



FlyBase *Drosophila* Metabolic  
Pathways Survey

## Survey Summary Sep 2022



## FlyBase *Drosophila* Metabolic Pathways Survey

### Introduction

We are currently writing a grant proposal which will, if successful, improve metabolic pathway resources for *Drosophila*. Please help us to understand the current needs of researchers in this field by answering the following questions.



## FlyBase *Drosophila* Metabolic Pathways Survey

### Questions

\* 1. Do you (or does your lab) work on *Drosophila* metabolism?

- Yes, it's the focus
- Yes, in part / sometimes
- No

\* 2. Which resources do you currently use to view *Drosophila* metabolic pathways? (Check all that apply)

- [KEGG](#)
- [BioCyc \(FlyCyc\)](#)
- [Reactome](#)
- None
- Other (please specify)

\* 3. Have you used the links on FlyBase gene pages to metabolic pathway pages at KEGG, BioCyc or Reactome? (e.g. see the [Pfk](#) report)

- Yes
- No, but I will now you've told me about them!
- No

\* 4. Are the current resources for viewing *Drosophila* metabolic pathways sufficient for your work?

- Yes
- No

\* 5. Rank the importance of the following (potential) features of a *Drosophila* metabolic pathway resource.

- The resource is specific for *Drosophila* (i.e. pathway components not relevant to *Drosophila* are excluded, whereas *Drosophila*-specific aspects are highlighted)
- Free and unrestricted access
- Genes/gene products are labeled with fly gene symbols
- Enzymes/reactions are labeled with Enzyme Commission (EC) numbers
- Chemical structures of metabolites are shown/accessible
- Pathways are manually curated/reviewed using available experimental evidence in flies, rather than computed entirely by orthology
- Integration with FlyBase, allowing direct access to related data, stocks, tools etc.
- Equivalent pathways at alternative resources are easily accessed/compared
- Pathways are linked to related metabolomic datasets
- Tissue/cell-specific pathways are included
- Paralogs of metabolic genes are included
- Pathway data (e.g. experimental evidence, gene symbols) are kept up to date
- Pathways are underpinned by, and linked to, Gene Ontology (GO) annotations

- Other (please rank here and specify in the box below)

