Q1 How often do you use FlyBase?

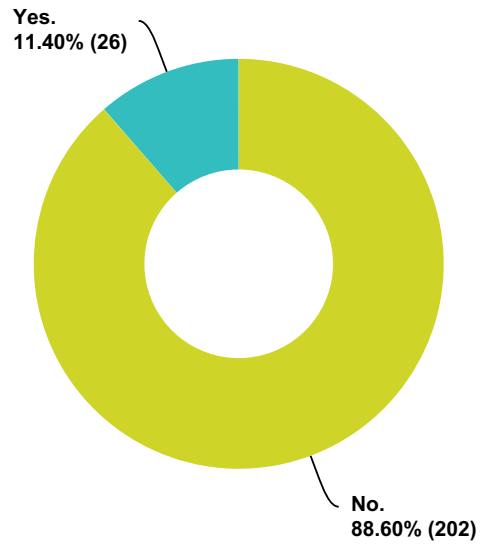**Answered: 235   Skipped: 3**
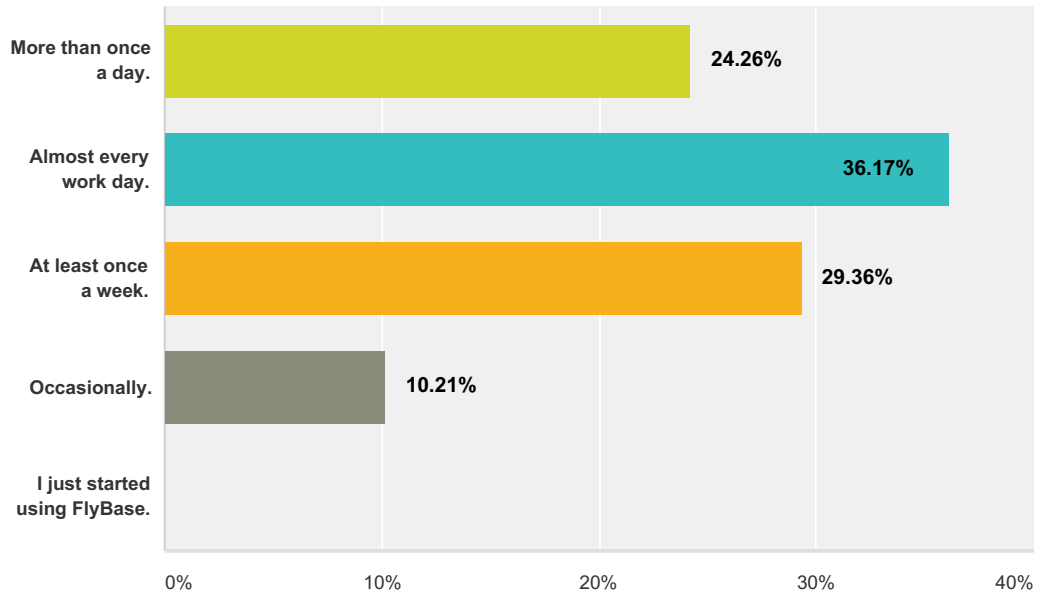
Answer Choices	Responses	
More than once a day.	**24.26%**	57
Almost every work day.	**36.17%**	85
At least once a week.	**29.36%**	69
Occasionally.	**10.21%**	24
I just started using FlyBase.	**0.00%**	0
Total		**235**

Q2 Could question 1 be improved?

Answered: 228   Skipped: 10

Yes.
11.40% (26)

No.
88.60% (202)

Answer Choices	Responses	
No.	**88.60%**	202
Yes.	**11.40%**	26
Total		**228**

Q3 What role does FlyBase play in these activities?

