

ADRC 2017

Reaching across the MODs: enhanced orthology data and future prospects



Cross-MOD resources

- Links to MOD gene reports from DIOPT/ FlyBase ortholog search
- Alliance of Genome Resources (AGR)
- Links from FlyBase to two new resources:
 - -Gene2Function
 - -MARRVEL

Orthology is the key approach for comparison of genes across organisms

- But determining orthology can be a tricky business
- Different methods:
 - Phylogenetic
 - Sequence comparison
 - Graph-based, other, combinations
- Different goals:
 - Exclusive (highly selective, high precision)
 - Inclusive (casts a wide net -- high sensitivity, high recall)
 - Intermediate (balancing act)

Determination of orthology: compilation of multiple algorithms

- No one best algorithm: different algorithms are appropriate for different applications.
- The result: a multitude of algorithms for making orthology calls.



• Flexible alternative: compilation of multiple algorithms (HCOP, DIOPT).

DIOPT multi-algorithm approach

DIOPT - DRSC Integrative Ortholog Prediction Tool

http://www.flyrnai.org/diopt

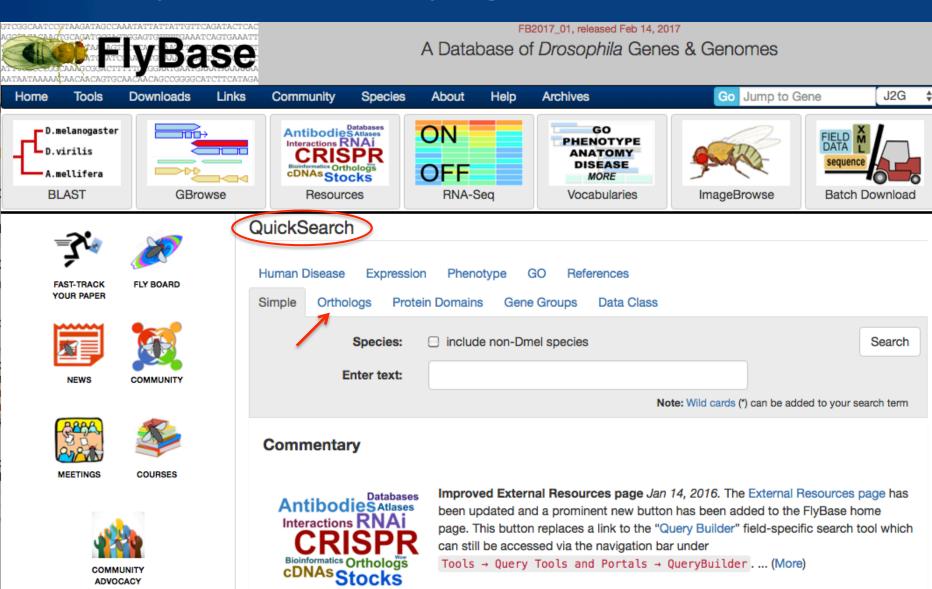
- FlyBase has added data from DIOPT; a tool developed by the DRSC
- DIOPT uses a scoring system:
 - Number of algorithms that call a given ortholog pair
 - Compared to the number of algorithms that include those 2 species
- Link to DIOPT from the FlyBase 'Orthologs' query
 - Can access documentation from the DIOPT query page

