**FlyBase Community Advisory Group
Introductory Survey**

Results - November 2014

Response rate

We received responses from 457/561 registered members (81%).

Introduction

Welcome to the FlyBase Community Advisory Group!

The FlyBase team is continually working to improve the amount and usefulness of data in FlyBase, and our aim in setting up this group is to get more feedback from the community to make sure that the decisions we make will be helpful for the greatest number of Drosophila researchers. To do this we plan to send you up to six surveys a year on a variety of different topics, depending on what we are working on. These could include questions on:

- What kind of data we should collect
- How we integrate data produced using new techniques
- How these data should be displayed on the website
- Finding and extracting data on the website

We look forward to working with you to ensure that FlyBase continues to make accessing Drosophila-related research as easy and intuitive as possible.

The first survey

In this introductory survey we will begin by asking you a few questions about how you and your lab use FlyBase and where you think we could improve. Different research groups interact with FlyBase in different ways, so having an idea of what interests you will enable us to target specific surveys to the right group of people in the future.

Part 1: How you use FlyBase

1. When you come to FlyBase, what kind of data are you usually looking for? Tick as many as apply.

- Phenotype
- Expression
- Literature
- Stocks
- Clones
- Computed gene summaries

- RNAi lines
- Mutant alleles
- Transgenic constructs
- Anatomy information
- Genomic/map information (e.g. gene structure)
- Gene Ontology

- Link-outs
- Genetic interactions
- Sequence files
- People
- Human Disease
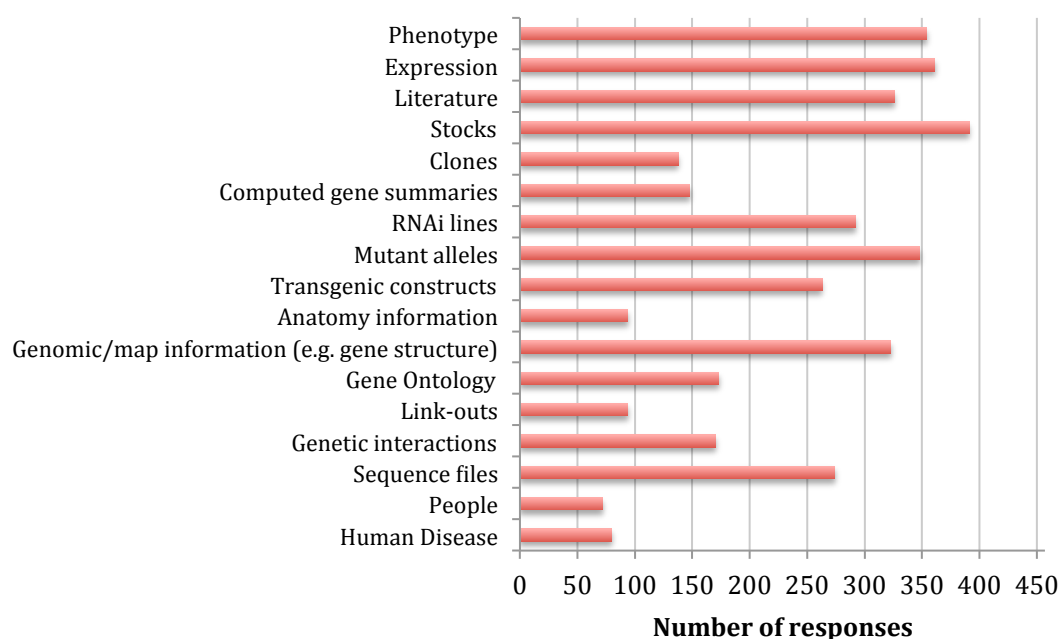
2. How often do you use FlyBase to:

- Extract detailed info about small numbers of genes (or alleles, etc.)
- Extract or download 'bulk' genome-scale information
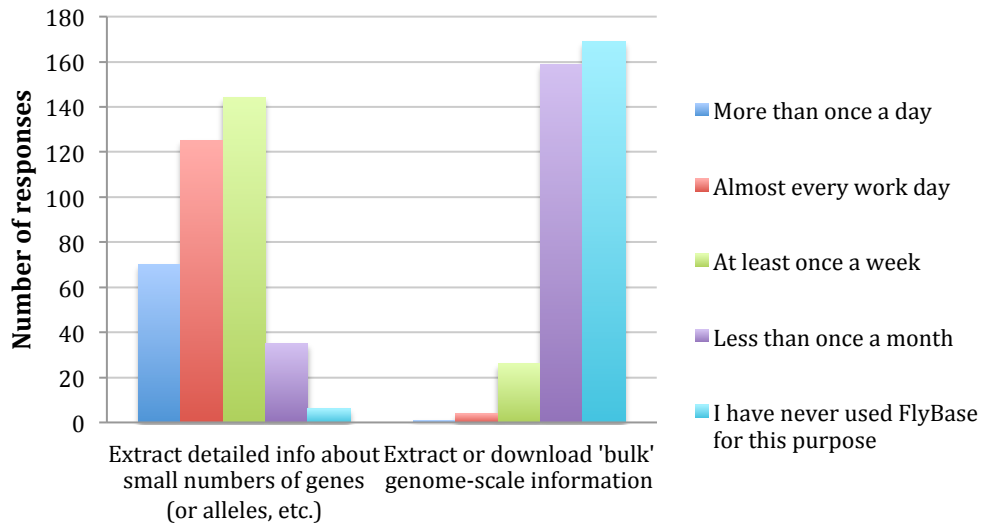
3. FlyBase provides data and links to many other Drosophila resources. In order to facilitate these collaborations please indicate which of the following databases you use. Tick as many as apply.
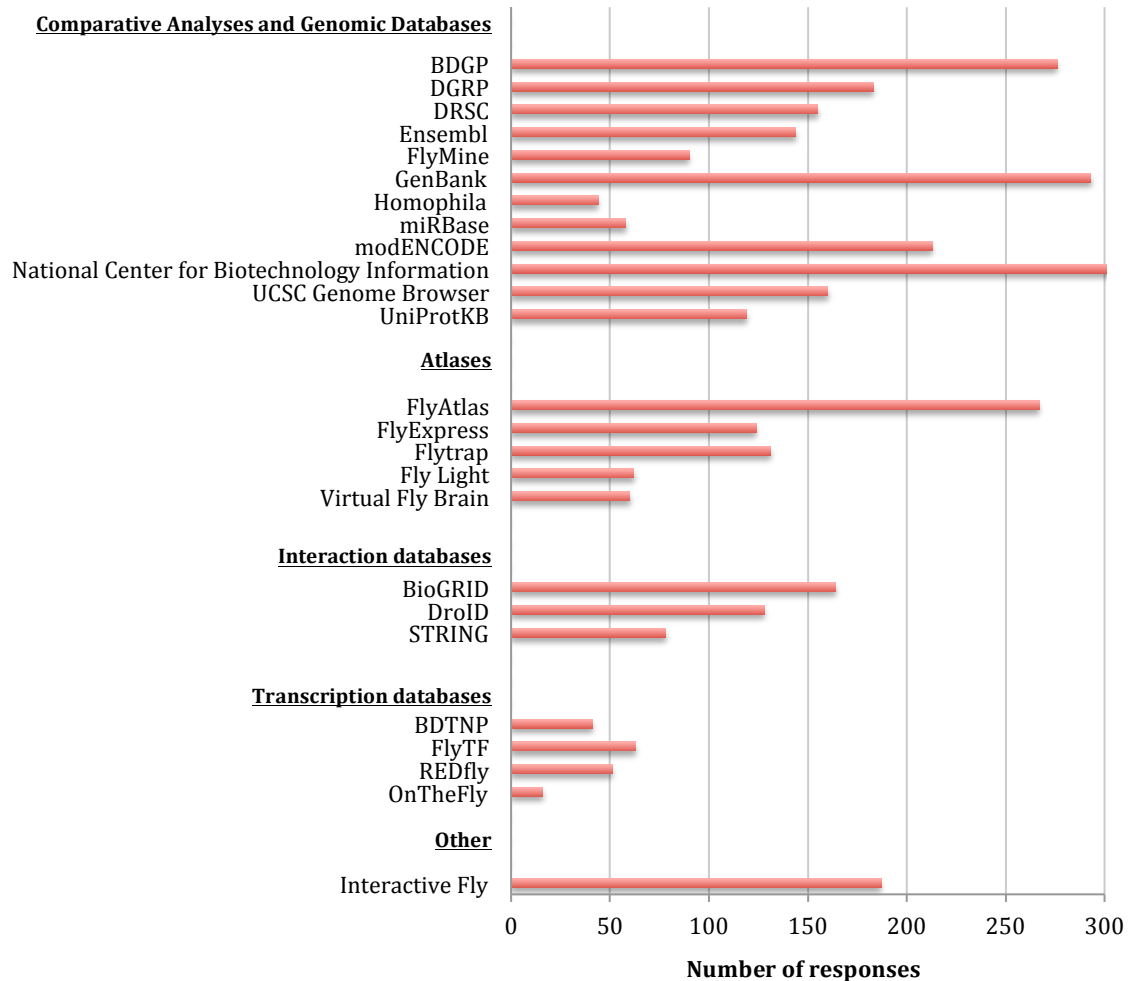
4. Are there any data or functionalities available in a resource you indicated in question 3 that you would like to see incorporated into FlyBase?