Answered: 205   Skipped: 33
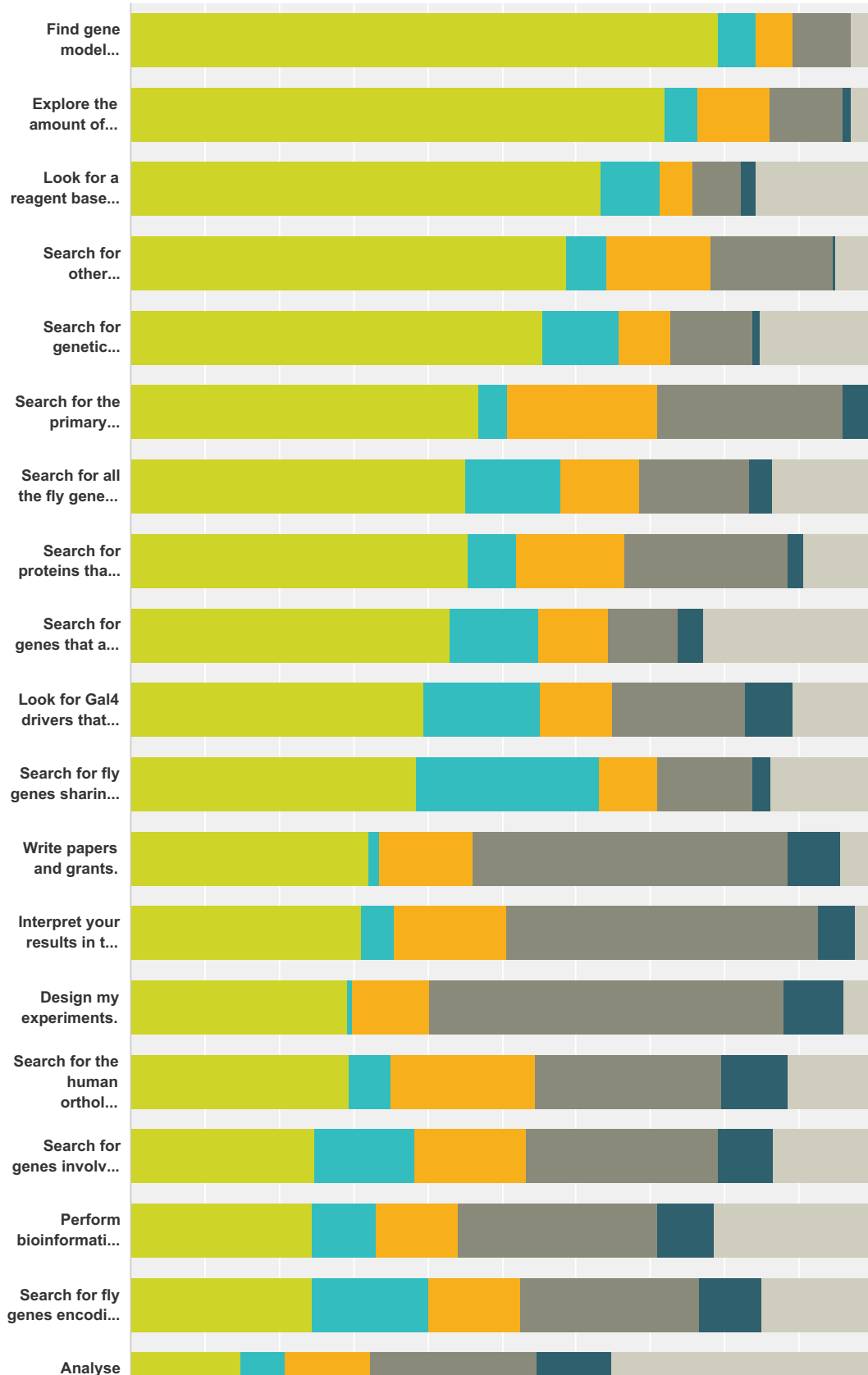
2016 General FlyBase survey
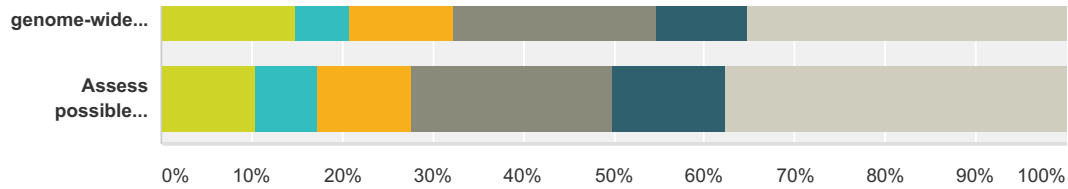
Legend:
- I need FlyBase to do this, and easily find the information I need.
- I need FlyBase to do this, but have difficulty finding the information I need.
- I generally do this with FlyBase, but can also do it with other resources.
- I use a variety of resources to do this, including FlyBase.
- I use another resource to do this.
- I do not do this type of work.

	I need FlyBase to do this, and easily find the information I need.	I need FlyBase to do this, but have difficulty finding the information I need.	I generally do this with FlyBase, but can also do it with other resources.	I use a variety of resources to do this, including FlyBase.	I use another resource to do this.	I do not do this type of work.	Total
Find gene model information for a gene, including alternative transcript and proteins.	79.21% 160	4.95% 10	4.95% 10	7.92% 16	0.00% 0	2.97% 6	202
Explore the amount of knowledge and reagents available for a gene.	71.92% 146	4.43% 9	9.85% 20	9.85% 20	0.99% 2	2.96% 6	203
Look for a reagent based on genomic location.	63.37% 128	7.92% 16	4.46% 9	6.44% 13	1.98% 4	15.84% 32	202
Search for other Drosophila resources.	58.71% 118	5.47% 11	13.93% 28	16.42% 33	0.50% 1	4.98% 10	201
Search for genetic interactions between mutant alleles.	55.56% 110	10.10% 20	7.07% 14	11.11% 22	1.01% 2	15.15% 30	198
Search for the primary research papers studying a particular gene.	46.80% 95	3.94% 8	20.20% 41	25.12% 51	3.94% 8	0.00% 0	203
Search for all the fly genes encoding a particular kind of protein, e.g. tubulins.	45.10% 92	12.75% 26	10.78% 22	14.71% 30	2.94% 6	13.73% 28	204
Search for proteins that interact with a given fly gene's protein product.	45.50% 91	6.50% 13	14.50% 29	22.00% 44	2.00% 4	9.50% 19	200
Search for genes that are expressed with a similar temporal profile during development.	43.07% 87	11.88% 24	9.41% 19	9.41% 19	3.47% 7	22.77% 46	202
Look for Gal4 drivers that drive expression in a particular tissue.	39.41% 80	15.76% 32	9.85% 20	17.73% 36	6.40% 13	10.84% 22	203

Search for fly genes sharing a particular phenotype.	**38.42%** 78	**24.63%** 50	**7.88%** 16	**12.81%** 26	**2.46%** 5	**13.79%** 28	203
Write papers and grants.	**32.00%** 64	**1.50%** 3	**12.50%** 25	**42.50%** 85	**7.00%** 14	**4.50%** 9	200
Interpret your results in the context of current knowledge.	**31.03%** 63	**4.43%** 9	**15.27%** 31	**41.87%** 85	**4.93%** 10	**2.46%** 5	203
Design my experiments.	**29.35%** 59	**0.50%** 1	**10.45%** 21	**47.76%** 96	**7.96%** 16	**3.98%** 8	201
Search for the human ortholog of a Drosophila gene.	**29.50%** 59	**5.50%** 11	**19.50%** 39	**25.00%** 50	**9.00%** 18	**11.50%** 23	200
Search for genes involved in a particular biological process, e.g. cell death.	**24.88%** 50	**13.43%** 27	**14.93%** 30	**25.87%** 52	**7.46%** 15	**13.43%** 27	201
Perform bioinformatic analysis of Drosophila genes.	**24.50%** 49	**8.50%** 17	**11.00%** 22	**27.00%** 54	**7.50%** 15	**21.50%** 43	200
Search for fly genes encoding a protein with a particular domain.	**24.50%** 49	**15.50%** 31	**12.50%** 25	**24.00%** 48	**8.50%** 17	**15.00%** 30	200
Analyse genome-wide data sets.	**14.93%** 30	**5.97%** 12	**11.44%** 23	**22.39%** 45	**9.95%** 20	**35.32%** 71	201
Assess possible functions of Human genes, e.g. GWAS candidates.	**10.40%** 21	**6.93%** 14	**10.40%** 21	**22.28%** 45	**12.38%** 25	**37.62%** 76	202

