

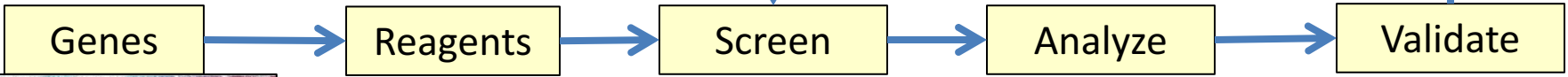
*DRSC/TRiP Informatics Tools for
Functional Genomics Studies
- 2018 Update*

Claire Yanhui Hu

April 13th 2018

DRSC/TRiP Informatics Tools

GSA functional genomics workshop 2015



DRSC Drosophila RNAi Screening Center

DIOPT DIOPT-DRSC Integrative Orthology Prediction Tool

DRSC - UP TORR Drosophila RNAi Screening Center

UP-TORR - Updated Targets of RNAi Reagents

DRSC Drosophila RNAi Screening Center

DIOPT-DIST DIOPT-DIST: DIOPT Diseases and Traits DRSC Disease Gene Query Tool

RSVP RNAi Stock Validation & Phenotypes



COMPLEAT protein COMPLEX Enrichment Analysis Tool

DRSC Drosophila RNAi Screening Center

FlyPrimerBank Search FlyPrimerBank for PCR Primers in D. melanogaster

Signed PPI

Online GESS

GLAD Gene List Annotation for Drosophila

CRISPRs

DGEP

High Resolution Melt Analysis

HRMA

New Look of DRSC/TRiP Web Site

DRSC/TRiP Functional Genomics Resources

Home

Technologies ▾

Online Tools ▾

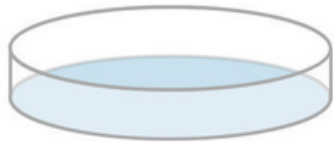
Protocols ▾

Reagents ▾

Equipment ▾

Publications

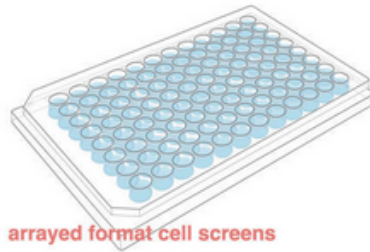
About ▾



pooled format cell screens



CRISPR libraries
wildtype or modified cells



arrayed format cell screens



RNAi or CRISPR
wildtype or modified cells

Made with © BioRender

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:

- [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](#)

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

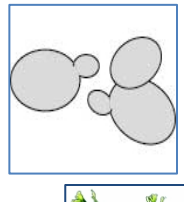
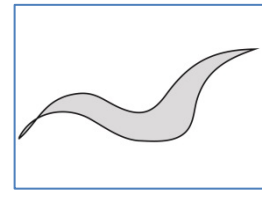
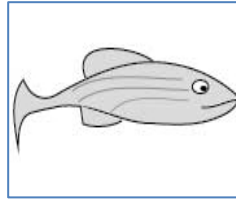
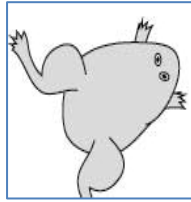
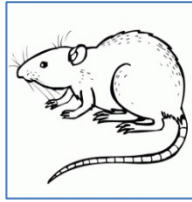
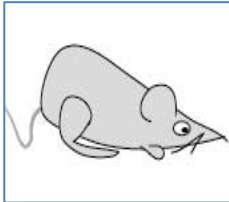
Topics

New features of old tools

- DIOPT

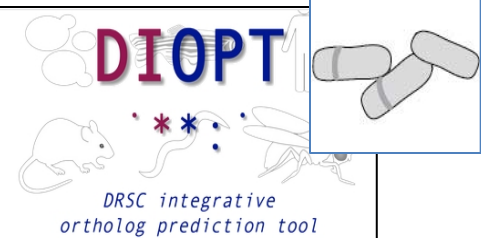
New tools

- Gene2Function
- MIST
- iProteinDB



DRSC/TRiP Functional Genomics Resources

10 species, 17 algorithms



About the DRSC

Other Online Tools

DIOPT - DRSC Integrative Ortholog Prediction Tool

New

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

Version 7.1 (March 2018)

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

[Documentation](#)

[Tutorial Video](#)

[Add New Submission](#)

Select Species:

Input Species:

Output Species:

Reverse

- Choose different species
- Choose same input and output species
- Set output species
- Adjust filters to

Enter Genes and/or

upd2

- Xenopus tropicalis (Western clawed frog)
- Homo sapiens (Human)
- Mus musculus (Mouse)
- Rattus norvegicus (Rat)
- Arabidopsis thaliana (Thale cress)**

separate; see [help](#)):

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 - \(vs 9\)](#)

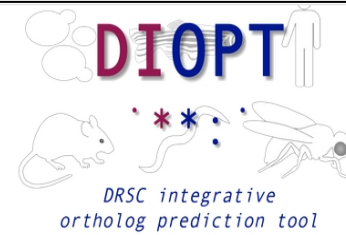
[User Submission](#)

[ZFIN](#)

Improvements

- Add tutorial video
- Add species eg. Arabidopsis thaliana
- Add prediction algorithms
- Add paralog search
- Add all species search
- Allow user to submit missing relationships
- Allow user to add feedback

Or upload from file:



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 [Zhang, et. al.](#)

[Documentation](#)

[Tutorial Video](#)

[Add New Submission](#)

Select Species:

Input Species:

Output Species:

Reverse

- Choose different species
- Choose same input and output species
- Set output species
- Adjust filters to

Enter Genes and/or

Or upload from file

upd2

separate; see [help](#):

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](#)

Search Term	Thale Cress	Fission yeast	Budding yeast	Worm	Fly	Zebrafish	Frog	Rat	Mouse	Human
ATG1	AT3G61960 (6 of 9)	atg1 (9 of 12)	ATG1 (10 of 15)	unc-51 (11 of 15)	Atg1 (13 of 15)	ulk1b (11 of 15)	ulk1 (6 of 12)	Ulk1 (14 of 14)	Ulk1 (16 of 16)	NA
ATP2B1	ACA4, ACA11 (8 of 9)	SPAPB2B4.04c (10 of 12)	PMC1 (12 of 15)	mca-3 (11 of 15)	PMCA (13 of 15)	atp2b1a (15 of 15)	atp2b2 (4 of 12)	Atp2b1 (11 of 14)	Atp2b1 (13 of 16)	NA
BRAF	AT4G24480, CTR1 (2 of 9)	----	----	lin-45 (11 of 15)	Raf (14 of 15)	braf (14 of 15)	braf (8 of 12)	Braf (9 of 14)	Braf (14 of 16)	NA
BRCA1	BARD1, BRCA1 (2 of 9)	SPCC548.05c (1 of 12)	CBF2 (1 of 15)	brc-1 (3 of 15)	CG10916, Sce, nopo, CG44271, CG5098 (1 of 15)	lnx1, lnx2b, rnf2, si:ch211-165g14.1, bard1, ftr73, LOC101882614 (1 of 15)	brca1 (3 of 12)	Brca1 (13 of 14)	Brca1 (13 of 16)	NA

