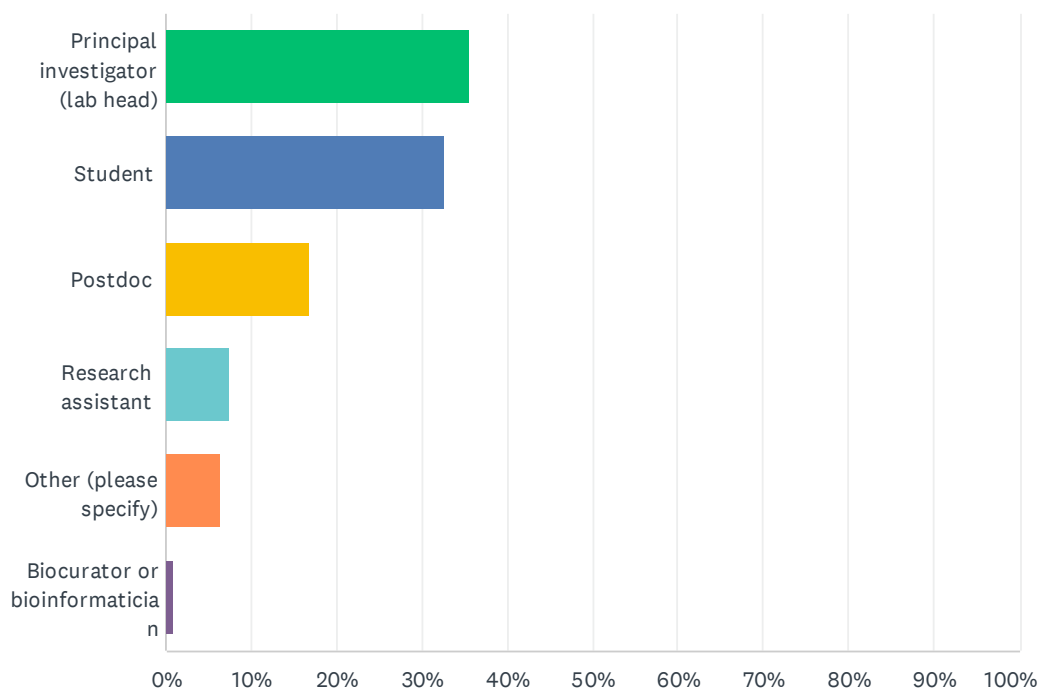


Q1 What is your position?

Answered: 638 Skipped: 12



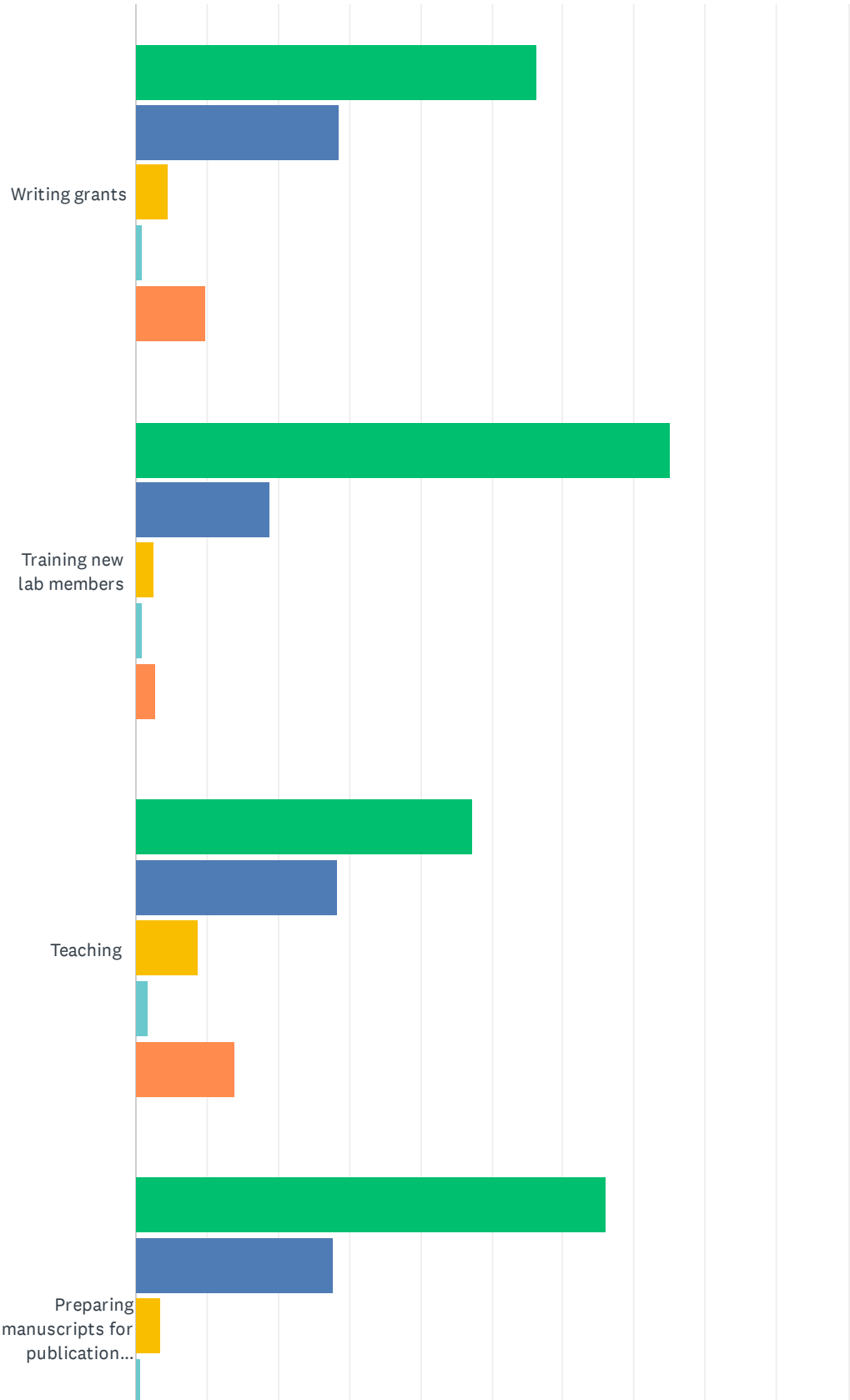
ANSWER CHOICES	RESPONSES	
Principal investigator (lab head)	35.58%	227
Student	32.60%	208
Postdoc	16.93%	108
Research assistant	7.52%	48
Other (please specify)	6.43%	41
Biocurator or bioinformatician	0.94%	6
TOTAL		638

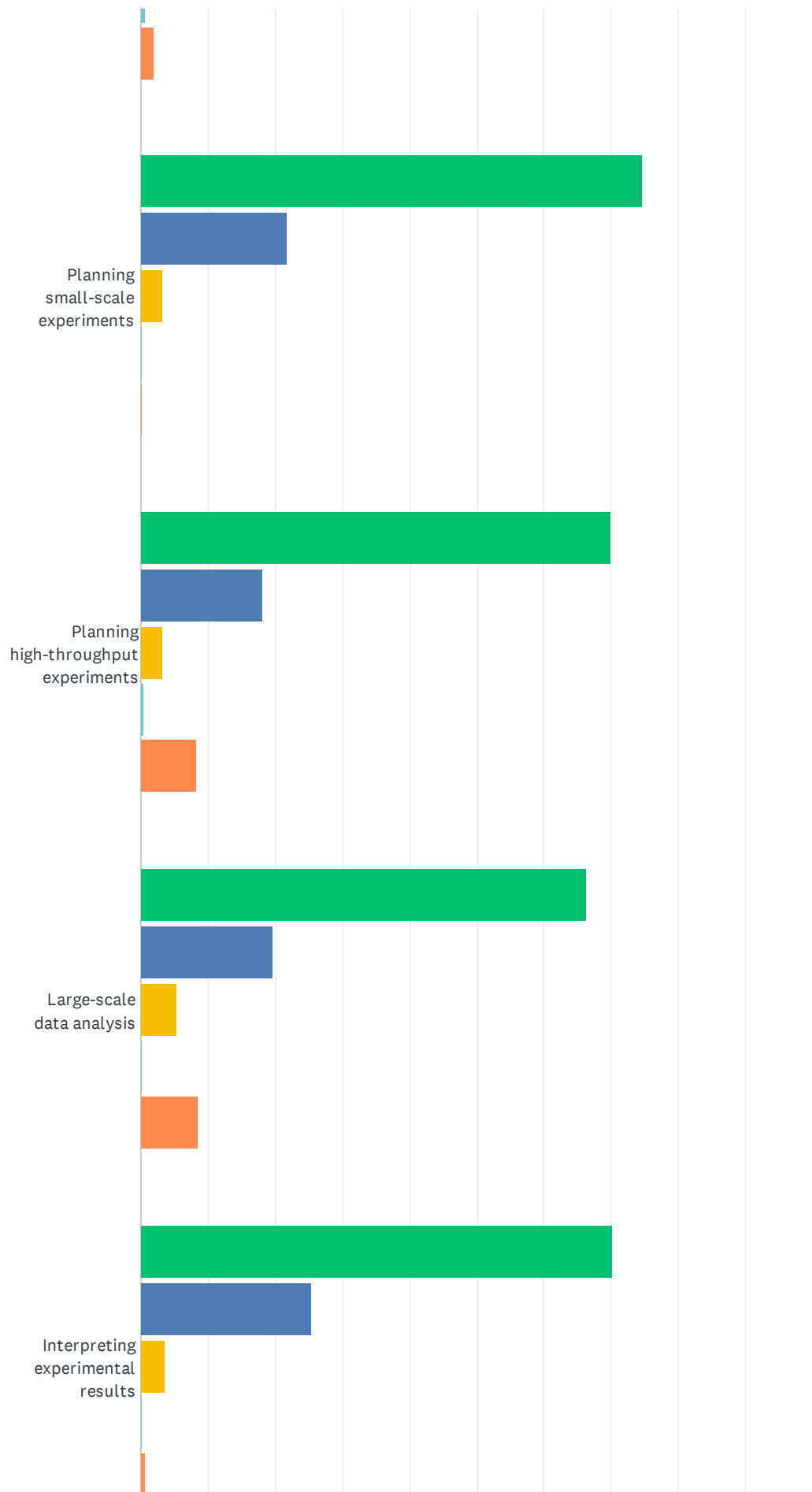
#	OTHER (PLEASE SPECIFY)	DATE
1	Lab manager	11/13/2025 10:44 AM
2	PhD	11/13/2025 10:21 AM
3	Associate professor	11/13/2025 1:57 AM
4	Subject librarian	11/12/2025 8:53 PM
5	Research Technician	11/11/2025 4:51 PM
6	Lecturer	11/7/2025 11:27 PM
7	Professor of Biology and PI	11/7/2025 2:21 PM
8	Independent Researcher	11/7/2025 10:46 AM