Q4 Is there a better way to phrase the possible roles that FlyBase plays?

Answered: 196   Skipped: 42

Yes.
15.31% (30)

No.
84.69% (166)
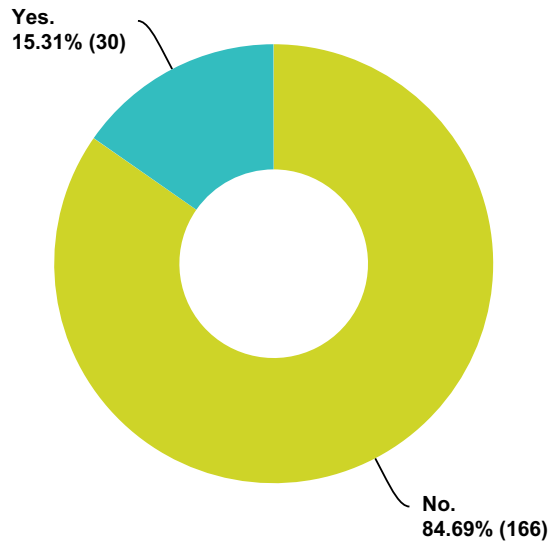
Answer Choices	Responses	
No.	84.69%	166
Yes.	15.31%	30
Total		**196**

Q5 Do you have any other suggestions for how to improve question 3?

Answered: 195   Skipped: 43

Yes.
12.82% (25)

No.
87.18% (170)
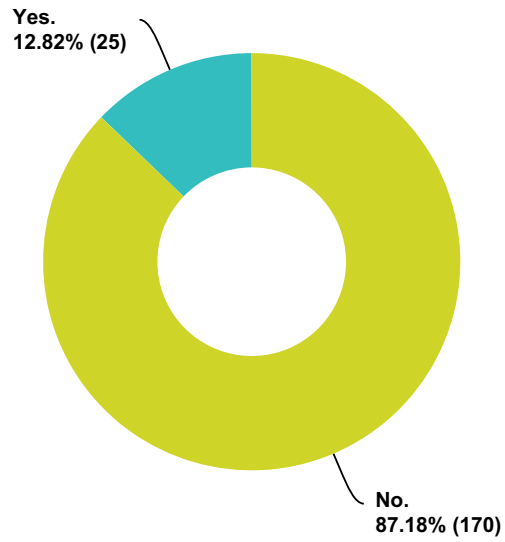
Answer Choices	Responses	
No.	**87.18%**	170
Yes.	**12.82%**	25
Total		195

Q6 Please give us feedback on these recent additions to FlyBase:

Answered: 195   Skipped: 43
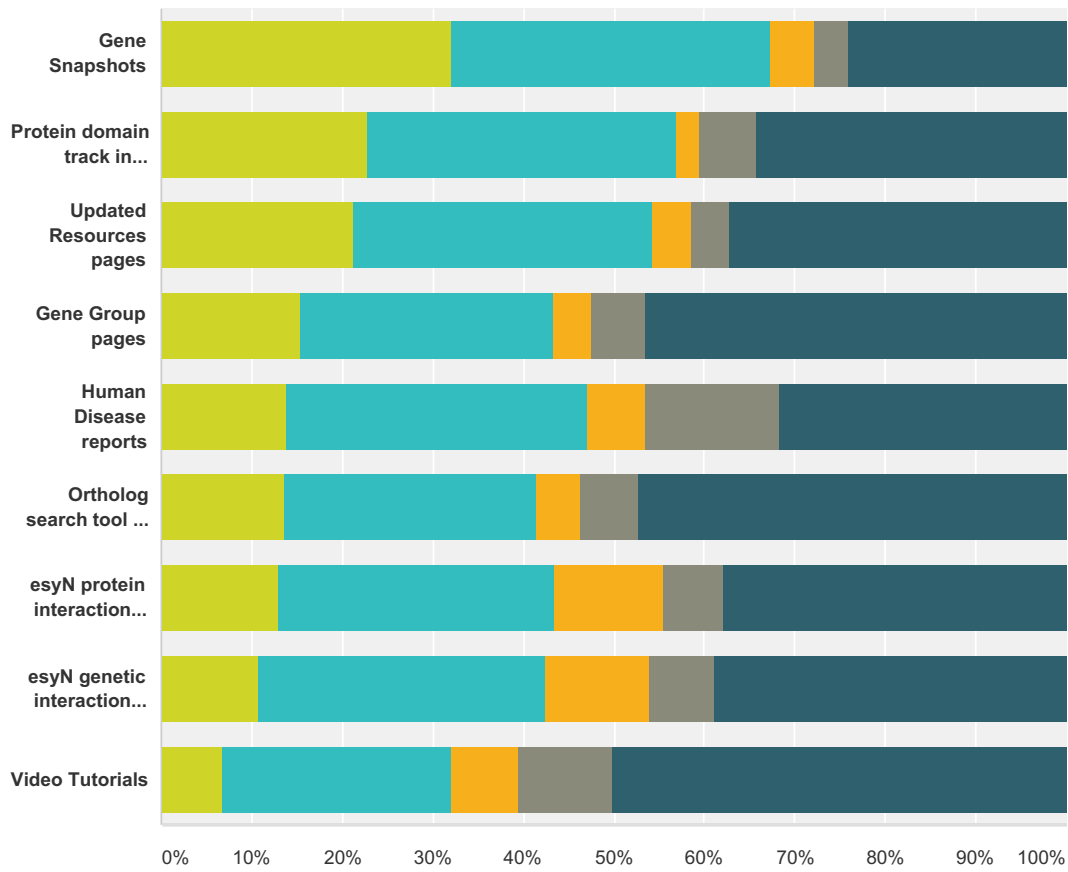
- ▮ This is great, I find it very helpful and use it frequently.
- ▮ This is great, I find it very helpful and use it occasionally.
- ▮ This would be very valuable, but needs improvement.   ▮ I would not use this in my work.
- ▮ I had not noticed that this had been added, but it looks useful.