**6. Do you have any other comments/suggestions about the provision of metabolic pathway resources for *Drosophila*?**

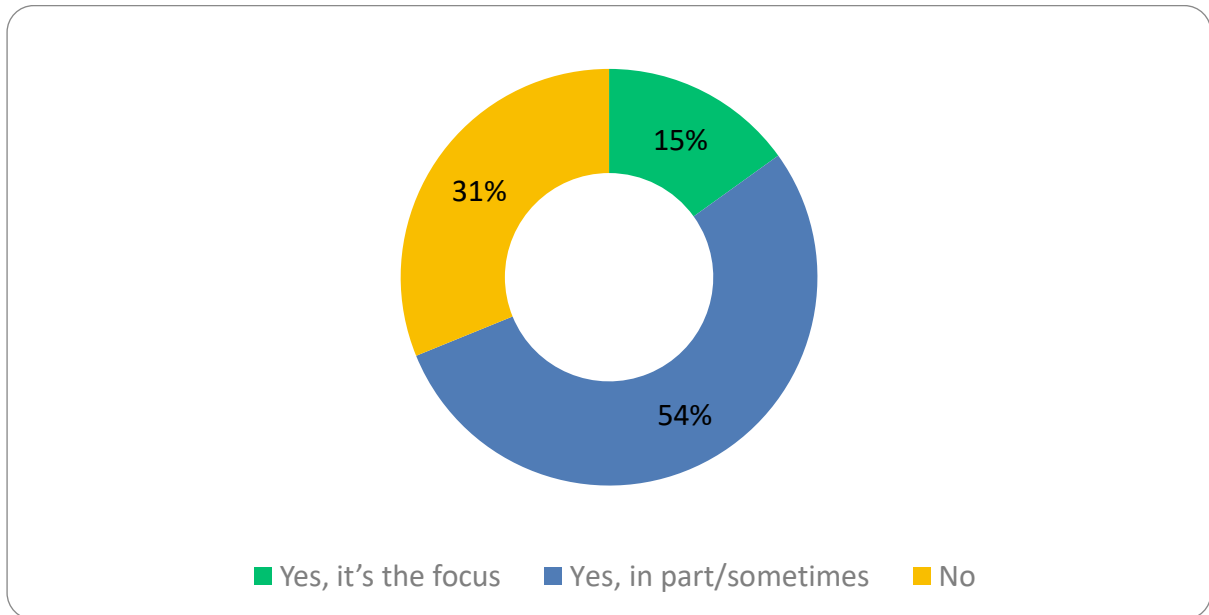


# FlyBase *Drosophila* Metabolic Pathways Survey

## Responses

### Q1: Do you (or does your lab) work on *Drosophila* metabolism?

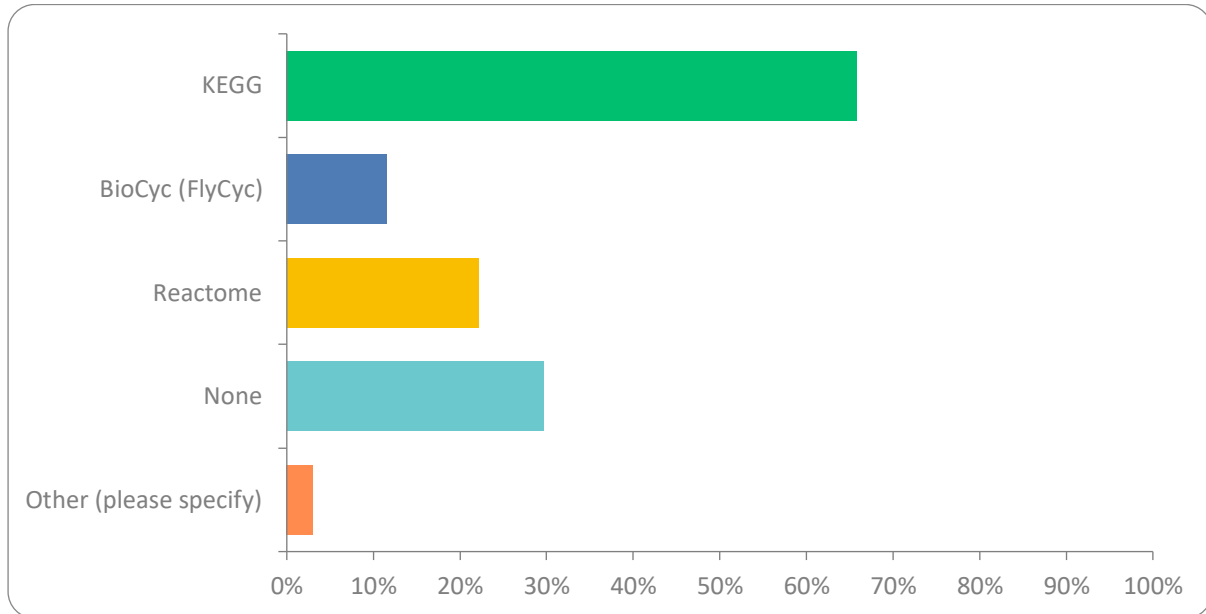
Answered: 199 Skipped: 0



ANSWER CHOICES	RESPONSES	
Yes, it's the focus	15.08%	30
Yes, in part/sometimes	53.77%	107
No	31.16%	62
TOTAL		199

