

*Online Bioinformatics Resources  
at DRSC/TRiP*

*Claire Yanhui Hu*

*June 11<sup>th</sup> 2020*

*Boston Area Drosophila Meeting*

# DRSC/TRiP Functional Genomics Resources

- Home
- Technologies ▾
- Online Tools ▾
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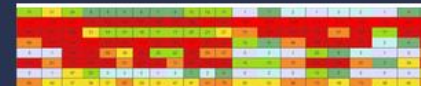
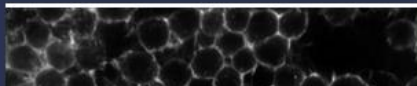


## DRSC/TRiP Functional Genomics Resources

The DRSC/TRiP-FGR site joins the *Drosophila* RNAi Screening Center (DRSC) and Transgenic RNAi Project (TRiP). Check out our [Technologies](#), [Online Tools](#), and other pages to learn more.

Quick **direct** links to our most popular online search tools:

- [iProteinDB](#) - post translational modification tool
- [DIOPT](#) ortholog search tool
- [Gene Lookup](#) search of DRSC/TRiP reagents, data, etc.
- [UP-TORR](#) batch search all public fly RNAi reagents
- [RSVP](#) search of in vivo fly RNAi data
- [Find CRISPR](#) gRNA search
- [Search and Nominate](#) genes for TRiP-CRISPR fly stocks
- [Nominate](#) genes for **CRIMIC** production



<https://fgr.hms.harvard.edu/>

<https://flyrnai.org/>

**Multi-Species****[DIOPT ortholog search](#)**

10 species, 18 algorithms  
[[Demo Video](#)]

**[Gene2Function](#)**

orthologs & gene info summaries (orthologs, GO, publications, & more)

**[BioLitMine](#)**

literature mining tool (genes, pathways, people, MeSH terms)

**[MIST](#)**

protein-protein & genetic interactions (multi-source)  
[[Demo Video](#)]

**[MARRVEL](#)**  
Connect human gene variants to ortholog info (multi-source)

**[DIOPT-DIST](#)**  
Connect disease genes to ortholog info or vice versa (OMIM & GWAS)

**Fly CRISPR****fly sgRNA database/LIMS**

**[TRiP sgRNA LIMS](#)**  
nominate or track TRiP-KO & -OE fly stock production

**Find CRISPRs**

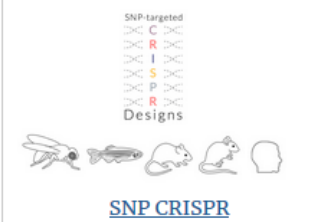
**[Find CRISPRs](#)**  
fly sgRNA design with genome view

**CRISPR 3**

**[Find CRISPRs 3](#)**  
find CRISPRs

**CRIMIC CRISPR MiMIC Gene Trap**

**[CRIMIC](#)**  
nominate for GDP gene trap fly stocks

**[SNP CRISPR](#)**

design allele-specific sgRNA for major model organisms

**Fly RNAi**
**UP-TORR**

**[UP-TORR](#)**  
cell and in vivo RNAi reagent search

**SnapDragon**

**[SnapDragon](#)**  
design dsRNAs for fly cell RNAi

**RSVP Plus**

**[RSVP Plus](#)**  
in vivo CRISPR & RNAi phenotype data

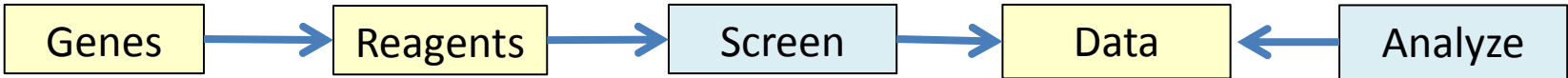
**Screen Summary**

**[Screen Summary](#)**  
browse DRSC cell RNAi screen data sets

**[GeneLookup](#)**  
(search DRSC & TRiP reagents by gene)

**[TRiP Batch Query](#)**  
(make a TRiP fly stock list from a g

<https://flyrnai.org/>



**DIOPT**

**UP-TORR**

**FlyRNAi  
cell based  
screen data**

**COMPLEAT**

**DIOPT-DIST**

**FlyPrimerBank**

**RSVP Plus  
In vivo data**

**Signed PPI**

**Gene2Function**

**Find CRISPR  
tool  
(3 versions)**

**DGET  
Bulk RNA-seq**

**Directed PPI**

**BioLitMine**

**SNP-CRISPR  
Designs**

**scRNA  
sc or snRNA-seq**

**Online GESS**

**GLAD**

**sgRNA  
transgenic fly  
LIMs**

**MIST  
interaction data**

**BioLitMine**

**iProteinDB  
PTM data**

□ Fly only  
 □ Multiple organisms

# DIOPT and Gene2Function

Examples of gene focused tools

# DRSC/TRiP Functional Genomics Resources



About the DRSC Other Online Tools

## DIOPT - DRSC Integrative Ortholog Prediction Tool

New

- + Add Arabidopsis thaliana
- + Add 3 prediction algorithms (Hieranoid, OrthoFinder, OrthoInspector)
- + Allow user to submit missing relationships
- + Allow user to add feedback

Version 7.1 (March 2018)

Details of this tool are published in [Hu, et. al.](#)

[Documentation](#)

[Tutorial Video](#)

[Add New Submission](#)

Select Species:

Input Species: Drosophila melanogaster (Fly)  
 Output Species: Homo sapiens (Human) Reverse

- Choose different
- Choose same in
- Set output speci
- Adjust filters to

- Schizosaccharomyces pombe (Fission yeast)
- Saccharomyces cerevisiae (Yeast)
- Caenorhabditis elegans (Worm)
- Drosophila melanogaster (Fly)
- Danio rerio (Zebrafish)
- Xenopus tropicalis (Western clawed frog)
- Homo sapiens (Human)**
- Mus musculus (Mouse)
- Rattus norvegicus (Rat)
- All (All)
- Arabidopsis thaliana (Thale cress)

Enter Genes and/or proteins (separate by comma; see [help](#)):

Or upload from file:

No file selected.

Search Field:

- All
  Entrez GeneID
  GenBank
  Gene name
  Uniprot ID
  Ensembl ID
  HGNC
  MGI ID
  Flybase ID
  Wormbase ID
  ZFIN ID
  Xenbase ID
  SGD ID
  CG Number
  Locus\_tag
  Genolevures
  RGD ID
  Pombase ID
  Amplicon
  TRIP stock

Select prediction tool(s): (2)


- All
- [Compara - \(vs 91\)](#)
- [eggNOG - \(vs 4.5\)](#)
- [HGNC](#)
- [Hieranoid - \(vs 2\)](#)
- [HomoloGene - \(vs 68\)](#)
- [Inparanoid - \(vs 8\)](#)
- [Isobase - \(vs 2\)](#)
- [OMA](#)
- [OrthoDB - \(vs 9.1\)](#)
- [OrthoFinder](#)
- [OrthoInspector - \(vs 2.21\)](#)
- [orthoMCL - \(vs 5\)](#)
- [Panther - \(vs 13.1\)](#)
- [Phylome - \(vs 4\)](#)
- [RoundUp](#)
- [TreeFam - \(vs 9\)](#)
- [User Submission](#)
- [ZFIN](#)

Additional Filter:

- None
- Return only best match when there is more than one match per input gene or protein
- Exclude low score (score > 1, unless only match score is 1)
- Exclude low scores (score > 2, unless only match score is 1 or 2)
- Exclude Low Ranked Scores

HARVARD MEDICAL SCHOOL Tools DRSC TRIP NEWS & EVENTS ORDER/SIGNUP

## DRSC/TRiP Functional Genomics Resources



About the DRSC Other Online Tools

### DIOPT - DRSC Integrative Ortholog Prediction Tool

New

- + Add Arabidopsis thaliana
- + Add 3 prediction algorithms (Hieranoid, OrthoFinder, OrthoInspector)
- + Allow user to submit missing relationships
- + Allow user to add feedback

Version 7.1 (March 2018)  
Details of this tool are published in *Hu, et. al.*

[Documentation](#) [Tutorial Video](#) [Add New Submission](#)

Select Species:  
Input Species:

Select prediction tool(s): (2)  
 All  
 [Compara - \(vs 91\)](#)  
 [eggNOG - \(vs 4.5\)](#)  
 HGNC

Usage:  
101,769 (6 month)



Model organism Aggregated Resources for Rare Variant Exploration

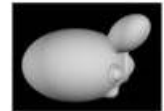
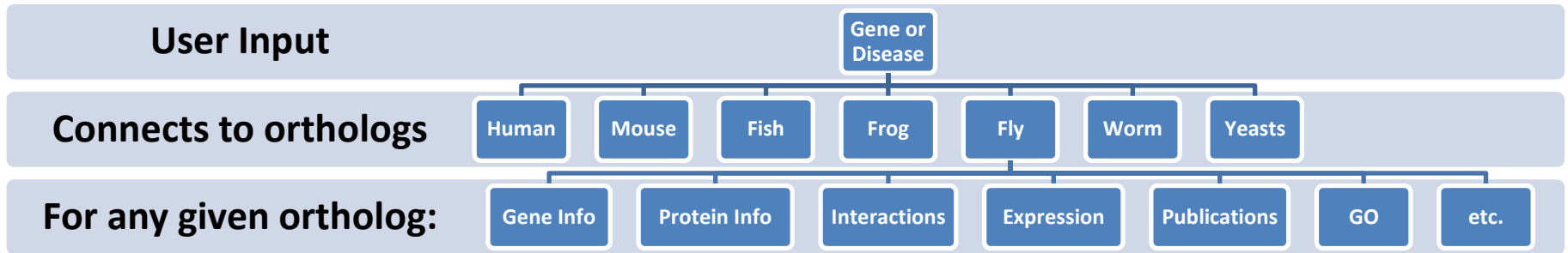
| Search Term | Fly GeneID | FlyBaseID                   | Fly Symbol | Species 2 | Human GeneID          | Human Species Gene ID | Human Symbol | DIOPT Score | Weighted Score | Rank     | Best Score | Best Score Reverse | Prediction Derived From   | Alignment & Scores   | Feedback  |
|-------------|------------|-----------------------------|------------|-----------|-----------------------|-----------------------|--------------|-------------|----------------|----------|------------|--------------------|---|----------------------|---|
| Dmtn        | 40792      | <a href="#">FBgn0037443</a> | Dmtn       | Human     | <a href="#">9911</a>  | <a href="#">24239</a> | TMCC2        | 11          | 10.79          | high     | Yes        | Yes                | Compara, eggNOG, Hieranoid, Inparanoid, OrthoDB, OrthoInspector, orthoMCL, Panther, Phylome, RoundUp, TreeFam | <a href="#">View</a> | <a href="#">Add</a>                             |
| Dmtn        | 40792      | <a href="#">FBgn0037443</a> | Dmtn       | Human     | <a href="#">23023</a> | <a href="#">29116</a> | TMCC1        | 11          | 10.79          | high     | Yes        | Yes                | Compara, eggNOG, Hieranoid, Inparanoid, OrthoDB, OrthoInspector, orthoMCL, Panther, Phylome, RoundUp, TreeFam | <a href="#">View</a> | <a href="#">Add</a>                             |
| Dmtn        | 40792      | <a href="#">FBgn0037443</a> | Dmtn       | Human     | <a href="#">57458</a> | <a href="#">29199</a> | TMCC3        | 9           | 8.96           | moderate | No         | Yes                | eggNOG, Hieranoid, Inparanoid, OrthoDB, OrthoInspector, Panther, Phylome, RoundUp, TreeFam                    | <a href="#">View</a> | <a href="#">Add</a>                             |
| Dmtn        | 40792      | <a href="#">FBgn0037443</a> | Dmtn       | Human     | <a href="#">1527</a>  | <a href="#">2563</a>  | TEX28        | 6           | 5.81           | moderate | No         | Yes                | Compara, eggNOG, OrthoDB, Panther, Phylome, TreeFam   | <a href="#">View</a> | <a href="#">Add</a>                             |
| Dn          |            |                             |            |           |                       |                       | MIR7844      | 1           | 0.93           | low      | No         | Yes                | Compara   |                      | (1) <a href="#">Show</a><br><a href="#">Add</a> |