	This is great, I find it very helpful and use it frequently.	This is great, I find it very helpful and use it occasionally.	This would be very valuable, but needs improvement.	I would not use this in my work.	I had not noticed that this had been added, but it looks useful.	Total	Weighted Average
Gene Snapshots	**32.09%** 60	**35.29%** 66	**4.81%** 9	**3.74%** 7	**24.06%** 45	187	2.52
Protein domain track in Gbrowse	**22.80%** 44	**34.20%** 66	**2.59%** 5	**6.22%** 12	**34.20%** 66	193	2.95
Updated Resources pages	**21.24%** 41	**33.16%** 64	**4.15%** 8	**4.15%** 8	**37.31%** 72	193	3.03

Gene Group pages	**15.51%** 29	**27.81%** 52	**4.28%** 8	**5.88%** 11	**46.52%** 87	187	3.40
Human Disease reports	**13.76%** 26	**33.33%** 63	**6.35%** 12	**14.81%** 28	**31.75%** 60	189	3.17
Ortholog search tool via DIOPT	**13.68%** 26	**27.89%** 53	**4.74%** 9	**6.32%** 12	**47.37%** 90	190	3.46
esyN protein interaction diagram	**12.95%** 25	**30.57%** 59	**11.92%** 23	**6.74%** 13	**37.82%** 73	193	3.26
esyN genetic interaction diagram	**10.88%** 21	**31.61%** 61	**11.40%** 22	**7.25%** 14	**38.86%** 75	193	3.32
Video Tutorials	**6.84%** 13	**25.26%** 48	**7.37%** 14	**10.53%** 20	**50.00%** 95	190	3.72

Q7 Could question 6 be improved?

Yes.
9.73% (18)

No.
90.27% (167)
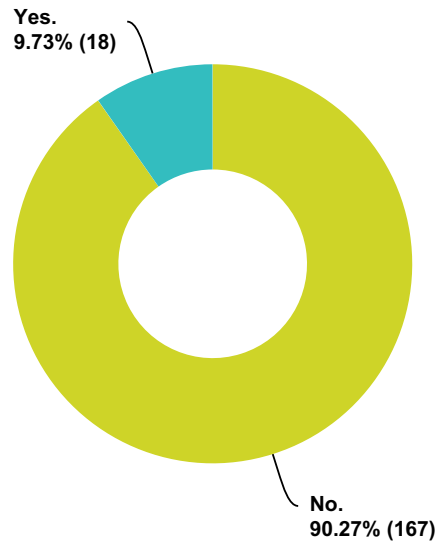
Answer Choices	Responses	
No.	**90.27%**	167
Yes.	**9.73%**	18
Total		**185**

Q8 Have you used the contact FlyBase form?

Answered: 198   Skipped: 40

Yes.
26.26% (52)

No.
73.74% (146)
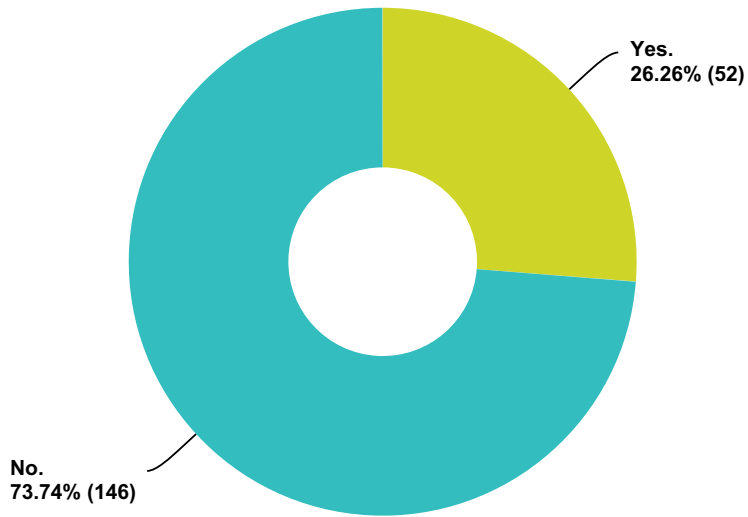
Answer Choices	Responses	
Yes.	**26.26%**	52
No.	**73.74%**	146
Total		**198**

Q9 What were the reasons you contacted FlyBase?