[68 responses]

5. If you could change one thing in FlyBase what would it be?

[260 responses]

Part 2: The automatically generated gene summary

In the second part of this survey we would like to ask your opinion on a subject we are currently reviewing. Each gene report contains an automatically generated summary, providing the key information about that gene. These are found at the top of the 'Summaries' section of the gene report.
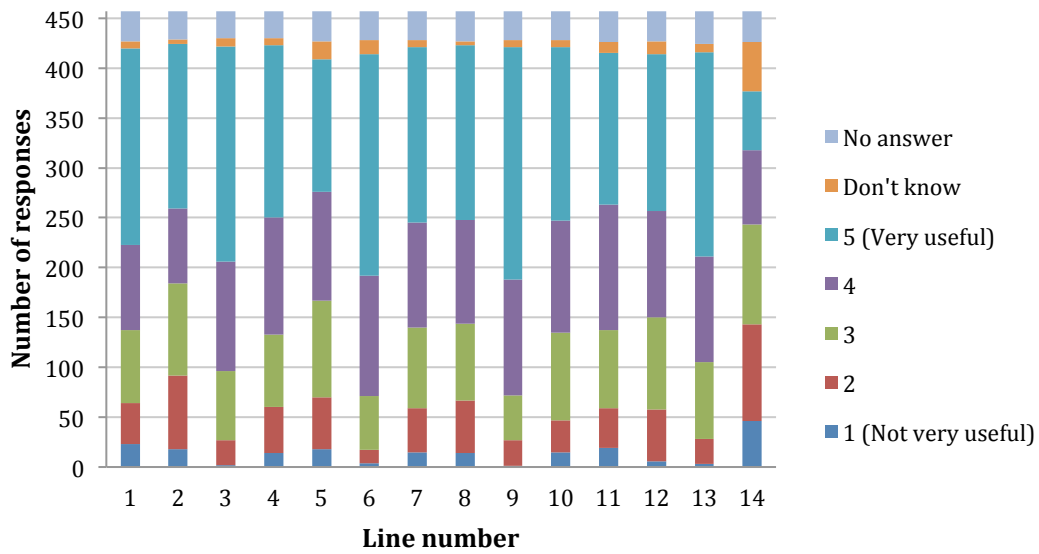
We will show you the sentences from the automated summaries for two different genes, one that has very little known about it, and one that is very well characterized. For each summary we would like you to rate how useful you find each sentence.

6a) All of the sentences from the automatically generated summary from the gene report of the relatively uncharacterized gene, CG2706, are shown and each one is numbered.

For each line of this summary indicate how useful you think that information is, where 5 is very useful and 1 is not useful at all.

1 • This gene is referred to in FlyBase by the symbol **Dmel\CG2076** (FBgn0030263)..