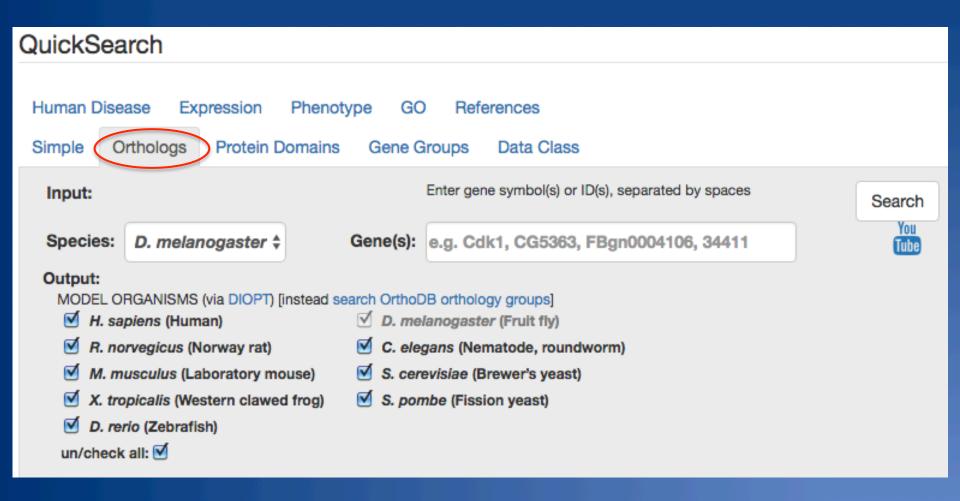
DIOPT Documentation

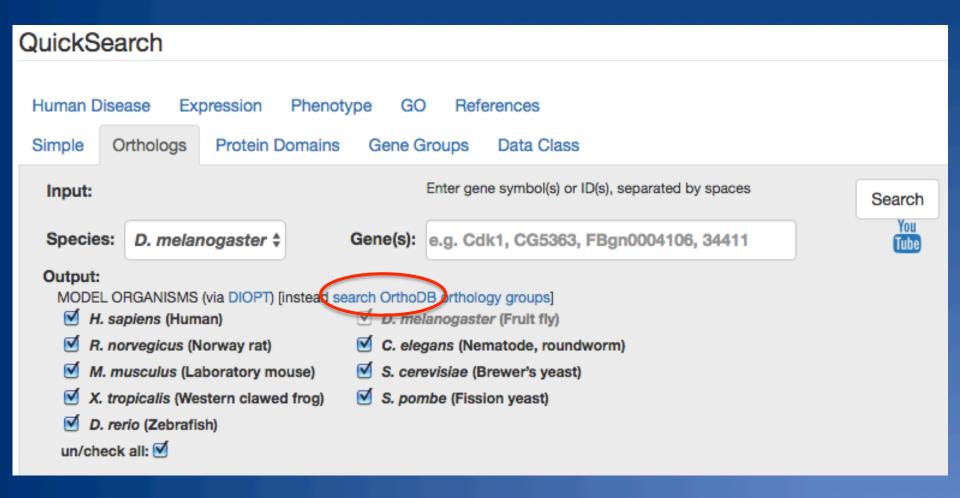
Prediction Method	Source	Prediction Algorithm	Coverage	DIOPT Weight*	PMID
Compara	Ensembl	Phylogenetic approach	70 species (vs.86)	0.931	19029536
<u>Homologene</u>	NCBI	Combination of BBH*, tree and synteny	21 species (vs. 68)	1	<u>11125071</u>
Inparanoid	Stockholm University, Sweden	BBH* approach to identify orthologs and in- paralogs	273 species (vs. 8)	1.005	11743721 25429972
<u>Isobase</u>	MIT	Sequence and PPI* network alignments	5 species (vs. 2, Nov. 2014)	0.957	21177658
OMA	CBRG, ETH Zurich	BBH*, global sequence alignments	1706 species (Oct 2014)	1.019	17545180
OrthoDB	University of Geneva	Phylogenetic approach	3027 species vs.9)	1.001	20972218 25428351

