Gene Gro

Gene Group Survey

Results – February 2015 Total number of responses – 382

Gene Groups in FlyBase

Many publications describe sets of genes that share a common biology. Comprehensive genome-wide studies and phylogenetic analyses are now commonplace, and the subunit composition of many multi-protein complexes are well characterized. FlyBase has been collating such data for Drosophila melanogaster as 'Gene Groups' as we believe that FlyBase users would benefit from being able to easily view and analyse acknowledged gene sets. We are in the process of making Gene Group pages available on the website, and we would appreciate your views on how to implement this resource.

For this current phase, we are limiting Gene Groups to:

- a. Gene families and/or gene products with shared molecular functions e.g. Ras GTPases, GPCRs, potassium channels;
- b. **Protein complexes** e.g. ribosomal complexes, 26S proteasome, ATAC complex;
- c. Gene arrays and gene complexes e.g. E(spl) complex.

Three databases that already provide gene group-type data are HGNC, TAIR and WormBase. These may be useful for you to look at to get a sense of the different ways such data might be presented.

HGNC

<u>TAIR</u> (you or your institution will require a subscription to see content) WormBase

Gene Group Report Proposal

The Gene Groups will be organized in a hierarchical structure e.g.

- > G PROTEIN COUPLED RECEPTORS
 - > CLASS A GPCRs
 - > AMINE RECEPTORS
 - > DOPAMINE RECEPTORS

Each level of the hierarchy will have its own Gene Group report page. All genes within that group will be displayed on that page.

The report page will include:

- a list of genes within the group;
- a short description, notes and links to source publications to give an over-view of how the group was collated;
- a set of "key" gene ontology terms to indicate what biological properties these genes are likely to share;
- relationships with other groups place within group hierarchy, links with related groups (e.g. wnt family and frizzled-like receptors) and links to orthologous groups in other databases.

A mock-up of a Gene Group report for Class B GPCRs is shown below.



