occurring in *trans*, most R-loops are thought to form in *cis* when nascent RNA reanneals to the template DNA.

There are many exceptions to this rule. The guide RNA of the CRISPR-Cas9 enzyme forms an RNA:DNA hybrid at its target site (Mitchell et al. 2020). Recently it has been shown that R-loops can form at the edges of double-strand breaks, and the prevention of their resolution results in persistent Rad52 foci (Ouyang et al. 2021, Yang et al. 2021). Finally, in plants some lncRNA can invade sites and form R-loops in *trans* (Ariel et al. 2020). It is likely that many more exceptions will be found as R-loop biology progresses. Therefore, it will become increasingly critical to differentiate between those R-loops that arise in *trans* versus those in *cis* as their formation, mode of action, size, and impact may be vastly different.

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