

**FlyBase Gene Ontology (GO)  
Survey**

# Survey Summary

## July 2023

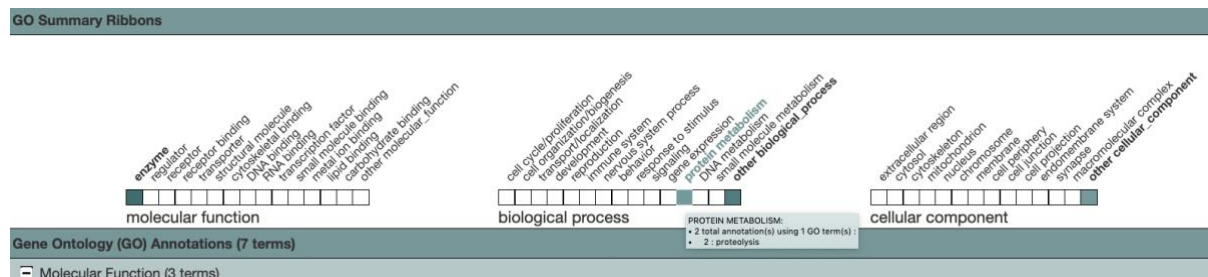


# FlyBase Gene Ontology (GO) Survey

## Introduction

The Gene Ontology (GO) is a structured set of standardized terms (controlled vocabulary) used to describe the biological properties of gene products. The GO is split into three aspects: molecular function, biological process and cellular component. The annotations are displayed on gene reports (e.g. [Damm gene report](#)) in two ways:

As a summary ribbon:

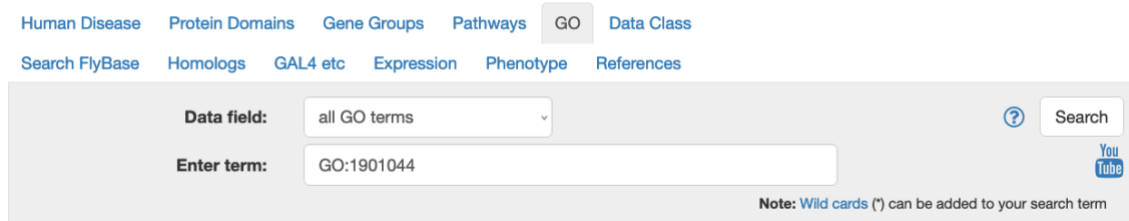


And as a table:

CV Term	Evidence	References
Terms Based on Experimental Evidence (3 terms)		
involved_in <a href="#">apoptotic process</a>	inferred from direct assay	( <a href="#">Harvey et al., 2001</a> )
involved_in <a href="#">programmed cell death</a>	inferred from genetic interaction with FLYBASE:hid; FB:FBgn0003997	( <a href="#">Harvey et al., 2001</a> )
involved_in <a href="#">proteolysis</a>	inferred from direct assay	( <a href="#">Harvey et al., 2001</a> )
Terms Based on Predictions or Assertions (2 terms)		
involved_in <a href="#">programmed cell death</a>	traceable author statement	( <a href="#">Richardson and Kumar, 2002</a> )
involved_in <a href="#">proteolysis</a>	inferred from electronic annotation with InterPro:IPR001309, InterPro:IPR002138, InterPro:IPR002398, InterPro:IPR011600 (assigned by InterPro)	( <a href="#">InterPro Project Members, 2004-</a> )

In FlyBase, GO annotations can be searched via the QuickSearch GO tab (a) and Vocabularies (b).

a) QuickSearch



The screenshot shows the FlyBase QuickSearch interface. At the top, there are navigation tabs: Human Disease, Protein Domains, Gene Groups, Pathways, GO (selected), and Data Class. Below these are sub-tabs: Search FlyBase, Homologs, GAL4 etc, Expression, Phenotype, and References. The main search area has a 'Data field:' dropdown menu set to 'all GO terms' and an 'Enter term:' text input field containing 'GO:1901044'. A 'Search' button is on the right, along with a help icon and a YouTube logo. A note at the bottom right states: 'Note: Wild cards (\*) can be added to your search term'.

b)



GO annotations are associated with genes by manual curation and via computational methods. Curators often add/remove annotations by reviewing a subject area or by curating research papers. The FlyBase GO curators would like to ask users of FlyBase how they use these annotations, introduce them to some GO resources that they may not be aware of, and target future projects to best suit the research community.



## FlyBase Gene Ontology (GO) Survey

### Questions

#### General questions about the use of GO annotation data

**Q1.** GO annotation data is available across species in many databases such as UniProtKB, FlyBase and via many bioinformatic tools. How often do you use any GO annotation data?

- Daily
- Weekly
- Monthly
- A few times a year
- Never

**Q2.** If you use GO annotation data, how do you use it? (Tick all that apply)

- Enrichment analysis
- For functional information on specific genes
- To get lists of genes associated with a particular molecular function (e.g. kinase activity), biological process (e.g. notch signaling pathway) or cellular component (e.g. nucleus)?
- Other (please specify)

**Q3.** If you search GO annotation data, what search tools do you use? (Tick all that apply)

- FlyBase Vocabularies tool
- FlyBase QuickSearch
- [AmiGO](#)
- [QuickGO](#)
- Other (please specify)

## GO annotation at FlyBase

The Gene Ontology has been in use for over 20 years ([Ashburner et. al., 2000](#)) and comprises over 40,000 GO terms. There is a very active effort by members of the GO consortium to improve the consistency and usability of the GO. The ontology and/or annotations may be revised to better reflect current biological knowledge. Many of these revisions result from global reviews of the ontology to address clear inconsistencies in usage and changes in annotation practices. (See [The Gene Ontology knowledgebase in 2023](#) for a summary of such efforts).