**Q2: Which resources do you currently use to view *Drosophila* metabolic pathways?  
(Check all that apply)**

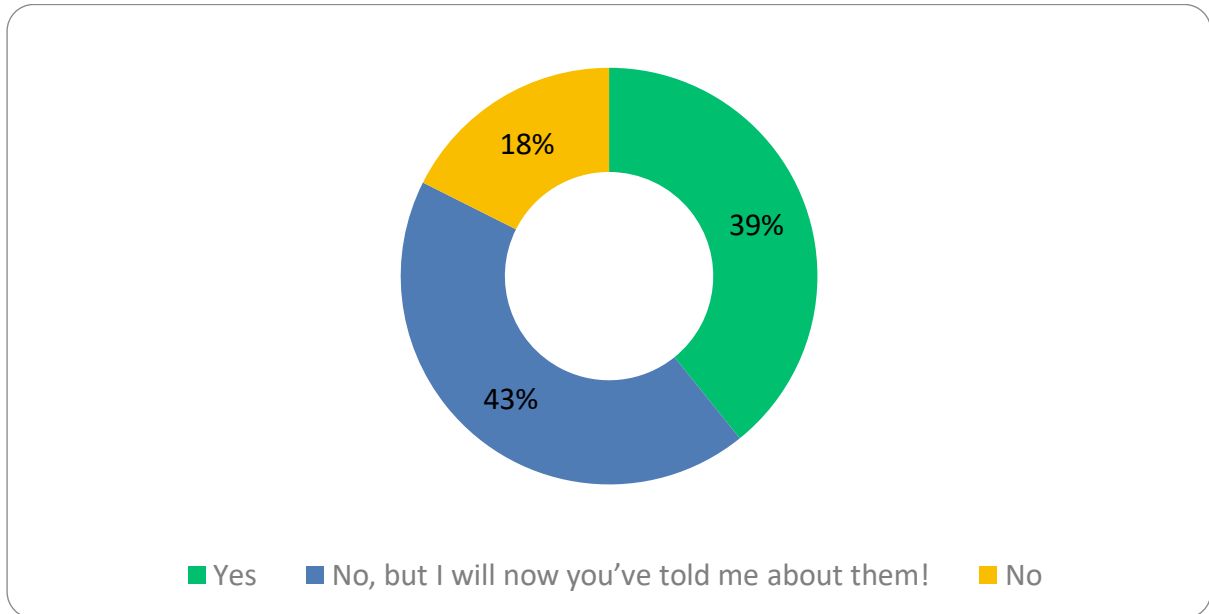
Answered: 199 Skipped: 0



ANSWER CHOICES	RESPONSES	
KEGG	65.83%	131
BioCyc (FlyCyc)	11.56%	23
Reactome	22.11%	44
None	29.65%	59
Other (please specify)	3.02%	6
<b>TOTAL</b>		<b>263</b>

**Q3: Have you used the links on FlyBase gene pages to metabolic pathway pages at KEGG, BioCyc or Reactome? (e.g. see the [Pfk](#) report)**

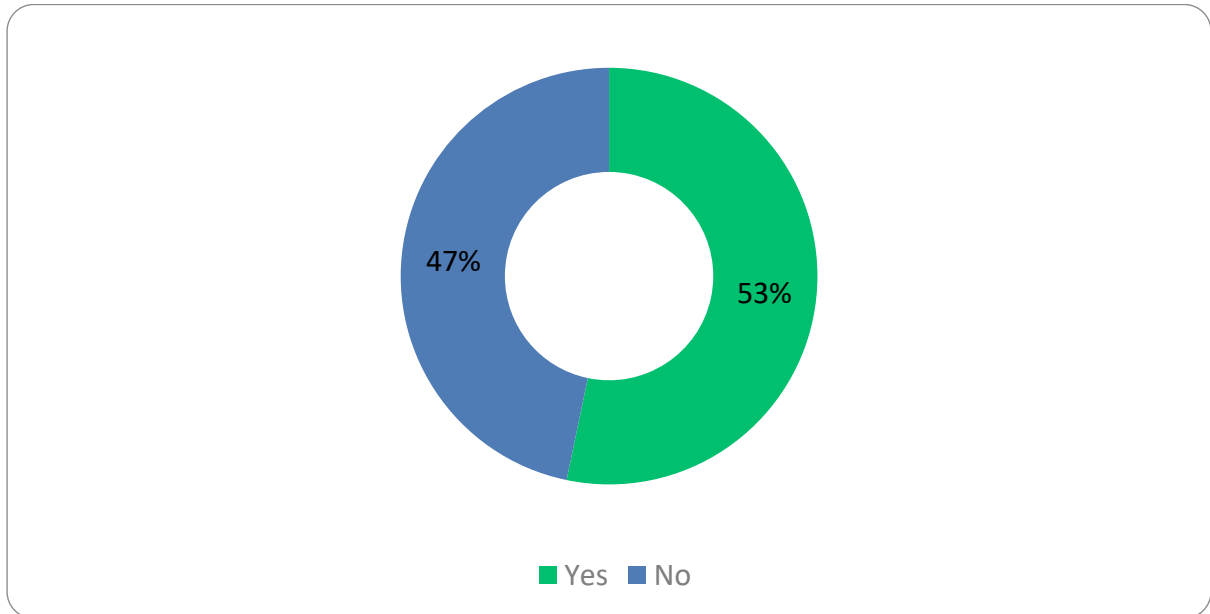
Answered: 199 Skipped: 0



ANSWER CHOICES	RESPONSES	
Yes	39.20%	78
No, but I will now you've told me about them!	43.22%	86
No	17.59%	35
TOTAL		199