Answered: 53   Skipped: 185

Q10 Were you satisfied with the:

Answered: 66   Skipped: 172
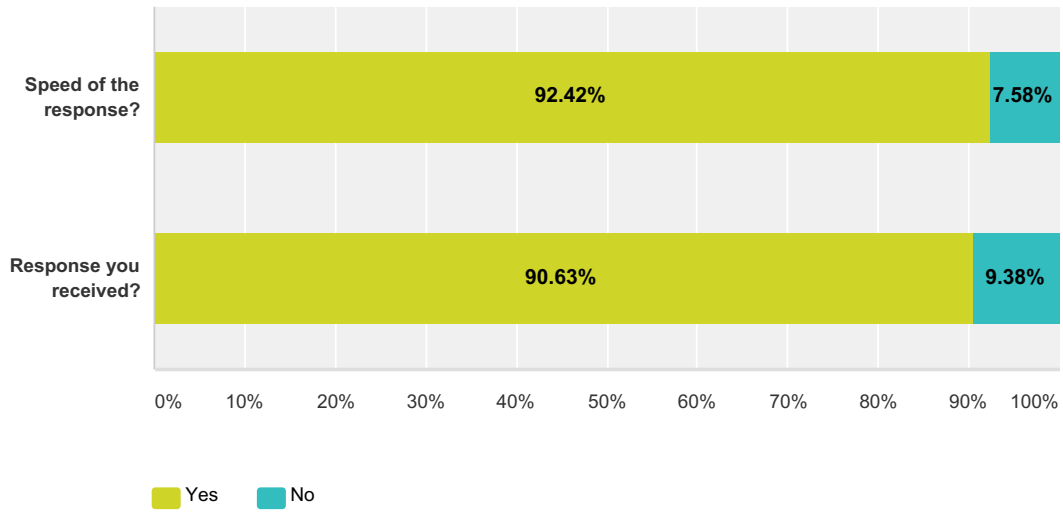
	Yes	No	Total	Weighted Average
Speed of the response?	**92.42%** 61	**7.58%** 5	66	1.08
Response you received?	**90.63%** 58	**9.38%** 6	64	1.09

13 / 25

Q11 Could questions 8-10 be improved?

Answered: 166   Skipped: 72

Yes.
9.04% (15)

No.
90.96% (151)
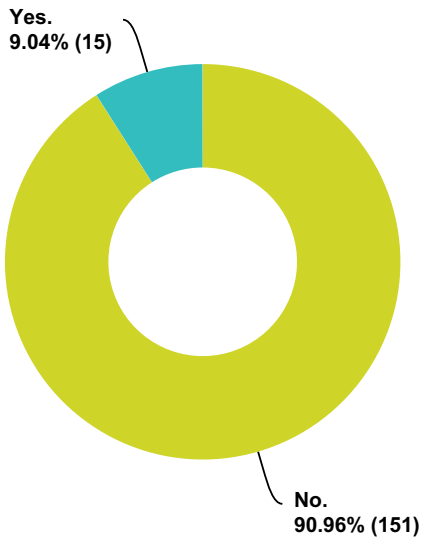
Answer Choices	Responses	
No.	**90.96%**	151
Yes.	**9.04%**	15
Total		**166**

Q12 Here is a list of possible additions to FlyBase that we are considering for the future. Please select up to 3 that would provide the greatest benefit for the work in your lab.

Answered: 192   Skipped: 46
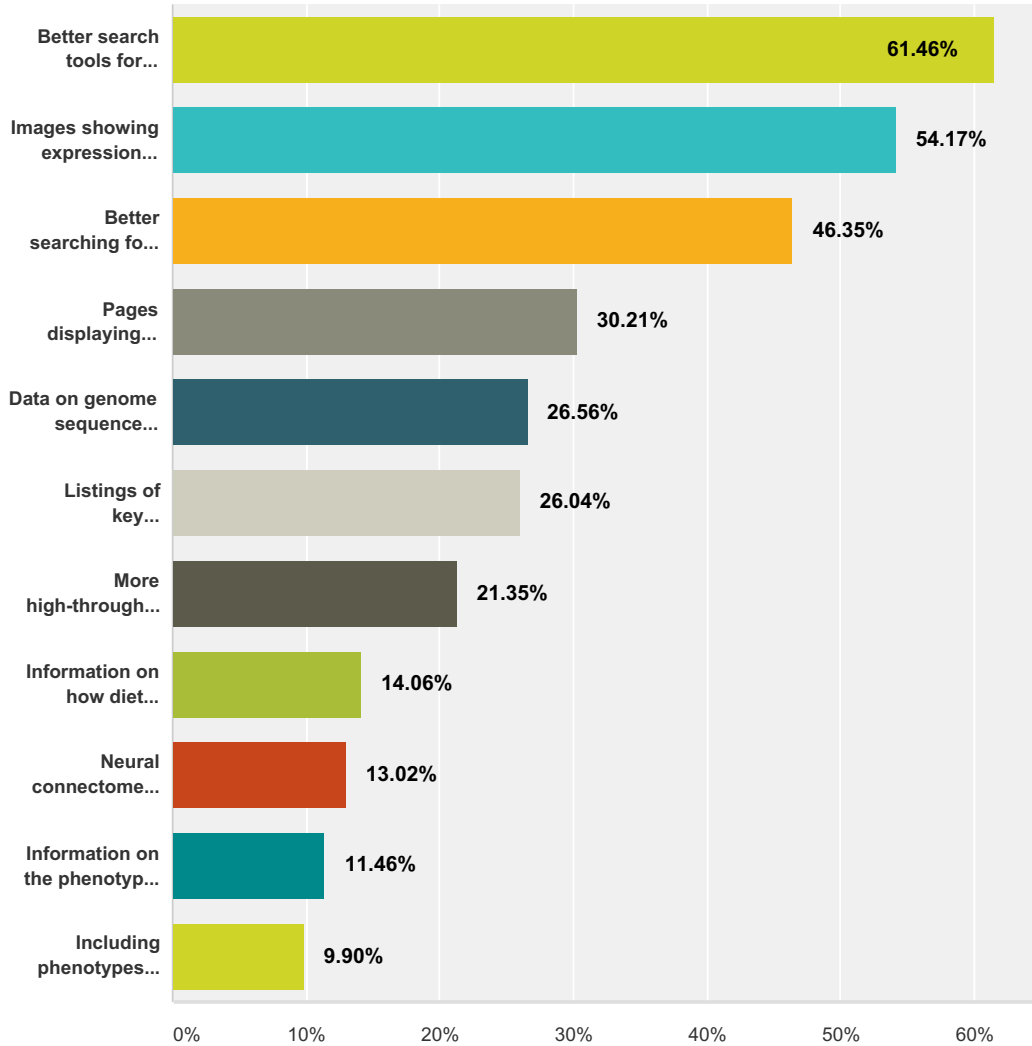
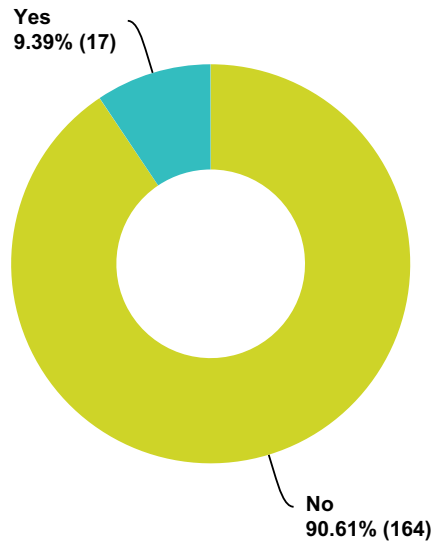| Answer Choices		Responses
Better search tools for finding GAL4 lines expressed in particular tissues.	**61.46%**	118
Images showing expression patterns.	**54.17%**	104
Better searching for genes having a specific mutant phenotype (e.g. wing notches).	**46.35%**	89
Pages displaying signalling pathways.	**30.21%**	58
Data on genome sequence variations from natural populations of D. melanogaster.	**26.56%**	51
Listings of key high-throughput studies for a gene, organised by assay, cell type, etc...	**26.04%**	50