Drosophila Cytokine Unpaired 2 Regulates Physiological Homeostasis by Remotely Controlling Insulin Secretion

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²Howard Hughes Medical Institute
Harvard Medical School, 77 Avenue Louis Pasteur, Boston, MA 02115, USA
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http://dx.doi.org/10.1016/j.cell.2012.08.019

SUMMARY
In *Drosophila*, the fat body (FB), a functional analog of the vertebrate adipose tissue, is the nutrient sensor that conveys the nutrient status to the insulin-producing cells (IPCs) in the fly brain to release *Drosophila* insulin-like peptides (Dilps). Dilp secretion in turn regulates energy balance and promotes systemic growth. We identify Unpaired 2 (Upd2), a protein with similarities to type I cytokines, as a secreted factor produced by the FB in the fed state. When *upd2* function is perturbed specifically in the FB, it results in a systemic reduction in growth and alters energy metabolism. Upd2 activates JAK/STAT signaling in a population of GABAergic neurons that project onto the IPCs. This activation relieves the inhibitory tone of the GABAergic neurons on the IPCs, resulting in the secretion of Dilps. Strikingly, we find that human Leptin can rescue the *upd2* mutant phenotypes, suggesting that Upd2 is the functional homolog of Leptin.

stored lipids and glycogen are broken down to generate energy

About the DRSC | Other Online Tools

DIOPT - DRSC Integrative Ortholog Prediction Tool

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

Your 1 query symbols mapped to 1 genes.

[Download the Results](#) (as a tab-delimited text file, named as ".xls").

Input Order	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
1	upd2	32805	FBgn0030904	upd2	Human	3952	6553	LEP	1	1	low	Yes	Yes	User_Submission	View	(1) Show Add

[Download the Results](#) (as a tab-delimited text file, named as ".xls").

Diopt New Submission

Scientist:

email:

publication (pmid preferred):

Input Species:

Output Species:

Input Gene:

Output Gene:

Comment:

About the DRSC | Other Online Tools

back to: [DIOPT - Ortholog Prediction Tool](#) / [DIOPT for Diseases and Traits](#)

Protein Alignment: upd2 and LEP

Sequence 1: NP_573277.2 Gene: upd2 FLYBASEID: FBgn0030904 Length: 370 Species: Drosophila melanogaster
 Sequence 2: NP_000221.1 Gene: LEP HGNCID: 6553 Length: 167 Species: Homo sapiens

Alignment Length: 57 Identity: 16/58 (28%)
 Similarity: 26/58 (45%) Gaps: 8/58 (14%)

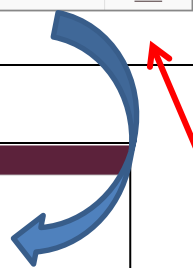
```

Fly      6  VMPPTKARHLRDOVALDYAYDE----DNSGRSSSSSSSSSSGG--DILPAFDVNP 55
          |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Human   110 VLAFSKSCHLPWASGLE-TLDSLGLVLEASGYSTEVVALSRLOGSLQDMLWOLDLSP 165
  
```

Known Domains:

Gene	Sequence	Domain	Region	External ID	Identity
upd2	NP_573277.2	Unpaired	108..327	CDD:292594	
LEP	NP_000221.1	Leptin	26..167	CDD:280242	16/58 (28%)

Blue background indicates that the domain is not in the aligned region.



Topics

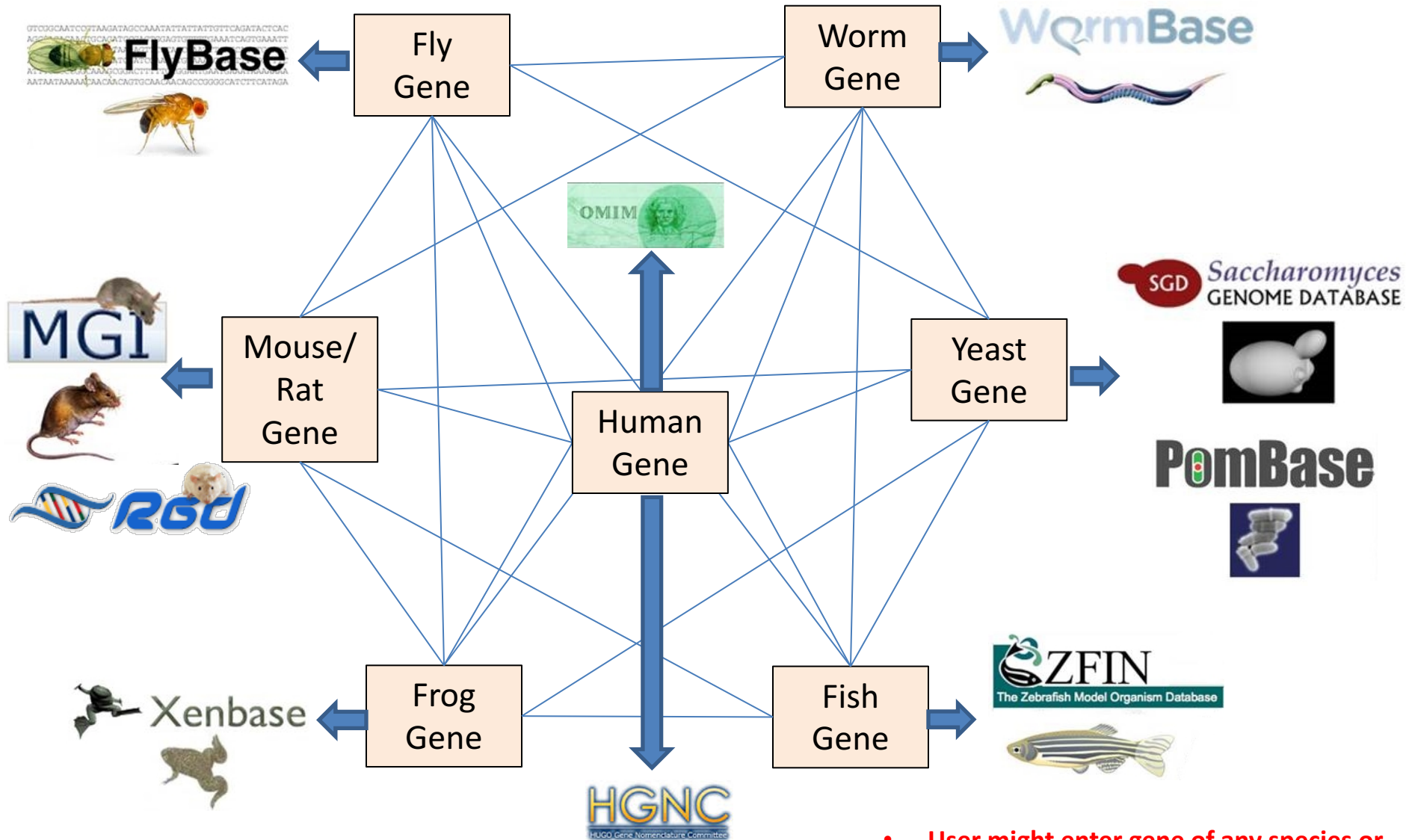
New features of old tools

- DIOPT

New tools

- Gene2Function
- MIST
- iProteinDB

Gene2Function: highly integrated system using DIOPT as hub to bring information together