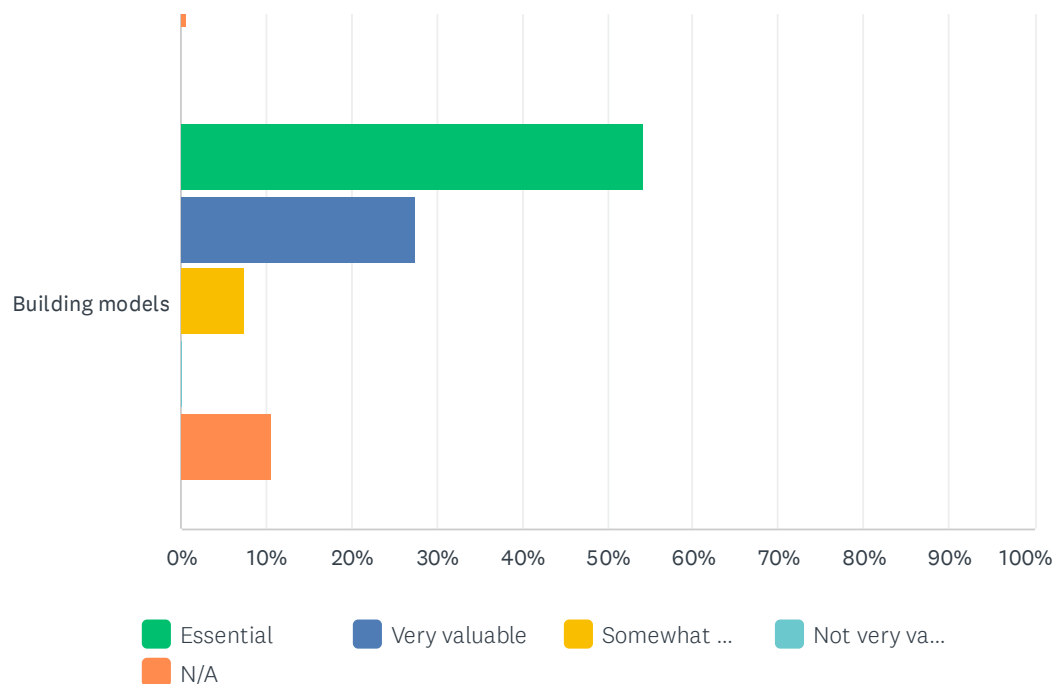
9	Assistant Professor	11/7/2025 9:32 AM
10	scientific officer zz	11/6/2025 12:21 PM
11	Staff Scientist	11/4/2025 1:04 PM
12	permanent research fellow - project leader in a team (but not PI)	11/1/2025 1:02 PM
13	research engineer	11/1/2025 11:42 AM
14		11/1/2025 8:14 AM
15	Research assistant professor	10/31/2025 8:46 PM
16	technicien	10/31/2025 1:38 PM
17	staff scientist	10/31/2025 12:57 PM
18	I was previously a research assistant working with Pombe	10/31/2025 12:43 PM
19	Lab Manager/staff scientist	10/31/2025 12:35 PM
20	Staff scientist	10/31/2025 11:52 AM
21	Research specialist	10/31/2025 11:51 AM
22	assistant professor	10/31/2025 12:11 AM
23	Research Associate	10/30/2025 7:35 PM
24	Research Associate professor (non tenure track)	10/30/2025 2:15 PM
25	researcher	10/30/2025 12:53 PM
26	Lab manager	10/30/2025 12:26 PM
27	Researcher in compony (formerly postdoc)	10/30/2025 12:06 PM
28	project leader, research scientist	10/27/2025 11:31 AM
29	faculty member	10/24/2025 4:24 AM
30	non tenured faculty	10/23/2025 7:58 PM
31	Researcher	10/23/2025 5:14 PM
32	Research Technician	10/23/2025 4:53 PM
33	Senior Staff Scientist	10/23/2025 4:51 PM
34	Research associate	10/23/2025 2:30 PM
35	Assistant Professor	10/23/2025 12:00 PM
36	associate professor	10/23/2025 10:50 AM
37	Staff scientist	10/23/2025 10:22 AM
38	Researcher	10/23/2025 10:21 AM
39	researcher in company	10/23/2025 10:11 AM
40	Former PhD student about to start a Postdoc	10/21/2025 1:02 PM
41	Research scientist (eqv to Research Associate Professor)	10/17/2025 3:02 PM

Q2 How valuable is PomBase for ...?

Answered: 648 Skipped: 2







	ESSENTIAL	VERY VALUABLE	SOMEWHAT VALUABLE	NOT VERY VALUABLE	N/A	TOTAL	WEIGHTED AVERAGE
Writing grants	56.36% 359	28.57% 182	4.40% 28	0.94% 6	9.73% 62	637	1.45
Training new lab members	75.08% 482	18.85% 121	2.49% 16	0.78% 5	2.80% 18	642	1.27
Teaching	47.34% 302	28.37% 181	8.78% 56	1.72% 11	13.79% 88	638	1.59
Preparing manuscripts for publication (e.g. finding references)	66.20% 427	27.75% 179	3.41% 22	0.62% 4	2.02% 13	645	1.37
Planning small-scale experiments	74.73% 482	21.71% 140	3.10% 20	0.16% 1	0.31% 2	645	1.28
Planning high-throughput experiments	69.95% 447	18.15% 116	3.13% 20	0.47% 3	8.29% 53	639	1.28
Large-scale data analysis	66.35% 422	19.65% 125	5.35% 34	0.16% 1	8.49% 54	636	1.34
Interpreting experimental results	70.08% 452	25.27% 163	3.72% 24	0.31% 2	0.62% 4	645	1.34
Building models	54.06% 346	27.50% 176	7.50% 48	0.31% 2	10.63% 68	640	1.49

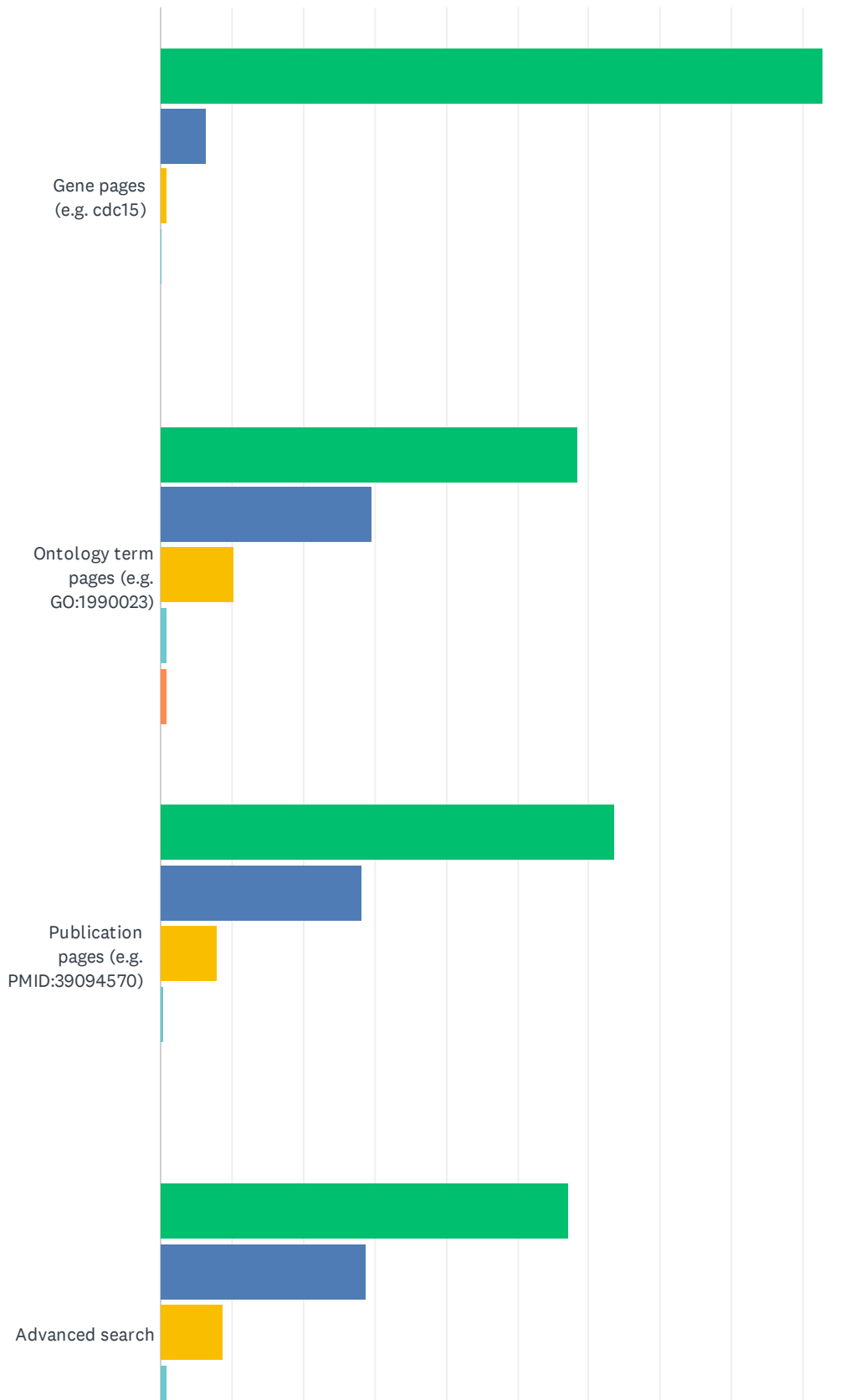
#	OTHER (PLEASE SPECIFY, ESPECIALLY IF YOU ARE NOT A FISSION YEAST RESEARCHER)	DATE
1	fission yeast research is impossible without pombase	11/16/2025 1:08 AM
2	Helps in preparing a base and the expand the ideology on which the work is based.	11/13/2025 5:12 AM
3	essential	11/13/2025 3:09 AM
4	PomBase is a very useful and important website for my research and work.	11/12/2025 6:17 AM
5	Given the high cost and the technical difficulty to obtain human meiocyte samples, especially	11/12/2025 1:55 AM

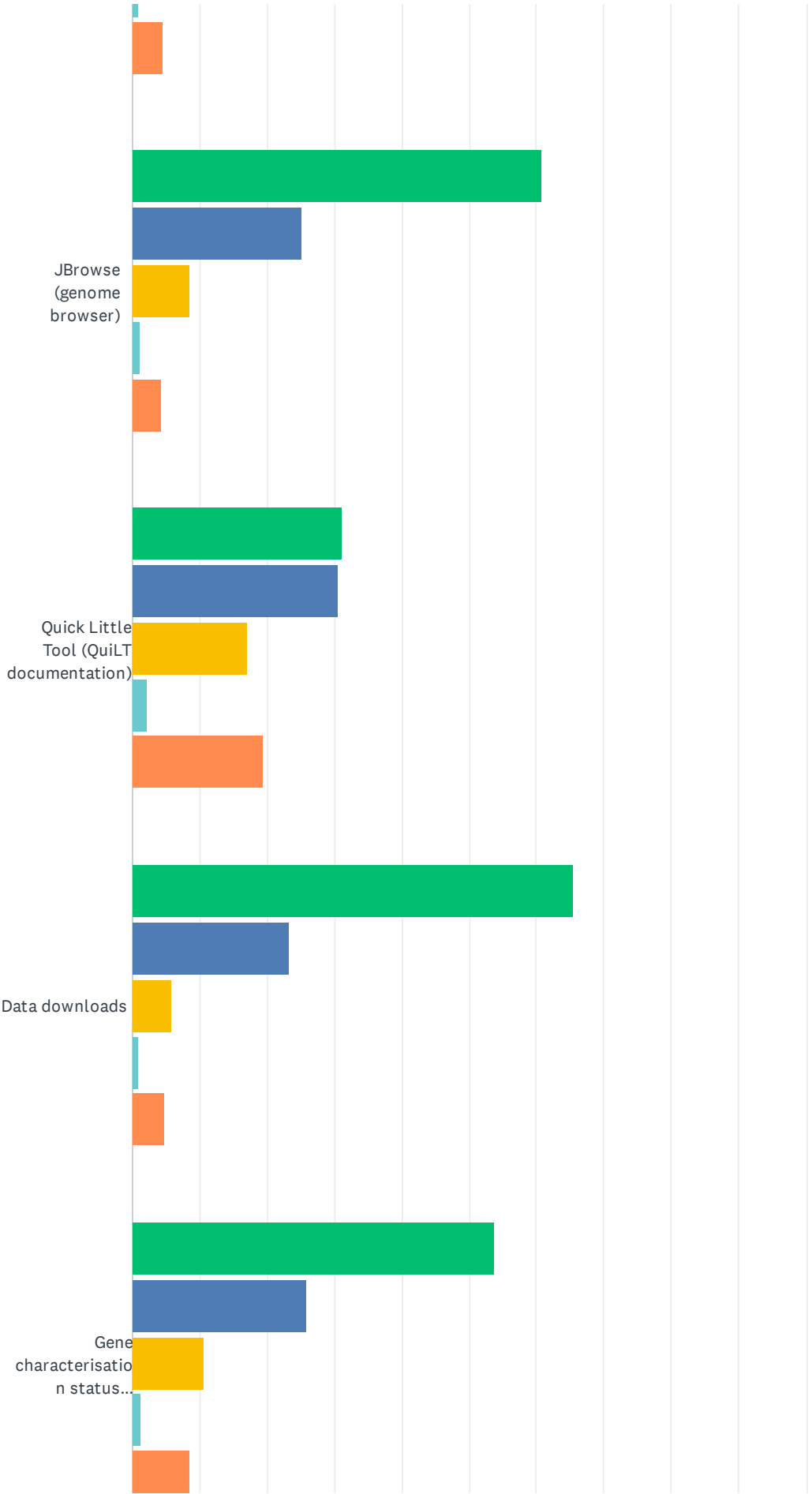
those harboring mutations, *S.pombe* still is the best genetically tractable model to study meiotic chromosome segregation. Many fundamental mechanisms have been revealed with the fission yeast system.