<https://www.flyrnai.org/diopt/>

# Gene2Function

**Problem:** Lots of info but separate databases, formats, etc.

**Solution:** Highly integrated and standardized resource





# Option1: search by gene

# Gene2Function



## Search by Gene

Species

Human

Step1: select species

Gene

Gene Name

Step2: enter gene symbol

### Filters

- None
- Exclude low score (score > 1, unless only match score is 1)
- Exclude low scores (score > 2, unless only match score is 1 or 2)
- Return only best match when there is more than one match per input gene or protein

filters

Search By Gene

## Search by Disease

Disease

Breast cancer

Search By Disease

# G2F Gene Search Result

- Orthologous genes, conservation, annotation, data and reagents

filters

- Filter:
- None
  - Exclude low score (score > 1, unless only match score is 1)
  - Exclude low scores (score > 2, unless only match score is 1 or 2)
  - Return only best match when there is more than one match per input gene or protein

Update Filter

Human disease annotation

DIOPT info

Publications

Evidence based gene ontology

Interactions

Phenotype & expression

PDB: 3D structure

ORF clones at PlasmID

Researchers

Result count: 7

Export (tab separated)

Export to Excel

| NCBI Gene ID | Symbol? | Human Disease Count?        | Species Name                             | Species specific gene ID | Species specific database | DIOPT Score? | Best Score? | Best Score reverse? | Confidence? | Publication Counts? | GO Component Count? | GO Function Count? | GO Process Count? | Protein Interaction Counts? | Genetic Interaction Counts? | Mine Phenotype Data? | Mine Expression Data? | Mine Disruption Phenotype? | RNAi Cell Data | Crispr Cell Data | 3D Structure? | ORF Clones? | Researchers? | Protein Alignment?                           |
|--------------|---------|-----------------------------|--|--------------------------|---------------------------|--------------|-------------|---------------------|-------------|---------------------|---------------------|--------------------|-------------------|-----------------------------|-----------------------------|----------------------|-----------------------|----------------------------|----------------|------------------|---------------|-------------|--------------|--|
| 7471         | WNT1    | 2<br>Drugbank: 0<br>MARRVEL | Human (Homo sapiens)                     | 12774                    | HGNC                      | 11/12        | Yes         | Yes                 | high        | 174                 | 1                   | 1                  | 19                | 13                          | 0                           | 0                    | 376                   | 0                          | 499            | 686              | 0             | 1           | 179          | [+] pairwise alignment                       |
| 22408        | Wnt1    |                             | Mouse (Mus musculus)                     | 98953                    | MGI                       | 11/12        | Yes         | Yes                 | high        | 585                 | 2                   | 4                  | 47                | 8                           | 6                           | 0                    | 0                     | 0                          | NA             | NA               | 0             | 0           | 442          | [+] pairwise alignment                       |
| 24881        | Wnt1    |                             | Rat (Rattus norvegicus)                  | 1597195                  | RGD                       | 7/10         | Yes         | Yes                 | high        | 0                   | 0                   | 0                  | 0                 | 0                           | 0                           | NA                   | NA                    | 0                          | NA             | NA               | 0             | 0           | 0            | [+] pairwise alignment                       |
| 100491444    | wnt1    |                             | Western clawed frog (Xenopus tropicalis) | XB-GENE-485280           | Xenbase                   | 9/9          | Yes         | Yes                 | high        | 0                   | 0                   | 0                  | 0                 | 0                           | 0                           | 14                   | 117                   | 0                          | NA             | NA               | 0             | 0           | 0            | [+] pairwise alignment                       |
| 30128        | wnt1    |                             | Zebrafish (Danio rerio)                  | ZDB-GENE-980526-526      | ZFIN                      | 11/12        | Yes         | Yes                 | high        | 0                   | 0                   | 0                  | 0                 | 0                           | 0                           | 0                    | 188                   | 0                          | NA             | NA               | 0             | 0           | 0            | [+] pairwise alignment                       |
| 34009        | wg      |                             | Fly (Drosophila melanogaster)            | FBgn0004009              | FLYBASE                   | NA           | -           | -                   |             | 1974                | 11                  | 8                  | 66                | 27                          | 131                         | 0                    | 0                     | 1                          | 48             | 0                | 0             | 0           | 845          | [+] multiple seq alignment of best orthologs |
| 173399       | cwn-1   |                             | Worm (Caenorhabditis elegans)            | WBGene00000857           | WormBase                  | 4/11         | Yes         | Yes                 | high        | 8                   | 0                   | 1                  | 10                | 2                           | 2                           | Wormbase             | Wormbase              | 1                          | NA             | NA               | 0             | 0           | 11           | [+] pairwise alignment                       |

Paralog Overview

Click To Load Paralogs

Disease Overview

Click To Load Disease Overview

Gene Annotation Overview

Click To Load Go Annotation Overview

Input gene is highlighted

<http://www.gene2function.org/>

Link to summary of last authors of all publications

Summary of Last Authors of Related Publications

Results Table

| Gene ID | Last Name | First Initial | Count Paper as Last Author | Recent Paper             | Year Recent Paper | Address In Recent Paper   |
|---------|-----------|---------------|----------------------------|--------------------------|-------------------|---|
| 34009   | Perrimon  | N             | 40                         | <a href="#">26245833</a> | 2015              | Department of Genetics Howard Hughes Medical Institute, Harvard Medical School, Boston, Massachusetts 02115 perrimon@receptor.med.harvard.edu.  |
| 34009   | Cohen     | SM            | 37                         | <a href="#">26226636</a> | 2015              | Institute of Molecular and Cell Biology, Singapore, Singapore.  |
| 34009   | Bienz     | M             | 35                         | <a href="#">22645652</a> | 2011              | NA  |
| 34009   | Nusse     | R             | 34                         | <a href="#">22203956</a> | 2012              | NA  |
| 34009   | Basler    | K             | 29                         | <a href="#">28369070</a> | 2017              | Institute of Molecular Life Sciences, University of Zurich, Zurich, Switzerland.  |
| 34009   | Vincent   | JP            | 28                         | <a href="#">26974662</a> | 2016              | The Francis Crick Institute, Mill Hill Laboratory, The Ridgeway, Mill Hill, London NW7 1AA, UK.   |
| 34009   | Irvine    | KD            | 19                         | <a href="#">23318637</a> | 2013              | NA  |
| 34009   | Cadigan   | KM            | 18                         | <a href="#">25188465</a> | 2014              | Department of Molecular, Cellular and Developmental Biology, University of Michigan, Ann Arbor, Michigan, United States of America.   |
| 34009   | Mlodzik   | M             | 17                         | <a href="#">26364750</a> | 2015              | Department of Developmental & Regenerative Biology and Graduate School of Biomedical Sciences, Icahn School of Medicine at Mount Sinai, One Gustave L. Levy Place, New York, NY 10029, USA; Department of Ophthalmology, Icahn School of Medicine at Mount Sina |
| 34009   | Morata    | G             | 17                         | <a href="#">24096487</a> | 2014              | Centro de Biología Molecular, CSIC-Universidad Autónoma de Madrid, Madrid, Spain.   |

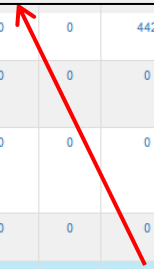
Filter:

- None
- Exclude low score (score > 1, unless only match score is 1)
- Exclude low scores (score > 2, unless only match score is 1)
- Return only best match when there is more than one match

Result count: 7  
[Export \(tab separated\)](#) [Export to Excel](#)

| NCBI Gene ID | Symbol? | Human Disease Count?             | Species Name         |
|--------------|---------|----------------------------------|----------------------|
| 7471         | WNT1    | 2<br><a href="#">Drugbank: 0</a> | Human (Homo sapiens) |
|              |         | <a href="#">MARRVEL</a>          |                      |

| Gene ID   | Symbol | Species                                  | Accession           | Database | 11/12 | Yes | Yes | high | 585  | 2  | 4 | 47 | 8  | 6   | 0                        | 0                        | 0 | NA | NA | 0 | 0 | 442 | [+] pairwise alignment                       |
|-----------|--------|--|---------------------|----------|-------|-----|-----|------|------|----|---|----|----|-----|--------------------------|--------------------------|---|----|----|---|---|-----|--|
| 22408     | Wnt1   | Mouse (Mus musculus)                     | 98953               | MGI      | 11/12 | Yes | Yes | high | 585  | 2  | 4 | 47 | 8  | 6   | 0                        | 0                        | 0 | NA | NA | 0 | 0 | 442 | [+] pairwise alignment                       |
| 24881     | Wnt1   | Rat (Rattus norvegicus)                  | 1597195             | RGD      | 7/10  | Yes | Yes | high | 0    | 0  | 0 | 0  | 0  | 0   | NA                       | NA                       | 0 | NA | NA | 0 | 0 | 0   | [+] pairwise alignment                       |
| 100491444 | wnt1   | Western clawed frog (Xenopus tropicalis) | XB-GENE-485280      | Xenbase  | 9/9   | Yes | Yes | high | 0    | 0  | 0 | 0  | 0  | 0   | 14                       | 117                      | 0 | NA | NA | 0 | 0 | 0   | [+] pairwise alignment                       |
| 30128     | wnt1   | Zebrafish (Danio rerio)                  | ZDB-GENE-980526-526 | ZFIN     | 11/12 | Yes | Yes | high | 0    | 0  | 0 | 0  | 0  | 0   | 0                        | 188                      | 0 | NA | NA | 0 | 0 | 0   | [+] pairwise alignment                       |
| 34009     | wg     | Fly (Drosophila melanogaster)            | FBgn0004009         | FLYBASE  | NA    | -   | -   |      | 1974 | 11 | 8 | 66 | 27 | 131 | 0                        | 0                        | 1 | 48 | 0  | 0 | 0 | 845 | [+] multiple seq alignment of best orthologs |
| 173399    | cwn-1  | Worm (Caenorhabditis elegans)            | WBGene00000857      | WormBase | 4/11  | Yes | Yes | high | 8    | 0  | 1 | 10 | 2  | 2   | <a href="#">Wormbase</a> | <a href="#">Wormbase</a> | 1 | NA | NA | 0 | 0 | 11  | [+] pairwise alignment                       |



Paralog Overview

[Click To Load Paralogs](#)

Disease Overview

[Click To Load Disease Overview](#)

Gene Annotation Overview

[Click To Load Go Annotation Overview](#)