- User might enter gene of any species or human disease term
- Blue edges are DIOPT relationships

Gene²Function



Search by Gene

Species

Human

Gene

EGFR

[Search By Gene](#)

Search by Disease

Disease

[Search By Disease](#)

gene search

- view orthologs
- view publications
- connect to GO terms
- connect to PPIs
- *and more*

Gene ID	Symbol	Human Protein Name	Species	Species ID	Species name	Species symbol	Species database	EGFP Score	Best Score	Confidence	Publication Count	GO Count	GO Function Count	GO Protein Count	Protein Interaction Count	Search	View	View	View	Protein
5271	FNKG2	FNKG2	Human	100936	MG2	13	NCBI	100	100	High	311	2	0	31	33	0	NA	NA	NA	31 (100% alignment)
5272	FNKG1	FNKG1	Human	100936	MG2	13	NCBI	100	100	High	311	2	0	31	33	0	NA	NA	NA	31 (100% alignment)
5273	FNKG3	FNKG3	Human	100936	MG2	13	NCBI	100	100	High	311	2	0	31	33	0	NA	NA	NA	31 (100% alignment)
5274	FNKG4	FNKG4	Human	100936	MG2	13	NCBI	100	100	High	311	2	0	31	33	0	NA	NA	NA	31 (100% alignment)
5275	FNKG5	FNKG5	Human	100936	MG2	13	NCBI	100	100	High	311	2	0	31	33	0	NA	NA	NA	31 (100% alignment)

Gene Ontology

Gene Info
 - Species: Human (Homo sapiens)
 - Symbol: FNKG2
 - Description: protein-coding gene (NCBI) (protein-coding gene)

Process

GO:0043025	snp	positive regulation of	GO:0043026	snp	negative regulation of
GO:0043029	expression	regulation of	GO:0043030	expression	regulation of
GO:0043032	expression	regulation of	GO:0043033	expression	regulation of
GO:0043036	expression	regulation of	GO:0043037	expression	regulation of

disease search

- refine search
- view associated genes
- connect to gene info

Gene ID	Symbol	Human Protein Name	Species	Species ID	Species name	Species symbol	Species database	EGFP Score	Best Score	Confidence	Publication Count	GO Count	GO Function Count	GO Protein Count	Protein Interaction Count	Search	View	View	View	Protein
1028	MG2A	MG2A	Human	100936	MG2	13	NCBI	100	100	High	311	2	0	31	33	0	NA	NA	NA	31 (100% alignment)
1029	MG2B	MG2B	Human	100936	MG2	13	NCBI	100	100	High	311	2	0	31	33	0	NA	NA	NA	31 (100% alignment)
1030	MG2C	MG2C	Human	100936	MG2	13	NCBI	100	100	High	311	2	0	31	33	0	NA	NA	NA	31 (100% alignment)
1031	MG2D	MG2D	Human	100936	MG2	13	NCBI	100	100	High	311	2	0	31	33	0	NA	NA	NA	31 (100% alignment)
1032	MG2E	MG2E	Human	100936	MG2	13	NCBI	100	100	High	311	2	0	31	33	0	NA	NA	NA	31 (100% alignment)

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

filters

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?	Publications 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 Drugbank .0 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	MGJ	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-465280	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

Input gene is highlighted

Paralog Overview

[Click To Load Paralogs](#)

Disease Overview

[Click To Load Disease Overview](#)

Gene Annotation Overview

[Click To Load Go Annotation Overview](#)

h21 -----MGLWALLPGWVSAITLLAL-----AALPAALANSSGR-----WVGIVNVASSTNLL--TDSKSLQLVLEPSE-QLLSRKRRLIRQNFGLIHSVSGGLQSAVRECKWQFNRR [101]
 mm1 -----MGLWALLPSWVSTLLAL-----TALPAALANSSGR-----WVGIVNIASSTNLL--TDSKSLQLVLEPSE-QLLSRKRRLIRQNFGLIHSVSGGLQSAVRECKWQFNRR [101]
 rn1 -----MGLWALLPSWVSAITLLAL-----TALPAALGANSSGR-----WVGIVNIASSTNLL--TDSKSLQLVLEPSE-QLLSRKRRLIRQNFGLIHSVSGGLQSAVRECKWQFNRR [101]
 xt1 -----MRILITFLVG-LKTIWLVLF-----SSLNTIYAVNNSGK-----WVGIVNVASAGNVLPGSDAQVPLVLDPSL-QLLSRKRRLIRQNFGLIQSITRGLHSAIREECKWQFNRR [102]
 dr1 -----MWSDIMRVLALLLA-VKAACVLLV-----SSLTIGAVNNSGR-----WVGIVNVASSGNLL--TNSKNVQLVLDPSL-ALLSRKRRLIRQNFGLIHLAAGLHTAIREECKWQFNRR [105]
 dm1 -----MDISYIFVICMLALCSGSSLSQVGEQKRSGRGSGMWMGLAKVGEFNNITP-----IMYMDFAHSTLRKRRLVDRNFVGLVGLVPGANLAIREECKWQFNRR [101]
 ce1 MLKSTQVILIFILLISIVESLSWAL-----GLAANRFDRDK-----PGTSCK-----SE-KGLTRRQMRFCCKNIDLMESVRSGLAAHAECCQFQFHRR [85]

NCBI Resources How To

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 US National Library of Medicine
 National Institutes of Health

PubMed [Search Box] [Advanced]

Article types: Clinical Trial, Review, Customize...