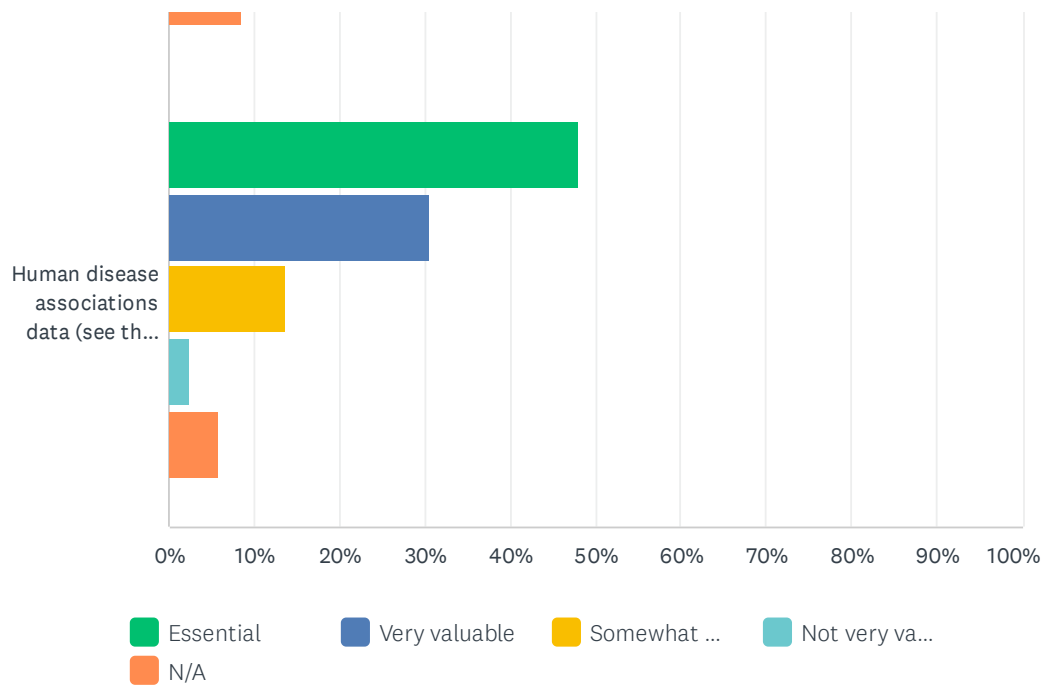
6	Discovering existing results on other scientific databases they link to. Using existing data minimizes wasted effort and funds on experiments that have already been done.	11/11/2025 9:26 AM
7	It is the main source of information for this organism	11/10/2025 3:11 PM
8	I am not a fission yeast researcher. However, unlike many other databases, Pombase, is just annotated in such a complete way that when I try to find data from other organisms, I start with pombase because it's usually there, a few clicks away.	11/10/2025 1:43 PM
9	PomBase has been an essential for planning experiments and interpreting data for research within my lab over the last 20 years.	11/10/2025 9:18 AM
10	It reduces the time and resources needed to devise and analyse the results of all experiments. Without Pombase every individual lab would need to find details about genes, mutant phenotypes, interactions, chromosomal location, primer design etc. It is also extremely useful for exploring the function of genes of interest identified in human and crop plant fungal pathogens because gene annotation in fungal pathogen databases is very poor.	11/4/2025 12:00 PM
11	Pombase has been essential for building new ideas and thinking about next projects!	10/31/2025 9:27 PM
12	Overall, Pombase is a great resource for reference genomes and annotations that I use for my bioinformatics work. It is also essential for getting sequences of genes/proteins for designing experiments and mutants.	10/23/2025 8:44 PM
13	I am an <i>S. japonicus</i> researcher who benefits greatly from being able to gain information about proteins and pathways that are conserved between <i>S. japonicus</i> and <i>S. pombe</i> and also identify differences between <i>S. japonicus</i> and <i>S. pombe</i> using PomBase.	10/23/2025 8:02 PM
14	Pombase is relevant and necessary to essentially anything I want to do with pombe	10/23/2025 7:40 PM
15	Pombase is a good tool to link genes from different fungal organism as this is a very well annotated database. This makes it really valuable outside the field of fission yeast alone.	10/23/2025 6:22 PM
16	I just want to say that I work in a small fission yeast lab in the Southeastern US, at a public college that serves underrepresented groups and minorities. Our lab works to train those who wouldn't have an opportunity to learn about cell biology and molecular research otherwise. PomBase has quite literally been an absolutely integral aspect of our research and training everybody in the lab. It is a central part of what we do.	10/23/2025 2:59 PM
17	correlations to counterparts in mammals	10/23/2025 2:12 PM
18	Specially useful for searching interaction networks and orthologs of genes of interest in other organisms.	10/23/2025 11:15 AM
19	To get current information especially news related to <i>S. pombe</i> or other fission yeasts.	10/23/2025 10:50 AM
20	I only use pombe as an occasional adjunct organism to other models - but its unique position between the simple and higher eukaryotes means that the research data and teaching examples that I draw from this are a vital bridge in everything I do - pombase is the key tool for exploring this data.	10/23/2025 10:37 AM
21	Daily using!!	10/21/2025 3:15 PM
22	PomBase is not only one of the (maybe the) best model organism databases in terms of usability, information quality, and exploring complexes or the literature, but also a fantastic tool to explain basics of molecular biology, gene organization, primer design and cloning principles to graduate school students. An invaluable resource.	10/21/2025 12:05 AM
23	Pombase is used daily in my lab for finding new readings and validating our current understanding of genes and proteins of interest.	10/18/2025 1:48 AM
24	I use PomBase every day for a variety of reasons	10/16/2025 2:49 PM

Q3 How valuable is each of these PomBase features for your work?