2 • It is a protein_coding_gene from *Drosophila melanogaster*.

3 • It has **2 annotated transcripts** and **2 polypeptides** (1 unique).

4 • **Gene sequence location** is **X:11090210..11092098**.

5 • It has the cytological map location **10A4**.

6 • Protein features are: Bax inhibitor 1-related.

7 • Its molecular function is unknown.

8 • The biological processes in which it is involved are not known.

9 • **5 alleles are reported.**

10 • No phenotypic data is available.

11 • The **phenotypic classes** of alleles include: viable; fertile. .

12 • Summary of **modENCODE Temporal Expression Profile**: Temporal profile ranges from a peak of very high expression to a trough of moderate expression. Peak expression observed in adult male stages.

13 • Summary of **FlyAtlas Anatomical Expression Data**: High or moderate levels of expression observed in all larval and adult organs/tissues. Expression at high levels in the following post-embryonic organs or tissues: adult eye, larval/adult midgut, larval/adult Malpighian tubules, adult heart, adult salivary gland, adult spermathecae, larval/adult carcass. Expression at moderate levels in the following post-embryonic organs or tissues: adult head; larval/adult central nervous system; adult crop; larval/adult hindgut; larval/adult fat body; larval salivary gland; larval trachea; adult ovary; adult male reproductive system.

14 • Comments on **Affy2 ProbeSet**: ProbeSet 1640185_at completely aligns to an exonic region of the only FlyBase-annotated transcript isoform of CG2076.
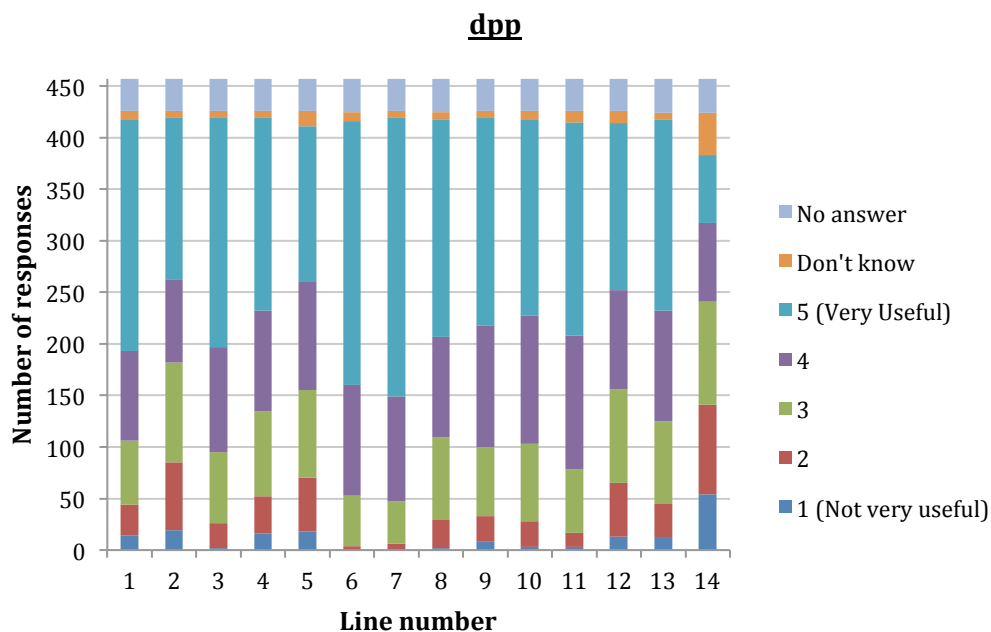
CG2076