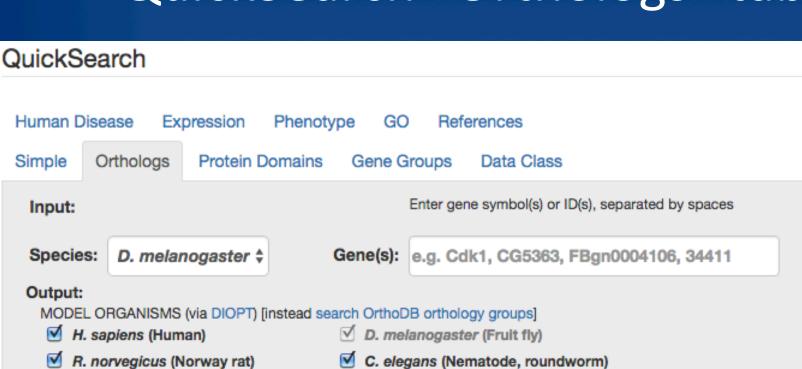
^{*}BBH = Best Blast Hits

FlyBase home page: QuickSearch







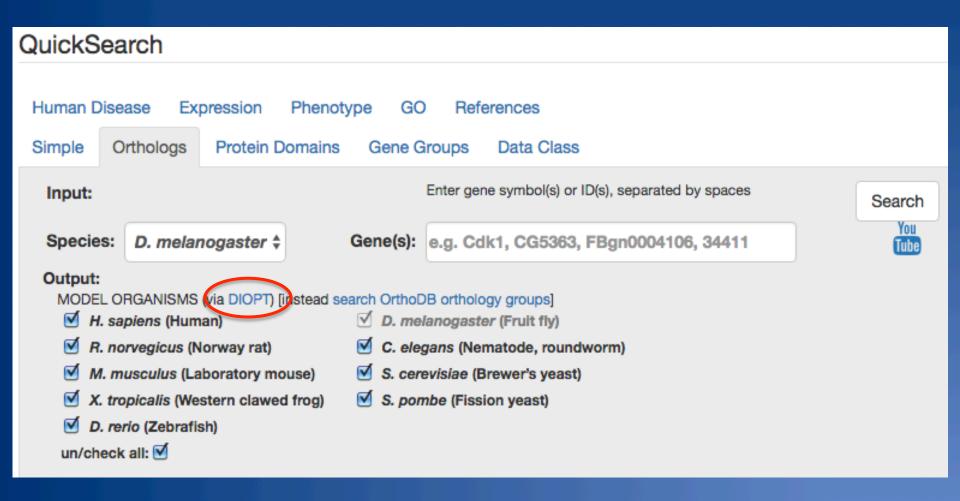




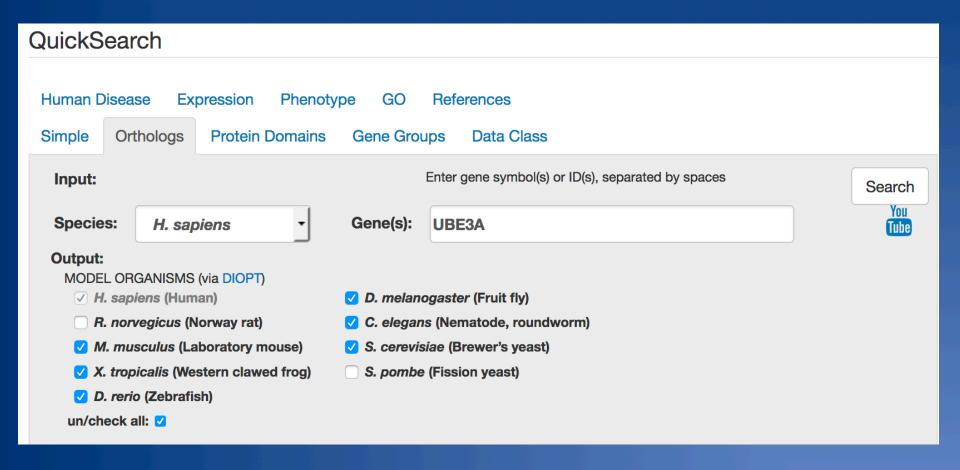
C. elegans (Nematode, roundworm)

- S. cerevisiae (Brewer's yeast)
- M. musculus (Laboratory mouse)
- S. pombe (Fission yeast)
- X. tropicalis (Western clawed frog)
- D. rerio (Zebrafish)

un/check all: M



Search with a human gene



Ortholog query output: human UBE3A

	Search Terr	m: UBE3A S	Species: Hon	no sapiens (Hum	nan) Gene: UBE3A Reports: NCBI Ensembl HGNC OMIM Transgene In Fly			
	Ortholog Cons				Via DIOPT (v6.0)			
Ortholog Gene	Ortholog Gene Reports	Score	Best Score	Best Rev Score	Source			
Mus musculus	s (Laboratory mouse)							
Ube3a	NCBI MGI	12 of 12	Yes	Yes (+)	Compara, eggNOG, HGNC, Homologene, Inparanoid, Isobase, OMA, orthoMCL, Panther, Phylome, RoundUp, TreeFam	(+)		
Hectd2	NCBI MGI	2 of 12	No	No (+)	eggNOG, orthoMCL	(+)		
Herc3	NCBI MGI	1 of 12	No	No (+)	eggNOG	(+)		
Herc4	NCBI MGI	1 of 12	No	No (+)	eggNOG	(+)		
Herc6	NCBI MGI	1 of 12	No	No (+)	eggNOG	(+)		
Xenopus trop	icalis (Western clawed	frog)						
ube3a	NCBI Xenbase	6 of 7	Yes	Yes (+)	Compara, eggNOG, Homologene, OMA, Phylome, TreeFam	(+)		
herc3	NCBI Xenbase	1 of 7	No	No (+)	eggNOG	(+)		
herc4	NCBI Xenbase	1 of 7	No	No (+)	eggNOG	(+)		
herc6	NCBI Xenbase	1 of 7	No	No (+)	eggNOG	(+)		
Danio rerio (Z	ebrafish)							
ube3a	NCBI ZFIN	9 of 11	Yes	Yes (+)	Compara, eggNOG, Homologene, OMA, orthoMCL, Panther, Phylome, TreeFam, ZFIN	(+)		
hectd2	NCBI ZFIN	2 of 11	No	No (+)	eggNOG, orthoMCL	(+)		
herc3	NCBI ZFIN	1 of 11	No	No (+)	eggNOG	(+)		
herc4	NCBI ZFIN	1 of 11	No	No (+)	eggNOG	(+)		
Drosophila m	elanogaster (Fruit fly)							
Ube3a	NCBI FlyBase	10 of 11	Yes	Yes (+)	Compara, eggNOG, Homologene, Inparanoid, OMA, orthoMCL, Panther, Phylome, RoundUp, TreeFam	(+)		
Sherpa	NCBI FlyBase	1 of 11	No	No (+)	eggNOG	(+)		
Caenorhabdit	is elegans (Nematode, I	roundworm) - no ortholo	ogs found				
Saccharomyc	es cerevisiae (Brewer's	yeast)						
HUL4	NCBI SGD	4 of 10	Yes	No (+)	Compara, eggNOG, orthoMCL, Panther	(+)		