The FlyBase GO curators work as part of the GO consortium in these review projects. They also work to improve the accuracy of GO annotation by topic-directed reviews and targeted annotation projects.

The following section has some questions relating to the work of FlyBase GO curators.

**Q4.** We have grant funding (MRC, UK) to improve the ontology and GO annotation in several areas. To help with prioritization, please choose 3 of these projects.

- Mitochondrial proteins and processes.
- mRNA localization and localized translation
- Phase separation and non-membrane bounded organelles
- Circadian rhythm
- Review of orthologs human metastatic cancer-associated proteins
- Processes involved in collective cell migration
- Planar cell polarity
- Host-virus processes
- Are there any other specific topics for which you would like to see a focussed GO review?

**Q5.** Do you know that GO annotation topic-directed reviews provide the basis for the FlyBase [Gene Groups](#) and [Signaling Pathways](#) resources?

- Yes
- No
- Don't know what these resources are

**Q6.** Would you find it useful to have regular updates about current GO annotation targets and projects at FlyBase?

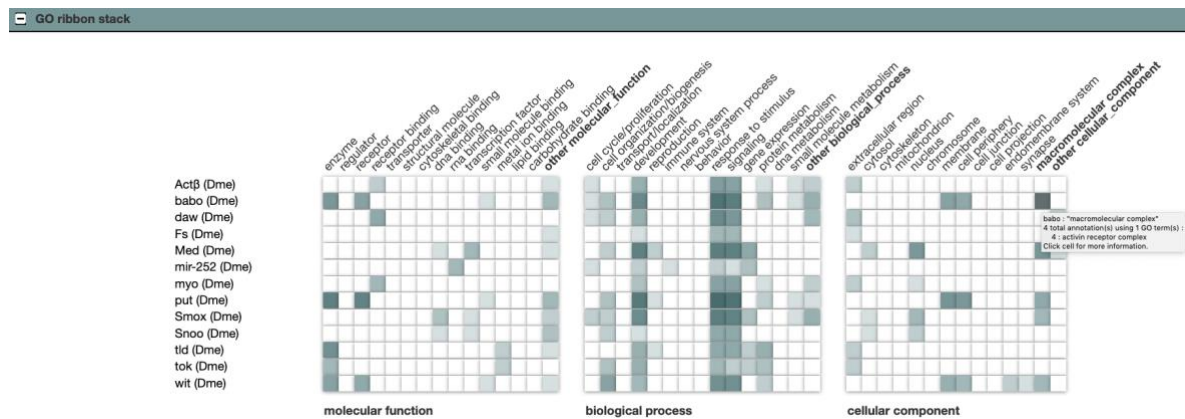
- Yes
- No
- No opinion

**Q7.** If you answered yes to Q6, how would you prefer us to communicate this information?  
(chose 1-3 options)

- Newsletter
- New in this Release
- Twitter
- FlyBase wiki
- Publication
- Other (please specify)

## GO tools

You can compare what is known about the function of a set of genes using the GO ribbons stack. For example, a high-level overview of the functions of all the members of the Activin Signaling Pathway is shown below:



Please go to the page displaying [this GO ribbon](#). Mouse-over and click one of the colored cells to see the detailed information.

You can also generate a GO ribbon for any set of ≤100 genes via a FlyBase HitList. Follow the example below to do this:

- i) From the homepage select the 'Protein Domains' tab of QuickSearch.
- ii) Start typing 'Actin family' into the search box and pick the matching term. Click the 'Search' button.

### QuickSearch

Human Disease Protein Domains Gene Groups Pathways GO Data Class

Search FlyBase Homologs GAL4 etc Expression Phenotype References

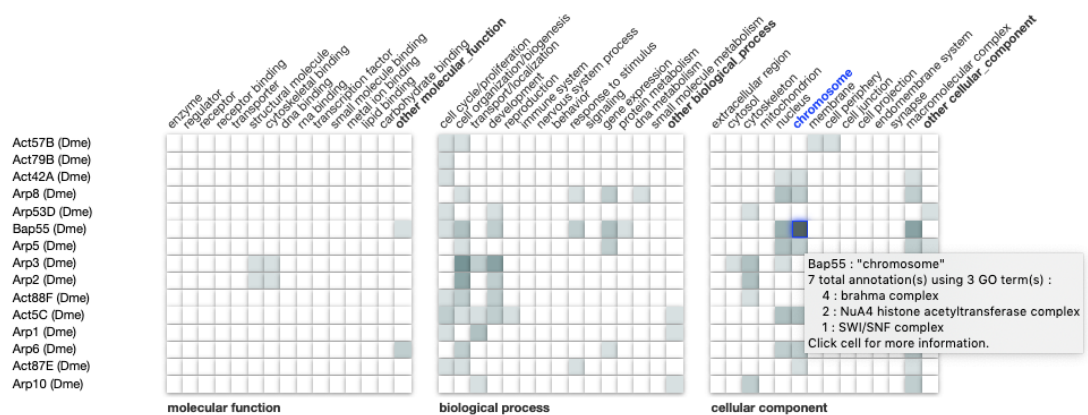
Search using InterPro IDs or signatures, including protein domains, families, repeats, and sites:  Search

Protein domain:

Note: Wild cards (\*) can be added to your search term

iii) You should see a HitList with 15 genes. Select 'GO Ribbon Stack Viewer' from the dropdown 'Export' menu.

iv) Use the 'GO ribbon stack viewer' to compare the annotations of actin family proteins. Mouse-over and click colored cells for more detail. Can you use the stack to see which genes encode cytoskeletal components vs nuclear chromatin remodeling components?