Horizontal Vertical

### Go Slim

Beta  
[Export \(tab separated\)](#) [Export to Excel](#)

| HCBI Gene ID | Symbol | Species   | aging | anatomical structure development | anatomical structure formation involved in morphogenesis | biological process | biogenetic process | cell adhesion | cell cycle | cell death | cell differentiation | cell morphogenesis | cell motility | cell proliferation | cell-cell signaling | cellular component assembly | cellular nitrogen compound metabolic process | cellular protein modification process | cytoskeleton organization | developmental maturation | DNA metabolic process | embryo development | growth | immune system process | locomotion | neurological system process | pigmentation | reproduction | response to stress | signal transduction | DNA binding | enzyme binding | ion binding | molecular function | signal transduction | cell |   |
|--------------|--------|-----------|-------|----------------------------------|--|--------------------|--------------------|---------------|------------|------------|----------------------|--------------------|---------------|--------------------|---------------------|-----------------------------|--|---------------------------------------|---------------------------|--------------------------|-----------------------|--------------------|--------|-----------------------|------------|-----------------------------|--------------|--------------|--------------------|---------------------|-------------|----------------|-------------|--------------------|---------------------|------|---|
| 7471         | WNT1   | Human     | 1     | 2                                | 0  | 19                 | 3                  | 0             | 2          | 0          | 1                    | 0                  | 0             | 0                  | 3                   | 3                           | 1  | 3                                     | 0                         | 0                        | 0                     | 0                  | 0      | 0                     | 0          | 0                           | 0            | 0            | 2                  | 7                   | 1           | 0              | 0           | 1                  | 0                   | 1    |   |
| 22408        | Wnt1   | Mouse     | 0     | 28                               | 4  | 47                 | 4                  | 2             | 0          | 0          | 1                    | 14                 | 0             | 0                  | 3                   | 6                           | 0  | 4                                     | 2                         | 0                        | 1                     | 0                  | 5      | 0                     | 2          | 0                           | 0            | 0            | 1                  | 7                   | 0           | 0              | 0           | 4                  | 1                   | 1    |   |
| 24881        | Wnt1   | Rat       | 0     | 2                                | 0  | 3                  | 0                  | 0             | 0          | 0          | 0                    | 1                  | 0             | 0                  | 0                   | 0                           | 0  | 0                                     | 0                         | 0                        | 0                     | 0                  | 0      | 0                     | 0          | 0                           | 0            | 0            | 0                  | 0                   | 0           | 0              | 0           | 0                  | 0                   | 0    |   |
| 30128        | wnt1   | Zebrafish | 0     | 5                                | 0  | 5                  | 0                  | 0             | 0          | 0          | 0                    | 0                  | 0             | 0                  | 0                   | 0                           | 0  | 0                                     | 0                         | 0                        | 1                     | 0                  | 0      | 0                     | 0          | 0                           | 0            | 0            | 0                  | 0                   | 0           | 0              | 0           | 0                  | 0                   |      |   |
| 34009        | wg     | Fly       | 0     | 45                               | 3  | 68                 | 3                  | 0             | 0          | 1          | 2                    | 14                 | 1             | 0                  | 5                   | 5                           | 4  | 3                                     | 0                         | 1                        | 0                     | 1                  | 5      | 2                     | 5          | 0                           | 1            | 1            | 2                  | 0                   | 5           | 0              | 0           | 1                  | 8                   | 0    | 8 |
| 173399       | cwn-1  | Worm      | 0     | 7                                | 0  | 10                 | 0                  | 0             | 0          | 0          | 0                    | 7                  | 0             | 8                  | 0                   | 0                           | 0  | 0                                     | 0                         | 0                        | 0                     | 0                  | 0      | 8                     | 0          | 0                           | 0            | 0            | 0                  | 0                   | 1           | 0              | 1           | 0                  | 0                   | 0    |   |

### Go Terms Full

Beta  
[Export \(tab separated\)](#) [Export to Excel](#)

| HCBI Gene ID | Symbol | Species   | actin filament bundle assembly | animal organ regeneration | anaphor/polar body formation | asocytoblastomeric neuron signaling | bone development | brain segmentation | branch fusion | branching involved in vascular bud morphogenesis | canonical Wnt: signaling pathway | canonical Wnt: signaling pathway | canonical Wnt: signaling pathway | caraboside differentiation | cell fate specification | cell proliferation in midbrain | cell-cell signaling | central response to peptide hormone stimulus | cerabullin development | cerabullin formation | compound eye morphogenesis | cupule pattern formation | determination of genital disc primordium | dorsal development | dorsal closure | dorsal closure, elongation of leading edge cells | ecoderm development | embryonic pattern formation | embryonic axis specification | epidermis brain development | epithelial cell proliferation | epithelial cell type specification | filopodium assembly | forebrain anterior-posterior axis morphogenesis | fourth ventricle development | general disc: anterior-posterior pattern formation | general disc: sexually dimorphic development | heart development | heart formation | hematopoietic stem cell proliferation | hindbrain development | hindgut morphogenesis | histoblast morphogenesis | intestinal disc development | intestinal disc-derived line | intraneuron migration | lateral disc | lateral plate |   |
|--------------|--------|-----------|--------------------------------|---------------------------|------------------------------|-------------------------------------|------------------|--------------------|---------------|--|----------------------------------|----------------------------------|----------------------------------|----------------------------|-------------------------|--------------------------------|---------------------|--|------------------------|----------------------|----------------------------|--------------------------|--|--------------------|----------------|--|---------------------|-----------------------------|------------------------------|-----------------------------|-------------------------------|------------------------------------|---------------------|---|------------------------------|--|--|-------------------|-----------------|---------------------------------------|-----------------------|-----------------------|--------------------------|-----------------------------|------------------------------|-----------------------|--------------|---------------|---|
| 7471         | WNT1   | Human     | 0                              | 0                         | 0                            | 1                                   | 0                | 0                  | 0             | 1  | 0                                | 1                                | 0                                | 0                          | 0                       | 0                              | 0                   | 0  | 0                      | 0                    | 0                          | 0                        | 0  | 0                  | 0              | 0  | 0                   | 0                           | 0                            | 0                           | 0                             | 0                                  | 0                   | 0   | 0                            | 0  | 0  | 0                 | 0               | 0                                     | 0                     | 0                     | 0                        | 0                           | 0                            | 0                     |              |               |   |
| 22408        | Wnt1   | Mouse     | 0                              | 0                         | 1                            | 0                                   | 0                | 1                  | 0             | 2  | 1                                | 0                                | 0                                | 1                          | 1                       | 1                              | 0                   | 0  | 0                      | 0                    | 0                          | 0                        | 0  | 0                  | 0              | 1  | 1                   | 0                           | 0                            | 0                           | 0                             | 1                                  | 0                   | 0   | 0                            | 0  | 0  | 0                 | 0               | 0                                     | 0                     | 0                     | 0                        | 0                           | 0                            | 0                     | 0            | 0             | 0 |
| 24881        | Wnt1   | Rat       | 0                              | 1                         | 0                            | 0                                   | 0                | 0                  | 0             | 0  | 0                                | 0                                | 0                                | 0                          | 1                       | 0                              | 0                   | 0  | 0                      | 0                    | 0                          | 0                        | 0  | 0                  | 0              | 0  | 0                   | 0                           | 0                            | 0                           | 0                             | 0                                  | 0                   | 0   | 0                            | 0  | 0  | 0                 | 0               | 0                                     | 0                     | 0                     | 0                        | 0                           | 0                            | 0                     | 0            | 0             |   |
| 30128        | wnt1   | Zebrafish | 0                              | 0                         | 0                            | 0                                   | 1                | 0                  | 0             | 0  | 0                                | 0                                | 0                                | 0                          | 0                       | 0                              | 0                   | 0  | 0                      | 0                    | 0                          | 0                        | 0  | 0                  | 0              | 0  | 0                   | 0                           | 0                            | 0                           | 0                             | 0                                  | 0                   | 0   | 0                            | 0  | 0  | 0                 | 0               | 0                                     | 0                     | 0                     | 0                        | 0                           | 0                            | 0                     | 0            | 0             |   |
| 34009        | wg     | Fly       | 1                              | 0                         | 1                            | 0                                   | 0                | 1                  | 0             | 1  | 2                                | 0                                | 0                                | 1                          | 0                       | 0                              | 0                   | 0  | 0                      | 0                    | 1                          | 1                        | 1  | 0                  | 0              | 1  | 1                   | 1                           | 1                            | 0                           | 0                             | 1                                  | 1                   | 1   | 1                            | 0  | 0  | 0                 | 1               | 1                                     | 1                     | 1                     | 0                        | 0                           | 1                            | 1                     | 0            | 0             |   |
| 173399       | cwn-1  | Worm      | 0                              | 0                         | 0                            | 0                                   | 0                | 0                  | 0             | 0  | 0                                | 0                                | 0                                | 1                          | 0                       | 0                              | 0                   | 0  | 0                      | 0                    | 0                          | 0                        | 0  | 0                  | 0              | 0  | 0                   | 0                           | 0                            | 0                           | 0                             | 0                                  | 0                   | 0   | 0                            | 0  | 0  | 0                 | 0               | 0                                     | 0                     | 0                     | 0                        | 0                           | 0                            | 2                     | 0            | 0             |   |

# GO Slim

| GO Term  | GO ID      | WNT1 - 7471 - Human | Wnt1 - 22408 - Mouse | Wnt1 - 24881 - Rat | wnt1 - 30128 - Zebrafish | wg - 34009 - Fly | cwn-1 - 173399 - Worm |
|--|------------|---------------------|----------------------|--------------------|--------------------------|------------------|-----------------------|
| aging  | GO:0007568 | 1                   | 0                    | 0                  | 0                        | 0                | 0                     |
| anatomical structure development                         | GO:0048856 | 2                   | 28                   | 2                  | 5                        | 45               | 7                     |
| anatomical structure formation involved in morphogenesis | GO:0048646 | 0                   | 4                    | 0                  | 0                        | 3                | 0                     |
| biological_process                                       | GO:0008150 | 19                  | 47                   | 3                  | 5                        | 66               | 10                    |
| biosynthetic process                                     | GO:0009058 | 3                   | 4                    | 0                  | 0                        | 3                | 0                     |
| catabolic process  | GO:0009056 | 0                   | 2                    | 0                  | 0                        | 0                | 0                     |
| cell adhesion  | GO:0007155 | 2                   | 0                    | 0                  | 0                        | 0                | 0                     |
| cell cycle   | GO:0007049 | 0                   | 0                    | 0                  | 0                        | 1                | 0                     |
| cell death   | GO:0008219 | 1                   | 1                    | 0                  | 0                        | 2                | 0                     |
| cell differentiation                                     | GO:0030154 | 0                   | 14                   | 1                  | 0                        | 14               | 7                     |
| cell morphogenesis                                       | GO:0000902 | 0                   | 0                    | 0                  | 0                        | 1                | 0                     |
| cell motility  | GO:0048870 | 0                   | 0                    | 0                  | 0                        | 0                | 8                     |
| cell proliferation                                       | GO:0008283 | 3                   | 3                    | 0                  | 0                        | 5                | 0                     |
| cell-cell signaling                                      | GO:0007267 | 3                   | 6                    | 0                  | 0                        | 5                | 0                     |
| cellular component assembly                              | GO:0022607 | 1                   | 0                    | 0                  | 0                        | 4                | 0                     |
| cellular nitrogen compound metabolic process             | GO:0034641 | 3                   | 4                    | 0                  | 0                        | 3                | 0                     |
| cellular protein modification process                    | GO:0006464 | 0                   | 2                    | 0                  | 0                        | 0                | 0                     |
| cytoskeleton organization                                | GO:0007010 | 0                   | 0                    | 0                  | 0                        | 1                | 0                     |