Format: Summary Sort by: Most Recent Per page: 20 Send to

Selected items: 1 to 20 of 198

1. Ras-activated Dsor1 promotes Wnt signaling in Drosophila development. Hall ET, Verheyen EM. J Cell Sci. 2015 Dec 15;128(24):4499-501. doi: 10.1242/jcs.175240. Epub 2015 Nov 5. PMID: 26542023 Free Article Similar articles

2. Wingless mediated apoptosis: How cone cells direct the death of peripheral ommatidia in the developing Drosophila eye. Kumar SR, Patel H, Tomlinson A. Dev Biol. 2015 Nov 15;407(2):183-94. doi: 10.1016/j.ydbio.2015.09.017. Epub 2015 Sep 30. PMID: 26428511 Free PMC Article Similar articles

3. Intersex (ix) mutations of Drosophila melanogaster cause nonrandom cell death in genital disc and can induce tumours in genitals in response to decapentaplegic (dpp/disk) mutations. Chatterjee RN, Chatterjee P, Kuthe S, Acharyya-Ari M, Chatterjee R. J Genet. 2015 Jun;94(2):207-20. PMID: 26174668 Free Article Similar articles

4. Gain of cis-regulatory activities underlies novel domains of wingless gene expression in Drosophila. Koshikawa S, Giorgianni MW, Vaccaro K, Kassner VA, Yoder JH, Werner T, Carroll SB. Proc Natl Acad Sci U S A. 2015 Jun 16;112(24):7524-9. doi: 10.1073/pnas.1509022112. Epub 2015 Jun 1. PMID: 26034272 Free PMC Article Similar articles

h21 -----GRDLRFMLNHNNEAGRITVFSSEMRQCECKCHGMSGCTVRCWMRLPTLRAVGDVLRDRFDGASRVLYGNR-----GSN [264]
 mm1 -----GRDLRFMLNHNNEAGRITVFSSEMRQCECKCHGMSGCTVRCWMRLPTLRAVGDVLRDRFDGASRVLYGNR-----GSN [264]
 rn1 -----GRDLRFMLNHNNEAGRITVFSSEMRQCECKCHGMSGCTVRCWMRLPTLRAVGDVLRDRFDGASRVLYGNR-----GNN [264]
 xt1 -----GRDLKYLVLNHNNAAGRLTVLTEMREQCECKCHGMSGCSLRTCWMRL [264]
 dr1 -----GRDLRYLTLNHNNEAGRMTVAASEMRQCECKCHGMSGCTVRCWMRL [264]
 dm1 -----GRNLRKMLNHNNEAGRLHVQAEEMRQCECKCHGMSGCTVRCWMRL [264]
 ce1 LGPSQLSADGMMHMLNHNNAAGRQVLEKSLRLECECKCHGMSGCEMRTCDWLSL [264]

See data for this gene in MARRVEL

Export (tab separated) Export to Excel

Disease_Term	Source	Rank	Other Values
{Osteoporosis, early-onset, susceptibility to, autosomal dominant}, 615221 (3)	OMIM	high	<ul style="list-style-type: none"> Genome region : 12q13.12 OMIM_ID : 164820 OMIM gene ID OMIM_ID : 615221 OMIM phenotype ID
Osteogenesis imperfecta, type XV, 615220 (3)	OMIM	high	<ul style="list-style-type: none"> Genome region : 12q13.12 OMIM_ID : 164820 OMIM gene ID OMIM_ID : 615220 OMIM phenotype ID

GenomeCRISPR

Home About Help API Submission

Screens sgRNAs Gene info

Tabular view Tree view

Target gene: WNT1

Each row represents one screening experiment

Screen ID	Cell line	Cas-9 variant	Screen type	Screen	Performance
GCR1671 (Wang et al.)	KBM7	hSpCas9	negative selection	viability	
GCR2031 (Wang et al.)	Jiyoye	hSpCas9	negative selection	viability	
GCR1788 (Wang et al.)	Raji	hSpCas9	negative selection	viability	
GCR1630 (Wang et al.)	K562	hSpCas9	negative selection	viability	
GCR1658 (Hart et al.)	DLD1	hSpCas9	negative selection	viability	
GCR3286 (Hart et al.)	GBM cells	hSpCas9	negative selection	viability after 5 days	

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	26245833	2015	Department of Genetics Howard Hughes Medical Institute, Harvard Medical School, Boston, Massachusetts 02115 perimon@receptor.med.harvard.edu.
34009	Cohen	SM	37	26226636	2015	Institute of Molecular and Cell Biology, Singapore, Singapore.
34009	Bienz	M	35	22645652	2011	NA
34009	Nusse	R	34	22203956	2012	NA
34009	Basler	K	29	28369070	2017	Institute of Molecular Life Sciences, University of Zurich, Zurich, Switzerland.
34009	Vincent	JP	28	26974662	2016	The Francis Crick Institute, Mill Hill Laboratory, The Ridgeway, Mill Hill, London NW7 1AA, UK.
34009	Irvine	KD	19	23318637	2013	NA
34009	Cadigan	KM	18	25188465	2014	Department of Molecular, Cellular and Developmental Biology, University of Michigan, Ann Arbor, Michigan, United States of America.
34009	Mlodzik	M	17	26364750	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 Sinai
34009	Morata	G	17	24096487	2014	Centro de Biología Molecular, CSIC-Universidad Autónoma de Madrid, Madrid, Spain.





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

Examples Using G2F

Genev	GWAS Traits	GWAS publications	Publications Gene Ontology	Information about orthologs	Suggested species for follow up
IGSF9B 	Schizophrenia 	25056061	0/0	higher expression in the nervous system in worm and fly. 34 fly paper and 2 mouse paper. Disruption neuronal phenotype in fly	fly mouse worm
NT5DC2	Bipolar disorder Schizophrenia	21926972 25056061 23974872	0/0	expressed in the nervous system in frog, fish and fly. Partially lethal in fly. 3 fly papers, 2 mouse papers and 1 rat paper	fly mouse fish rat
PPDPF	Prostate cancer	23535732	0/0	fish: GO-cell proliferation. 4 fish papers	fish
COQ10B	Schizophrenia	25056061	0/0	yeast (S.c.): GO-mitochondrion/ubiquinone binding. rich genetic-interaction data in yeast	yeast (sc)
NTN5	Bipolar disorder diarrhoeal disease at age 1 diarrhoeal disease at age 2	21926972 27559109 27559109	0/0	100 fly papers, 36 worm papers and 2 fish papers	fly worm fish
SAMD10 	Prostate cancer	23535732	0/0	fly: GO - EGFR pathway; regulates Ras protein signal transduction; compound eye cone cell differentiation; positive regulation of ERK1 and ERK2 cascade. 5 fly papers	fly
ABHD16B 	Prostate cancer	23535732	0/0	fly paper: A genetic screen in Drosophila identifying novel components of the hedgehog signaling pathway.	fly
C2orf69	Schizophrenia	23974872	0/0	fly: expressed in the nervous system and rich in PPI data	fly
FAM26D	Pelvic organ prolapse (moderate/severe)	26545240	0/0	worm: disruption phenotype - Uncoordinated locomotion with mutants showing reduced forward velocity, muscle force and power production	worm
ASPHD1	Schizophrenia	25056061	0/0	expressed in nervous system in fish, fly and worm. 5 fly papers	fish fly Worm
ACBD7	Hippocampal sclerosis	25188341	0/0	yeast (S.c.): rich interaction data; GO:chronological cell aging/long-chain fatty acid transport	yeast (sc)
NDUFC2-KCTD14	Pelvic organ prolapse	26545240	0/0	rat: NADH dehydrogenase (ubiquinone) activity; fly: phenotype-partial lethal; mouse-paper (mitochondria)	rat fly mouse

Topics

New features of old tools

- DIOPT

New tools

- Gene2Function
- MIST
- iProteinDB

Public resources

- using Drosophila gene *mnb* as example

DIP

mentha

Database of Interacting Proteins

Search by: [protein] [sequence] [motif] [article] [DMEs] [pathBLAST]

THE DIP DATABASE

The DIP™ database catalogs experimentally determined interactions between proteins. It contains 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 (DIP) and The Database of Interacting Proteins (DIP).