Answered: 647 Skipped: 3



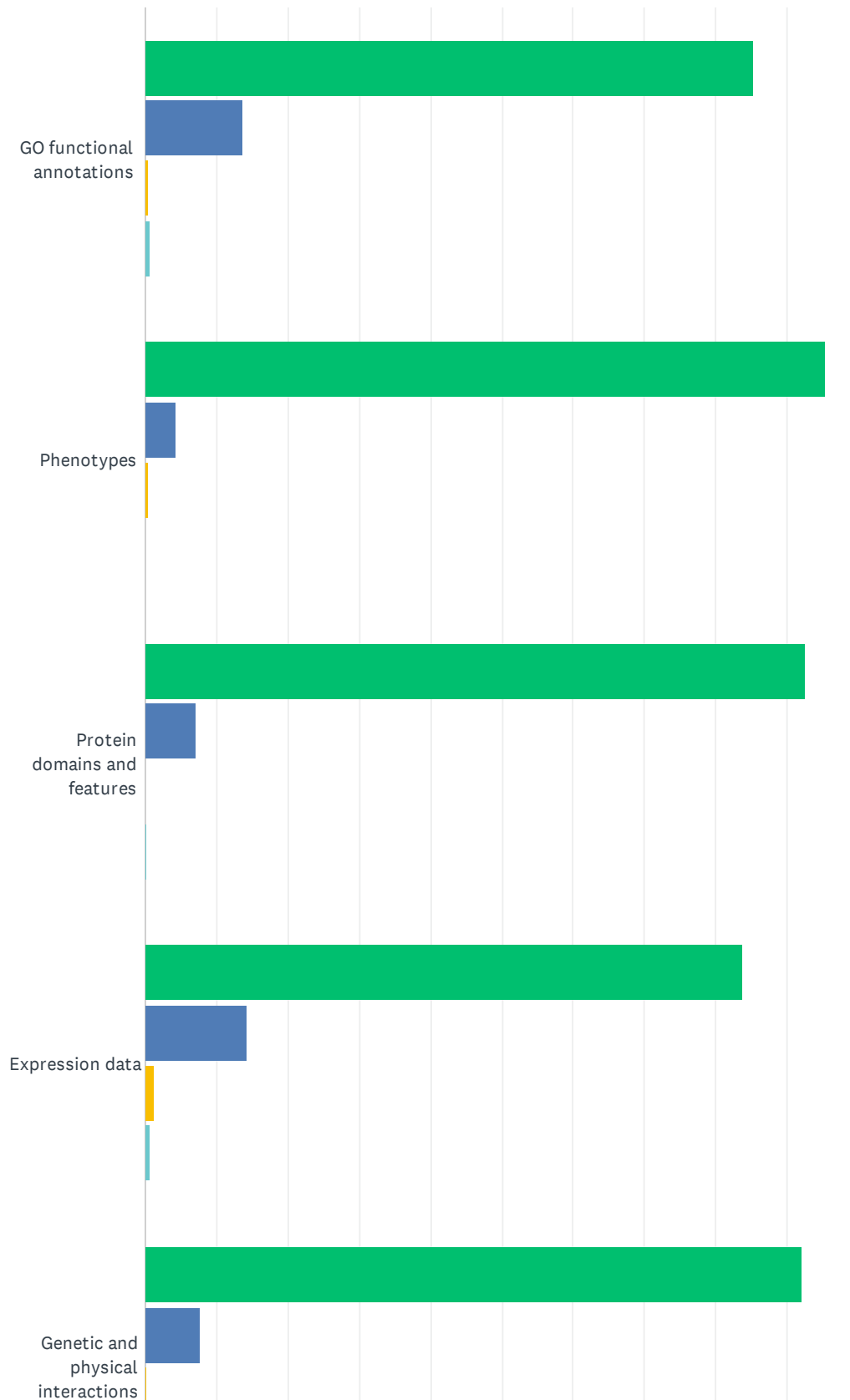


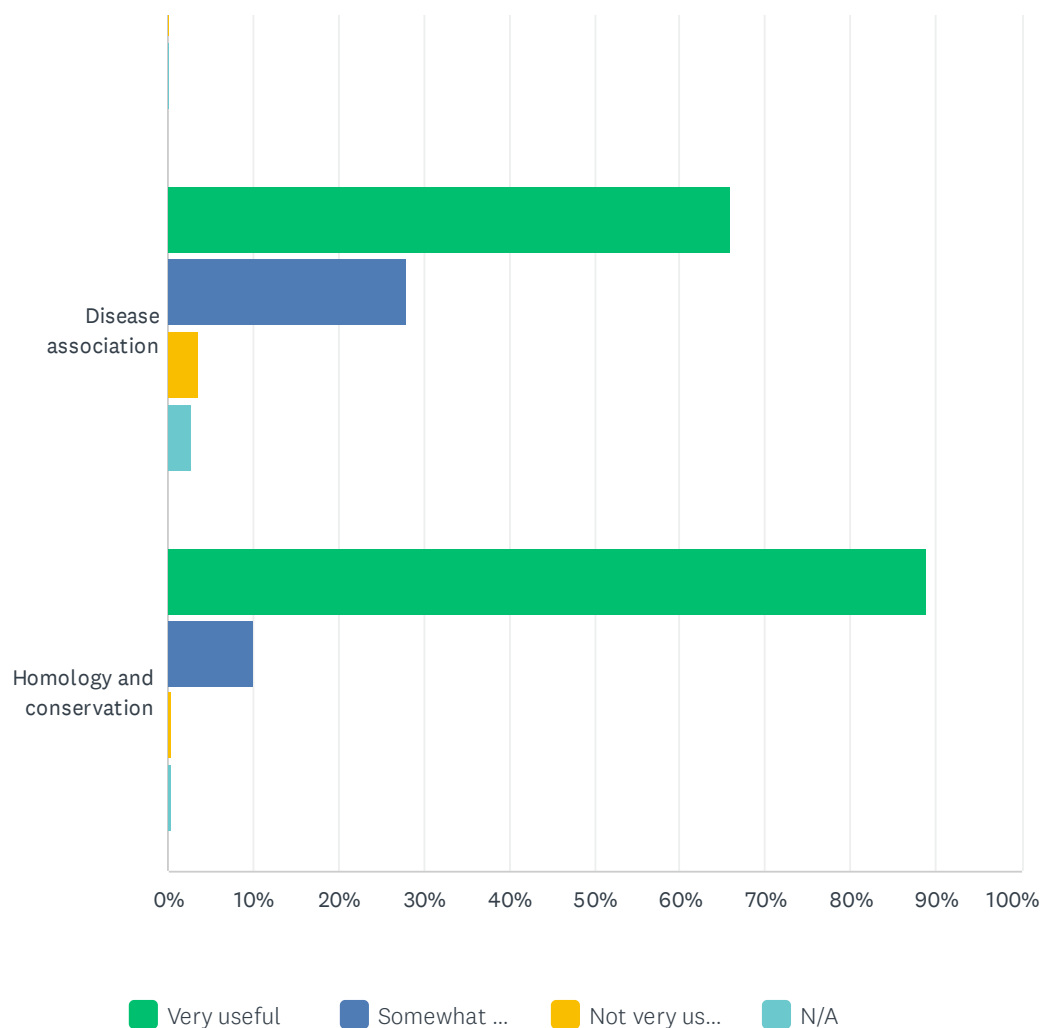


	ESSENTIAL	VERY VALUABLE	SOMEWHAT VALUABLE	NOT VERY VALUABLE	N/A	TOTAL	WEIGHTED AVERAGE
Gene pages (e.g. cdc15)	92.72% 599	6.35% 41	0.77% 5	0.15% 1	0.00% 0	646	1.08
Ontology term pages (e.g. GO:1990023)	58.32% 375	29.55% 190	10.26% 66	0.93% 6	0.93% 6	643	1.53
Publication pages (e.g. PMID:39094570)	63.51% 409	28.11% 181	7.92% 51	0.47% 3	0.00% 0	644	1.45
Advanced search	57.08% 363	28.77% 183	8.81% 56	0.79% 5	4.56% 29	636	1.51
JBrowse (genome browser)	60.82% 388	25.24% 161	8.62% 55	1.10% 7	4.23% 27	638	1.48
Quick Little Tool (QuiLT documentation)	31.02% 197	30.55% 194	17.01% 108	2.05% 13	19.37% 123	635	1.88
Data downloads	65.41% 418	23.32% 149	5.79% 37	0.78% 5	4.69% 30	639	1.39
Gene characterisation status tracker	53.82% 345	25.74% 165	10.76% 69	1.25% 8	8.42% 54	641	1.56
Human disease associations data (see the disease ontology slim)	47.89% 307	30.42% 195	13.57% 87	2.34% 15	5.77% 37	641	1.69

Q4 How useful are the different types of data displayed on gene pages?

Answered: 646 Skipped: 4

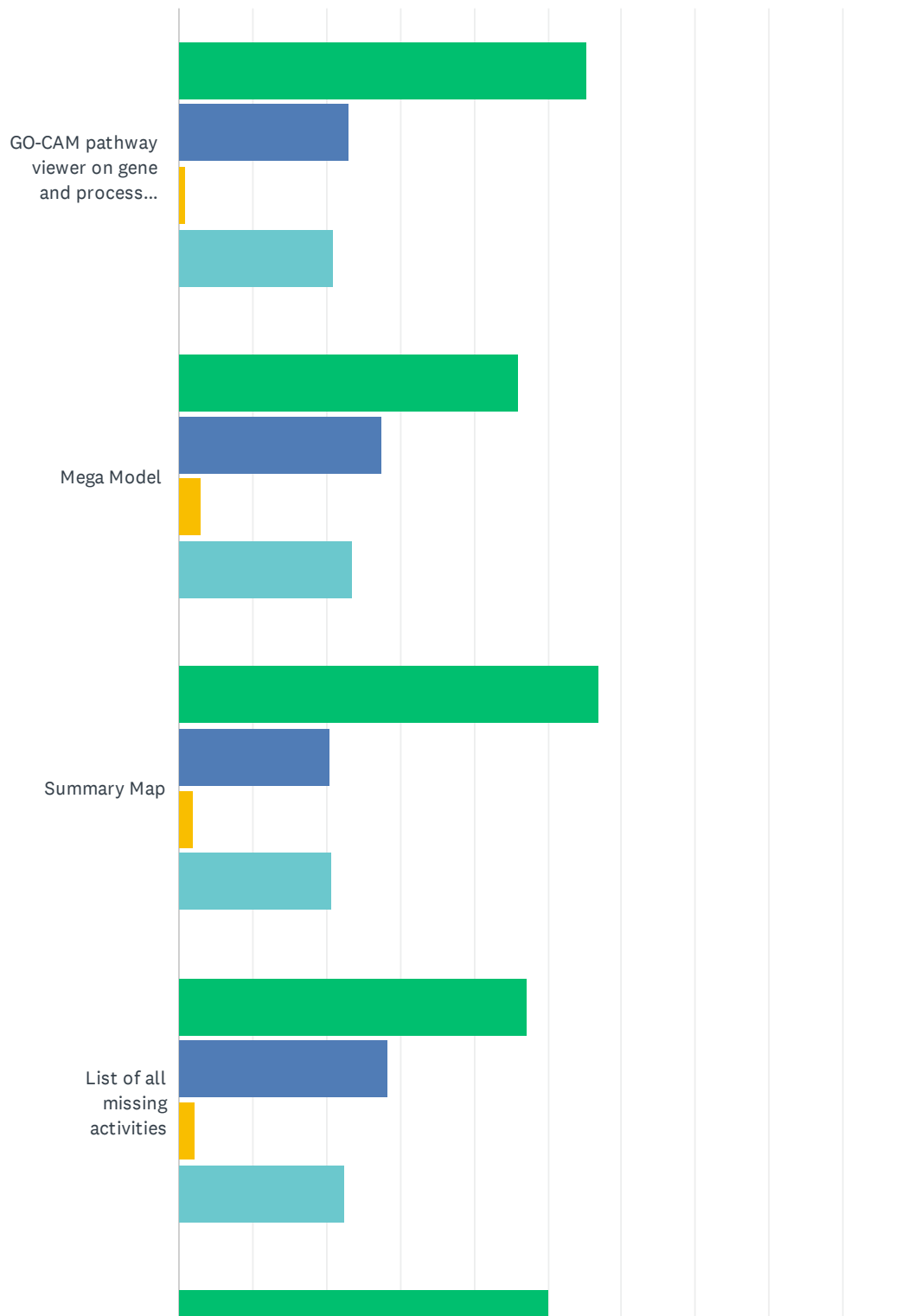


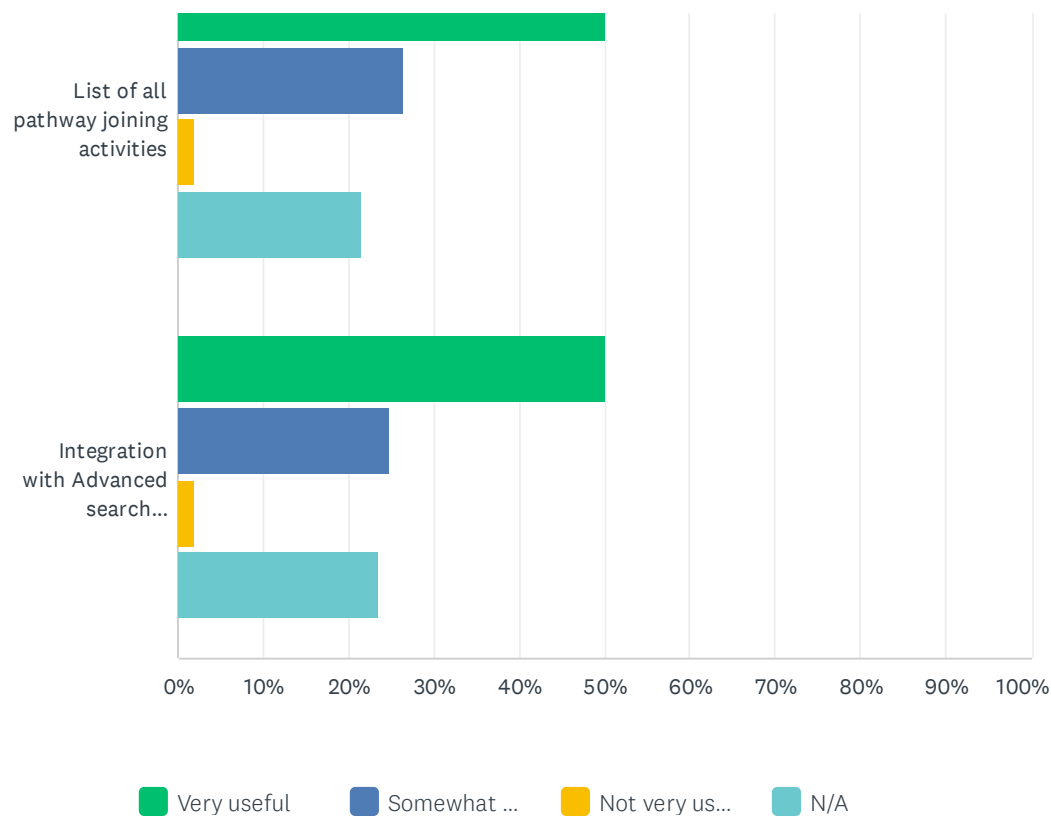


	VERY USEFUL	SOMEWHAT USEFUL	NOT VERY USEFUL	N/A	TOTAL	WEIGHTED AVERAGE
GO functional annotations	85.29% 551	13.62% 88	0.46% 3	0.62% 4	646	1.15
Phenotypes	95.34% 614	4.19% 27	0.47% 3	0.00% 0	644	1.05
Protein domains and features	92.56% 597	7.13% 46	0.00% 0	0.31% 2	645	1.07
Expression data	83.85% 540	14.29% 92	1.24% 8	0.62% 4	644	1.17
Genetic and physical interactions	92.08% 593	7.61% 49	0.16% 1	0.16% 1	644	1.08
Disease association	65.79% 423	27.84% 179	3.58% 23	2.80% 18	643	1.36
Homology and conservation	88.96% 572	10.11% 65	0.47% 3	0.47% 3	643	1.11

Q5 At the start of the year, we have publicly released GO-CAM pathways on PomBase. We have since added several new pathways, and new tools making use of GO-CAM. How useful is each of these GO-CAM-related features for your work?