**Q4: Are the current resources for viewing *Drosophila* metabolic pathways sufficient for your work?**

Answered: 199 Skipped: 0

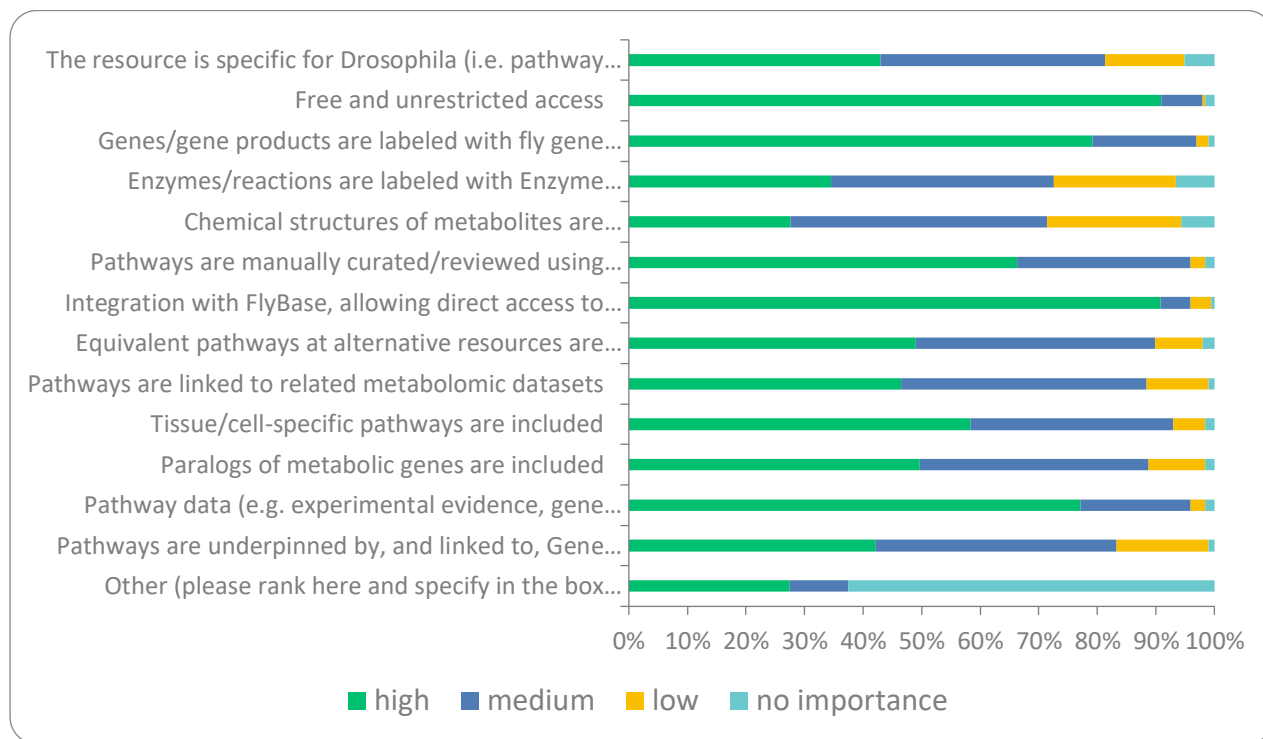


ANSWER CHOICES	RESPONSES	
Yes	53.27%	106
No	46.73%	93
TOTAL		199



**Q5: Rank the importance of the following (potential) features of a *Drosophila* metabolic pathway resource.**

Answered: 199 Skipped: 0



	HIGH	MEDIUM	LOW	NO IMPORTANCE
The resource is specific for <i>Drosophila</i> (i.e. pathway components not relevant to <i>Drosophila</i> are excluded, whereas <i>Drosophila</i> -specific aspects are highlighted)	42.93% 85	38.38% 76	13.64% 27	5.05% 10
Free and unrestricted access	90.91% 180	7.07% 14	0.51% 1	1.52% 3
Genes/gene products are labeled with fly gene symbols	79.19% 156	17.77% 35	2.03% 4	1.02% 2
Enzymes/reactions are labeled with Enzyme Commission (EC) numbers	34.52% 68	38.07% 75	20.81% 41	6.60% 13
Chemical structures of metabolites are shown/accessible	27.55% 54	43.88% 86	22.96% 45	5.61% 11
Pathways are manually curated/reviewed using available experimental evidence in flies, rather than computed entirely by orthology	66.33% 130	29.59% 58	2.55% 5	1.53% 3
Integration with FlyBase, allowing direct access to related data, stocks, tools etc.	90.86% 179	5.08% 10	3.55% 7	0.51% 1

Equivalent pathways at alternative resources are easily accessed/compared	48.99% 97	40.91% 81	8.08% 16	2.02% 4
Pathways are linked to related metabolomic datasets	46.46% 92	41.92% 83	10.61% 21	1.01% 2
Tissue/cell-specific pathways are included	58.29% 116	34.67% 69	5.53% 11	1.51% 3
Paralogs of metabolic genes are included	49.74% 97	38.97% 76	9.74% 19	1.54% 3
Pathway data (e.g. experimental evidence, gene symbols) are kept up to date	77.16% 152	18.78% 37	2.54% 5	1.52% 3
Pathways are underpinned by, and linked to, Gene Ontology (GO) annotations	42.13% 83	41.12% 81	15.74% 31	1.02% 2
Other (please rank here and specify in the box below)	27.50% 11	10.0% 4	0% 0	62.50% 25