DIP PAGES

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

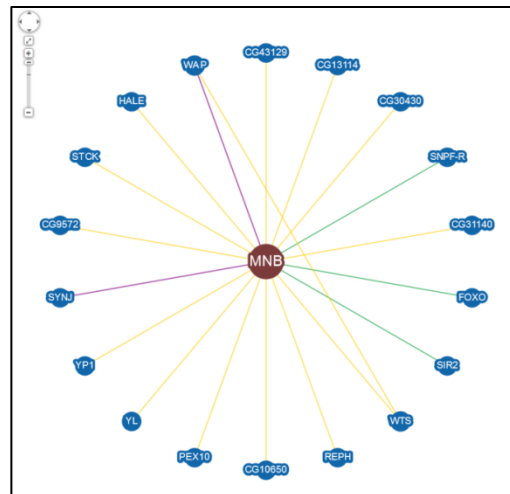
FlyBase A Database of *Drosophila* Genes & Genomes

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

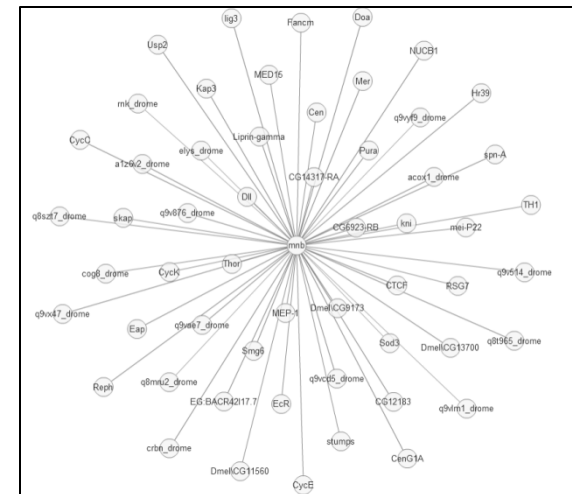
GO PHENOTYPE ANATOMY DISEASE MORE

genetic

BioGRID



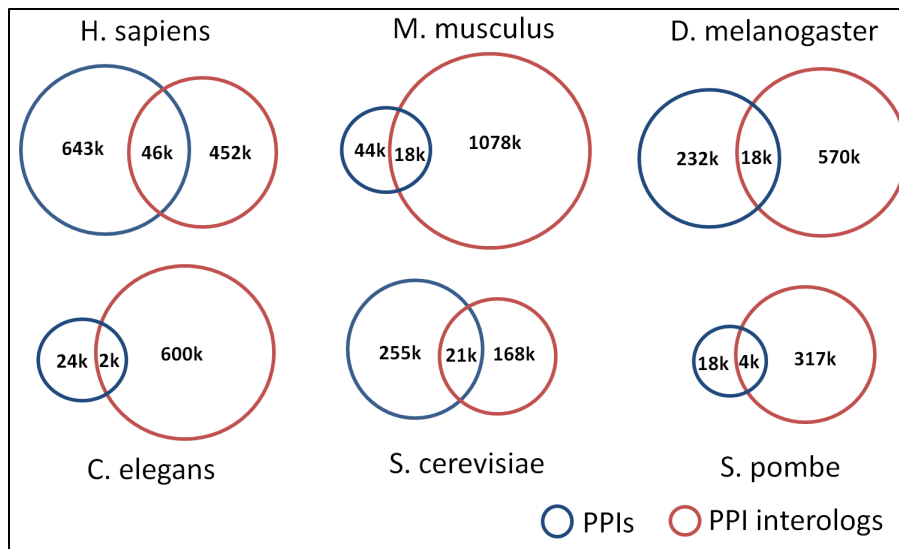
IntAct



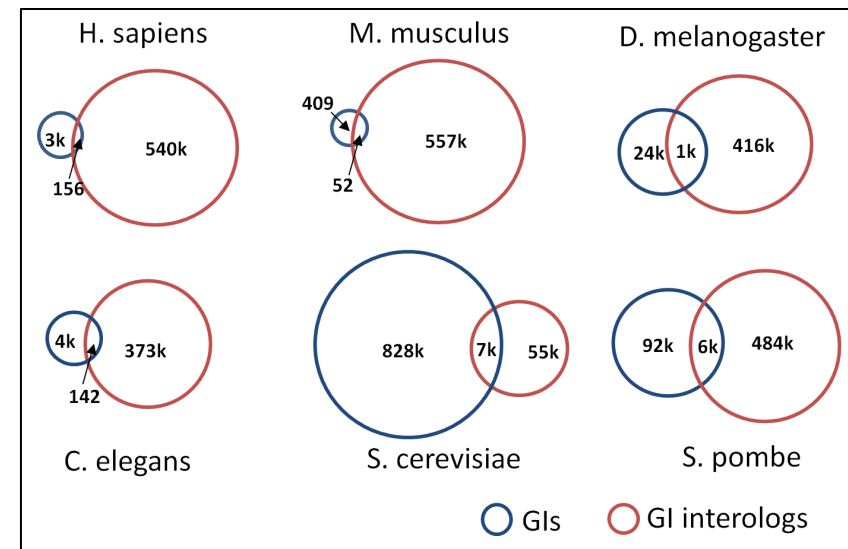
MIST (Molecular Interaction Search Tool)

Data Source	PPI	Genetic	PPI-interolog	Genetic-interolog	Batch search	Pair-search	Filters	Functional prediction
DIP	Yes							
DroID	Yes	Yes	Yes					
BioGrid	Yes	Yes						
IntAct	Yes	Yes						
FlyBase	Yes	Yes						
HPRD	Yes							
PomBase	Yes							
mentha	Yes							
HumanMAPK	Yes							
MIST	Yes	Yes	Yes	Yes	Yes	Yes	Yes	

Protein-Protein Interactions



Genetic Interactions





MIST

Molecular Interaction Search Tool
@ Harvard Medical School

[Home](#)[Statistics](#)[About/Help](#)[Example files](#)

Human Drosophila (*D. melanogaster*) Mouse Rat *C. elegans* *S. cerevisiae* *S. pombe* Zebrafish (*D. rerio*) *X. laevis* *X. tropicalis*

Search:

Protein List

Protein Pairs

Find Interactors

Copy/Paste : [Example](#)

CSW

Upload from the file:

Browse...