Gene Group: CLASS B GPCRs

Home	Tools	Files	Species	Documents	Resources	News	Help	Archives	Jump to Gene G
General Inforn	nation		loi -	ee n onen-					
Name Symbol				SS B GPCRs		pecies		D. melano	
	iowod		GPC	I.09.15		lyBase ID	mhore	FBgg0000 25	0005
Date Last Revi Description	leweu		Z012	1.00.10	P	lumber of me	inbers	2 5	
Description of	Gene Group			s B or secretin-like GPCRs Methuselah-type). (Adapte		ong N-termina	domain. Fa	mily B GPCRs can be d	ivided into three subfamilies: B1, B2 a
Notes on Grou	up membership)	stan	is also a member of the ca	dherin family. Harmar (2001) classifie	es stan as a	Family B GPCR. This ag	grees with the HGNC gene family em and classes stan as an atypical Gf
(ey GO Terms	5		oldo	sinoacon ana io ano groupin	g ddoptod floro. Er ot d	i., (2010) doo	a oligitay diri	or one oldoomodilon by the	and classes starr as an atypical of
Molecular Fun	ection								
	led receptor act	ivity						(FlyBas	e, 2014-)
Biological Pro									
ellular Comp	led receptor sig	naling pathwa	ay					(FlyBas	e, 2014-)
	nent of plasma	membrane						(FlvRas	e, 2014-)
Related Gene		Hombrano						(i i) Dao	0, 2011 /
arent group(s	s)		G P	ROTEIN COUPLED RECE	PTORS				
Component group(s)			CLA	CLASS B GPCRs, SUBFAMILY B1 CLASS B GPCRs, SUBFAMILY B2					
elated group(s)				METHUSELAH-TYPE RECEPTORS NEUROPEPTIDES, PEPTIDE AND PROTEIN HORMONES					
+/-] Members			IVE	onor or ribed, FEF fibe	ALD I NOTEIN HORN	OHLO			
or all membe						Download a	nd Export H	outtons	
CLASS B GPC	Rs, SUBFAMIL	Y B1							
Gene Symbol	.,		ne Name					Additional Data	
Dh31-R		Diu	retic hormone 31	Receptor					
Dh44-R1		Diu	retic hormone 44	receptor 1					
0h44-R2			retic hormone 44	receptor 2					
nec odfe			ctor	factor roos-t					
odfr CLASS B GPC	Rs, SUBFAMIL		ment-dispersing	actor receptor	1				
Gene Symbol	ita, dobi Ailii		ne Name						
CG11318									
CG15556									
Cirl				t receptor for α-latrotoxin					
tan JETHUSELAH	I-TYPE RECEP		rry night						
Gene Symbol	RECEP		ne Name						
nth			thuselah						
nthl1		met	thuselah-like 1						
mthl2			thuselah-like 2						
mthl3 mthl4			thuselah-like 3 thuselah-like 4						
nthi5			thuselah-like 5						
nthl6			thuselah-like 6						
mthl7			thuselah-like 7						
mthl8			thuselah-like 8						
mthl9 mthl10			thuselah-like 9						
mthl11			thuselah-like 10 thuselah-like 11						
mthl12			thuselah-like 12						
mthl13		met	thuselah-like 13						
mthl14			thuselah-like 14						
nthi15	lete	met	thuselah-like 15						
[+/-] External o			HG	NC.					
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			Wo	rmBase					
				WormBase Secretin					
Mhan ac	-(-)		0.0	WormBase Methusel CD family detabase	ah Class GPCRs				
Other resource	e(s) s and Seconda	ny IDe	GP	CR family database					
Synonym(s)	a and aeconds	ny IDS							
, ,,,,(0)			Fan	nily B GPCR					
				nily 2 GPCR					
			Sec	retin receptor family					
+/-] Reference					10				
Research paper				Li et al., 2013, Gene 519(1): 112. Comparative genomic analysis and evolution of family-B G protein-coupled receptors from six model insect species. [FBrf0221117]					
			Cor						
				Patel et al., 2012, J. Exp. Zool. B Mol. Dev. Evol. 318(5): 368–387. Dramatic expansion and developmental expression diversification of the methuselah gene family during recent Drosophila evolution.					
					opmental expression d	iversification o	f the methus	selah gene family during	recent Drosophila evolution.
Review				[FBrf0218628] Hauser et al., 2006, Prog. Neurobiol. 80(1): 119.					
COVIEW						fly Drosophila	melanogast	er and the honev bee Ar	ois mellifera. [FBrf0193587]
				ser et al., 2006, Brief. Fun	ct. Genomic. Proteomic	c. 4(4): 32133	30.		
								aster by exploiting genor	nic data. [FBrf0195077]
			lder	ntifying neuropeptide and p	roteiir normone recepto	is in Diosoph		,,	
				ntifying neuropeptide and p mar et al., 2001, Genome l					
			Har Fan	mar et al., 2001, Genome in hily-B G-protein-coupled re	Biol. 2(12): REVIEWS3 ceptors. [FBrf0147071]	013.			
			Har Fan Bro	mar et al., 2001, Genome l	Biol. 2(12): REVIEWS3 ceptors. [FBrf0147071] Cell Biol. 150(2): F83F	013.		,	,

Question 1: Attribution of Gene Group members

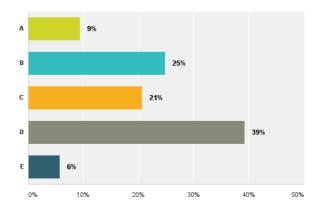
FlyBase Gene Groups are intended to reflect the current consensus within the research literature. Referenced notes are provided in the "Notes on Group membership" section to explain the criteria for membership where necessary.

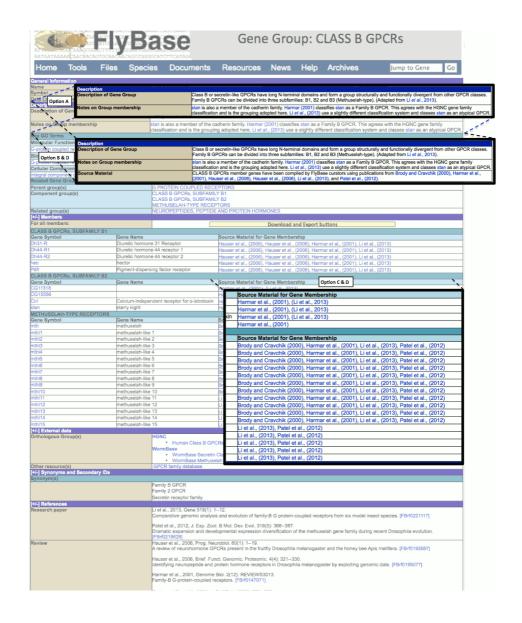
Gene Groups are often compiled from multiple publications. Each publication may not list the exact same set of genes owing to their year of publication or focus, for example.