**Q8.** As shown above, GO ribbons provide a high-level overview on Gene, Gene group and Signaling pathway pages. Do you think these ribbons are:

- Useful
- Not useful
- Don't know
- Comment or suggestions on GO ribbons

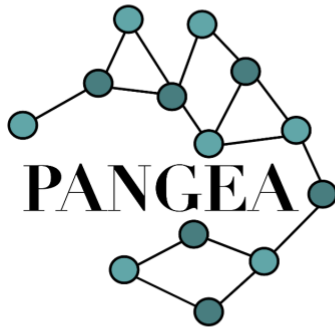
Gene Set Enrichment Analysis (GSEA) is a computational method often used in the analysis of medium/high-throughput experiments such as RNAi screens, microarray or proteomics to look for statistically significant biological trends or groups.

**Q9.** Have you used any of these Enrichment Tools? (tick as many as apply)

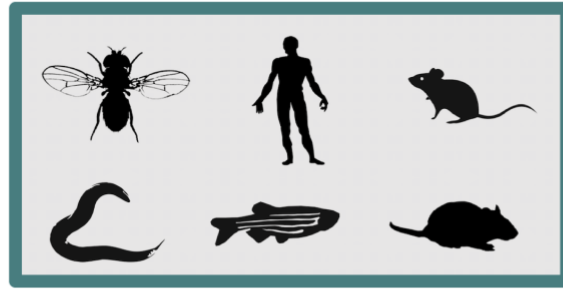
- [DAVID](#)
- [GORilla](#)
- [GO Term Finder](#)
- [GO/PANTHER](#)
- [g:Profiler/g:GOST](#)
- [WebGestalt](#)
- [PANGEA](#)
- Other (please specify)

**Q10.** Have you heard of [PANGEA](#) - an enrichment tool developed by the DRSC and FlyBase?

## A gene set classification and enrichment tool



for



major research organisms

*Link to PANGEA can be found on the sidebar of the Homepage or, for gene lists generated in FlyBase, using the HitList export menu. For more information and a video tutorial see*

*<https://www.flyrnai.org/tools/pangea/web/about>.*

- Yes
- No – but I am going to try it
- No – don't want to use it

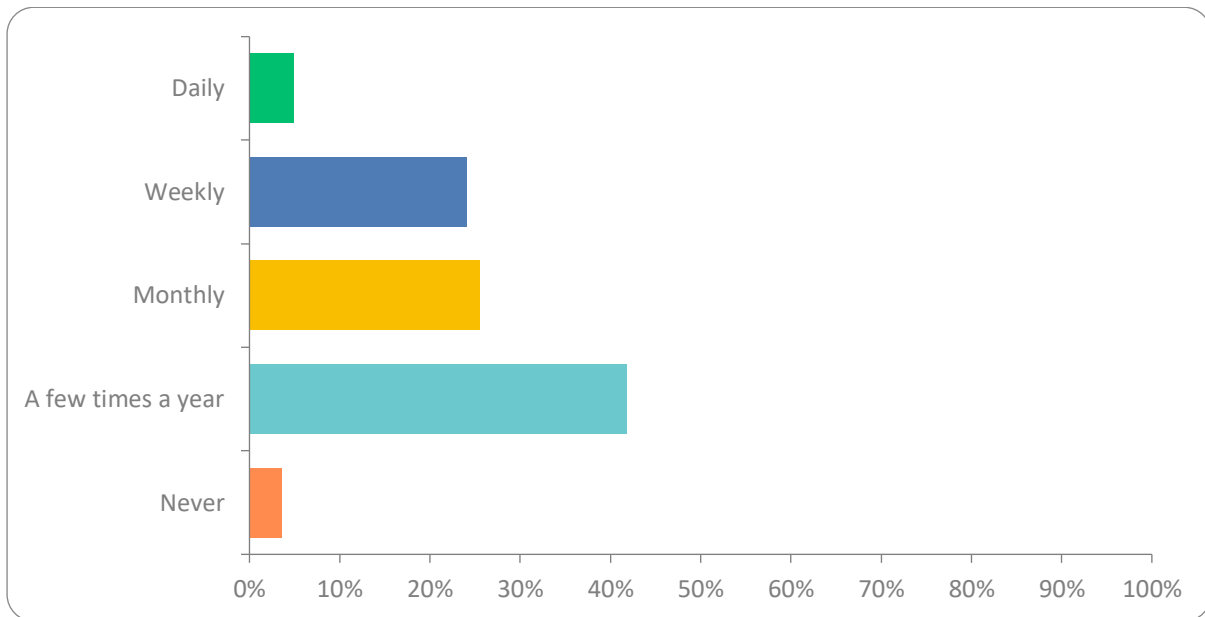


## FlyBase Gene Ontology (GO) Survey

### Responses

**Q1.** GO annotation data is available across species in many databases such as UniProtKB, FlyBase and via many bioinformatic tools. How often do you use any GO annotation data?