No file selected.

Choose Networks to Search: [Help](#)

Protein-protein interactions.

Interaction type

Filter By Rank

• Filter By Rank **Filter out Low Rank Results**

Other Filtering Options

• Filter By Interaction Type **Either**

Between Filters use: AND OR

Evidence Count is greater than

Number Of Papers is greater than

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

Interologs: protein-protein interactions from other species

Filter By Rank

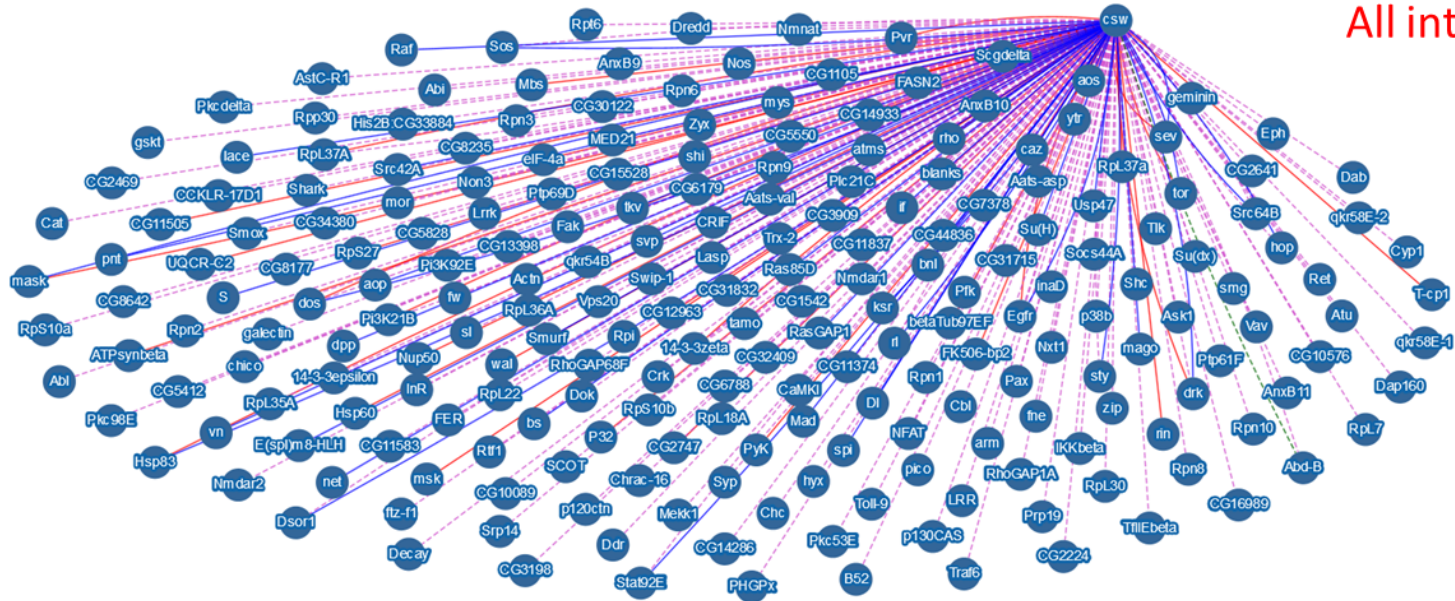
• Filter By Rank **None**

Other Filtering Options

• Filter By Number of Species

• Filter By Interaction Type **Either**

All interactions for csw

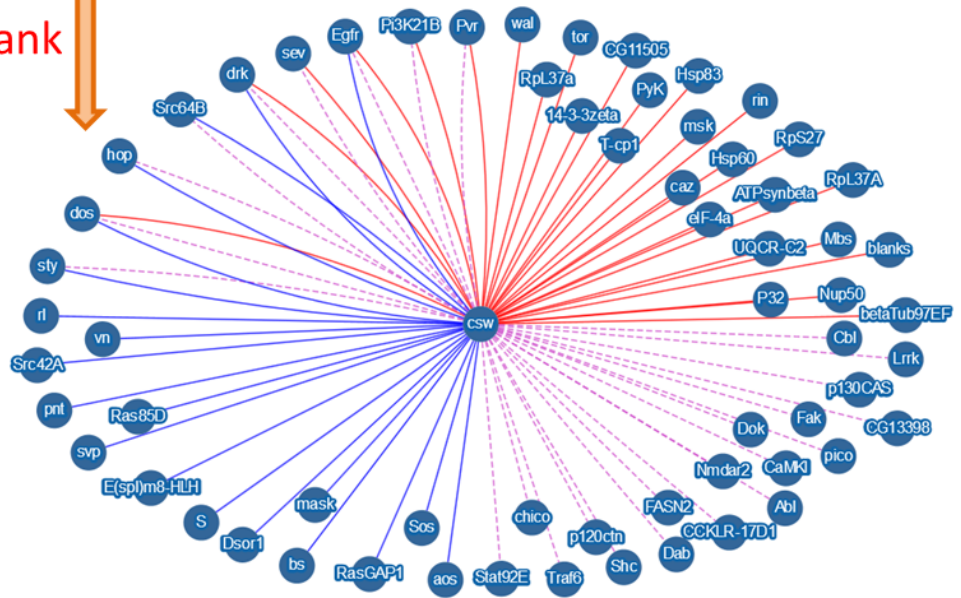


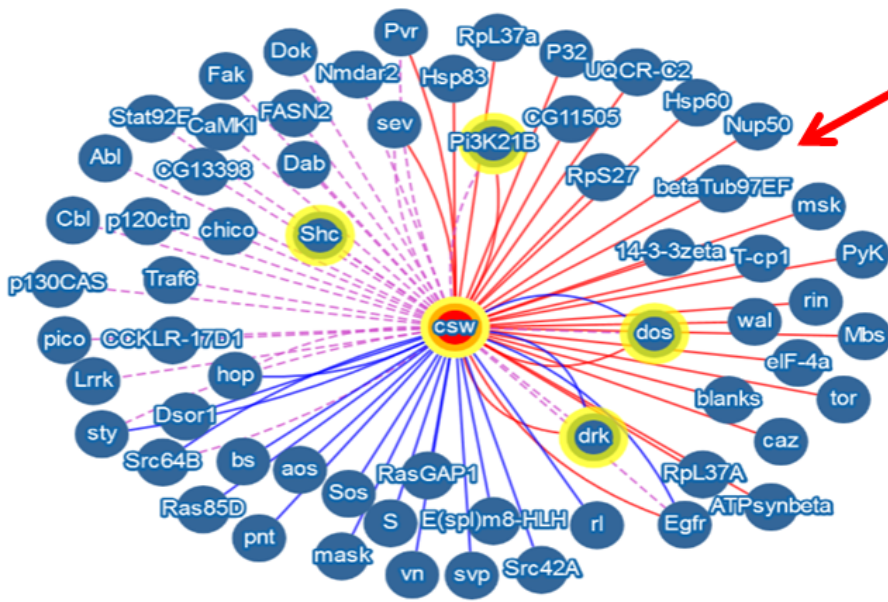
PPI	Red
Interologs	Purple
Genetic interactions	Blue
Interologs Genetic	Green