In addition to displaying all references in full at the bottom of the page and the "Notes on Group membership", we would like to know whether more detailed attribution should be displayed.

Choose your preferred option (illustration below).

- A. No further attribution is necessary
- B. Add a "Source Material" summary in Description section
- C. Add a "Source Material for Gene Membership" column to the Members table to show the source(s) of each gene
- D. Add a "Source Material" summary in Description section AND a "Source Material for Gene Membership" column to the Members table (i.e. B and C)
- E. Don't know





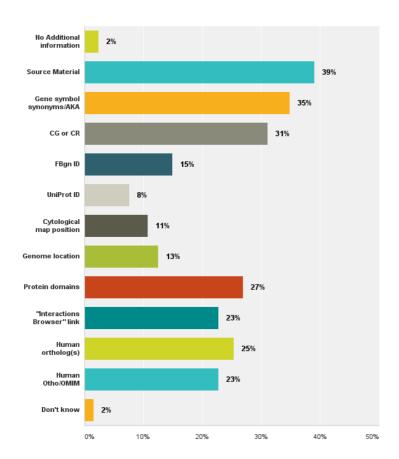
Question 2: Displaying information about member genes on the Gene Group Report

The Members table listing individual members of the group will contain the gene symbols and gene names. Additional information and links could be provided in columns to the right of the gene name field.



Which additional information and/or links would you like to see displayed in here? Select a maximum of THREE of the following options.

- No additional information (just want a list of genes)
- Source Material (as in Question 1)
- Gene symbol synonyms/AKA
- CG or CR annotation ID (hyperlinks to GBrowse view)
- FBgn ID
- UniProt ID
- Cytological map position
- Genome sequence location
- Protein domains
- Hyperlink to "Interactions Browser" showing physical/genetic interactions
- Human ortholog(s)
- Human ortholog(s) and any OMIM phenotype
- Don't know

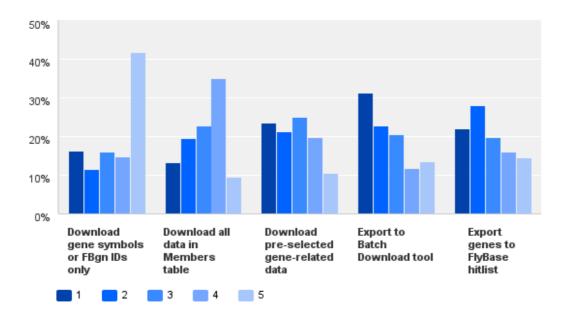


Question 3: Getting additional data on Gene Group members

In addition to the summary Members table referred to in Question 2, there will be buttons to download or export data on Gene Group members.

Which download or export tools would be most useful for you? (Rank 1-5, where 1 is the most useful and 5 is the least useful)

- · Download gene symbols or FBgn IDs only
- · Download all data shown in Members table
- Download data shown in Members table PLUS additional pre-selected generelated data e.g. all GO annotations, orthologs, protein domains (no user selection)
- Export genes to the Batch Download tool to specify gene-related data to download (user selected)
- Export genes to a standard FlyBase hitlist access to several query tools, conversion options and Analysis/Refinement tools



Question 4: Further Analyses of Gene Groups

We are interested in how you would want to further analyse or compare data within and between Gene Groups. Your answers could help us develop tools to facilitate this analysis.

Of the options listed below, pick the types of data that you would be most likely to compare or analyse (a maximum of THREE).

- Protein-protein interactions
- Genetic interactions
- Phenotypic data
- Expression patterns
- Genomic position
- Sequence alignment/similarity
- Domain structure or organization
- Find orthologous gene sets
- Gene Ontology terms
- Don't know
- Other (please specify)