# GO

| GO ID  | WNT1 - 7471 - Human | Wnt1 - 22408 - Mouse | Wnt1 - 24881 - Rat | wnt1 - 30128 - Zebrafish | wg - 34009 - Fly | cwn-1 - 173399 - Worm |   |
|--|---------------------|----------------------|--------------------|--------------------------|------------------|-----------------------|---|
| actin filament bundle assembly   | GO:0051017          | 0                    | 0                  | 0                        | 0                | 1                     | 0 |
| animal organ regeneration  | GO:0031100          | 0                    | 0                  | 1                        | 0                | 0                     | 0 |
| anterior/posterior pattern specification, imaginal disc                                  | GO:0007448          | 0                    | 0                  | 0                        | 0                | 1                     | 0 |
| astrocyte-dopaminergic neuron signaling  | GO:0036520          | 0                    | 1                  | 0                        | 0                | 0                     | 0 |
| bone development   | GO:0060348          | 1                    | 0                  | 0                        | 0                | 0                     | 0 |
| brain segmentation   | GO:0035284          | 0                    | 0                  | 0                        | 1                | 0                     | 0 |
| branch fusion, open tracheal system  | GO:0035147          | 0                    | 0                  | 0                        | 0                | 1                     | 0 |
| branching involved in ureteric bud morphogenesis   | GO:0001658          | 0                    | 1                  | 0                        | 0                | 0                     | 0 |
| branching morphogenesis of an epithelial tube  | GO:0048754          | 0                    | 0                  | 0                        | 0                | 1                     | 0 |
| canonical Wnt signaling pathway  | GO:0060070          | 1                    | 2                  | 0                        | 0                | 2                     | 0 |
| canonical Wnt signaling pathway involved in midbrain dopaminergic neuron differentiation | GO:1904954          | 0                    | 1                  | 0                        | 0                | 0                     | 0 |
| canonical Wnt signaling pathway involved in negative regulation of apoptotic process     | GO:0044336          | 1                    | 0                  | 0                        | 0                | 0                     | 0 |
| cardioblast differentiation  | GO:0010002          | 0                    | 0                  | 0                        | 0                | 1                     | 0 |
| cell fate specification  | GO:0001708          | 0                    | 0                  | 0                        | 0                | 0                     | 1 |
| cell proliferation in midbrain   | GO:0033278          | 0                    | 1                  | 0                        | 0                | 0                     | 0 |

<http://www.gene2function.org/>

## Biological Literature Mining Tool for Human and Model Organisms



Find relationships between genes, MeSH terms, pathways, and people from PubMed literature

### Single Term Search

Step 1 - what do you want to find?

Gene to MeSH Terms

Step 2 - select organism

—select organism—

Step 3 - enter search term (case-insensitive)

Enter gene name, symbol, or Entrez gene ID

[+] Filter Options

Search

Reset

# Gene: **wg** > MeSH Terms

## Query Information

Entrez Gene ID: 34009

Gene: wingless (wg)

Organism: Fruit fly (taxon ID: 7227)

Displaying: mesh\_cat:A results

## Download

## Other View

[Show Word Cloud.](#)

## Search Another Gene

Note that the search will be performed in the same organism. To do a different search, [click here](#).

Search

- Show top ten results
- Show results with at least this many publications:

10

- Show all results
- Show selected mesh categories

- All
- Anatomy
- Organisms
- Diseases
- Chemicals and Drugs
- Analytical, Diagnostic and Therapeutic Techniques, and Equipment
- Psychiatry and Psychology
- Phenomena and Processes

| Descriptor ID | MeSH Categories | MeSH Term                         | Recent Publications (max. 10)  | Publications Count |
|---------------|-----------------|-----------------------------------|--|--------------------|
| D014921       | (A) - Anatomy   | Wings, Animal                     | 30194291, 29938762, 29895891, 29225023, 29028797, 28829945, 28754838, 28671979, 28671940, 28619822 | 503                |
| D004625       | (A) - Anatomy   | Embryo, Nonmammalian              | 30630823, 30095068, 29518114, 29408853, 29357360, 28093727, 27183005, 27138857, 27068109, 26628090 | 272                |
| D005123       | (A) - Anatomy   | Eye                               | 29530880, 28619822, 28376317, 28032862, 25849899, 25781970, 24509725, 24086596, 24039600, 23222441 | 142                |
| D005121       | (A) - Anatomy   | Extremities                       | 29938762, 21497759, 21478472, 21320482, 20816798, 19605497, 18613734, 18194655, 18184724, 17654717 | 99                 |
| D008648       | (A) - Anatomy   | Mesoderm                          | 27599298, 27068109, 26245833, 24980505, 24496448, 23380635, 22371299, 21382367, 19088091, 18407256 | 96                 |
| D013234       | (A) - Anatomy   | Stem Cells                        | 30389852, 29938758, 29714689, 29440430, 28923062, 28698559, 27392294, 27364467, 27137186, 26994311 | 82                 |
| D002460       | (A) - Anatomy   | Cell Line                         | 29719260, 27528688, 26974125, 26887613, 26738424, 26312500, 26305360, 26008746, 25267296, 25139856 | 74                 |
| D009474       | (A) - Anatomy   | Neurons                           | 30202077, 29895891, 28958816, 28645846, 27307238, 27068458, 26199408, 25139856, 25015062, 24957133 | 71                 |
| D002478       | (A) - Anatomy   | Cells, Cultured                   | 30194291, 29533772, 29408853, 28698559, 28347816, 26364750, 25188465, 25155749, 24821423, 23197537 | 58                 |
| D004817       | (A) - Anatomy   | Epidermis                         | 28506986, 24795868, 19906854, 18614578, 18485238, 18077590, 17611224, 17267442, 16125166, 15936749 | 58                 |
| D017956       | (A) - Anatomy   | Photoreceptor Cells, Invertebrate | 26386564, 26160900, 26025917, 25892303, 24961796, 24781186, 22952997, 22095083, 20008573, 19268449 | 57                 |
| D002462       | (A) - Anatomy   | Cell Membrane                     | 27959917, 26199408, 25848770, 25010066, 24390349, 22108505, 21900504, 21666802, 20627080, 20226663 | 53                 |
| D002490       | (A) - Anatomy   | Central Nervous System            | 27095493, 24913688, 24314314, 23886579,  | 53                 |
| D009132       | (A) - Anatomy   |                                   |  |                    |

<https://www.flyrnai.org/tools/biolitmine/>

# Gene: wg > MeSH Terms

## Query Information

Entrez Gene ID: 34009  
 Gene: wingless (wg)  
 Organism: Fruit fly (taxon ID: 7227)  
 Displaying: mesh\_cat:A results

## Download

## Other View

Show Word Cloud.

## Search Another Gene

Note that the search will be performed in the same organism. To do a different search, click here.

wg

Search

- Show top ten results
- Show results with at least this many publications:

10

- Show all results
- Show selected mesh categories

All

Anatomy

Organisms

Diseases

Chemicals and Drugs

Analytical, Diagnostic and Therapeutic Techniques, and Equipment

Psychiatry and Psychology

Phenomena and Processes

| Descriptor ID | MeSH Categories | MeSH Term     | Recent Publications (max. 10)   | Publications Count |
|---------------|-----------------|---------------|---|--------------------|
| D014921       | (A) - Anatomy   | Wings, Animal | 30194291, 29938762, 29895891, 29225023, 29028797, 28829945, 28754838, 28671979, | 503                |



|         |               |         |   |    |
|---------|---------------|---------|---|----|
| D009132 | (A) - Anatomy | Muscles | 30630823, 24850114, 26845150, 26237646, 25135939, 24979807, 24814146, 24594656, | 52 |
|---------|---------------|---------|---|----|



# Find CRISPR Tool

Examples of reagent focused tools

# DRSC Find CRISPRs

To find CRISPRs, enter the gene ID, symbol, or chromosome:location. Then select tracks and click the 'Submit' button.

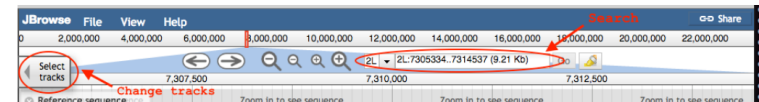
This will take you to the JBrowse view. If you want to change tracks or search for another gene in JBrowse, type a gene ID, symbol, or chromosome:location over the coordinates directly in JBrowse. In the upper left-hand corner of the JBrowse view, click "Select Tracks" to change your track selections.

Version: 3.0.2 (Jan 2017)

### \*\*NEW\*\* features:

- Based on Fly Genome Assembly 6
- Added a "seedScore" to each CRISPR (ranging from 12 to 15). This number indicates the uniqueness of the bp-end of a CRISPR excluding PAM. For example, a seed score of 12 means that CRISPR has a unique 12-bp end excluding PAM, whereas a seed score of 13 means that CRISPR has a unique 13-bp excluding PAM.
- Bug fix: gene names on the mitochondrion genome show more than just "mt"

# Version 1



1. Enter Gene ID, Symbol, or Chromosome:Location

esg

2. Select Tracks

- Targets CDS, No Predicted Off-Targets (preferred)
- Targets UTR, No Predicted Off-Targets (preferred)
- Targets Intron, No Predicted Off-Targets (preferred)
- Targets UTR/CDS Boundary or Intron/Exon Boundary, No Predicted Off-Targets (preferred)
- Targets Intergenic Region, No Predicted Off-Targets (preferred)
- Targets CDS, UTR, Boundary, Intron, or Intergenic Region, One to Three Predicted Non-CDS Off-Targets
- Targets CDS, UTR, Boundary, Intron, or Intergenic Region, One to Three Predicted CDS Off-Targets
- Targets CDS, UTR, Boundary, Intron, or Intergenic Region, More than Three Predicted Off-Targets

3. Select mismatch stringency for off-targets

- 5 Mismatches (most stringent)
- 4 mismatches
- 3 mismatches (least stringent)

Submit

CRISPR (Efficiency:5.82 Frameshift:64.7 OT:0 seedScore:12)

**Primary Data**

- Name: (Efficiency:5.82 Frameshift:64.7 OT:0 seedScore:12)
- Type: CRISPR
- Description: FBgn0001981  
GGACACATTGCGACTCATACGGG
- Position: 2L:15335252..15335274 (+ strand)
- Length: 23 bp

**Attributes**

- Seq\_id: 2L
- Region sequence: >2L 2L:15335252..15335274 (+ strand) class=CRISPR length=23  
GGACACATTGCGACTCATACGGG

OK

<https://www.flyrnai.org/crispr/>

## Find CRISPRs

### » Search by gene

To find CRISPRs within a gene, enter the gene symbol, select tracks of interest, then click the 'Submit' button.

### » Search by sequence

If you have a sequence and want to find nearby CRISPRs, enter the sequence into the textbox to BLAST it before viewing it on JBrowse. If the sequence is a significant hit, it will show as a highlight.

Both search functions will take you to a summary page with a table and embedded JBrowse view. If you want to zoom in or shift the location on the genome, click on "Full-screen view".