|		
More high-throughput ChIP-Seq data in GBrowse.	**21.35%**	41
Information on how diet affects signaling pathways and/or longevity.	**14.06%**	27
Neural connectome data.	**13.02%**	25
Information on the phenotypic effects of drug treatments.	**11.46%**	22
Including phenotypes caused by inactivating or activating specific neurons.	**9.90%**	19
Total Respondents: 192		

Q13 Could question 12 be improved?

Answered: 181   Skipped: 57

**Yes
9.39% (17)**

**No
90.61% (164)**

Answer Choices	Responses	
No	**90.61%**	164
Yes	**9.39%**	17
Total		**181**

Q14 FlyBase, several of the other major NHGRI-funded model organism databases (MODs, including Saccharomyces Genome Database, WormBase, Zebrafish Model Organism Database, Mouse Genome Database and Rat Genome Database), and the GO Consortium are beginning a project to produce a consolidated web resource (called the Alliance of Genome Resources -- AGR) that provides improved cross-organism querying and report functionality. In this context, please indicate the utility to your work of each of the following cross-organism queries or reports we're considering implementing for the first release of the AGR:
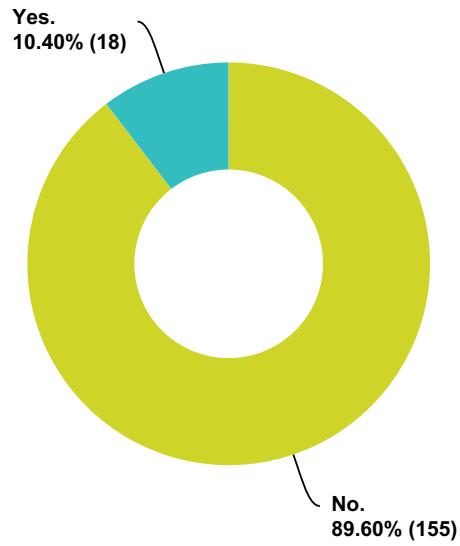
Answered: 189   Skipped: 49
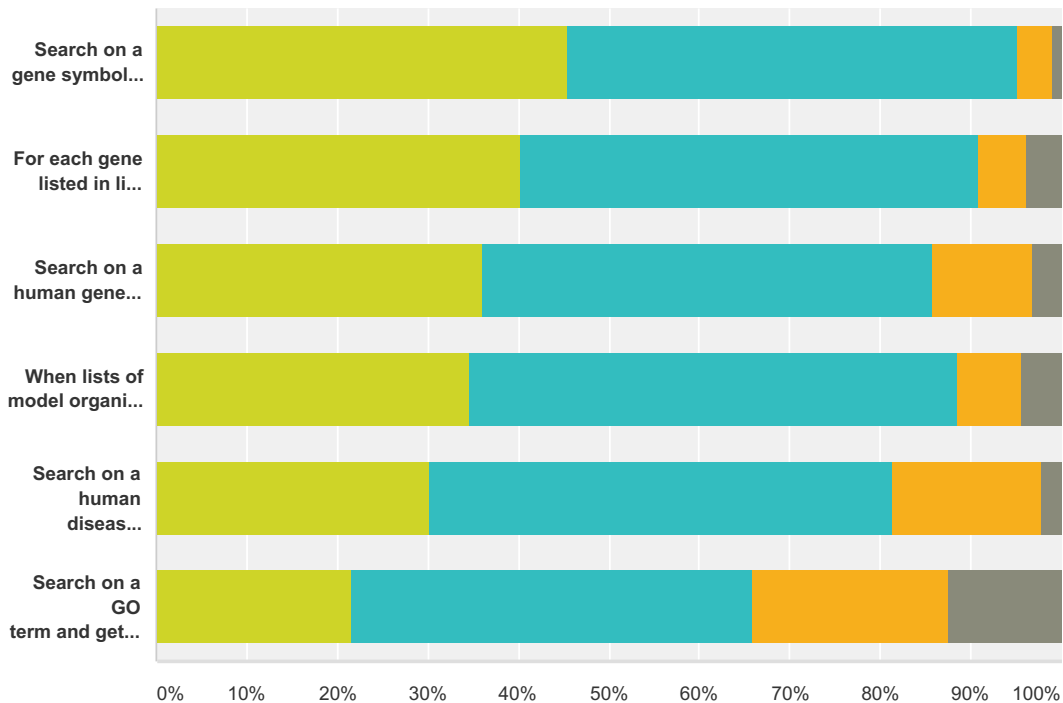
Legend:
- This is great, I find it very helpful and I'd use it frequently.
- This is great, I find it very helpful and I'd use it occasionally.
- I would not use this in my work.
- I don't think this is worth implementing.