Answered: 631 Skipped: 19

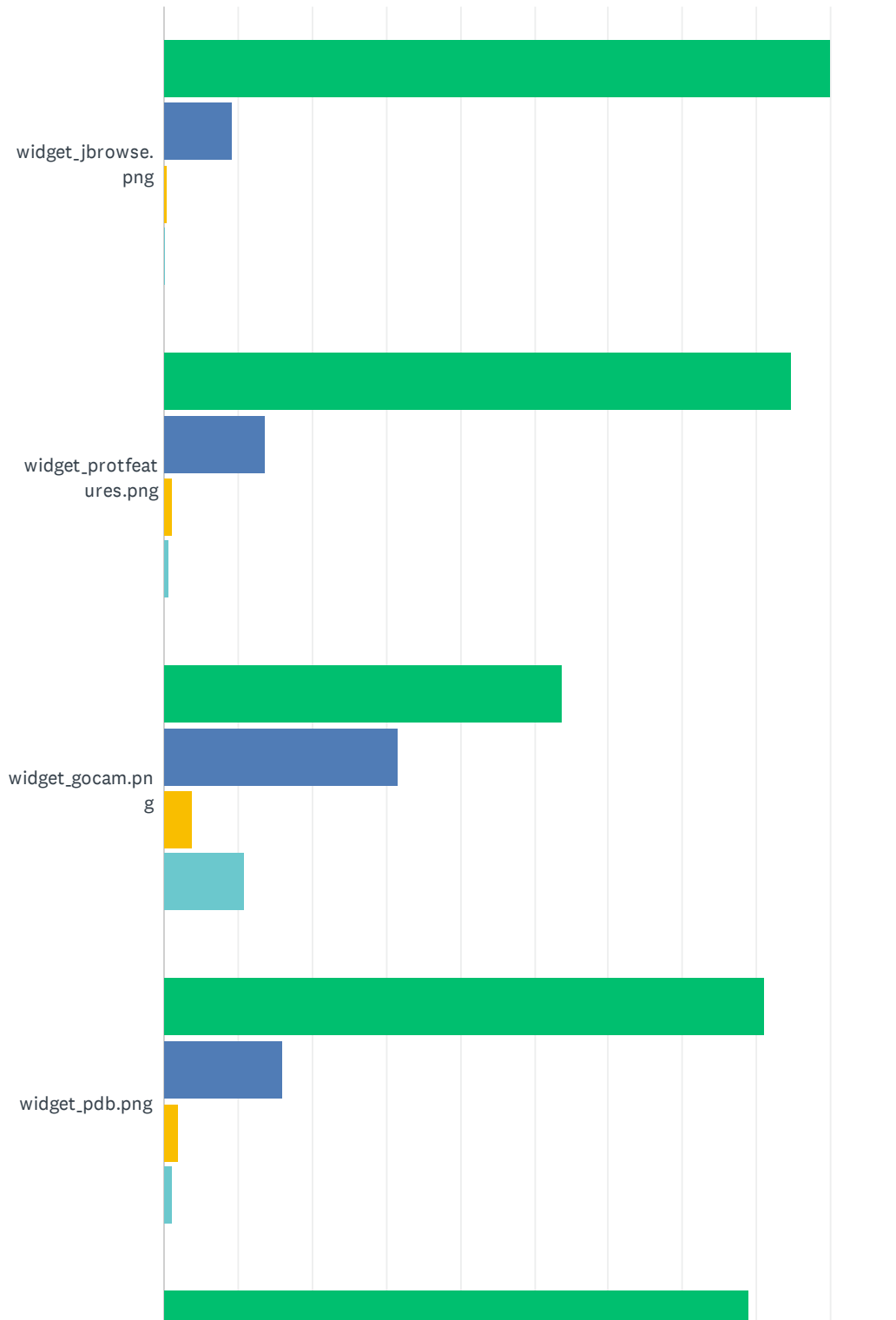


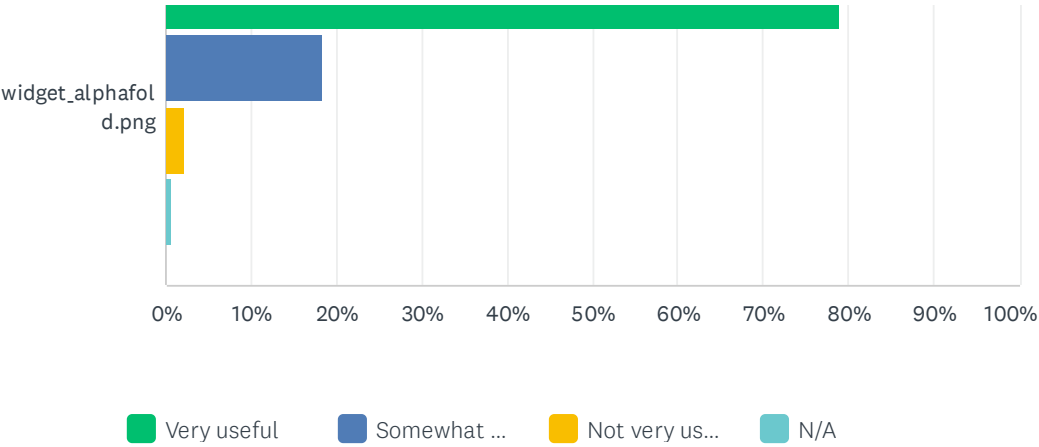


	VERY USEFUL	SOMEWHAT USEFUL	NOT VERY USEFUL	N/A	TOTAL	WEIGHTED AVERAGE
GO-CAM pathway viewer on gene and process pages	55.18% 346	23.13% 145	0.80% 5	20.89% 131	627	1.31
Mega Model	46.10% 290	27.50% 173	3.02% 19	23.37% 147	629	1.44
Summary Map	56.94% 357	20.41% 128	1.91% 12	20.73% 130	627	1.31
List of all missing activities	47.21% 296	28.39% 178	2.07% 13	22.33% 140	627	1.42
List of all pathway joining activities	50.16% 315	26.43% 166	1.91% 12	21.50% 135	628	1.39
Integration with Advanced search functionalities	50.08% 313	24.64% 154	1.92% 12	23.36% 146	625	1.37

Q6 The summary section at the top of the gene pages contains an embedded viewer that can display various widgets. Not all genes have all viewers available. See cdc15 (image below) for an example with all 5 viewers available. How useful are each of these viewers?

Answered: 644 Skipped: 6

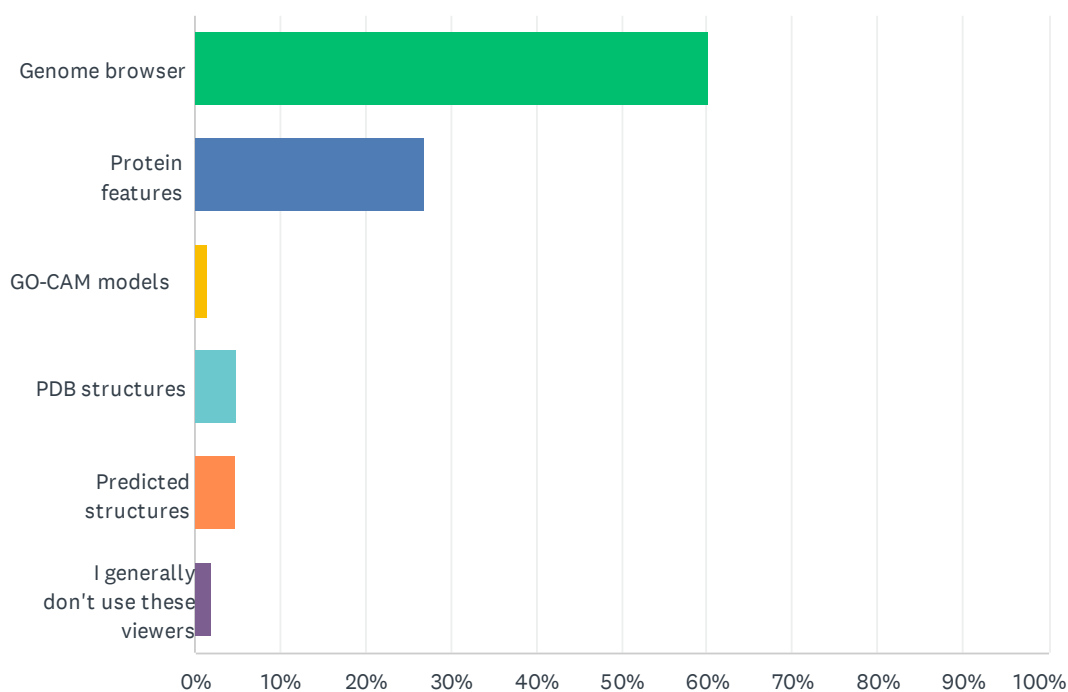




	VERY USEFUL	SOMEWHAT USEFUL	NOT VERY USEFUL	N/A	TOTAL	WEIGHTED AVERAGE
Genome browser	90.03% 578	9.19% 59	0.47% 3	0.31% 2	642	1.10
Protein features	84.56% 542	13.73% 88	1.09% 7	0.62% 4	641	1.16
GO-CAM models	53.83% 344	31.46% 201	3.91% 25	10.80% 69	639	1.44
PDB structures	81.03% 521	16.02% 103	1.87% 12	1.09% 7	643	1.20
Predicted structure	78.94% 506	18.25% 117	2.18% 14	0.62% 4	641	1.23

Q7 Which of these viewers do you use the most?

Answered: 640 Skipped: 10



ANSWER CHOICES	RESPONSES	
Genome browser	60.16%	385
Protein features	26.88%	172
GO-CAM models	1.56%	10
PDB structures	4.84%	31
Predicted structures	4.69%	30
I generally don't use these viewers	1.88%	12
TOTAL		640

Q8 Can you think of any improvements that would make the PomBase interface clearer or more practical?

Answered: 223 Skipped: 427

#	RESPONSES	DATE
1	Not currently	11/19/2025 12:18 PM
2	In built GO analysis tool	11/19/2025 7:01 AM
3	i think alot of information is already available to used PomBase	11/18/2025 3:44 PM
4	N/A	11/18/2025 3:04 AM
5	No	11/17/2025 5:07 PM
6	nope	11/17/2025 4:40 PM
7	No	11/17/2025 4:15 PM
8	Pombase is an essential database and everything is just perfect! The only small improvement could be related to the section devoted to particular genomic elements, like centromeres, could contain possibility to view relevant sequences.	11/17/2025 4:12 PM
9	More curations will help	11/17/2025 1:16 PM
10	A detailed schematic version of all the different interconnected signalling pathways a gene/protein is involved in	11/17/2025 10:36 AM
11	no	11/17/2025 6:34 AM
12	no	11/17/2025 2:39 AM
13	It's fine now	11/16/2025 4:08 PM
14	I like it the way it is.	11/16/2025 1:08 AM
15	No, it's already pretty useful	11/15/2025 1:34 PM
16	at the moment, I always use search in the interface, I think would be better to make a larger place for "search"	11/15/2025 1:15 AM
17	NoN	11/14/2025 4:41 AM
18	Integration of 3D genomics data (such as Hi-C, Micro-C, HiChIP)	11/14/2025 3:38 AM
19	I think PomBase is constantly evolving and upgrading to standards I haven't thought of yet. A fantastic, essential resource.	11/13/2025 5:34 PM
20	Link introduction documents to every icon and chart.	11/13/2025 4:56 PM
21	Ok	11/13/2025 1:06 PM
22	No	11/13/2025 8:54 AM
23	-	11/13/2025 8:11 AM
24	No, the pombase moderators constantly improve from researchers feedback already	11/13/2025 7:01 AM
25	incorporate AI for further analysis and study	11/13/2025 6:30 AM
26	Addition of literature papers , from organisms other than fission yeast. It would help researchers gain more insight about their work and hence aid in research.	11/13/2025 5:12 AM
27	I am using it with satisfaction.	11/13/2025 3:51 AM
28	yes	11/13/2025 3:09 AM

29	A direct link to the very first paper that discovered the gene up front or at least indicate so.	11/13/2025 12:17 AM
30	no	11/13/2025 12:11 AM
31	N/A	11/12/2025 10:14 PM
32	Provide an API to access data rather than files.	11/12/2025 9:18 PM
33	No, it is amazing for the purposes I use it for	11/12/2025 8:27 PM
34	very good as is!	11/12/2025 8:15 PM
35	Perhaps tutorials could be nice to allow for early researchers to use Pombase without needing a mentor	11/12/2025 8:12 PM
36	NA	11/12/2025 8:07 PM
37	I am unsure about this right now, but will give a thought and send in my suggestions if I come up with something. I am so used to using the current features as they are, I haven't thought about how to improve them.	11/12/2025 7:41 PM
38	The system is very clear and useful	11/12/2025 7:04 PM
39	A way to search for specific strains (ex. 968 h90, 972 h-, 972 FY1181, etc.) Being able to use these names that are commonly found in papers to search the website or even include a new strain database tab that includes name identifiers so they become searchable. Would be nice to be have a strain catalogue that tells you the mutations in the strain too. For molecular genetics	11/12/2025 6:45 PM
40	NA.	11/12/2025 9:01 AM
41	NA	11/12/2025 8:45 AM
42	May add the localization of gene product	11/12/2025 8:40 AM
43	no	11/12/2025 8:36 AM
44	NO	11/12/2025 7:53 AM
45	it is very suitable to use now	11/12/2025 7:48 AM
46	no	11/12/2025 7:27 AM
47	no	11/12/2025 6:38 AM
48	no	11/12/2025 6:38 AM
49	no	11/12/2025 6:37 AM
50	no	11/12/2025 6:35 AM
51	no	11/12/2025 6:17 AM
52	Nothing	11/12/2025 6:03 AM
53	No	11/12/2025 4:35 AM
54	no	11/12/2025 3:04 AM
55	Non.	11/12/2025 3:00 AM
56	No, It's perfect!	11/12/2025 2:50 AM
57	no	11/12/2025 2:03 AM
58	Temporarily unavailable.	11/12/2025 2:00 AM
59	no	11/12/2025 1:34 AM
60	Not yet	11/11/2025 11:59 PM
61	A small summary paragraph about each gene on the gene page. Also a variant viewer - for any gene highlights residues that have snps in different strains. These are features I often used in	11/11/2025 9:26 AM

SGD. Also for proteins including the alphafold structure Id and PLDDT in one of the bulk downloads would be handy but maybe niche.