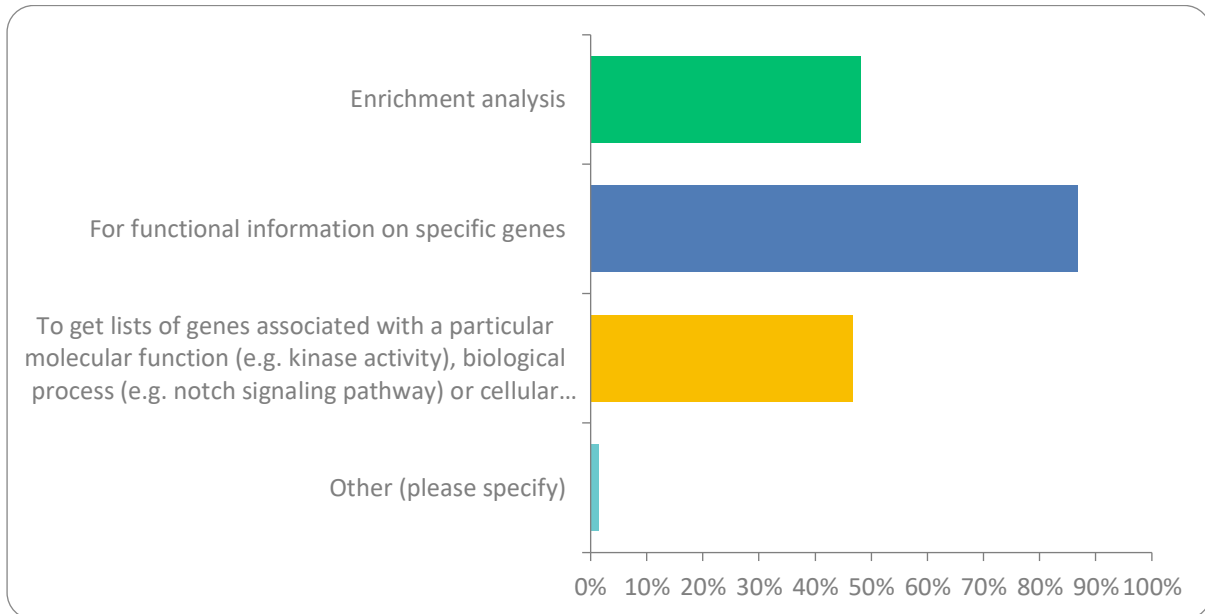
Answered: 141 Skipped: 1



ANSWER CHOICES	RESPONSES	
Daily	4.96%	7
Weekly	24.11%	34
Monthly	25.53%	36
A few times a year	41.84%	59
Never	3.55%	5
<b>TOTAL</b>		<b>141</b>

**Q2. If you use GO annotation data, how do you use it? (Tick all that apply)**

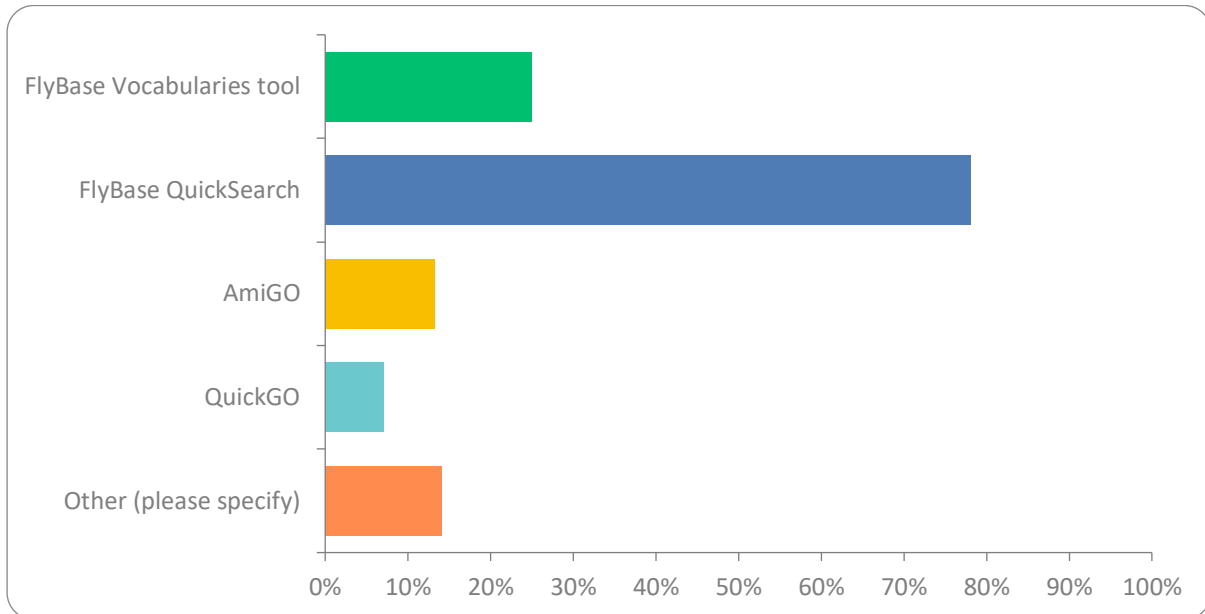
Answered: 137 Skipped: 5



ANSWER CHOICES	RESPONSES	
Enrichment analysis	48.18%	66
For functional information on specific genes	86.86%	119
To get lists of genes associated with a particular molecular function (e.g. kinase activity), biological process (e.g. notch signaling pathway) or cellular component (e.g. nucleus)?	46.72%	64
Other (please specify)	1.46%	2
<b>TOTAL</b>		<b>251</b>