Ortholog query output: human UBE3A

Sea	rch Term: UBE3A S	pecies: H o	mo sapie	ens (Human)	Gene: UBE3A Reports: NCBI Ensembl HGNC OMIM Transg					
Ortholog	Ortholog Cono		Via DIOPT (v6.0)							
Ortholog Gene	Ortholog Gene Reports	Score	Best Score	Best Rev Score	Source					
Mus mus	culus (Laboratory	mouse)								
Ube3a	NCBI MGI	12 of 12	Yes	Yes (+)	Compara, eggNOG, HGNC, Homologene, Inparanoid, Isobase, OMA, orthoMCL, Panther, Phylome, RoundUp, TreeFam					
Hectd2	NCBI MGI	2 of 12	No	No (+)	eggNOG, orthoMCL					
Herc3	NCBI MGI	1 of 12	No	No (+)	eggNOG					
Herc4	NCBI MGI	1 of 12	No	No (+)	eggNOG					
Herc6	NCBI MGI	1 of 12	No	No (+)	eggNOG					
Xenopus	tropicalis (Westerr	n clawed fi	rog)							
ube3a	NCBI Xenbase	6 of 7	Yes	Yes (+)	Compara, eggNOG, Homologene, OMA, Phylome, TreeFam					
herc3	NCBI Xenbase	1 of 7	No	No (+)	eggNOG					
herc4	NCBI Xenbase	1 of 7	No	No (+)	eggNOG					
herc6	NCBI Xenbase	1 of 7	No	No (+)	eggNOG					
Danio ren	io (Zebrafish)									
ube3a	NCBI ZFIN	9 of 11	Yes	Yes (+)	Compara, eggNOG, Homologene, OMA, orthoMCL, Panther, Phylome, TreeFam, ZFIN					
hectd2	NCBI ZFIN	2 of 11	No	No (+)	eggNOG, orthoMCL					
herc3	NCBI ZFIN	1 of 11	No	No (+)	eggNOG					
herc4	NCBI ZFIN	1 of 11	No	No (+)	eggNOG					

Ortholog query output: human UBE3A

	Search Ter	m: UBE3A S	pecies: <i>Hon</i>	no sapiens (Hun	nan) Gene: UBE3A Reports: NCBI Ensembl HGNC OMIM Transgene In Fly	
	Ortholog Comp				Via DIOPT (v6.0)	
Ortholog Gene	Ortholog Gene Reports	Score	Best Score	Best Rev Score	Source	Align
Mus musculu	s (Laboratory mouse)	_				
Ube3a	NCBI MGI	12 of 12	Yes	Yes (+)	Compara, eggNOG, HGNC, Homologene, Inparanoid, Isobase, OMA, orthoMCL, Panther, Phylome, RoundUp, TreeFam	(+)
Hectd2	NCBI MGI	2 of 12	No	No (+)	eggNOG, orthoMCL	(+)
Herc3	NCBI MGI	1 of 12	No	No (+)	eggNOG	(+)
Herc4	NCBI MGI	1 of 12	No	No (+)	eggNOG	(+)
Herc6	NCBI MGI	1 of 12	No	No (+)	eggNOG	(+)
Xenopus trop	icalis (Western clawed	frog)				
ube3a	NCBI Xenbase	6 of 7	Yes	Yes (+)	Compara, eggNOG, Homologene, OMA, Phylome, TreeFam	(+)
herc3	NCBI Xenbase	1 of 7	No	No (+)	eggNOG	(+)
herc4	NCBI Xenbase	1 of 7	No	No (+)	eggNOG	(+)
herc6	NCBI Xenbase	1 of 7	No	No (+)	eggNOG	(+)
Danio rerio (Z	ebrafish)	_				
ube3a	NCBI ZFIN	9 of 11	Yes	Yes (+)	Compara, eggNOG, Homologene, OMA, orthoMCL, Panther, Phylome, TreeFam, ZFIN	(+)
hectd2	NCBI ZFIN	2 of 11	No	No (+)	eggNOG, orthoMCL	(+)
herc3	NCBI ZFIN	1 of 11	No	No (+)	eggNOG	(+)
herc4	NCBI ZFIN	1 of 11	No	No (+)	eggNOG	(+)
Drosophila m	elanogaster (Fruit fly)	_				
Ube3a	NCBI FlyBase	10 of 11	Yes	Yes (+)	Compara, eggNOG, Homologene, Inparanoid, OMA, orthoMCL, Panther, Phylome, RoundUp, TreeFam	(+)
Sherpa	NCBI FlyBase	1 of 11	No	No (+)	eggNOG	(+)
Caenorhabdit	is elegans (Nematode,	roundworm)	- no ortholo	ogs found		
Saccharomyo	es cerevisiae (Brewer's	s yeast)				
HUL4	NCBI SGD	4 of 10	Yes	No (+)	Compara, eggNOG, orthoMCL, Panther	(+)