62	No	11/11/2025 8:15 AM
63	The interface is very user-friendly as is.	11/10/2025 10:56 PM
64	None	11/10/2025 3:11 PM
65	I don't know why my PomBase pages always open to the protein structure, which I am not as interested in. I don't know how to change it as clearing all my browser data does not fix the problem.	11/10/2025 2:12 PM
66	Pombase is already one of the clearers databases, which is why even though I'm not a fission yeast researcher, I always start with PomBase	11/10/2025 1:43 PM
67	No	11/10/2025 11:43 AM
68	I like all the current functions. I can't think any improvements.	11/10/2025 10:25 AM
69	N/A	11/10/2025 10:04 AM
70	The term, exon, is used in a wrong way. Please correct it.	11/10/2025 9:41 AM
71	none	11/10/2025 9:18 AM
72	I think that the Pombase gene page should retain the previous default setting of displaying the "Genome browser" when opening a gene page, because "Predicted structures" and "Protein Features" always have slow loading speeds.	11/8/2025 1:47 PM
73	a need of a system that checks regularly S. pombe/related publications to update the literature entries automatically	11/8/2025 12:40 PM
74	no	11/8/2025 11:59 AM
75	..	11/7/2025 11:27 PM
76	No, the interface is very user-friendly	11/7/2025 3:03 PM
77	No, I don't think any major improvements are needed. The PomBase interface is already very clear and easy to use. The layout is intuitive, the tools are well organized, and the search functions work smoothly. Moreover, as more data become available over time, the platform will continue to improve and become even more useful for researchers.	11/7/2025 2:29 PM
78	No	11/7/2025 10:46 AM
79	No improvements needed PomBase is a crucial part of my PhD and is incredibky helpful!	11/7/2025 9:57 AM
80	None	11/7/2025 9:32 AM
81	Already very essential for student. Future developments of the interactive tools for teaching activities will even make it better.	11/7/2025 9:07 AM
82	more quantitative biophysical numbers than already exist, e.g. for proteins: affinities of proteins, dwell times of interactions, reported copy numbers etc.	11/7/2025 9:03 AM
83	generating more valuable details about the interactions between more proteins	11/7/2025 9:02 AM
84	an AI asistant	11/5/2025 11:45 AM
85	On the gene pages, for some genes, the phenotyps lists can be very long, as a result of high throughput screens.	11/5/2025 11:45 AM
86	No idea at this moment	11/5/2025 8:44 AM
87	The PomBase userinterface is already excellent, it might be useful to have the Uniprot ID higher up, close to the Systematic ID	11/4/2025 7:50 PM
88	No	11/4/2025 6:39 PM
89	it's great	11/4/2025 12:46 PM
90	I have not used GO-CAM so much but I expect that it will be something that I use much more	11/4/2025 12:00 PM

	frequently in future.	
91	Nothing in particular comes to mind, but navigating the database can be challenging if you're not familiar with it.	11/3/2025 8:59 PM
92	Not really. Pombase is one of the most important tool in our research. It keeps improving and new features are always welcome, but as such, I could not pick something that I really miss.	11/3/2025 3:18 PM
93	N/A	11/3/2025 12:48 PM
94	A very minor comment - when looking at the relevant links to papers at the bottom of a gene page, it really clutters them up by having the same batch of papers which were big screens every time, which rarely have anything specific to offer about whatever gene you're looking at.	11/3/2025 12:35 PM
95	Integrated features with other fungal databases, especially for phylogenetic analyses	11/3/2025 9:39 AM
96	No suggestions	11/3/2025 8:53 AM
97	It is already pretty good!	11/3/2025 4:20 AM
98	It's perfect	11/3/2025 3:49 AM
99	None	11/3/2025 12:59 AM
100	no	11/3/2025 12:50 AM
101	No.	11/2/2025 11:36 AM
102	No.	11/2/2025 8:47 AM
103	verything is good!	11/2/2025 4:00 AM
104	The current interface is perfect!	11/2/2025 12:24 AM
105	A pop-up bubble that appears as your mouse hovers over certain features, explaining what can be done using that feature in short.	11/1/2025 4:03 PM
106	see protein-protein interaction in a map like STRING and links to references like in BioGrid	11/1/2025 1:02 PM
107	Already very good and useful. There's lots of cool upgrades but quite time consuming to keep up with the changes and upgrades, would be great to have some tutorial document or youtube video to learn from.	11/1/2025 12:41 PM
108	Not at this time	11/1/2025 6:36 AM
109	nothing	11/1/2025 5:56 AM
110	Can't think of any.	10/31/2025 9:27 PM
111	Not right now	10/31/2025 8:46 PM
112	If we can search in pombase with sequence like ncbi that would be helpful	10/31/2025 7:14 PM
113	I find it very easy to navigate compared to other databases	10/31/2025 6:40 PM
114	Yes, while using Genome browser , zoom-in is easy but inconvenient to zoom-out.	10/31/2025 5:05 PM
115	None, it's great!	10/31/2025 4:32 PM
116	It would be greatly appreciated if the information could be updated to the most recent date.	10/31/2025 3:18 PM
117	NO	10/31/2025 3:13 PM
118	To mark in genome browser different things, in example, integrations of auxotrophy genes (ura4, ade6...) in heterochromatin domains as otr1, imr1, tel(1L) an so on.	10/31/2025 3:12 PM
119	no	10/31/2025 1:38 PM
120	No	10/31/2025 1:26 PM
121	NA	10/31/2025 12:57 PM
122	the phenotypes have different names for very similar phenotypes. It would be good if we could group these somehow for the purposes of advanced search, for example if you want all genes	10/31/2025 12:23 PM

	that show decreased growth in nitrogen starvation and G0, which nearly overlap but not quite?	
123	-	10/31/2025 11:51 AM
124	No	10/31/2025 11:24 AM
125	Keep building the mega model! That's been very helpful for big picture thinking.	10/31/2025 11:21 AM
126	I am very happy with the current interface.	10/31/2025 11:19 AM
127	Honestly, not much. Modernize the interface if I had to choose.	10/31/2025 11:15 AM
128	I think that it is perfect as it is	10/31/2025 11:11 AM
129	nothing	10/31/2025 12:11 AM
130	great as it is	10/30/2025 9:07 PM
131	smoother user interface	10/30/2025 8:52 PM
132	It would be nice to have a designated curator to compile information for ease of access. For example, myo2-E1(G345R aa) is listed under both "abolished protein localization to actomyosin contractile ring" and "normal protein localization to actomyosin contractile ring"...	10/30/2025 7:35 PM
133	No	10/30/2025 6:17 PM
134	No	10/30/2025 2:15 PM
135	I would not alter the interface - it is one of the best for accessing genome data.	10/30/2025 1:37 PM
136	One thing that I think is missing or would be useful is a short functional description of the gene/protein, especially if you look up genes/proteins you never worked with or are in general new to yourself.	10/30/2025 1:22 PM
137	For phenotype and interaction data it would be useful to know if it was manual or high throughput	10/30/2025 12:58 PM
138	I think it is already very useful	10/30/2025 12:26 PM
139	No its perfect	10/30/2025 12:11 PM
140	More general and useful interface might be insufficient than Uniprot or other BIG platforms. More specific interface for the pombe researchers might be the key for the future.	10/30/2025 12:06 PM
141	I think that the interface is really user-friendly	10/30/2025 11:49 AM
142	N/A	10/30/2025 11:46 AM
143	The home page can be a little overwhelming to a new user. The welcome message is great, but there are links underneath it to the "tools", "genome browser", etc. which can all be accessed from the drop downs at the top of the page (I think). The news section is incredibly useful and I would suggest putting it on its own tab/drop down menu, but I'm not sure what you would replace it with on the home page.	10/28/2025 8:33 PM
144	No	10/28/2025 11:17 AM
145	I think it is an excellent platform. Its continuous updates have been very useful.	10/28/2025 10:59 AM
146	It would be great to have a more direct disease association annotation	10/28/2025 10:42 AM
147	I want to know the relationship between phenotype and publication.	10/28/2025 9:44 AM
148	n	10/27/2025 2:29 PM
149	no	10/27/2025 9:04 AM
150	None, looks great as it is	10/27/2025 8:29 AM
151	Nothing at the moment. Pombase is already very user-friendly.	10/25/2025 1:38 PM
152	Availability of protein sequence NCBI accessions (not gene names). As an example, pdc201 should appear plainly spelled out as NP_594083.1. NCBI accessions should then be available in the option for download of a list of genes.	10/24/2025 4:09 PM

153	I think that everything is very clear	10/24/2025 1:12 PM
154	no	10/24/2025 5:50 AM
155	improve JBbrowser	10/24/2025 5:35 AM
156	No	10/24/2025 4:39 AM
157	No improvements needed	10/24/2025 3:19 AM
158	I want references(link of papers) at phenotype of each mutant. I want to know whether those phenotypes were obtained through comprehensive analysis or observed by disrupting a single gene.	10/24/2025 2:13 AM
159	None, the interface is very friendly.	10/23/2025 11:41 PM
160	I'm used to finding the downloads page for the genome sequence/annotation data. But it was a bit hard to find at first and takes some time for students I mentor to get used to. If there was an option under downloads at the top bar that leads to the main genome dataset page directly, that might make it more new user friendly? Not sure if this is better but just a suggestion	10/23/2025 8:44 PM
161	Too much information is presented together. Unreliable data from high throughput screen are presented as facts, leading to numerous inconsistent data for individual genes. It needs more curation instead of packing in everything that comes out	10/23/2025 7:58 PM
162	Na	10/23/2025 7:53 PM
163	The current interface is great/better than most, I can't think of improvements	10/23/2025 7:40 PM
164	At the end of the page for each gene in the publication list it would be great to have a link going immediately to the publication in a new window, rather than going to a new pombase window with the abstract.	10/23/2025 6:22 PM
165	sometimes I cant find an easy link to genome browser that I feel was easier to access before.	10/23/2025 5:49 PM
166	I think it is quite informative and intuitive as it is now.	10/23/2025 4:22 PM
167	A tutorial page with general instructions. Some of the features are not easy to figure out.	10/23/2025 3:51 PM
168	No	10/23/2025 3:49 PM
169	No, it is a great resource as is!	10/23/2025 3:43 PM
170	I think a more detailed summary of what each gene does would be helpful. For example SGD has a small paragraph summarizing the gene functions for each entry, and I find this very useful to get an idea of what a gene does, in conjunction with the GO annotations.	10/23/2025 3:32 PM
171	Frankly, I think the work at PomBase has been fantastic and I could not personally improve upon the site.	10/23/2025 2:59 PM
172	better linking the external data resources (some are older, like PombeTV, and linking out and then searching becomes challenging at times) -perhaps an initiative to have PIs of external resources that are >10 yr old to provide a statement or resource that aligns that previous resource with newer datasets	10/23/2025 2:57 PM
173	-	10/23/2025 2:42 PM
174	Not currently	10/23/2025 2:30 PM
175	To make Genome browser more user friendly or include more tutorials for available features	10/23/2025 2:06 PM
176	n/a	10/23/2025 1:46 PM
177	With all the new tools available, I feel like I could use a tutorial or a video to learn about the tools and how to apply them.	10/23/2025 1:21 PM
178	We're very satisfied with the current database — it meets all our needs.	10/23/2025 1:12 PM
179	No	10/23/2025 12:24 PM
180	Maybe, it might be a good idea to include a small microscopy image or a section showing the normal location of the protein in question in a wildtype cell.	10/23/2025 11:59 AM