2016 General FlyBase survey

	This is great, I find it very helpful and I'd use it frequently.	This is great, I find it very helpful and I'd use it occasionally.	I would not use this in my work.	I don't think this is worth implementing.	Total	Weighted Average
Search on a gene symbol from any of the AGR model organisms and get a list of orthologous genes for all the others.	**45.50%** 86	**49.74%** 94	**3.70%** 7	**1.06%** 2	189	1.60
For each gene listed in lists of genes, link to a commonly formatted report. At least initially, each of these reports would linktothe respective model organism database gene for more extensive and organism-specific data.	**40.32%** 75	**50.54%** 94	**5.38%** 10	**3.76%** 7	186	1.73
Search on a human gene symbol and get a list of orthologous genes from all AGR model organisms.	**35.98%** 68	**49.74%** 94	**11.11%** 21	**3.17%** 6	189	1.81
When lists of model organism genes are presented in any context (e.g., items 1-4 above), for each gene include GO information and some indication of how well the gene has been characterized.	**34.59%** 64	**54.05%** 100	**7.03%** 13	**4.32%** 8	185	1.81
Search on a human disease name and get a list of genes from AGR model organisms that have been associated with that disease.	**30.32%** 57	**51.06%** 96	**16.49%** 31	**2.13%** 4	188	1.90
Search on a GO term and get a list of all AGR model organisms that are associated with that term.	**21.62%** 40	**44.32%** 82	**21.62%** 40	**12.43%** 23	185	2.25

Q15 Could question 14 be improved?

Yes.
10.40% (18)

No.
89.60% (155)

Answer Choices	Responses	
No.	**89.60%**	155
Yes.	**10.40%**	18
Total		**173**

Q16 Which terms best describe your position?

Answered: 192   Skipped: 46
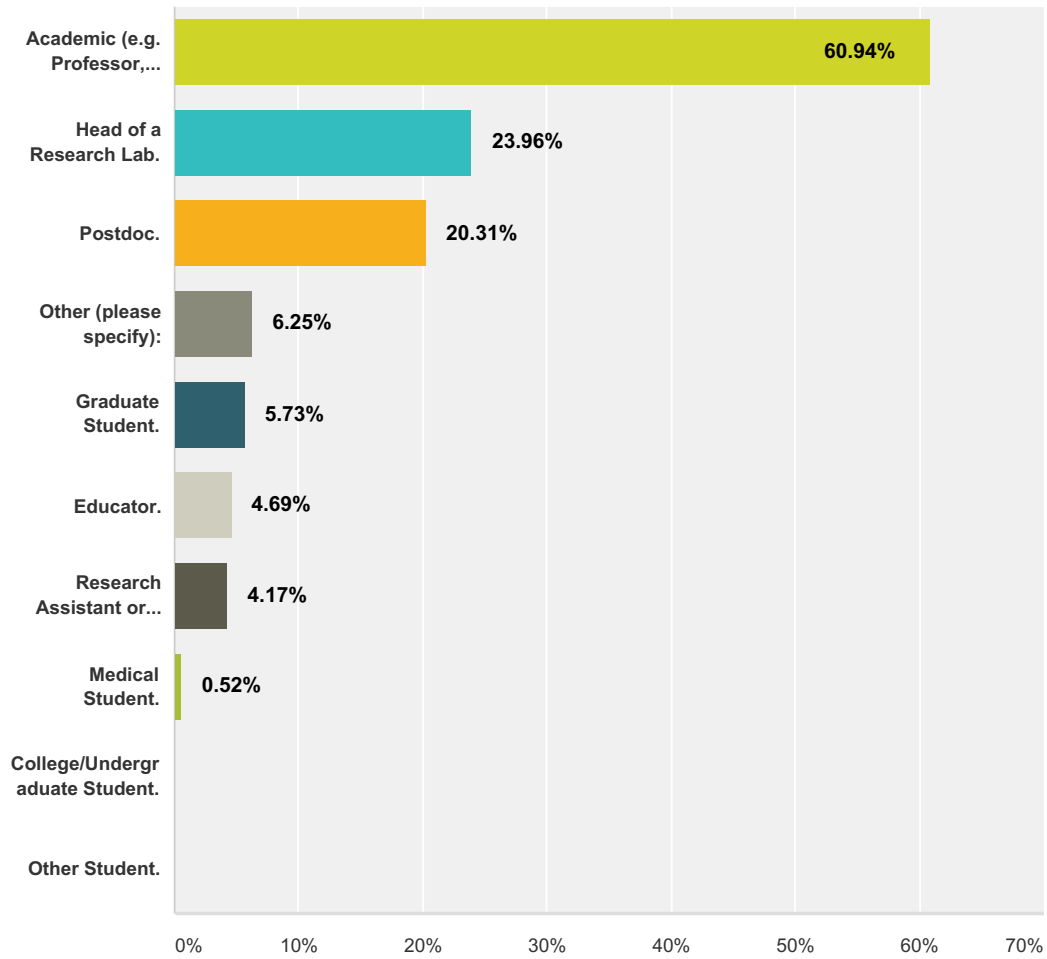
Answer Choices	Responses	
Academic (e.g. Professor, Lecturer).	**60.94%**	117
Head of a Research Lab.	**23.96%**	46
Postdoc.	**20.31%**	39
Other (please specify):	**6.25%**	12
Graduate Student.	**5.73%**	11
Educator.	**4.69%**	9
Research Assistant or Technician.	**4.17%**	8
Medical Student.	**0.52%**	1
College/Undergraduate Student.	**0.00%**	0
Other Student.	**0.00%**	0