### \*\*NEW\*\* features:

- Variant Search (data sources below)
- Summary table of all CRISPRs within gene/location of interest
- Searching by design sequence
- Batch search by gene
- "seedScore" available for each CRISPR (ranging from 12 to 15), indicating its unique bp-end excluding PAM
- Machine Learning based efficiency prediction ?
- Updated JBrowse to version 1.13.0
- Updated FlyBase release 6.14 -> 6.24

### Search by gene

#### 1. Enter Gene ID or Symbol

#### 2. Select Tracks

##### No Predicted Off-Targets (preferred)

- CDS
- UTR
- Intron
- UTR/CDS Boundary or Intron/Exon Boundary
- Intergenic Region

##### 1 - 3 Predicted Off-Targets

- CDS, UTR, Boundary, Intron, or Intergic Region (Non-CDS Off-Targets)
- CDS, UTR, Boundary, Intron, or Intergic Region (CDS Off-Targets)

##### >3 Predicted Off-Targets

- CDS, UTR, Boundary, Intron, or Intergic Region

#### 3. Select Mismatch Stringency

- 5 Mismatches (most stringent)
- 4 mismatches
- 3 mismatches (least stringent)

### Batch search by gene

#### 1. Enter one Gene ID or Symbol per line

#### 2. Select Tracks

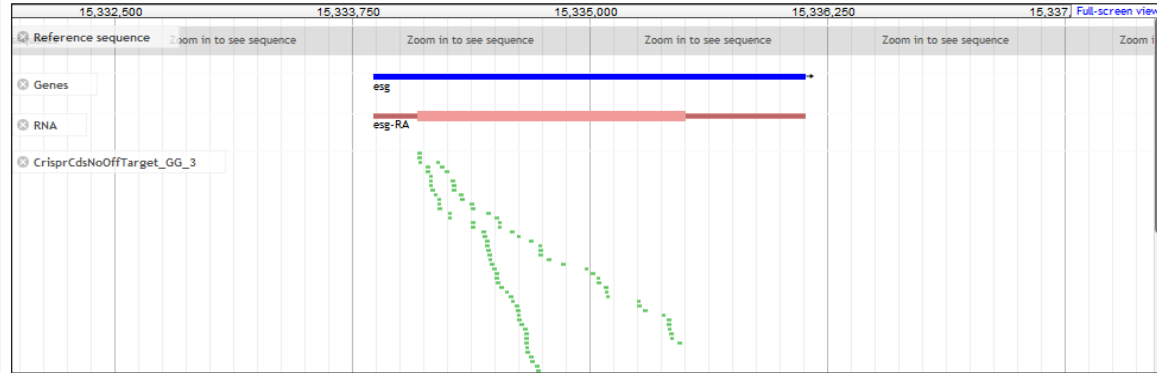
##### No Predicted Off-Targets (preferred)

- CDS
- UTR

<https://www.flyrnai.org/crispr3/>

### JBrowse:

Double click to zoom, or hold **shift** and press the up or down arrow keys.



Browser:  
click to view each sgRNA design

### Filter Results:

#### Location

Current Start: 15331971

Current Stop: 15338035

Start Position:

Stop Position:

Filter Reset

#### Cutoff

Note: This filter only affects table results.

Score:

Efficiency Score

>

Cutoff Value:

Filter Reset

#### Exon Location

Search by exon name or isoform.

Search: Use sample term

Submit

Filters:  
Genome location  
Exon name/isoform  
Various scores

Export:

Copy CSV Excel

Search:

| FBgn                     | CRISPR Sequence | Housden Efficiency Score | Machine Learning Efficiency Score | Frameshift Score | Seed Region | Off Target Score | U6 Terminator | Chr     | Start | End      | Strand   | Domains | SNPs in Cas9 attP2 Stock | SNPs in Cas9 attP40 Stock | SNPs in S2R+ Cell Line |
|--------------------------|-----------------|--------------------------|-----------------------------------|------------------|-------------|------------------|---------------|---------|-------|----------|----------|---------|--------------------------|---------------------------|------------------------|
| <input type="checkbox"/> | FBgn0001981     | GCATACCGTGAAGACATGTTGG   | 3.44                              | 0.55             | 51.63       | 12               | 0             | none    | 2L    | 15334096 | 15334118 | +       | 0                        | 0                         | 0                      |
| <input type="checkbox"/> | FBgn0001981     | TACCGTGAAGACATGTTGGTGG   | 4.21                              | 0.48             | 48.11       | 12               | 0.03          | none    | 2L    | 15334099 | 15334121 | +       | 0                        | 0                         | 0                      |
| <input type="checkbox"/> | FBgn0001981     | CTCCACCAACATGTCTCCACGG   | 9.35                              | 0.74             | 52.73       | 12               | 0.06          | none    | 2L    | 15334101 | 15334123 | -       | 0                        | 0                         | 0                      |
| <input type="checkbox"/> | FBgn0001981     | TAACTGGGCGCTTTTATGCGGG   | 5.63                              | 0.38             | 59.96       | 13               | 0.3           | present | 2L    | 15334141 | 15334163 | -       | 0                        | 0                         | 0                      |
| <input type="checkbox"/> | FBgn0001981     | TAACTGGGCGCTTTTATGCGGG   | 9.11                              | 0.51             | 59.23       | 12               | 0.11          | present | 2L    | 15334142 | 15334164 | -       | 0                        | 0                         | 0                      |
| <input type="checkbox"/> | FBgn0001981     | CCCAGTTAATACCAAGTTCGAGG  | 3.84                              | 0.28             | 62.17       | 14               | 0.11          | none    | 2L    | 15334156 | 15334178 | +       | 0                        | 0                         | 0                      |
| <input type="checkbox"/> | FBgn0001981     | CCTCGAACTGGTAATTAAGTGGG  | 4.23                              | 0.61             | 66.11       | 12               | 0.01          | none    | 2L    | 15334156 | 15334178 | -       | 0                        | 0                         | 0                      |
| <input type="checkbox"/> | FBgn0001981     | GCCTCGAACTGGTAATTAAGTGG  | 3.84                              | 0.47             | 66.95       | 15               | 0.12          | none    | 2L    | 15334157 | 15334179 | -       | 0                        | 0                         | 0                      |
| <input type="checkbox"/> | FBgn0001981     | GATTTTGAGGCGCTCGAACTGG   | 4.83                              | 0.49             | 62.64       | 12               | 0.22          | present | 2L    | 15334168 | 15334190 | -       | 0                        | 0                         | 0                      |
| <input type="checkbox"/> | FBgn0001981     | GGGTGTACTGTGATTTGAGG     | 5.79                              | 0.22             | 61.88       | 12               | 0.21          | present | 2L    | 15334181 | 15334203 | -       | 0                        | 0                         | 0                      |
| <input type="checkbox"/> | FBgn0001981     | TAACACCCCAATGAGCCGAGG    | 4.06                              | 0.3              | 55.37       | 12               | 0.13          | none    | 2L    | 15334195 | 15334217 | +       | 0                        | 0                         | 0                      |
| <input type="checkbox"/> | FBgn0001981     | ACAAATCCTGGCGCTATTGGG    | 3.65                              | 0.50             | 65.11       | 13               | 0.24          | none    | 2L    | 15334201 | 15334223 | -       | 0                        | 0                         | 0                      |
| <input type="checkbox"/> | FBgn0001981     | CACAATCCTGGCGCTATTGGG    | 4.80                              | 0.35             | 64.30       | 12               | 0.04          | none    | 2L    | 15334202 | 15334224 | -       | 0                        | 0                         | 0                      |

Table:  
Info of all relevant sgRNA designs synchronized with browser, Searchable, exportable

<https://www.flyrnai.org/crispr3/>

# SNP Annotation

Export:

Search:

| <input type="checkbox"/> | FBgn        | CRISPR Sequence         | Housden Efficiency Score | Machine Learning Efficiency Score | Frameshift Score | Seed Region | Off Target Score | U6 Terminator | Chr | Start    | End      | Strand | Cut Frame                | Start Codon Distance         | Domains | SNPs in Cas9 attP2 Stock | SNPs in Cas9 attP40 Stock | SNPs in S2R+ Cell Line |
|--------------------------|-------------|-------------------------|--------------------------|-----------------------------------|------------------|-------------|------------------|---------------|-----|----------|----------|--------|--------------------------|------------------------------|---------|--------------------------|---------------------------|------------------------|
| <input type="checkbox"/> | FBgn0003731 | GGGCCGAACTGCTGCGGTATAGG | 4.97                     | 0.45                              | 52.77            | 12          | 0                | none          | 2R  | 21547758 | 21547780 | -      | Egfr-PB: 2               | Egfr-PB: 170                 | 0       | 2                        | 1                         | 0                      |
| <input type="checkbox"/> | FBgn0003731 | ATTACCGGAACCTCAGAGATCGG | 4.47                     | 0.51                              | 57.76            | 12          | 0                | none          | 2R  | 21554881 | 21554903 | +      | Egfr-PA: 2<br>Egfr-PB: 2 | Egfr-PA: 218<br>Egfr-PB: 365 | 4       | 1                        | 0                         | 0                      |
| <input type="checkbox"/> | FBgn0003731 | CTGAGGTCCAAATTCGTGGG    | 6.55                     | 0.24                              | 48.39            | 12          | 0                | none          | 2R  | 21554952 | 21554974 | -      | Egfr-PA: 2<br>Egfr-PB: 2 | Egfr-PA: 278<br>Egfr-PB: 425 | 6       | 0                        | 0                         | 0                      |
| <input type="checkbox"/> | FBgn0003731 | GACAACATACGGGAGGTCACCGG | 7.20                     | 0.59                              | 68.43            | 12          | 0                | none          | 2R  | 21554982 | 21555004 | +      | Egfr-PA: 1<br>Egfr-PB: 1 | Egfr-PA: 319<br>Egfr-PB: 466 | 6       | 0                        | 0                         | 0                      |
| <input type="checkbox"/> | FBgn0003731 | TTTAAGACATCGGTAGATCGGG  | 3.77                     | 0.32                              | 72.98            | 12          | 0                | none          | 2R  | 21555289 | 21555311 | -      | Egfr-PA: 1<br>Egfr-PB: 1 | Egfr-PA: 478<br>Egfr-PB: 625 | 6       | 1                        | 1                         | 0                      |
| <input type="checkbox"/> | FBgn0003731 | ATTTAAGACATCGGTAGATCGG  | 5.46                     | 0.34                              | 77.26            | 12          | 0                | none          | 2R  | 21555290 | 21555312 | -      | Egfr-PA: 2<br>Egfr-PB: 2 | Egfr-PA: 479<br>Egfr-PB: 626 | 6       | 1                        | 1                         | 0                      |

<https://www.flyrnai.org/crispr3/>

SNP info:  
 TRiP Cas9 injection stocks  
 S2R+ cell line  
 CRiMIC injection stocks

## CRISPR GuideXpress for Anopheles gambiae

### » Search for Orthologs

To search for orthologous genes between *Drosophila Melanogaster* and *Anopheles gambiae* (Gene set: AgamP4.12) enter an FBgn, Gene Symbol, or VectorBase ID, select methods, then click the 'submit' button.

### » Search for AgamP4 CRISPR Designs

To search for CRISPR knockout designs in *Anopheles gambiae* (Assembly: AgamP4) enter a VectorBase ID or genomic location, then click the 'submit' button. Results shown on a summary page with a table and embedded JBrowse view.