**Q3. If you search GO annotation data, what search tools do you use? (Tick all that apply)**

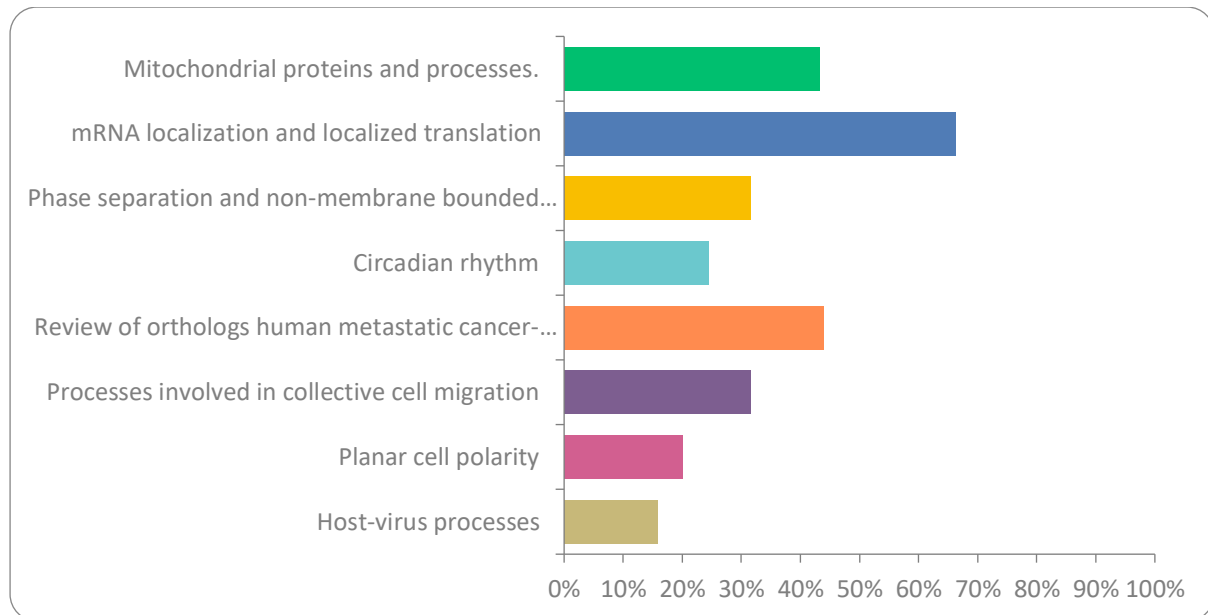
Answered: 128 Skipped: 14



ANSWER CHOICES	RESPONSES	
FlyBase Vocabularies tool	25.00%	32
FlyBase QuickSearch	78.12%	100
AmiGO	13.28%	17
QuickGO	7.03%	9
Other (please specify)	14.06%	18
<b>TOTAL</b>		<b>176</b>

**Q4.** We have grant funding (MRC, UK) to improve the ontology and GO annotation in several areas. To help with prioritization, please choose 3 of these projects.