Total Respondents: 192

Q17 Could question 16 be improved?

Answered: 178 Skipped: 60

Yes.
7.30% (13)

No.
92.70% (165)
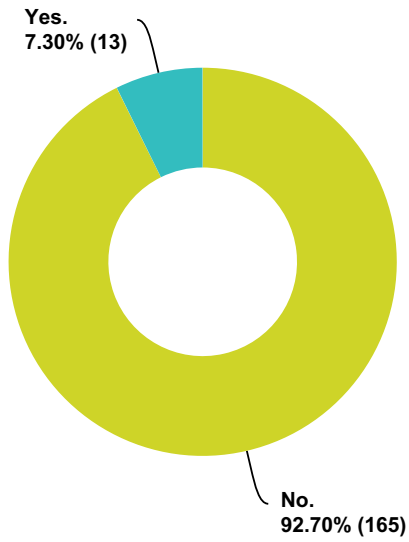
Answer Choices	Responses	
No.	92.70%	165
Yes.	7.30%	13
Total		**178**

Q18 Where do you work?

Answered: 192 Skipped: 46
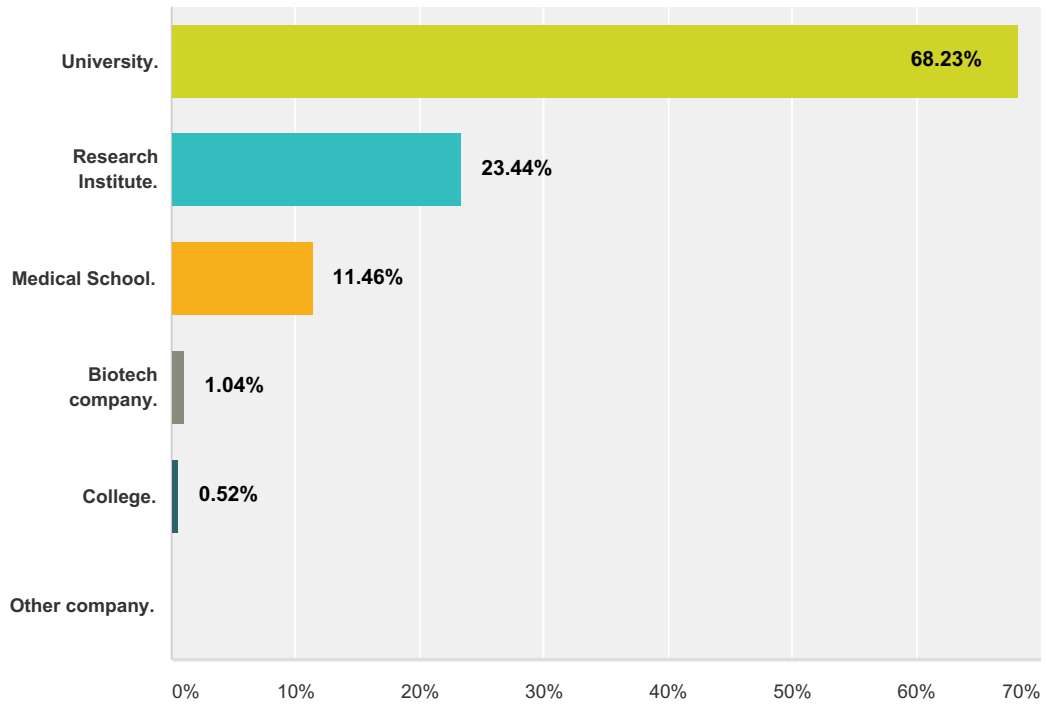
Answer Choices	Responses	
University.	**68.23%**	131
Research Institute.	**23.44%**	45
Medical School.	**11.46%**	22
Biotech company.	**1.04%**	2
College.	**0.52%**	1
Other company.	**0.00%**	0
Total Respondents: 192		

Q19 Could question 18 be improved?

Answered: 176   Skipped: 62

Yes
2.84% (5)

No
97.16% (171)
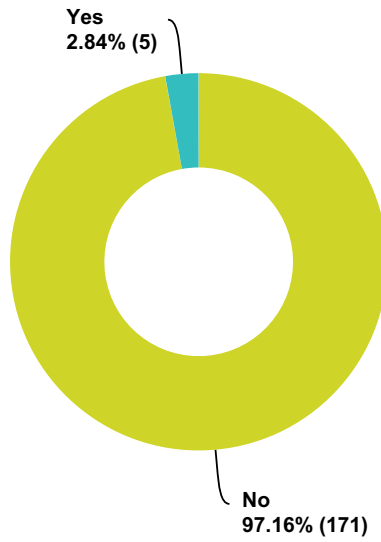
Answer Choices	Responses	
No	**97.16%**	171
Yes	**2.84%**	5
Total		**176**