MIST filter by rank



Interactions of high/moderate rank for csw





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
 - ERET-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-ChlGrb2-Shc complex, Ecr receptor gamma.P1 stimulated

Click to highlight
the nodes of
protein complex

Go to Mapping table

Protein Protein Interactions

Export table

Export interaction tables

Export all tables

Show 10 entries

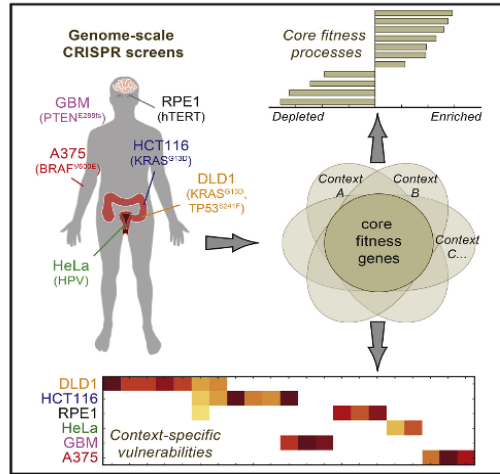
Search:

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) affinity chromatography technology(MI:0004) anti bait coimmunoprecipitation(MI:0006)
45278	csw	32045	Hsp60	22028469	high	DrolD, FlyBase		anti tag coimmunoprecipitation(MI:0007) peptide massfingerprinting(MI:0082)
45278	csw	32446	RpL37a	22028469	high	DrolD, FlyBase		anti tag coimmunoprecipitation(MI:0007) peptide massfingerprinting(MI:0082)

List view with
detailed
information

High-Resolution CRISPR Screens Reveal Fitness Genes and Genotype-Specific Cancer Liabilities

Graphical Abstract



Authors

Traver Hart, Megha Chandrashekar, Michael Aregger, ..., Daniel Durocher, Stephane Angers, Jason Moffat

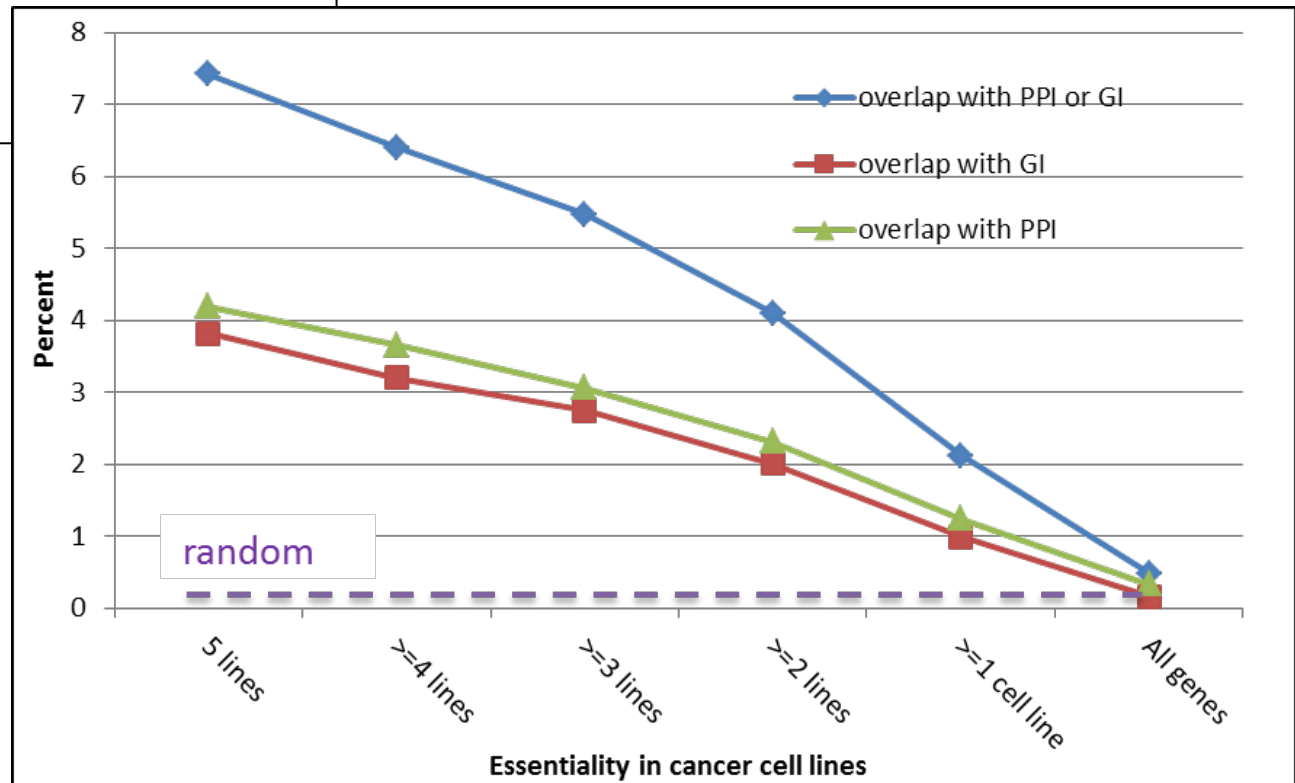
Correspondence

j.moffat@utoronto.ca

In Brief

CRISPR knockout screens for essential genes reveal oncogenic drivers specific to different cancer cell lines as well as unexpected metabolic and signaling dependencies that may guide future therapeutic targeting.