CRISPR design in *Drosophila Melanogaster*: <https://www.flyrnai.org/crispr3>

### \*\*NEW\*\* features:

- Search for orthologous genes between *Drosophila Melanogaster* and *Anopheles gambiae*
- Search for *Anopheles gambiae* CRISPR designs
- Batch search by gRNA sequences
- Machine Learning based efficiency prediction ?
- CRISPR Distance to Start Codon + % Coverage
- CRISPR Transcript Isoform Hits

### Ortholog Search

#### Fly ⇌ Mosquito

Enter one ID per line.

FBgn(s) or Gene Name(s):

Ortholog Prediction Tools:

All

Search

#### Mosquito ⇌ Fly

Enter one ID per line.

VectorBase ID(s):

Ortholog Prediction Tools:

All

Search

### CRISPR Search

#### Search by Gene

Search by gene location.

VectorBase ID:

Search

#### Search by Location

Search by genomic location.

Chromosome:

Start:

Stop:

Search

### CRISPR Batch Search

#### Search by Gene

Enter one VectorBase ID per line.

<https://www.flyrnai.org/tools/fly2mosquito/>

Enter one gRNA sequence per line.



# MIST – Molecular Interaction Search Tool

Examples of data focused tools

# Public resources

- using *Drosophila* gene *mnb* as example

DIP

mentha

Database of Interacting Proteins

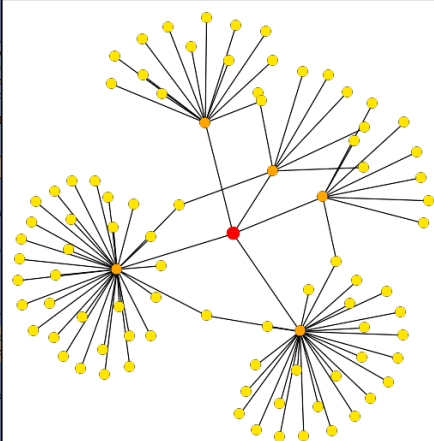
**THE DIP DATABASE**

The DIP™ database catalogs experimentally determined interactions between proteins. It combines a consistent set of protein-protein interactions. The data stored within the DIP database were curated using computational approaches that utilize the knowledge about the protein-protein interaction DIP data. Please, check the [reference](#) page to find articles describing the DIP database in greater detail.

This page serves also as an access point to other projects related to DIP, such as The Database of Interacting Proteins and The Database of Interacting Genes.

**DIP PAGES**

- NEWS**: Announcements about the most recent additions and changes to the database.
- REGISTRATION ACCOUNT**: Registration and account maintenance. Registration is required to gain access of the academic community. Trial accounts for the commercial users are also available.
- STATISTICS**: Detailed information about the current state of the database as well as some statistics.
- SATELLITES**: DIP-related projects, such as [DLRP](#) and [JDIP](#).
- SERVICES**: DIP-derived services.
- ARTICLES**: DIP in press. Both, papers published on DIP as well as a list of publications related to DIP.
- SEARCH**: Database search. This is the starting point of the database exploration. Once the interaction network can be explored by interactively following the interactions.
- LINKS**: Links to other protein interaction databases and related sites.
- FILES**: Download the complete DIP dataset as well as specialized DIP subsets and associated files.
- HELP**: A short description of the DIP database.



Links | Tools | Developers | Download | About/Guide | Contacts | Home

**mentha**  
the interactome browser

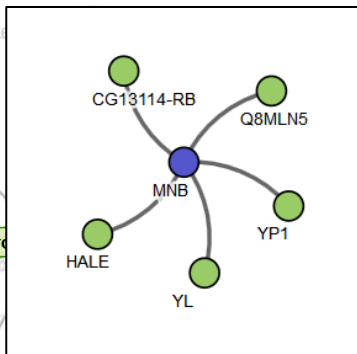
Example | Advanced Tools | Help

Genes, uniprot IDs, keywords  search

Organism: All (including those not listed)

Last update: 23rd July 2017  
89193 proteins; 661298 interactions; 48456 publications

When you click list in the Protein Bag you will be presented with all interactors!

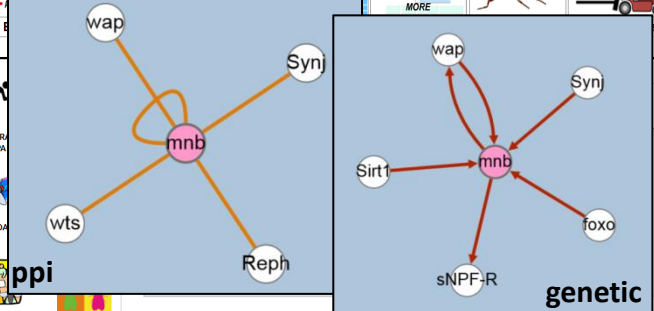


Try out the beta release of "FlyBase 2.0" at [beta.flybase.org](http://beta.flybase.org)

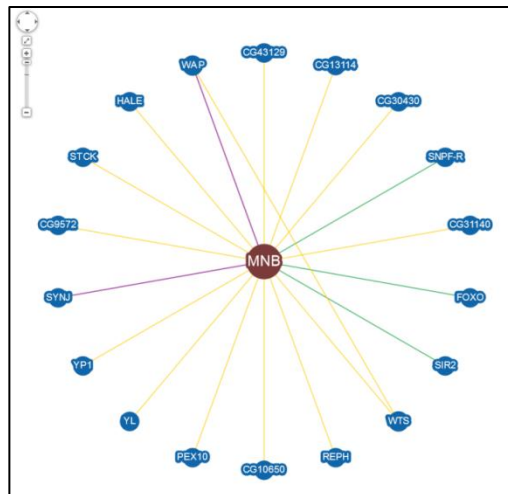
**FlyBase** A Database of *Drosophila* Genes & Genomes

Home Tools Downloads Links Community Species About Help Archives Jump to Gene Go

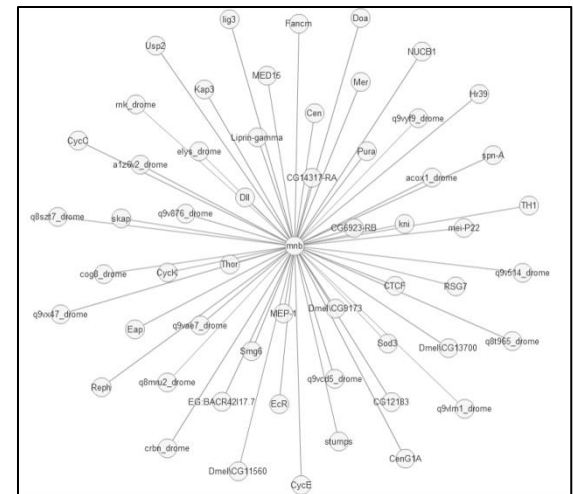
Wap, Synj, Sirt1, Wts, Reph, sNPF-R, genetic



BioGRID



IntAct

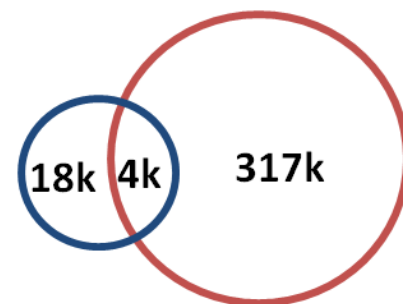
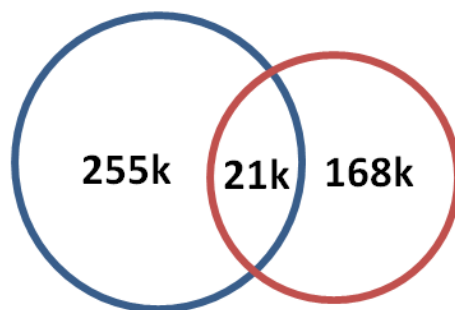
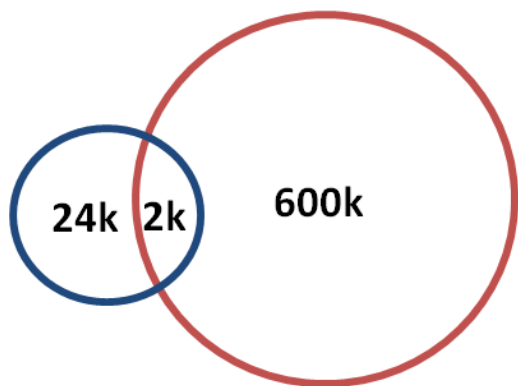
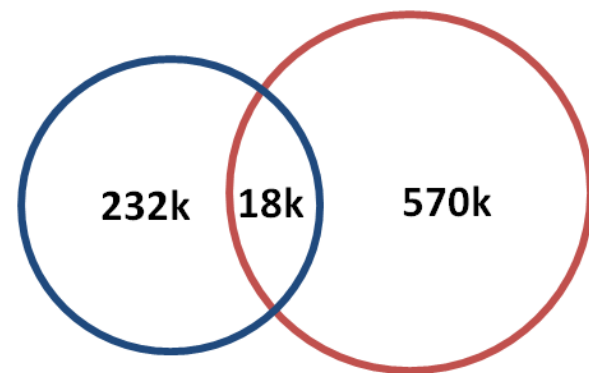
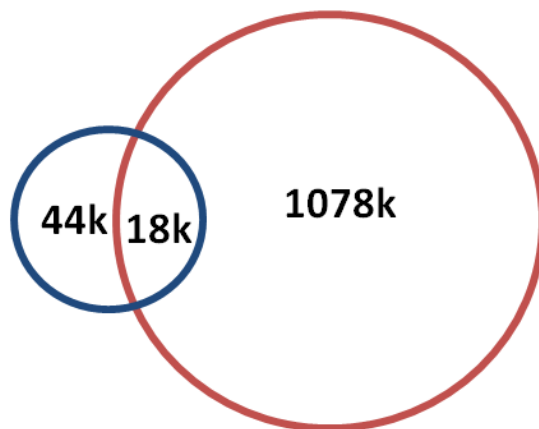
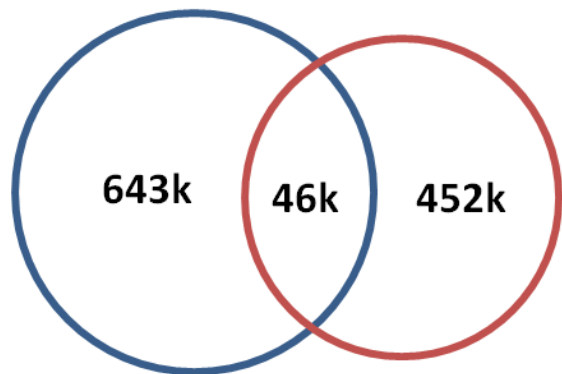




H. sapiens

M. musculus

D. melanogaster



C. elegans

S. cerevisiae

S. pombe

○ PPIs

○ PPI interologs



# MIST

Molecular Interaction Search Tool  
@ Harvard Medical School

Search:  Protein List  Protein Pairs

Find Interactors

Copy/Paste : [Example](#)

CSW

Upload from the file:  
 No file selected.

Choose Networks to Search: [Help](#) -

Protein-protein interactions.