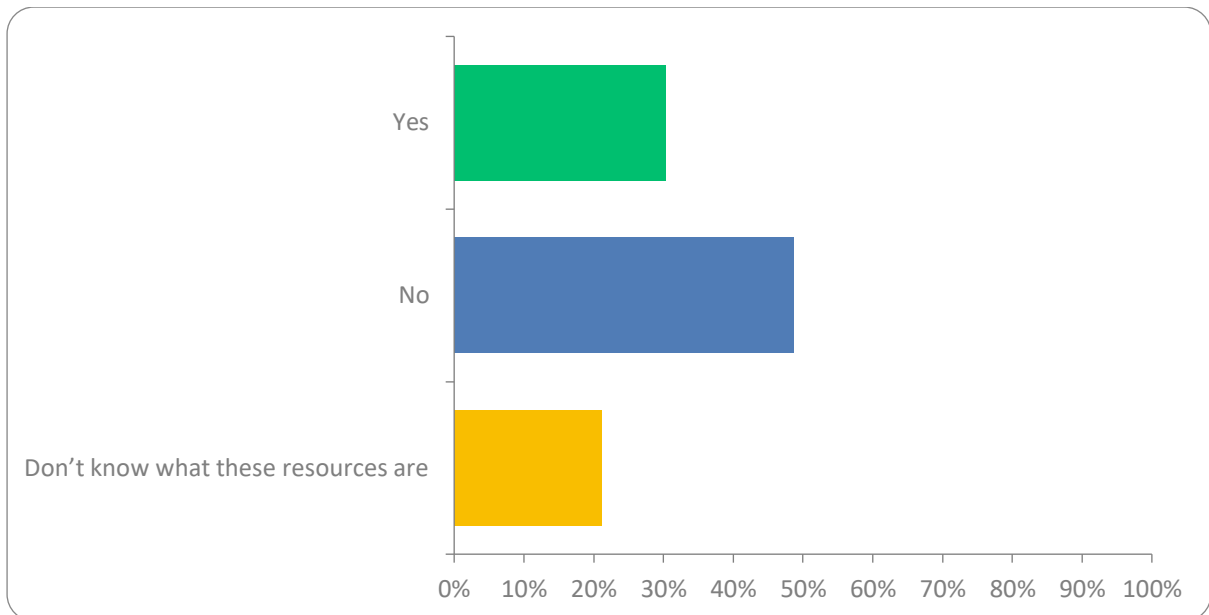
Answered: 139 Skipped: 3



ANSWER CHOICES	RESPONSES	
Mitochondrial proteins and processes.	43.17%	60
mRNA localization and localized translation	66.19%	92
Phase separation and non-membrane bounded organelles	31.65%	44
Circadian rhythm	24.46%	34
Review of orthologs human metastatic cancer-associated proteins	43.88%	61
Processes involved in collective cell migration	31.65%	44
Planar cell polarity	20.14%	28
Host-virus processes	15.83%	22
<b>TOTAL</b>		<b>385</b>

**Q5.** Do you know that GO annotation topic-directed reviews provide the basis for the FlyBase [Gene Groups](#) and [Signaling Pathways](#) resources?

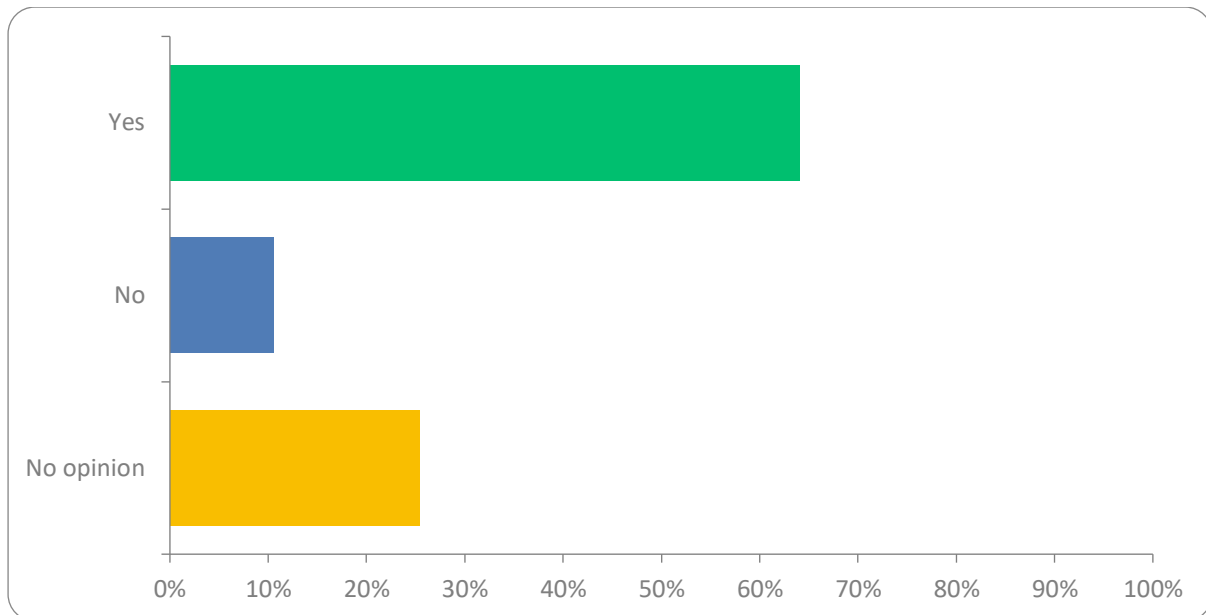
Answered: 142 Skipped: 0



ANSWER CHOICES	RESPONSES	
Yes	30.28%	43
No	48.59%	69
Don't know what these resources are	21.13%	30
<b>TOTAL</b>		<b>142</b>