Ube3a gene report

General Information

Symbol	Dmel\Ube3a	Species	D. melanogaster
Name	Ubiquitin protein ligase E3A	Annotation symbol	CG6190
Feature type	protein_coding_gene	FlyBase ID	FBgn0061469
Gene Model Status	Current	Stock availability	7 publicly available
Also Known As	dube3a, As		



- Interactions and Pathways
- Expression Data
- Alleles and Phenotypes
- Orthologs ← —
- Human Orthologs (via DIOPT v6) (5)
- Orthologs (via OrthoDB v7) (34)
- Human Disease Model Data
- Gene Model and Products
- Genomic Location and Detailed Mapping Data
- Stocks and Reagents
- Other Information
- External Crossreferences and Linkouts
- Synonyms and Secondary IDs (19)
- References (63)

Ortholog table in Ube3a gene report

☐ Model Organism Orti	hologs (via D	IOPT v6)	(31)														
Homo sapiens (Human)																	
Species\Gene Symbol	NCBI Gene	Score	Best score	Best reverse score	Source										Α	lign	Transgene in Fly
					eggNOG Compara	Homologene	Inparanoid	Isobase	OMA	OrthoDB	Panther	Phylome	RoundUp	TreeFam	ZFIN		
Hsap\UBE3A	7337	10 of 11	Yes	Yes	Y Y	$ \mathbf{Z} $	丞		Y (S	\checkmark	V	⋖			Yes
Hsap\HECTD2	143279	2 of 11	No	Yes													
Hsap\HERC6	55008	1 of 11	No	No													
Hsap\HERC4	26091	1 of 11	No	No													
Xenopus tropicalis (Wes																	_
Species\Gene Symbol	NCBI Gene	Score	Best score	Best reverse score	Source										Α	lign	Transgene in Fly
Xtro\ube3a	407881	7 of 7	Yes	Yes	Y Y	\checkmark		ı	Y (₹		≰		₹			
Xtro\herc6Xtro\herc6	100487734	1 of 7	No	No													
Xtro\herc4	100036667	1 of 7	No	No													
		2															
Saccharomyces cerevisi	ae (Brewer's	yeast)															
Species\Gene Symbol	NCBI Gene	Score	Best score	Best reverse score	Source										Al	ign	Transgene in Fly
Scer\HUL4	853494	5 of 10	Yes	Yes	S S					V	'			⋖			

Cross-MOD resources

- Links to MOD gene reports from DIOPT/ FlyBase ortholog search
- Alliance of Genome Resources (AGR)
- Links from FlyBase to two new resources:
 - -Gene2Function
 - -MARRVEL

COMING SOON: Alliance of Genome Resources (AGR)





AGR proposed gene report

Common report format for all (model organisms plus human)

GAK

Symbol GAK

Name cyclin G associated kinase

Synonyms DNAJC26, auxilin-2, FLJ40395, FLJ16629, DNAJ26, OTTHUMP00000217314,

OTTHUMP00000147520, MGC99654, cyclin-G-associated kinase

Biotype protein coding gene

Description In all eukaryotes, the cell cycle is governed by cyclin-dependent protein kinases (CDKs),

whose activities are regulated by cyclins and CDK inhibitors in a diverse array of

mechanisms that involve the control of phosphorylation and dephosphorylation of Ser,

Genomic Ensembl:ENSG00000178950

Resources NCBIGene:2580

UniProtKB:B4DS37 UniProtKB:D6RAQ7 **Species**

Homo sapiens

Primary Source HGNC:4113

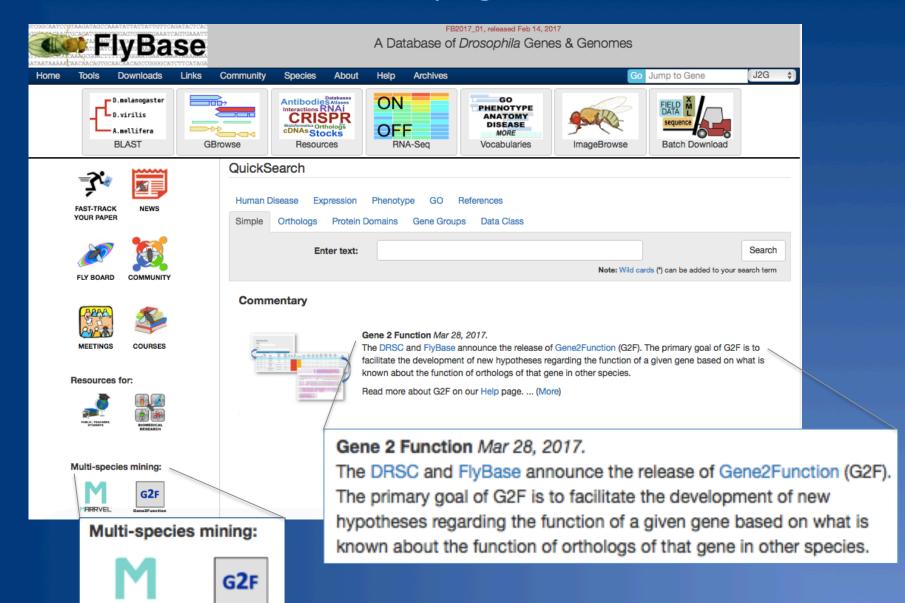
AGR gene report: ortholog table Simplifies navigation between species