Filter By Rank  
 • Filter By Rank

Other Filtering Options  
 • Filter By Interaction Type

Between Filters use:  AND  OR

Evidence Count is greater than

Number Of Papers is greater than

Interologs: protein-protein interactions from other species

Filter By Rank  
 • Filter By Rank

Other Filtering Options  
 • Filter By Number of Species

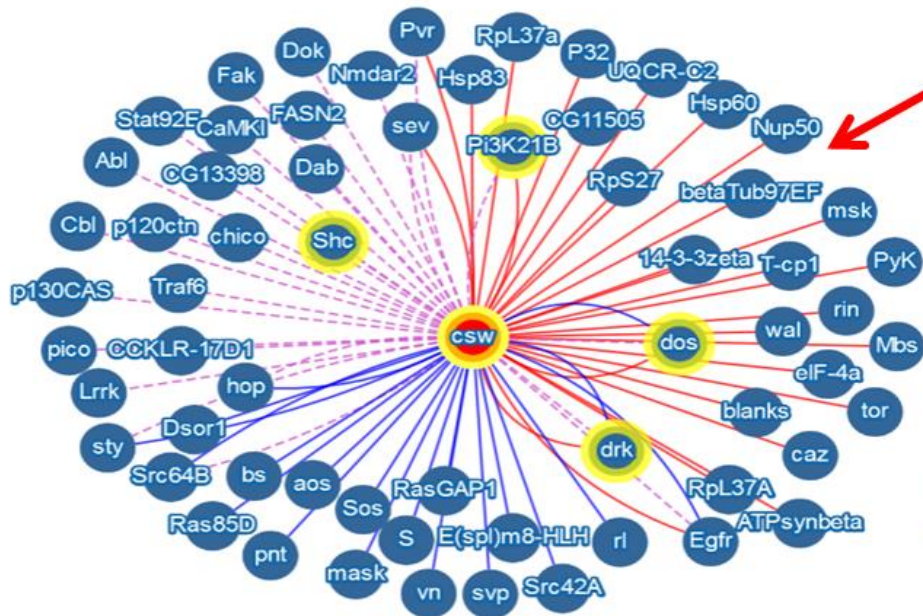
Filter By Interaction Type

Support single gene, multiple genes and gene pairs

Covers 10 model organisms

Interaction type

User has the option to filter the interactions based on rank, reference count, evidence type and count



Network view,  
edges are  
colored for  
different  
interaction type

- PPI
- Interologs
- Genetic interactions
- Interologs Genetic
- Kinase Substrate
- Phospho Correlation
- Exp. Correlation
- Phenotype Correl.

Change Layout -

Search Graph

Complex Groups

- details
- p130Cas-ER-alpha-cSrc-kinase- PI3-kinase p85-subunit complex
  - Ternary complex (Abl1, Dok1, Nck1)
  - SHC3-GAB1 complex
  - Cd2ap-Fyn complex
  - FRET-Shc-Grb2-Gab2-P85Pi3K-Shp2 complex
  - CNK1-SRC-RAF1 complex
  - Shc-Grb2-mSos1 complex, EGF stimulated
  - PLC-gamma-2-SLP-76-Lyn-Grb2 complex
  - EGF-Ncore
  - ITGA6-ITGB4-FYN complex
  - PSD95-FYN-NR2A complex
  - SLP-76-Cbl-Grb2-Shc complex, EGF receptor gamma.P1 stimulated

Click to highlight  
the nodes of  
protein complex

Go to Mapping table

Protein Protein Interactions

Export table

Export interaction tables

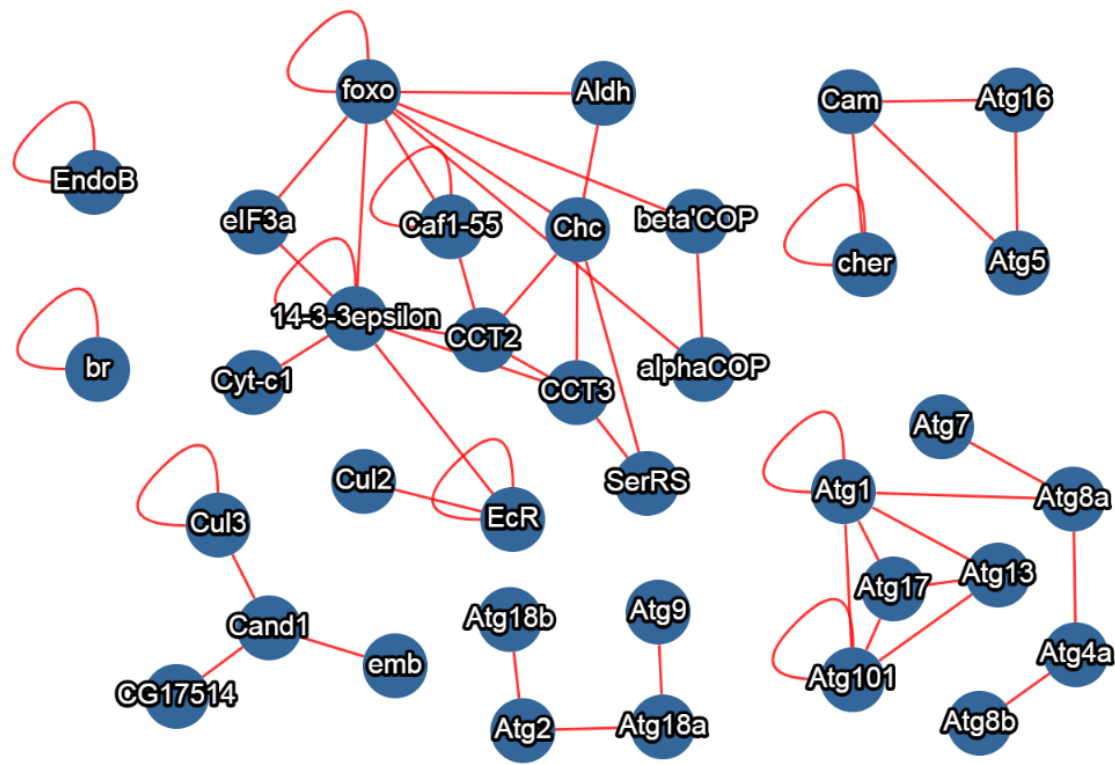
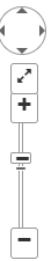
Show 10 entries

Search:

| Entrez GeneID A | Symbol A | Entrez GeneID B | Symbol B | PubMed ID | Rank | Source Databases                | Direct | Indirect  |
|-----------------|----------|-----------------|----------|-----------|------|---------------------------------|--------|---|
| 45278           | csw      | 32039           | sev      | 9582352   | high | BioGrid, DrolD, FlyBase, mentha |        | western blot(MI:0113)<br>affinity chromatography technology(MI:0004)<br>anti bait<br>coimmunoprecipitation(MI:0006) |
| 45278           | csw      | 32045           | Hsp60    | 22028469  | high | DrolD, FlyBase                  |        | anti tag<br>coimmunoprecipitation(MI:0007)<br>peptide<br>massfingerprinting(MI:0082)                                |
| 45278           | csw      | 32446           | RpL37a   | 22028469  | high | DrolD, FlyBase                  |        | massfingerprinting(MI:0082)   |

List view with  
detailed  
information

<https://fgrtools.hms.harvard.edu/MIST/>



**Edge Color**

|                      |        |
|----------------------|--------|
| PPI                  | Red    |
| Interologs           | Purple |
| Genetic interactions | Blue   |
| Interologs Genetic   | Green  |

**Node Color**

|  |        |
|--|--------|
| RPKM less than or equal to 1                     | Green  |
| RPKM greater than 1, less than or equal to 10    | Yellow |
| RPKM greater than 10, less than or equal to 1000 | Orange |
| RPKM greater than 1000                           | Red    |

**Node Shape**

|                       |
|-----------------------|
| Triangle - Input Gene |
| Circle - Interactor   |

Change Layout ▾

Download Network 📄

Search Graph

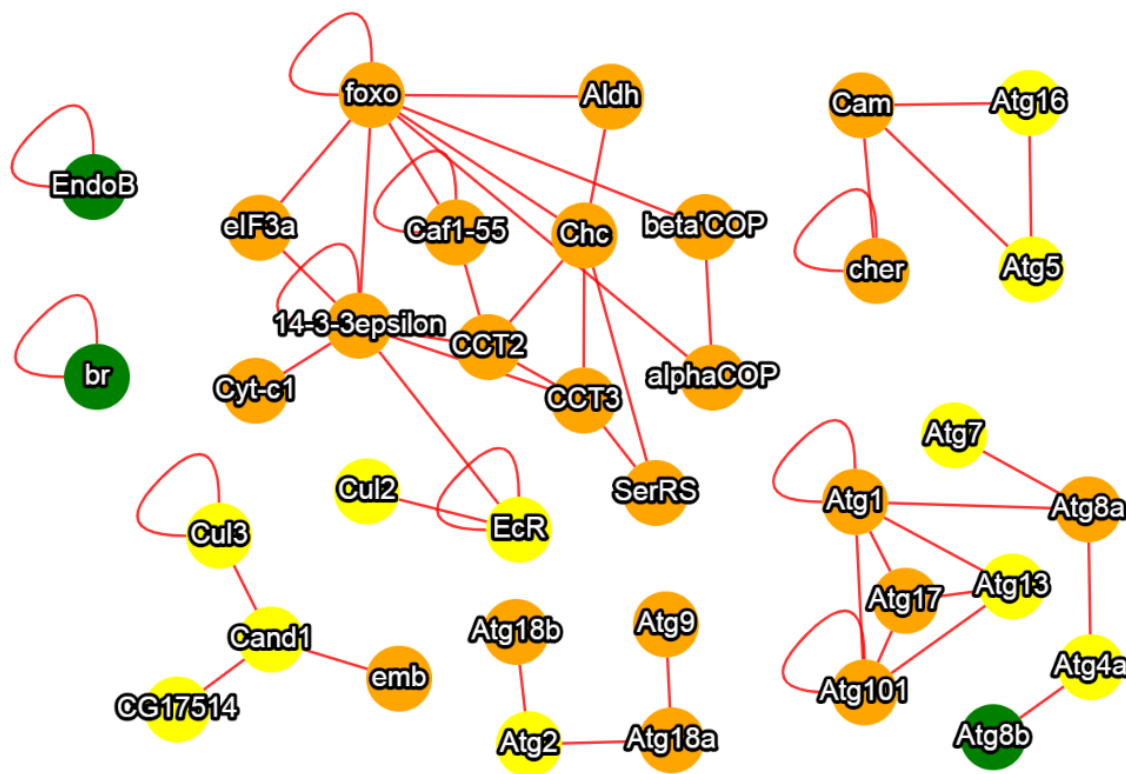
**Complex Groups**

- details
- CAND1-CUL2-RBX1 complex
  - determination of adult lifespan
  - putative complex without known function
  - synaptic vesicle coating
  - Coatamer-Arf1 complex
  - Apg16L-Apg12-Apg5 complex
  - regulation of immune system process
  - retrograde vesicle-mediated transport, Golgi to ER
  - larval midgut histolysis
  - CAND1-CUL3-RBX1 complex
  - CCT complex (chaperonin containing TCP1 complex)

**modENCODE Tissue Expression RPKMs**

- details
- salivary gland, larvae L3 wandering
  - salivary gland, white prepupae
  - digestive system, larvae L3 wandering
  - digestive system, 1-day adult
  - digestive system, 4-day adult
  - digestive system, 20-day adult
  - fat body, larvae L3 wandering
  - fat body, white prepupae
  - fat body, pupae P8
  - carcass, larvae L3 wandering
  - carcass, 1-day adult
  - carcass, 4-day adult