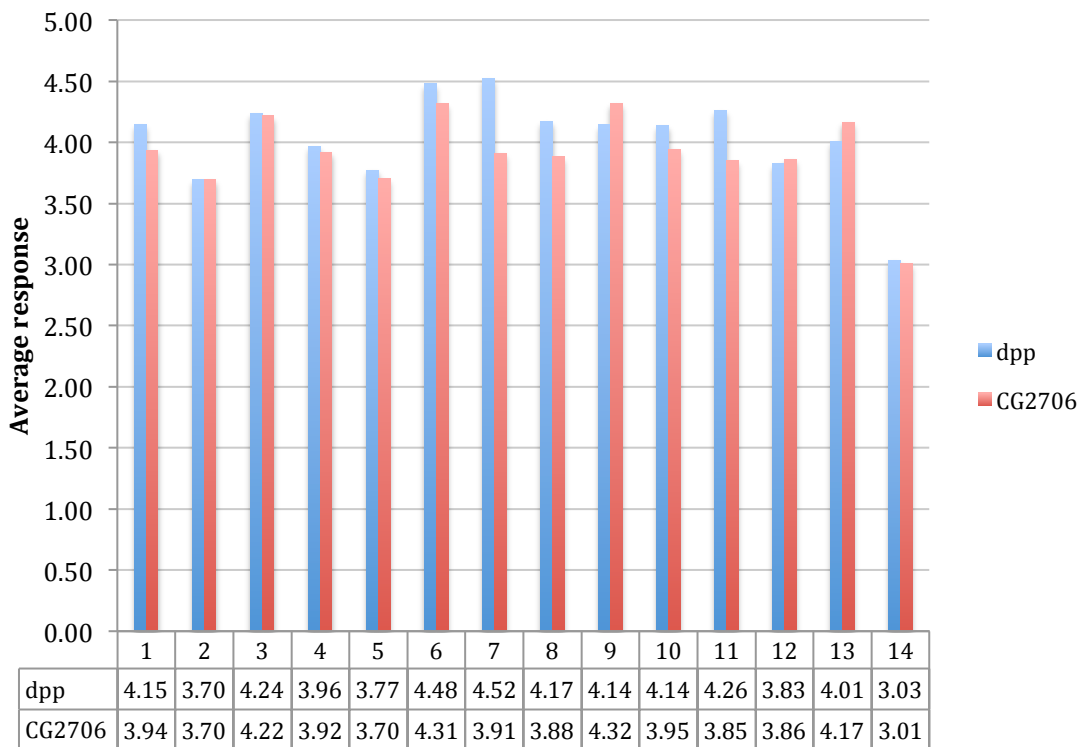| Line	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Average response	3.94	3.70	4.22	3.92	3.70	4.31	3.91	3.88	4.32	3.95	3.85	3.86	4.17	3.01

b) All of the sentences from the automatically generated summary from the gene report of the very well-studied gene, dpp, are shown and each one is numbered. Is the value of the different lines the same for this summary? For each line of this summary indicate how useful you think that information is, where 5 is very useful and 1 is not useful at all.

1. • The gene **decapentaplegic** is referred to in FlyBase by the symbol **Dmel\dpp** (CG9885, FBgn0000490).
2. • It is a protein_coding_gene from *Drosophila melanogaster*.
3. • It has **4 annotated transcripts** and **4 polypeptides** (1 unique).
4. • **Gene sequence location** is **2L:2428372..2459823**.
5. • It has the cytological map location **22F1-22F3**.
6. • **Protein features** are: Cystine-knot cytokine; Inhibin, alpha subunit; Transforming growth factor beta, conserved site; Transforming growth factor-beta, C-terminal; Transforming growth factor-beta, N-terminal; Transforming growth factor-beta-related.
7. • Its **molecular function** is described by: transforming growth factor beta receptor binding; heparin binding; morphogen activity; collagen binding; protein homodimerization activity; protein binding; growth factor activity; protein heterodimerization activity.
8. • It is involved in the **biological process** described with 76 unique terms, many of which group under: single-organism developmental process; biological regulation; multi-organism reproductive process; open tracheal system development; regulation of developmental process; post-embryonic organ morphogenesis; sensory organ development; dorsal/ventral axis specification; cell fate commitment; system development.
9. • **305 alleles are reported**.
10. • The **phenotypes** of these alleles manifest in: organ system; organ system subdivision; adult segment; portion of tissue; non-connected developing system; imaginal precursor; thoracic segment; external compound sense organ; late extended germ band embryo; integumentary specialisation.
11. • The **phenotypic classes** of alleles include: size defective; increased cell number; lethal - all die before end of larval stage; increased mortality during development; lethal - all die before end of P-stage; phenotype.
12. • Summary of **modENCODE Temporal Expression Profile**: Temporal profile ranges from a peak of moderate expression to a trough of very low expression. Peak expression observed at stages throughout embryogenesis, at stages throughout the pupal period, in adult male stages.
13. • Summary of **FlyAtlas Anatomical Expression Data**: Expression at high levels in the following post-embryonic organs or tissues: adult crop. Expression at moderate levels in the following post-embryonic organs or tissues: adult male accessory gland.
14. • Comments on **Affy2 ProbeSet**: ProbeSet 1630026_s_at completely aligns to an exonic region common to each of the 5 FlyBase-annotated transcript isoforms of dpp.