Orthology					
Species	Gene symbol	Score	Best score	Best reverse score	Method ❷ & ⑥ I ♠ O ፟ P R ♣ R ♣ Align
Homo sapiens	GAK [NCBI]	11 of 11	Yes	Yes	VIVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV
Homo sapiens	DNAJC6 [NCBI]	7 of 11	No	Yes	✓ □ ✓ □ ✓ ✓ ✓ ✓ □ ✓ View
Mus musculus	Gak [NCBI]	11 of 11	Yes	Yes	ZZZZZZZZZZZ View
Rattus norvegicus	Gak [NCBI]	8 of 8	Yes	Yes	✓ ✓ ✓ ✓ ✓ ✓ ✓ View
Mus musculus	Dnajc6 NCBI]	7 of 11	No	Yes	Z
Danio rerio	Gak [NCBI]	7 of 11	Yes	Yes	✓ ✓ □ ✓ ✓ ✓ □ □ ✓ ✓ View
Danio rerio	Dnajc6 NCBI]	5 of 11	No	Yes	☑ □ ☑ ☑ ☑ □ □ □ View
Caenorhabditis elegans	tag-257 [NCBI]	5 of 11	Yes	Yes	U U U U U U View
Caenorhabditis elegans	dnj-25 [NCBI]	5 of 11	No	Yes	U U U U U U U View
Saccharomyces cerevisiae	SWA2 [NCBI]	2 of 11	Yes	Yes	U U U U U View

Cross-MOD resources

- Links to MOD gene reports from DIOPT/ FlyBase ortholog search
- Alliance of Genome Resources (AGR)
- Links from FlyBase to two new resources:
 - -Gene2Function
 - -MARRVEL
- Feedback welcome!

New links from the home page: G2F and MARRVEL



Gene2Function

Gene 2 Function

http://www.gene2function.org

Same species that are included in DIOPT



Search By Disease
Disease
Disease Name
Search By Disease

- View orthologs & alignments
- View publications
- Connect to GO terms, PPIs, and more

- Refine search
- View associated genes
- Connect to gene info

Gene2Function gene output is based on the DIOPT ortholog table

Gene ID	Symbol	Human Disease Terms	Species Name	Species specific gene ID	Species specific database	DIOPT Score	Best Score	Best Score reverse	Confidence
7337	UBE3A	4	Human (Homo sapiens)	12496	HGNC	12	Yes	Yes	high
22215	Ube3a	NA	Mouse (Mus musculus)	105098	MGI		-	-	
361585	Ube3a	NA	Rat (Rattus norvegicus)	1306361	RGD	10	Yes	Yes	high
407881	ube3a	NA	Western clawed frog (Xenopus tropicalis)	XB-GENE-948557	Xenbase	7	Yes	Yes	high
792398	ube3a	NA	Zebrafish (Danio rerio)	ZDB-GENE- 041114-190	ZFIN	10	Yes	Yes	high
39266	Ube3a	NA	Fly (Drosophila melanogaster)	FBgn0061469	FLYBASE	11	Yes	Yes	high

G2F gene output: extended ortholog table

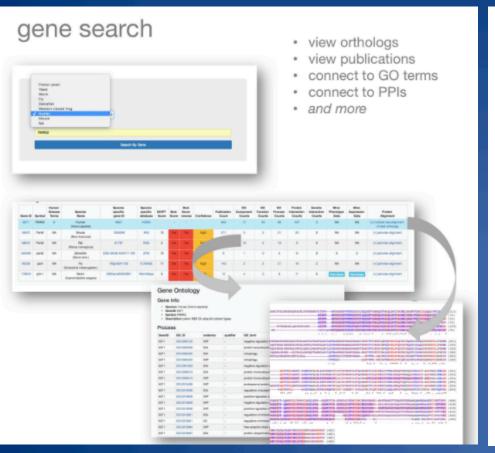
- Provides links to protein function data and related info
- Includes model organisms plus human