Reset Node Color    Export all tables



**Edge Color**

- PPI
- Interologs
- Genetic interactions
- Interologs Genetic

**Node Color**

- RPKM less than or equal to 1
- RPKM greater than 1, less than or equal to 10
- RPKM greater than 10, less than or equal to 1000
- RPKM greater than 1000

**Node Shape**

- Triangle - Input Gene
- Circle - Interactor

Change Layout ▾

Download Network ⬇

Search Graph

**Complex Groups**

details

- CAND1-CUL2-RBX1 complex
- determination of adult lifespan
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**modENCODE Tissue Expression RPKMs**

details

- salivary gland, larvae L3 wandering
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- fat body, larvae L3 wandering
- fat body, white prepupae
- fat body, pupae P8
- carcass, larvae L3 wandering
- carcass, 1-day adult
- carcass, 4-day adult

Reset Node Color

Export all tables

Digestive system 20-day adult

<https://fgrtools.hms.harvard.edu/MIST/>



# Single-Cell RNA-seq

Welcome to the single-cell RNA-seq data portal of DRSC/Perrimon lab

## Drosophila Data Sets

Gut Datasets

Blood Datasets

Abdomen Datasets

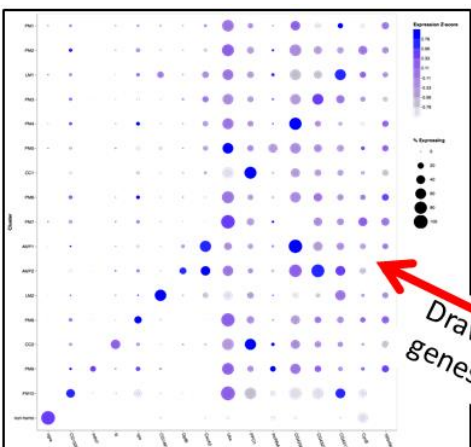
DRSC/TRiP Functional Genomics Resources

Visit the homepage to read [about us](#).

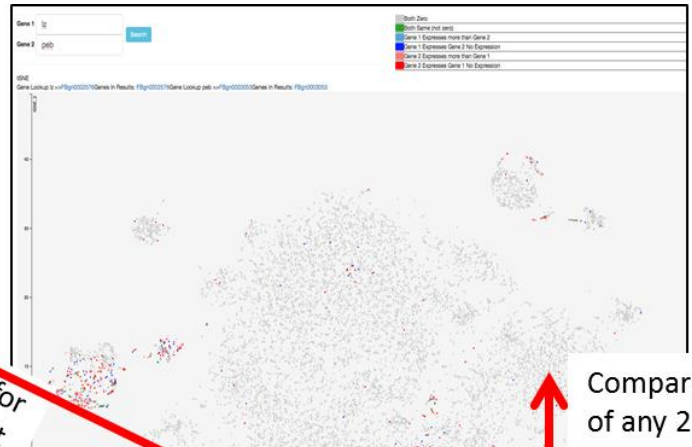
2019

[Back to top](#)

<https://www.flyrnai.org/scRNA>



Draw dot plot for genes of interest



Compare the expression of any 2 genes

Gene List Search Results

Cell Count Table

| Gene Name | Sample Type | PM1 | PM2 | LM1 | PM3 | PM4 | PM5 | CC1 | PM6 | PM7 | AMP1 | AMP2 | LM2 | CC2 | PM8 | PM9 | non-hemo |
|-----------|-------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|-----|-----|-----|-----|----------|
| lz        | PM1         | 1   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0    | 0    | 0   | 0   | 0   | 0   | 0        |
| lz        | PM2         | 0   | 1   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0    | 0    | 0   | 0   | 0   | 0   | 0        |
| lz        | LM1         | 0   | 0   | 1   | 0   | 0   | 0   | 0   | 0   | 0   | 0    | 0    | 0   | 0   | 0   | 0   | 0        |
| lz        | PM3         | 0   | 0   | 0   | 1   | 0   | 0   | 0   | 0   | 0   | 0    | 0    | 0   | 0   | 0   | 0   | 0        |
| lz        | PM4         | 0   | 0   | 0   | 0   | 1   | 0   | 0   | 0   | 0   | 0    | 0    | 0   | 0   | 0   | 0   | 0        |
| lz        | PM5         | 0   | 0   | 0   | 0   | 0   | 1   | 0   | 0   | 0   | 0    | 0    | 0   | 0   | 0   | 0   | 0        |
| lz        | CC1         | 0   | 0   | 0   | 0   | 0   | 0   | 1   | 0   | 0   | 0    | 0    | 0   | 0   | 0   | 0   | 0        |
| lz        | PM6         | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 1   | 0   | 0    | 0    | 0   | 0   | 0   | 0   | 0        |
| lz        | PM7         | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 1   | 0    | 0    | 0   | 0   | 0   | 0   | 0        |
| lz        | AMP1        | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 1    | 0    | 0   | 0   | 0   | 0   | 0        |
| lz        | AMP2        | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0    | 1    | 0   | 0   | 0   | 0   | 0        |
| lz        | LM2         | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0    | 0    | 1   | 0   | 0   | 0   | 0        |
| lz        | CC2         | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0    | 0    | 0   | 1   | 0   | 0   | 0        |
| lz        | PM8         | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0    | 0    | 0   | 0   | 1   | 0   | 0        |
| lz        | PM9         | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0    | 0    | 0   | 0   | 0   | 1   | 0        |
| lz        | PM10        | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0    | 0    | 0   | 0   | 0   | 0   | 1        |
| lz        | non-hemo    | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0    | 0    | 0   | 0   | 0   | 0   | 0        |

Get the statistics for genes of interest

DRSC RNA Seq explorer (Beta) Home Summary/Search Dot Plot Genes Search Two Genes Marker Genes Batch Query

Integration of Unwounded, Wounded, and Wasp infested 24 hr

Coordinate Ids

tSNE

Umap

Submit

Select tSNE or uMap

Select one or all samples

Select Condition / Sample

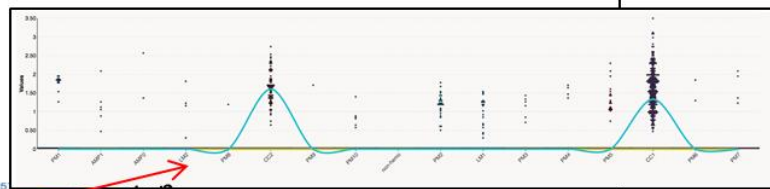
Wounded

Unwounded

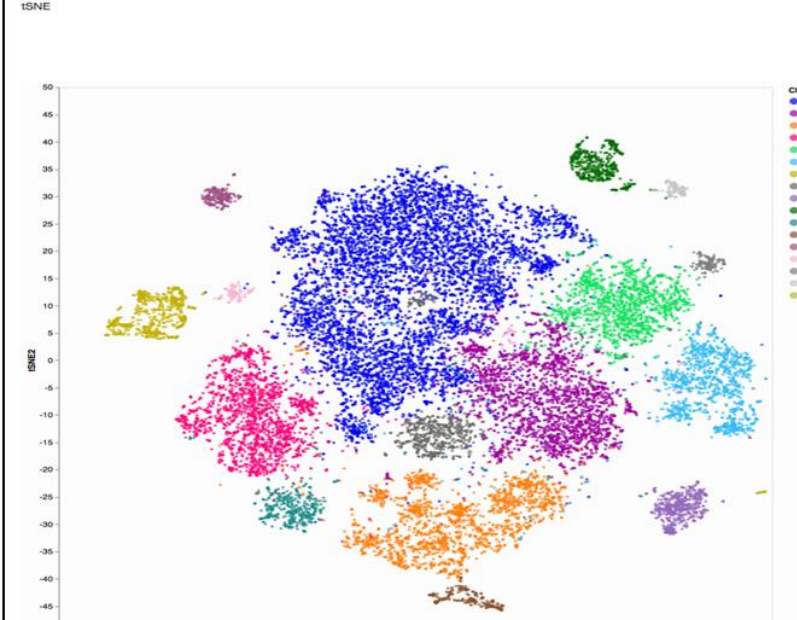
Wasp infested 24hr

all

Submit



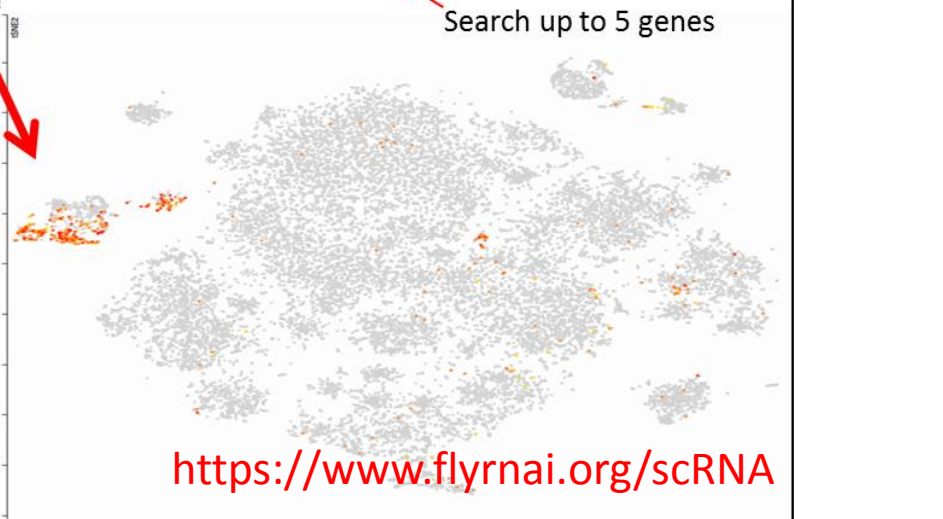
Plot distribution



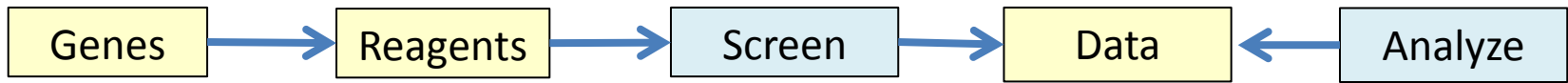
Gene Names (up to 5 comma separated) lz

Search

Search up to 5 genes



<https://www.flyrnai.org/scRNA>



**DIOPT**

**UP-TORR**

**FlyRNAi  
cell based  
screen data**

**COMPLEAT**

**DIOPT-DIST**

**FlyPrimerBank**

**RSVP Plus  
In vivo data**

**Signed PPI**

**Gene2Function**

**Find CRISPR  
tool  
(3 versions)**

**DGET  
Bulk RNA-seq**

**Directed PPI**

**BioLitMine**

**SNP-CRISPR  
Designs**

**scRNA  
sc or snRNA-seq**

**Online GESS**

**GLAD**

**sgRNA  
transgenic fly  
LIMs**

- Fly only
- Multiple organisms
- In process

**MIST  
interaction data**

**TF2TG**

**Paralog Explorer**

<https://fgr.hms.harvard.edu/>  
<https://flyrnai.org/>

**iProteinDB  
PTM data**

**Enrichment  
Tool**



# *Acknowledgements*



Norbert Perrimon



Stephanie Mohr



Aram Comjean



Jon Rodiger



Yifang Liu



Yue Gao

<https://fgr.hms.harvard.edu/>

<https://flyrnai.org/>