181	Along with genome browser, pombase can predict the linkages between the gene searched and nearby genes	10/23/2025 11:49 AM
182	no	10/23/2025 11:29 AM
183	The database is presently working extremely well, very intuitive and informative.	10/23/2025 11:21 AM
184	No.	10/23/2025 11:15 AM
185	I would suggest using different colours for the panels. E.g. blue for Gene ontology, pink for Phenotype and so on.	10/23/2025 11:11 AM
186	No	10/23/2025 10:58 AM
187	As an optional, homologous protein information to higher eukaryotes can be increased. Now there are only three (Homo sapiens, Schizosaccharomyces japonicus, and Saccharomyces cerevisiae) . Additionally, I am not very good at using English, so, basic instruction of using PomBase can be translated to various languages to enhance the accessibility of multiple contents. Because, from this survey form, I could know various functions I could have not recognized before.	10/23/2025 10:50 AM
188	It is easy to use already.	10/23/2025 10:48 AM
189	Now that I'm used to it it works perfectly for me.	10/23/2025 10:24 AM
190	The section of Phenotype in the Gene page is sometimes huge and hard to comprehend the overview. For instance, a summary matrix that quickly shows what conditions (nutrients, substances, temperature etc) are positive or negative on mutant strains would help a lot.	10/23/2025 10:22 AM
191	I think it's great!	10/23/2025 10:20 AM
192	I am currently not that research-active, so haven't delved very deep into new features yet. However, compared to other similar databases the Pombase one is much clearer laid out and more intuitive to use.	10/23/2025 10:19 AM
193	N/A	10/23/2025 10:11 AM
194	Having recently moved into working on other fungi has given me a renewed appreciation for the high quality user friendly Pombase interface	10/23/2025 10:03 AM
195	NA	10/23/2025 9:51 AM
196	I do not know how to use GO-CAM pathways.....	10/23/2025 9:51 AM
197	I would appreciate it if I could quickly check where the gene is located on the chromosome graphically (like the SGD).	10/23/2025 9:49 AM
198	I find it very practical	10/22/2025 2:12 PM
199	I find it sometimes difficult to find my way retrieving data sets (like gene list with functions). Eventually, I find them but it seem less intuitive	10/21/2025 5:42 PM
200	No, the interface is very clear and well laid out	10/21/2025 5:30 PM
201	Highlight the residues in the protein sequence (section sequence and transcripts) that are subject to PTM or mutation.	10/21/2025 3:15 PM
202	Color-coded interactions? (a bit like on BioGRID)?	10/21/2025 12:05 AM
203	I don't have suggestions, I quite like the interface.	10/20/2025 6:36 PM
204	include some tutorials for the students to get started	10/17/2025 7:03 PM
205	Maybe it is already fixed, but in past I could not export expression profiles over gene regions of interest...	10/17/2025 3:02 PM
206	It would be better if PomBase can perform GO enrichment analysis and other ontology enrichment analysis including their slim ontology enrichment analysis.	10/17/2025 4:37 AM
207	Sometimes I feel that there are a number of genetic or physical interacting factors in some genes. It would be helpful if some values were included for each of these factor.	10/17/2025 4:35 AM
208	None	10/17/2025 1:56 AM

209	As far as I know Pombase does not have a gene ontology enrichment tool. If true it would be a great feature to have.	10/17/2025 1:00 AM
210	no	10/16/2025 9:36 PM
211	highlight data found in external references, such as the location of the protein, for example.	10/16/2025 8:33 PM
212	No	10/16/2025 6:39 PM
213	None, it is perfect	10/16/2025 4:28 PM
214	I like it as it is	10/16/2025 4:16 PM
215	no	10/16/2025 3:44 PM
216	no	10/16/2025 2:49 PM
217	It's already very clear and practical as is	10/16/2025 1:47 PM
218	not really	10/16/2025 1:07 PM
219	Sorry, I have no idea. It is very comfortable.	10/16/2025 12:50 PM
220	For DNA binding proteins (for example transcription factors) it would be useful to include links to GEO databases of ChIP data to find genome binding sites.	10/16/2025 12:17 PM
221	I'd like to be able to get back to the top of page without scrolling.	10/16/2025 11:52 AM
222	The PomBase interface is great	10/13/2025 8:01 AM
223	na	10/12/2025 5:48 PM

Q9 Are there data, information, or functionalities, that you find difficult to locate in PomBase?

Answered: 225 Skipped: 425

#	RESPONSES	DATE
1	easy to used rather then other site	11/18/2025 3:44 PM
2	No	11/18/2025 2:53 PM
3	N/A	11/18/2025 3:04 AM
4	No	11/17/2025 5:07 PM
5	nope	11/17/2025 4:40 PM
6	No	11/17/2025 4:15 PM
7	Everything is clear	11/17/2025 4:12 PM
8	No	11/17/2025 1:16 PM
9	protein abundance	11/17/2025 6:34 AM
10	no	11/17/2025 2:39 AM
11	It is hoped that searching for the specific location of a certain chromosome can lead to the discovery of some unknown genes, rather than just searching for gene names or numbers.	11/16/2025 4:08 PM
12	No	11/16/2025 1:08 AM
13	Genotypic information sometimes are missing for some pombe strains.	11/15/2025 1:34 PM
14	Like I am working on heterochromatin, I always search dg dh sequences, these data are missing.	11/15/2025 1:15 AM
15	No	11/14/2025 4:41 AM
16	chromosome telomeres	11/14/2025 4:22 AM
17	No	11/13/2025 5:34 PM
18	Non-coding gene information. Cent, rDNA, and telomere.	11/13/2025 4:56 PM
19	No	11/13/2025 1:06 PM
20	Information regarding sequences related to repetitive and silenced genomic regions (i.e., mating type locus, centromeric repeats, telomeres) is hard to find and integrate into existing genome sequence/annotation files. Some advanced search options and general organism information can be hard to find.	11/13/2025 12:06 PM
21	search for phenotypes of well established mutants of a given gene (separation of function, interaction domain, site of PTM)	11/13/2025 10:17 AM
22	No	11/13/2025 8:54 AM
23	-	11/13/2025 8:11 AM
24	No	11/13/2025 7:01 AM
25	No	11/13/2025 5:12 AM
26	no problem	11/13/2025 3:51 AM
27	yes	11/13/2025 3:09 AM
28	No	11/13/2025 12:17 AM

29	no	11/13/2025 12:11 AM
30	Genome annotations for TSS and TES	11/12/2025 10:14 PM
31	A gz version of genome annotations	11/12/2025 9:00 PM
32	No	11/12/2025 8:27 PM
33	Nope, all functionalities are easy to find!	11/12/2025 8:12 PM
34	NA	11/12/2025 8:07 PM
35	No	11/12/2025 7:41 PM
36	Strain information like mentioned above	11/12/2025 6:45 PM
37	no	11/12/2025 9:27 AM
38	telomere information maybe should be updated GO term, KEGG term is difficult to be accumulated	11/12/2025 9:06 AM
39	NA.	11/12/2025 9:01 AM
40	NA	11/12/2025 8:45 AM
41	no	11/12/2025 8:40 AM
42	NO	11/12/2025 7:53 AM
43	No	11/12/2025 7:48 AM
44	no	11/12/2025 7:27 AM
45	no	11/12/2025 6:38 AM
46	no	11/12/2025 6:38 AM
47	no	11/12/2025 6:37 AM
48	no	11/12/2025 6:35 AM
49	no	11/12/2025 6:17 AM
50	A little difficult	11/12/2025 6:03 AM
51	No	11/12/2025 4:35 AM
52	no	11/12/2025 3:04 AM
53	No.	11/12/2025 3:00 AM
54	No	11/12/2025 2:50 AM
55	When I copy DNA or protein sequences, the sequences are always distributed incorrectly.	11/12/2025 2:03 AM
56	Temporarily unavailable.	11/12/2025 2:00 AM
57	no	11/12/2025 1:34 AM
58	No	11/11/2025 11:59 PM
59	Not really. They take great care to make it clear.	11/11/2025 9:26 AM
60	No	11/11/2025 8:15 AM
61	No, all is clear	11/11/2025 8:00 AM
62	No	11/10/2025 10:56 PM
63	When as a first time researcher find the latest genome reference	11/10/2025 3:11 PM
64	I did not know about the GO-CAM models. However, I am in the US and fighting in this fascist research hellscape has made exploring anything new that is not directly grant related very difficult.	11/10/2025 2:12 PM
65	N/a	11/10/2025 1:43 PM

66	No	11/10/2025 11:43 AM
67	None	11/10/2025 10:25 AM
68	N/A	11/10/2025 10:04 AM
69	Everything is easy and clear	11/10/2025 9:37 AM
70	no	11/10/2025 9:31 AM
71	none	11/10/2025 9:18 AM
72	NA	11/8/2025 1:47 PM
73	none	11/8/2025 12:40 PM
74	no	11/8/2025 11:59 AM
75	..	11/7/2025 11:27 PM
76	No	11/7/2025 3:03 PM
77	No, I don't find any data, information, or functionalities difficult to locate in PomBase. The platform is very well structured, and everything is clearly organized. It's easy to navigate and quickly find the information you're looking for.	11/7/2025 2:29 PM
78	It seems difficult to find homologs in <i>S. pombe</i> and other organisms as well.	11/7/2025 11:10 AM
79	No	11/7/2025 10:46 AM
80	No, everything I need is easily accessible and simple to find!	11/7/2025 9:57 AM
81	It used to be difficult to find genome sequence for NGS, now is OK!	11/7/2025 9:32 AM
82	None	11/7/2025 9:07 AM
83	no	11/7/2025 9:02 AM
84	sometimes	11/5/2025 11:45 AM
85	No.	11/5/2025 11:45 AM
86	No	11/5/2025 8:44 AM
87	No, everything is very easy to locate	11/4/2025 7:50 PM
88	No	11/4/2025 6:39 PM
89	No, it is well organised	11/4/2025 3:45 PM
90	No	11/4/2025 1:04 PM
91	no	11/4/2025 12:46 PM
92	Thinking ahead I wonder if genomewide data such as RNA-seq and ChIP-seq could be somehow integrated into the browser so that differences in RNA levels or protein occupancy in condition X, Y, or Z could be visualised across the window. But it would need good QC and internal normalisation.	11/4/2025 12:00 PM
93	no	11/4/2025 6:18 AM
94	It would be helpful if it were a bit more optimized for data scraping.	11/4/2025 2:30 AM
95	The GO-CAM and MegaModel can be challenging to find.	11/3/2025 8:59 PM
96	No	11/3/2025 3:18 PM
97	N/A	11/3/2025 12:48 PM
98	No	11/3/2025 8:53 AM
99	No	11/3/2025 4:51 AM
100	Not found yet!	11/3/2025 4:20 AM