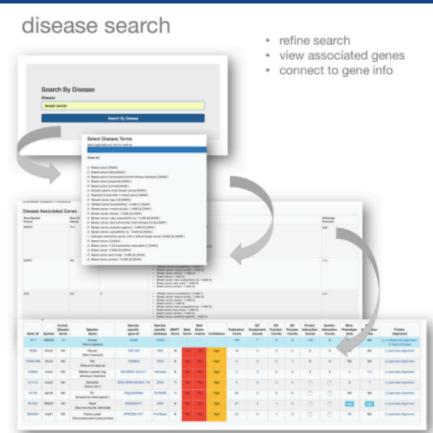
Symbol	Human Disease Terms	Species Name	Publication Count	GO Component Counts	GO Function Counts	GO Process Counts	Protein Interaction Counts	Protein Alignment
UBE3A	4	Human (Homo sapiens)	203	0	3	5	161	[+] pairwise alignment
Ube3a	NA	Mouse (Mus musculus)	130	2	3	9	3	[+] multiple seq alignment of best orthologs
Ube3a	NA	Rat (Rattus norvegicus)	4	0	0	0	1	[+] pairwise alignment
ube3a	NA	Western clawed frog (Xenopus tropicalis)	2	0	0	0	0	[+] pairwise alignment
ube3a	NA	Zebrafish (Danio rerio)	2	0	0	0	0	[+] pairwise alignment
Ube3a	NA	Fly (Drosophila melanogaster)	33	1	1	11	1	[+] pairwise alignment

G2F: Human disease terms include data from OMIM and GWAS Catalog

Symbol	Human Disease Terms	Species Name	Publication Count	GO Component Counts	GO Function Counts	GO Process Counts	Protein Interaction Counts	Protein Alignment
UBE3A	4	Human (Homo sapiens)	203	0	3	5	161	[+] pairwise alignment
Ube3a	NA	Mouse (Mus musculus)	130	2	3	9	3	[+] multiple seq alignment of best orthologs
Ube3a	NA	Rat (Rattus norvegicus)	4	0	0	0	1	[+] pairwise alignment
ube3a	NA	Western clawed frog (Xenopus tropicalis)	2	0	0	0	0	[+] pairwise alignment
ube3a	NA	Zebrafish (Danio rerio)	2	0	0	0	0	[+] pairwise alignment
Ube3a	NA	Fly (Drosophila melanogaster)	33	1	1	11	1	[+] pairwise alignment

Gene2Function overview





MARRVEL (http://marrvel.org/)

Model organism Aggregated Resources for Rare Variant ExpLoration

- Human gene reports: compilation of data from multiple sources; information on protein domains
- Emphasis on disease, natural variants, and variants associated with disease



Human Gene Symbol:

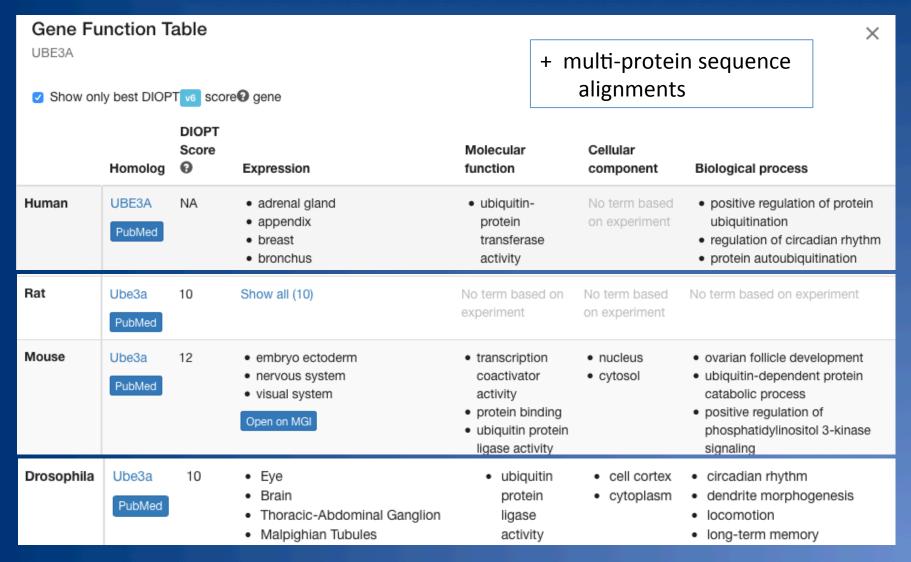
Please use official HGNC Gene Symbol. E.g. FBXL4

Human Variant (hg19):

E.g. 6:99365567 T>C

Example: 6:99365567 T>C / FBXL4 or 6:99365567 T>C or FBXL4

MARRVEL gene page includes model organisms in the Gene Function Table



MARRVEL by default shows only best hit or hits

UBE3A	inction T					×
Show on	Homolog	DIOPT Score	@ gene Expression	Molecular function	Cellular component	Biological process
Human	UBE3A PubMed	NA	adrenal glandappendixbreastbronchus	 ubiquitin- protein transferase activity 	No term based on experiment	 positive regulation of protein ubiquitination regulation of circadian rhythm protein autoubiquitination
Rat	Ube3a PubMed	10	Show all (10)	No term based on experiment	No term based on experiment	No term based on experiment
Mouse	Ube3a PubMed	12	embryo ectoderm nervous system visual system Open on MGI	 transcription coactivator activity protein binding ubiquitin protein ligase activity 	nucleuscytosol	 ovarian follicle development ubiquitin-dependent protein catabolic process positive regulation of phosphatidylinositol 3-kinase signaling
Drosophila	Ube3a PubMed	10	EyeBrainThoracic-Abdominal GanglionMalpighian Tubules	 ubiquitin protein ligase activity 	cell cortexcytoplasm	circadian rhythmdendrite morphogenesislocomotionlong-term memory