- Higher confident hits in the screens are more likely to interact with each other
- MIST can help set a cutoff as well as helps prioritize hits
- MIST can help generate hypotheses about the biological mechanisms for functionally related genes



Topics

New features of old tools

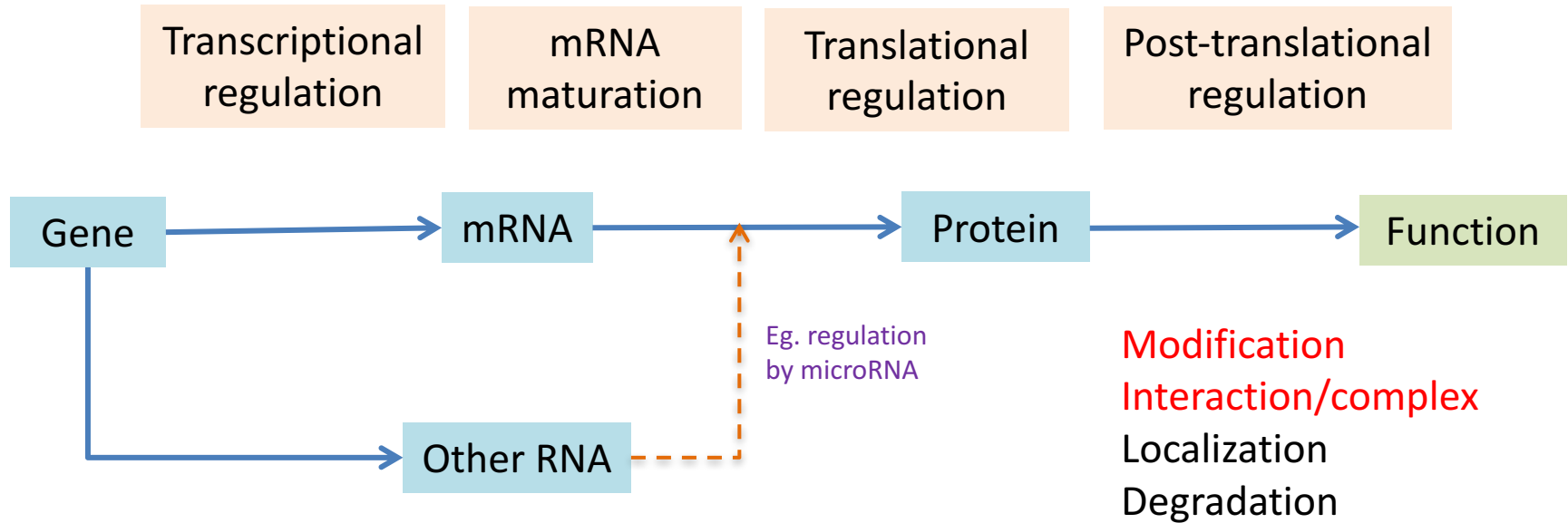
- DIOPT

New tools

- Gene2Function
- MIST
- **iProteinDB**

iProteinDB (integrated Protein DataBase)

- a resource for post-translational modification



iProteinDB

INTEGRATED PROTEIN DATABASE OF PTM FOR DROSOPHILA GENES

iProteinDB is an online integrated protein database and resource tool for providing information on post-translational modifications (PTMs) in *Drosophila melanogaster*. Comparative analysis is available with 5 other *Drosophila* species (*D. ananassae*, *D. pseudoobscura*, *D. simulans*, *D. virilis*, and *D. yakuba*), as well as the major model organisms and human.

SEARCH

Enter genes or proteins

Enter FBgn, gene symbol, gene annotation, or FBpp.

[Use sample terms](#)

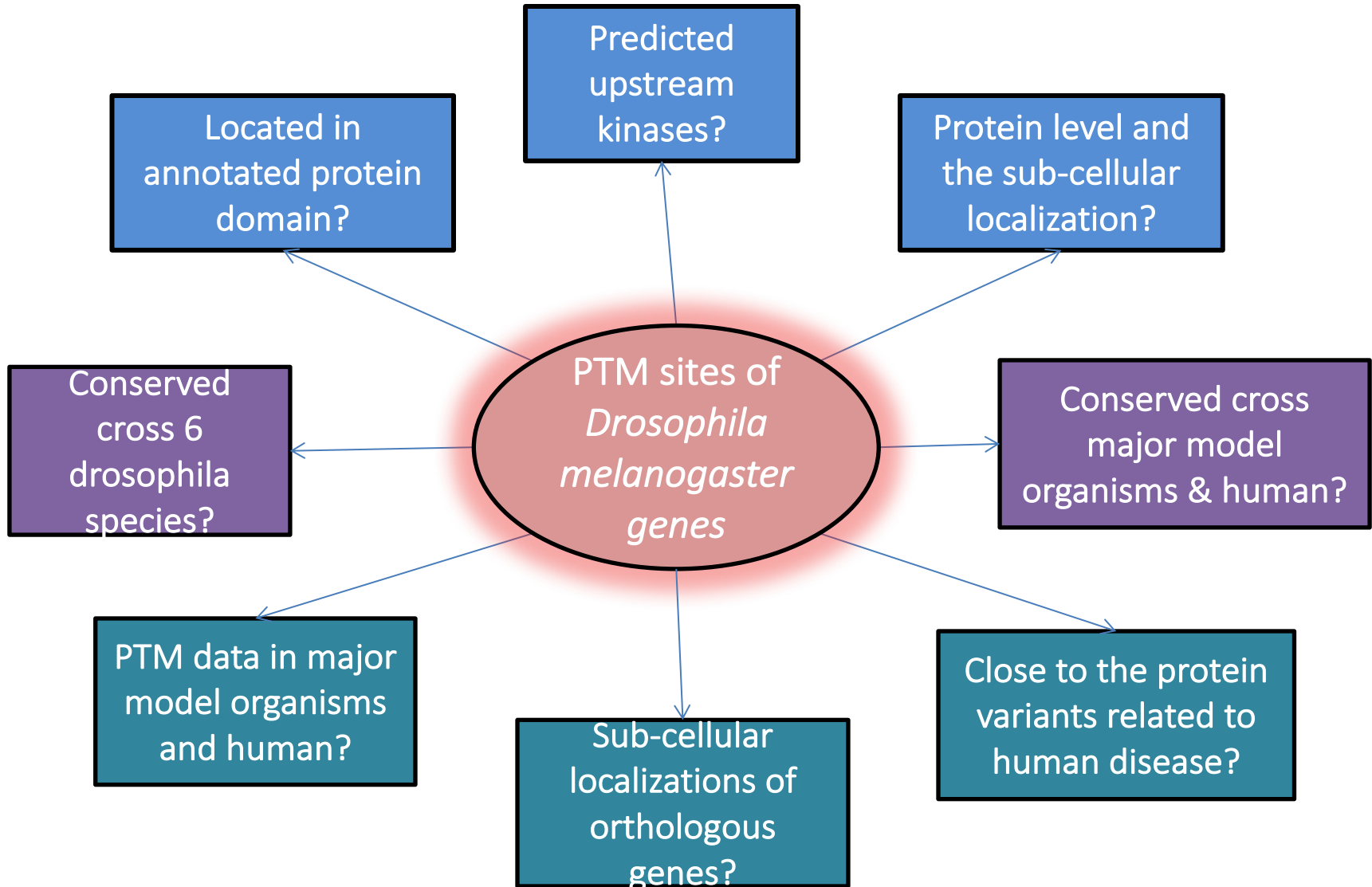
Act5C
AMPKalpha
SERCA
TER94
Sod1

Upload from file



1. Different IDs are supported: gene identifiers (FBgn), gene symbol and protein identifiers (FBpp)
2. Batch search is possible

iProteinDB Online Features



iProteinDB will be available soon at DRSC/TRiP website, stay tuned!