**Q6. Would you find it useful to have regular updates about current GO annotation targets and projects at FlyBase?**

Answered: 142 Skipped: 0

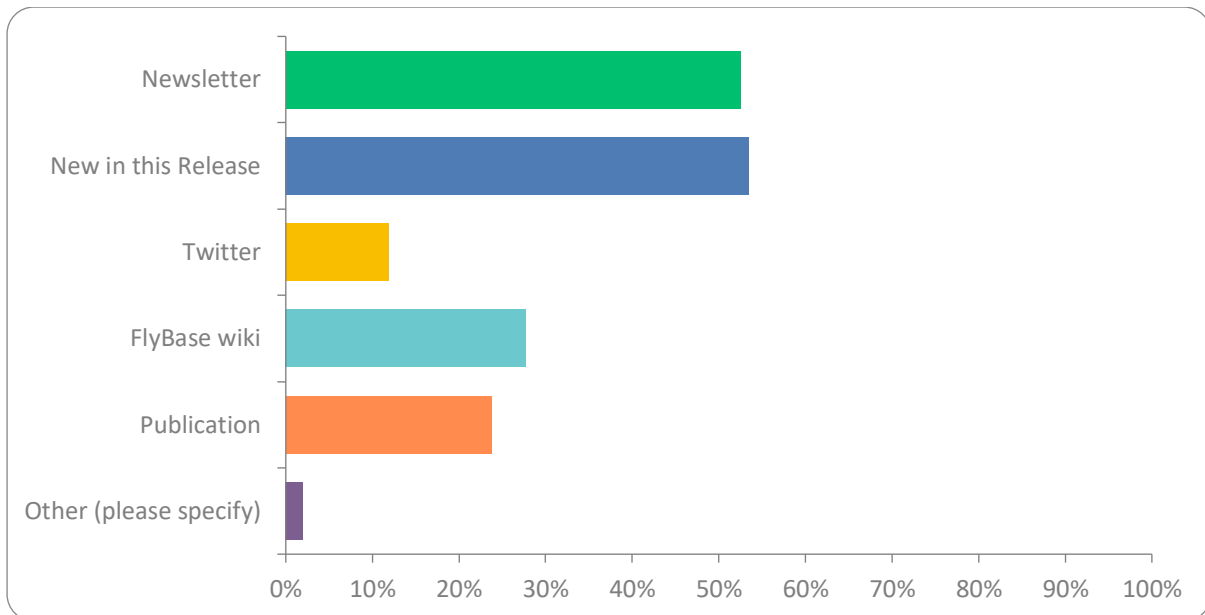


ANSWER CHOICES	RESPONSES	
Yes	64.08%	91
No	10.56%	15
No opinion	25.35%	36
<b>TOTAL</b>		<b>142</b>



**Q7. If you answered yes to Q6, how would you prefer us to communicate this information?  
(chose 1-3 options)**

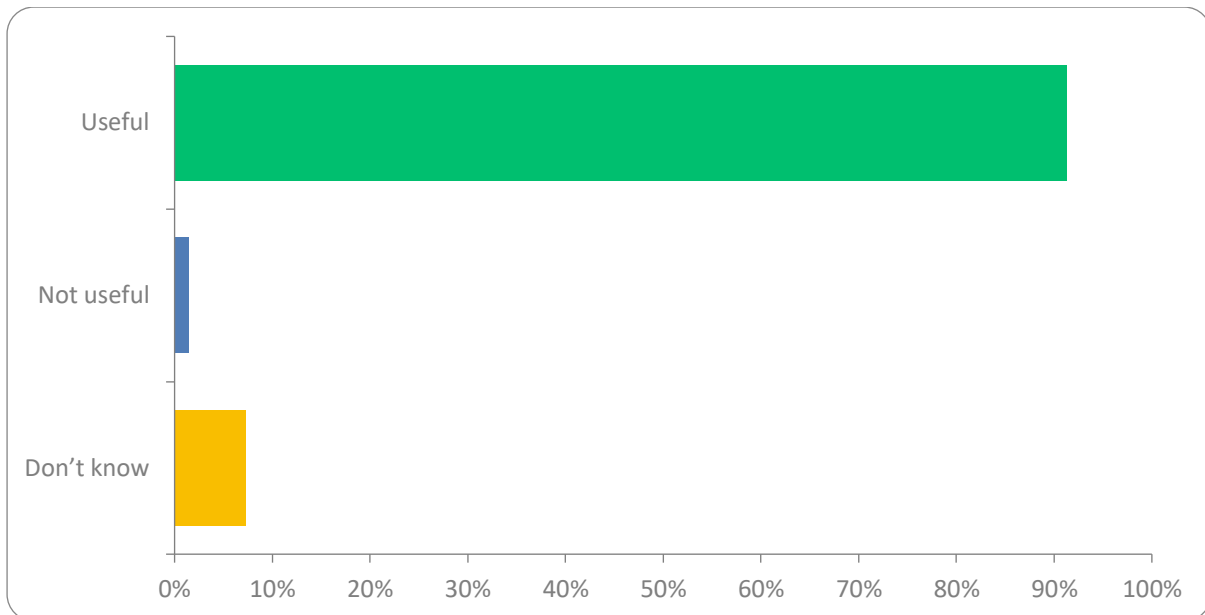
Answered: 101 Skipped: 41



ANSWER CHOICES	RESPONSES	
Newsletter	52.48%	53
New in this Release	53.47%	54
Twitter	11.88%	12
FlyBase wiki	27.72%	28
Publication	23.76%	24
Other (please specify)	1.98%	2
<b>TOTAL</b>		<b>173</b>

**Q8.** As shown above, GO ribbons provide a high-level overview on Gene, Gene group and Signaling pathway pages. Do you think these ribbons are:

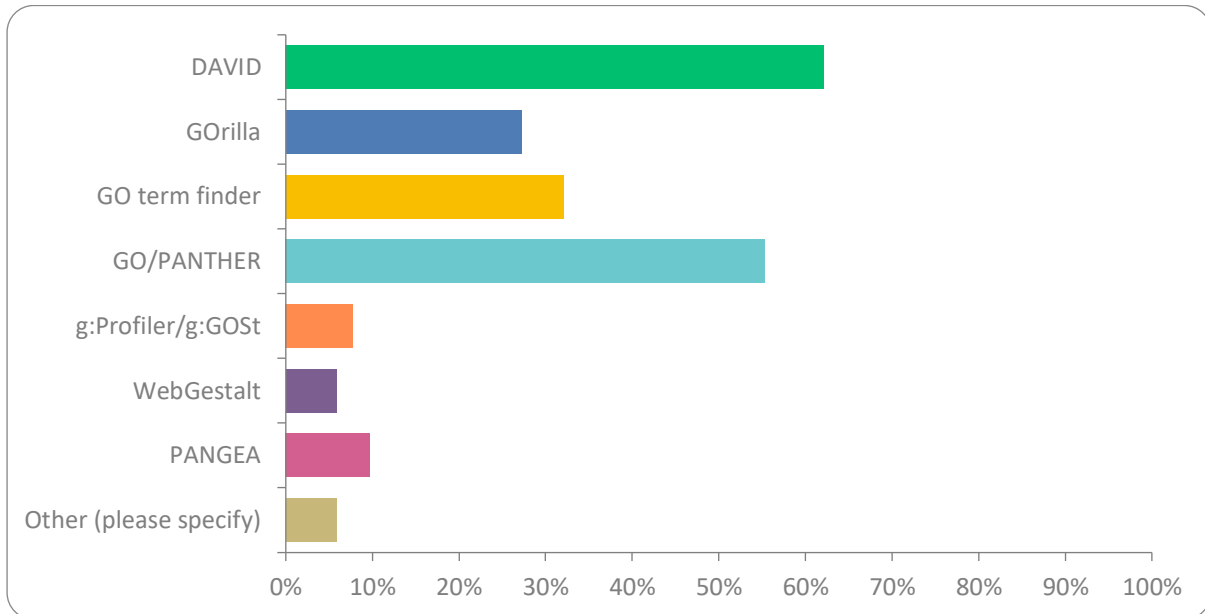
Answered: 138 Skipped: 4



ANSWER CHOICES	RESPONSES	
Useful	91.30%	126
Not useful	1.45%	2
Don't know	7.25%	10
<b>TOTAL</b>		<b>138</b>

**Q9. Have you used any of these Enrichment Tools? (tick as many as apply)**

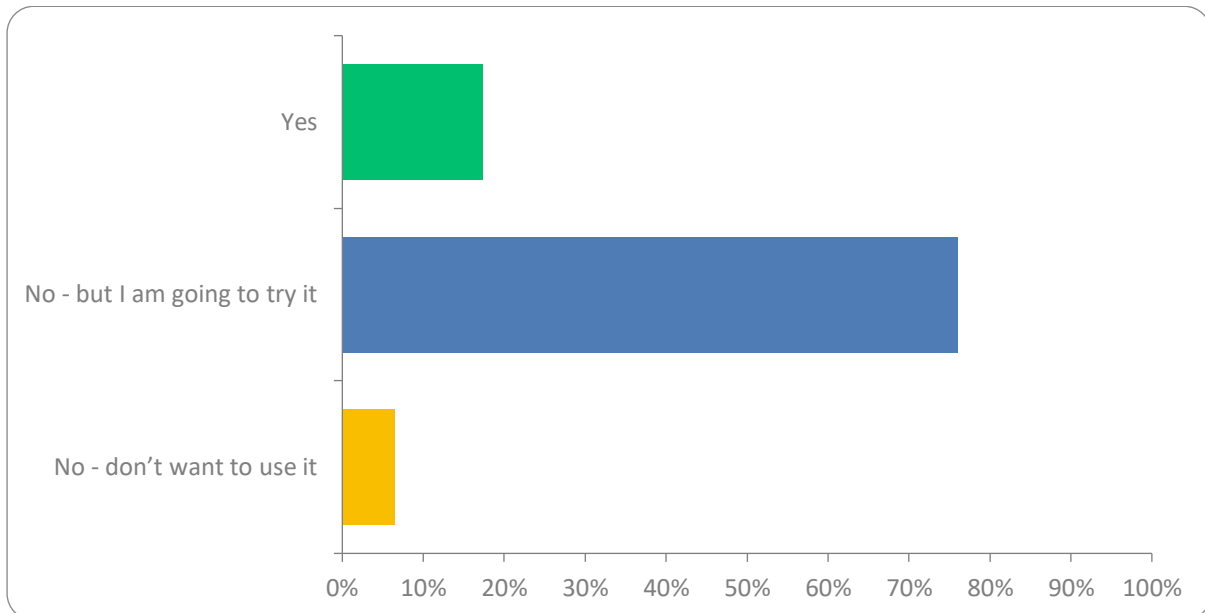
Answered: 103 Skipped: 39



ANSWER CHOICES	RESPONSES	
DAVID	62.14%	64
GOrilla	27.18%	28
GO term finder	32.04%	33
GO/PANTHER	55.34%	57
g:Profiler/g:GOS	7.77%	8
WebGestalt	5.83%	6
PANGEA	9.71%	10
Other (please specify)	5.83%	6
<b>TOTAL</b>		<b>212</b>

**Q10.** Have you heard of [PANGEA](https://www.flyrnai.org/tools/pangea/web/about) - an enrichment tool developed by the DRSC and FlyBase? Link to PANGEA can be found on the sidebar of the Homepage or, for gene lists generated in FlyBase, using the HitList export menu. For more information and a video tutorial see <https://www.flyrnai.org/tools/pangea/web/about>.

Answered: 138 Skipped: 4



ANSWER CHOICES	RESPONSES	
Yes	17.39%	24
No - but I am going to try it	76.09%	105
No - don't want to use it	6.52%	9
<b>TOTAL</b>		<b>138</b>