DIOPT: a note concerning filters

- FlyBase no filtering (yet)
- DIOPT removes hits of score = 1* (can override)
- Gene2Function removes hits = 1 or 2*
- MARRVEL shows only best hit or hits (can override)
- Alliance will filter

* Unless no higher score

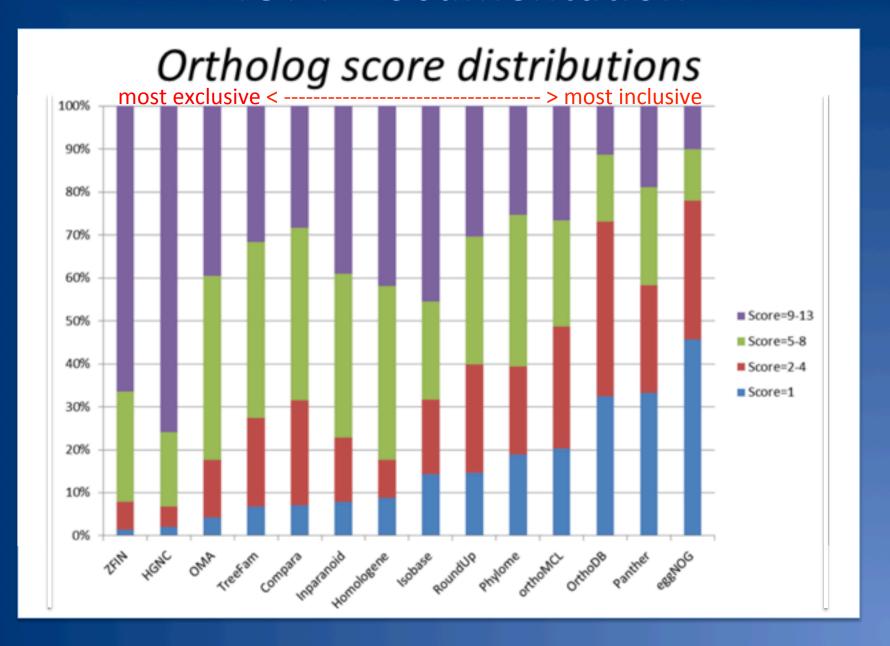
Good example: human ACTB

Thank you!

Fly Gdap1 has two high-scoring human orthologs

	Search Term:	Gdap1 S	pecies: Dra	osophila melan	ogaster (Fruit fly) Gene: Gdap1 Reports: NCBI FlyBase				
Ortholog			Via DIOPT (v6.0)						
Ortholog Gene	Ortholog Gene Reports	Score	Best Score	Best Rev Score	Source				
Homo sapiens (Human)									
GDAP1	NCBI Ensembl HGNC OMIM	10 of 11	Yes	Yes (+)	Compara, eggNOG, Homologene, Inparanoid, OMA, OrthoDB, orthoMCL, Phylome, RoundUp, TreeFam				
GDAP1L1	NCBI Ensembl HGNC	7 of 11	No	Yes (+)	Compara, eggNOG, Inparanoid, OrthoDB, Phylome, RoundUp, TreeFam				
EEF1G	NCBI Ensembl HGNC OMIM	1 of 11	No	No (+)	Panther				
GSTT2	NCBI Ensembl HGNC OMIM	1 of 11	No	No (+)	Phylome				
Mus musc	ulus (Laboratory mouse)								
Gdap1	NCBI MGI	10 of 11	Yes	Yes (+)	Compara, eggNOG, Homologene, Inparanoid, OMA, OrthoDB, orthoMCL, Phylome, RoundUp, TreeFam				
Gdap1l1	NCBI MGI	6 of 11	No	Yes (+)	Compara, eggNOG, Inparanoid, Phylome, RoundUp, TreeFam				
Eef1g	NCBI MGI	1 of 11	No	No (+)	Panther				
Gstt2	NCBI MGI	1 of 11	No	No (+)	Phylome				

DIOPT Documentation



Benchmarking of ortholog algorithms

Quest for Orthologs: Altenhoff et al. (2016)
 Standardized benchmarking in the quest for orthologs. Nat. Methods 13:425-30.

 DIOPT: Hu et al. (2011) An integrative approach to ortholog prediction for disease-focused and other functional studies. BMC Bioinformatics 12:357.