Pathways Project: Annotation Notebook Tables

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| **TABLE 1: Summary of the *tblastn* search results for the best scaffold match** | | | | | | | |
| **Range** | ***D. melanogaster*** | | **Target Species** | | **E-Value** | **Identities (%)** | **Subject Frame** |
| **Query Start** | **Query End** | **Subject Start** | **Subject End** |
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| **TABLE 2: *blastp* search results for the protein sequences of the genomic neighborhood of the target gene in the target species against the *D. melanogaster* reference protein database (refseq\_protein)** | | | | | | | |
|  | | **2nd Closest**  **Upstream** | **Closest**  **Upstream** | **Nested[[1]](#footnote-1)**  **Gene** | **Target**  **Gene** | **Closest Downstream** | **2nd Closest Downstream** |
| ***D. melanogaster*** | **Gene Symbol** |  |  |  |  |  |  |
| **Strand (+/-)** |  |  |  |  |  |  |
| **Target Species** | **NCBI RefSeq Gene (mRNA) Accession** |  |  |  |  |  |  |
| **NCBI RefSeq**  **Protein Accession** |  |  |  |  |  |  |
| **Strand (+/-)** |  |  |  |  |  |  |
| **Best *blastp* Result** | **Accession** |  |  |  |  |  |  |
| ***D. melanogaster* Gene Symbol[[2]](#footnote-2)** |  |  |  |  |  |  |
| **E-Value** |  |  |  |  |  |  |
| **Percent Identity** |  |  |  |  |  |  |
| **Are the genes in the two species orthologs? (yes/no)** | |  |  |  |  |  |  |

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| **TABLE 3: Isoforms with unique coding sequences in *D. melanogaster*** | |
| **Unique isoform(s) based on coding sequence** | **Other isoforms with identical coding sequences** |
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| **TABLE 4: Summary of *tblastn* CDS-by-CDS search results** | | | | | | | |
| **CDS** | **FlyBase ID** | **Query Length**  **Size (aa)** | ***D. melanogaster*** | | **Target Species** | | **Subject Frame** |
| **Query Start** | **Query End** | **Subject Start** | **Subject End** |
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| **TABLE 5: Gene Model for [insert isoform name here] in target species** | | | | | | |
| **CDS** | **FlyBase ID** | **Frame** | **Splice Acceptor Phase** | **Coordinates** | | **Splice**  **Donor**  **Phase** |
| **Start** | **End** |
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1. Leave column blank if target gene is not nested within another gene or another gene is not nested within your target gene. [↑](#footnote-ref-1)
2. If the *D. melanogaster* gene symbol of the best match is not provided in the “Description” column of the *blastp* results, you can identify it by clicking on the Accession Number (listed in the “Accession” column). In the new internet browser window that opens, scroll to the “FEATURES” section near the bottom. Next to the “CDS” feature you’ll see the gene symbol listed after “/gene=”. [↑](#footnote-ref-2)