dpp

Line	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Average response	4.15	3.70	4.24	3.96	3.77	4.48	4.52	4.17	4.14	4.14	4.26	3.83	4.01	3.03

Comparison between CG2076 and dpp

|	1	2	3	4	5	6	7	8	9	10	11	12	13	14
dpp	4.15	3.70	4.24	3.96	3.77	4.48	4.52	4.17	4.14	4.14	4.26	3.83	4.01	3.03
CG2706	3.94	3.70	4.22	3.92	3.70	4.31	3.91	3.88	4.32	3.95	3.85	3.86	4.17	3.01

Part 3: Receiving updates from FlyBase

Any new features and improvements that we introduce in response to your comments will only be useful if the community knows about them. Therefore in this final question we would like to know how useful you find the current methods we use to let you know about new features in FlyBase. We currently do this by documenting the changes in the Release Notes, and this can be accessed in a number of ways, including from the Navigation bar (see image) and the News section on the homepage.

Below is a list of existing and new methods that we could use to keep you up to date with the latest developments in FlyBase.

Rate each method based on how likely you are to use them, where 1 is very unlikely and 5 is very likely.

- Release Notes
- News section on the homepage
- Commentaries on the homepage
- Twitter
- Periodic emails (by subscribing to a mailing list)
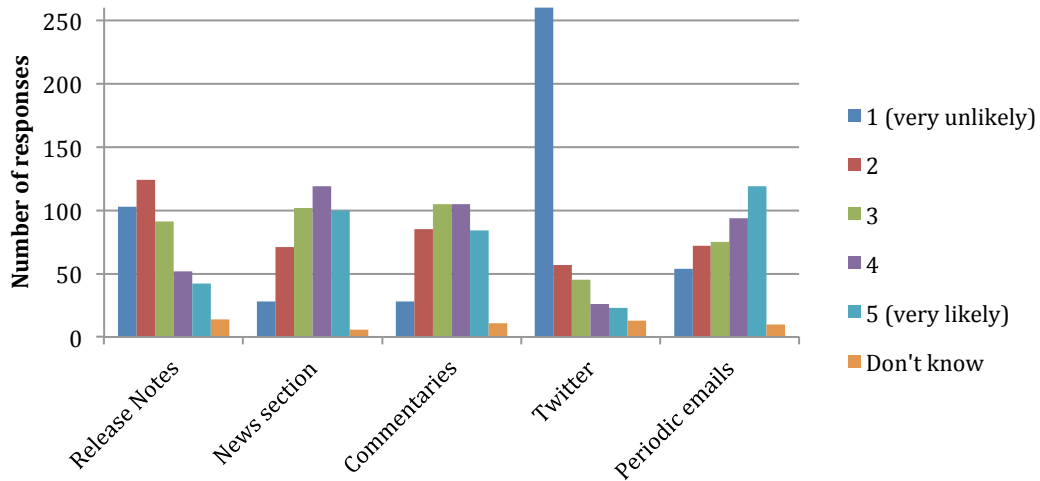
Method	Average response
Release Notes	2.53
News section	3.46
Commentaries	3.32
Twitter	1.77
Periodic emails	3.37

If you have any other additional suggestions for how FlyBase could better communicate with the community about new features and changes enter them in the box below.

[51 responses]