101	No	11/3/2025 3:49 AM
102	None	11/3/2025 12:59 AM
103	no	11/3/2025 12:50 AM
104	No.	11/3/2025 12:05 AM
105	No.	11/2/2025 11:36 AM
106	No.	11/2/2025 8:47 AM
107	No	11/2/2025 4:00 AM
108	No	11/1/2025 9:01 PM
109	No	11/1/2025 4:03 PM
110	protein-protein interaction conservation in eukaryotes	11/1/2025 1:02 PM
111	nothing	11/1/2025 5:56 AM
112	I feel as though it could be made easier to find homolog proteins in the search.	10/31/2025 9:27 PM
113	No	10/31/2025 8:46 PM
114	No	10/31/2025 7:14 PM
115	No	10/31/2025 6:40 PM
116	Using advance search	10/31/2025 5:05 PM
117	The gene expression could be hard to interpret, particularly if we want to know how it varies between different conditions.	10/31/2025 4:32 PM
118	No	10/31/2025 3:18 PM
119	NO	10/31/2025 3:13 PM
120	Not really. In general, It is easy to find data in PomBase. It is very well designed.	10/31/2025 3:12 PM
121	no	10/31/2025 1:38 PM
122	No	10/31/2025 1:26 PM
123	No	10/31/2025 12:57 PM
124	no	10/31/2025 12:29 PM
125	-	10/31/2025 11:51 AM
126	Imaging data could be displayed more clearly on gene pages	10/31/2025 11:24 AM
127	I generally get everything I need from you! Sometimes the physical interactions are difficult to interpret quickly.	10/31/2025 11:21 AM
128	No, most of them are easily accesible.	10/31/2025 11:19 AM
129	NO, everything is very straight forward and intuitive.	10/31/2025 11:15 AM
130	Not so far.	10/31/2025 11:11 AM
131	nothing	10/31/2025 12:11 AM
132	NO	10/30/2025 9:07 PM
133	I always forget that information about protein/gene mutations is nested under phenotypes.	10/30/2025 7:35 PM
134	No	10/30/2025 6:17 PM
135	No	10/30/2025 2:15 PM
136	No	10/30/2025 1:37 PM
137	No, there aren't	10/30/2025 12:26 PM

138	Uniprot ID	10/30/2025 12:11 PM
139	No	10/30/2025 11:49 AM
140	No, I think Pombase is very easy to use	10/30/2025 11:46 AM
141	I'm not sure if this exists already, but a bulk download feature (multiple genes at once) for orthologs in other fission yeast species could be useful.	10/28/2025 8:33 PM
142	No	10/28/2025 11:17 AM
143	No	10/28/2025 10:59 AM
144	Disease association	10/28/2025 10:42 AM
145	No	10/28/2025 9:44 AM
146	n	10/27/2025 2:29 PM
147	No	10/27/2025 11:56 AM
148	no	10/27/2025 9:04 AM
149	No	10/27/2025 8:29 AM
150	No	10/25/2025 1:38 PM
151	Very friendly searches	10/24/2025 1:32 PM
152	no	10/24/2025 1:12 PM
153	No.	10/24/2025 11:14 AM
154	no	10/24/2025 5:50 AM
155	no	10/24/2025 5:35 AM
156	No	10/24/2025 4:39 AM
157	none	10/24/2025 3:19 AM
158	no	10/24/2025 2:13 AM
159	No, I haven't had any problems.	10/23/2025 11:41 PM
160	no	10/23/2025 9:33 PM
161	I only really use pombase for genomic information and protein sequence information. All of those are easy to find and identify, but I don't like using it for phenotypes because the type of screen used isn't identified and knowing for example if a phenotype was found in a large screen versus and small mechanistic paper changes interpretation greatly.	10/23/2025 8:44 PM
162	The centromeres and telomeres sequences data and telomere to telomeres assembly are missing or buried. There is too much focus on Gene Ontology, which is unreliable. There should more focus on curating actual data and associate it with the proper gene.	10/23/2025 7:58 PM
163	Na	10/23/2025 7:53 PM
164	I think that some of the tools are apparent to experts in big data analysis but can be a little confusing to the naive among us	10/23/2025 7:48 PM
165	No	10/23/2025 7:01 PM
166	finding ortologs of genes in not innately clear	10/23/2025 6:22 PM
167	portein complexes is hit or miss.	10/23/2025 5:49 PM
168	No	10/23/2025 3:49 PM
169	No	10/23/2025 3:43 PM
170	No	10/23/2025 3:32 PM
171	I think the certain annotations for parts of proteins can be difficult to find.	10/23/2025 2:59 PM

172	-Very challenging to download data for ChIP seq, etc. Not sure why, but hard to find lists and files that would allow data use. -Also, GO terms is challenging to download annotation sets and directions	10/23/2025 2:57 PM
173	-	10/23/2025 2:42 PM
174	No	10/23/2025 2:30 PM
175	No, it's all very easy to locate.	10/23/2025 2:30 PM
176	No	10/23/2025 2:06 PM
177	very easy	10/23/2025 1:54 PM
178	n/a	10/23/2025 1:46 PM
179	The features I use most on Pombase are quite intuitive.	10/23/2025 1:21 PM
180	We're very satisfied with the current database — it meets all our needs.	10/23/2025 1:12 PM
181	No	10/23/2025 12:24 PM
182	Nothing!! Is perfect the interface and is very simple to find everything	10/23/2025 11:59 AM
183	No	10/23/2025 11:49 AM
184	This survey has actually been really useful for revealing some I didn't know about -is there a master document/guide somewhere that walks through each of these different features?	10/23/2025 11:29 AM
185	Not at all	10/23/2025 11:21 AM
186	No.	10/23/2025 11:15 AM
187	No, but the colour coding would simplify the orientation.	10/23/2025 11:11 AM
188	No	10/23/2025 10:58 AM
189	To get documented or putative protein modification sites.	10/23/2025 10:50 AM
190	No	10/23/2025 10:48 AM
191	I think it should be clearer which datasets to use for whole genome sequencing and RNAseq analysis. If I am correct there is no .gtf file which is required for some bioinformatics tool. Maybe a comprehensive approach to give which datasets to use for which commonly used tools?	10/23/2025 10:24 AM
192	Whereas most information is very easy to access, I find it difficult to collect information on how the mentioned functionalities were experimentally obtained (namely Methods). This information is almost invisible in PomBase.	10/23/2025 10:22 AM
193	Yes, it was difficult to find a downloadable file of the pombe genome to use on IGV.	10/23/2025 10:21 AM
194	Would love to have a direct link somewhere up on the landing page to Japonicus DB. I guess you now know who I am ;) But seriously, several people told me that it would be great to have it!	10/23/2025 10:20 AM
195	n/a	10/23/2025 10:19 AM
196	N/A	10/23/2025 10:11 AM
197	The consistency over the years has made all features easily accessible	10/23/2025 9:51 AM
198	No	10/22/2025 2:12 PM
199	see question 8	10/21/2025 5:42 PM
200	No	10/21/2025 5:30 PM
201	no	10/21/2025 3:15 PM
202	Alternative transcriptional start sites / integrating the different CAGE datasets to have a clearer idea of functional 5' and 3' end sites on genes	10/21/2025 12:05 AM
203	Well I hadn't previously used the GO-CAM models, so I will look at those more.	10/20/2025 6:36 PM

204	The pombe genome to upload to use in IGV.	10/18/2025 9:15 PM
205	homology to other species, cerevisiae or human for example	10/17/2025 7:03 PM
206	Somehow, it is really not easy to find information on centromeres - their genomic size and coordinates etc... And on total (typical) size of Ch III, as info their is on sequenced part, leaving one wonder how big are ribosomal DNA regions...	10/17/2025 3:02 PM
207	The FYPO.obo file is difficult to locate since the latest one is one the FYPO github page. It should be in the PomBase FTP server.	10/17/2025 4:37 AM
208	Nothing in particular.	10/17/2025 4:35 AM
209	None	10/17/2025 1:56 AM
210	I do find it hard to use the advance search tool to say pull up gene lists. I know I could read the documentation. But it would be nice if it were intuitive.	10/17/2025 1:00 AM
211	no	10/16/2025 9:36 PM
212	If they are known, the sequence where binds transcription factor (cis-region) or other motifs binding motifs ...	10/16/2025 8:33 PM
213	No	10/16/2025 6:39 PM
214	I still find moving around the genome browser or sending genome browser sequences to FASTA challenging but this might be me.	10/16/2025 4:31 PM
215	No	10/16/2025 4:28 PM
216	No, everything is easily accesible	10/16/2025 4:16 PM
217	no	10/16/2025 3:44 PM
218	no	10/16/2025 2:49 PM
219	no	10/16/2025 2:25 PM
220	the advanced search	10/16/2025 1:07 PM
221	No, there aren't	10/16/2025 12:50 PM
222	No	10/16/2025 12:44 PM
223	No	10/16/2025 12:17 PM
224	Things can be a little difficult to track down. Would be good if more terms were searchable. I often have to look around in the various tabs to track something down or if I'm showing someone a feature. (But this may just be my poor memory.)	10/16/2025 11:52 AM
225	na	10/12/2025 5:48 PM

Q10 If you have integrated PomBase data with your own tools or pipelines, do you have any suggestion to make the data easier to access or use?

Answered: 174 Skipped: 476

#	RESPONSES	DATE
1	no	11/19/2025 12:18 PM
2	Na	11/18/2025 2:53 PM
3	N/A	11/18/2025 3:04 AM
4	No	11/17/2025 5:07 PM
5	nope	11/17/2025 4:40 PM
6	No	11/17/2025 4:15 PM
7	Genomic coordinates and gene annotations for easy NGS data analysis.	11/17/2025 4:12 PM
8	no	11/17/2025 6:34 AM
9	no	11/17/2025 2:39 AM
10	No	11/16/2025 1:08 AM
11	Highlight the start codon and stop codon of genes, it will be handy	11/15/2025 1:34 PM
12	integrate NCBI-Blast, would be useful for alignment.	11/15/2025 1:15 AM
13	NA	11/14/2025 9:22 PM
14	No	11/14/2025 4:41 AM
15	No	11/13/2025 5:34 PM
16	N/A	11/13/2025 4:56 PM
17	Sorry	11/13/2025 1:06 PM
18	Integrating the existing GO annotation files with tools in R or analogous programs can be tricky. Furthermore, there doesn't seem to be a file or vignette for dealing with semantic similarities between related GO terms (besides the new GO-CAM models) which can lead to more subjective interpretations in pathway analyses. The GO slim information may be useful, however these are difficult to get as a single file from Pombase.	11/13/2025 12:06 PM
19	N/A	11/13/2025 8:54 AM
20	-	11/13/2025 8:11 AM
21	N/A	11/13/2025 7:01 AM
22	Allow each user to favourite certain genes which gives quicker access and even offline access to us. Adding protein - protein interactions/ prediction tool would be good too.	11/13/2025 5:12 AM
23	I am using it with satisfaction.	11/13/2025 3:51 AM
24	maybe	11/13/2025 3:09 AM
25	N/A	11/13/2025 12:17 AM
26	no	11/13/2025 12:11 AM
27	n/a	11/12/2025 10:14 PM
28	Upgrade biomart database so downloading data from r will be updated	11/12/2025 9:00 PM
29	N/A	11/12/2025 8:27 PM

30	Perhaps a universal file format? Some data have one type of format, whereas some have a different type of file format. One type would make it easier for computational and bioinformatic analysis	11/12/2025 8:12 PM
31	NA	11/12/2025 8:07 PM
32	We have not done that yet.	11/12/2025 7:41 PM
33	NA.	11/12/2025 9:01 AM
34	NA	11/12/2025 8:45 AM
35	no	11/12/2025 8:40 AM
36	NO	11/12/2025 7:53 AM
37	No	11/12/2025 7:48 AM
38	no	11/12/2025 7:27 AM
39	no	11/12/2025 6:38 AM
40	no	11/12/2025 6:38 AM
41	no	11/12/2025 6:37 AM
42	no	11/12/2025 6:35 AM
43	no	11/12/2025 6:17 AM
44	Nothing	11/12/2025 6:03 AM
45	No	11/12/2025 4:35 AM
46	no	11/12/2025 3:04 AM
47	No.	11/12/2025 3:00 AM
48	No	11/12/2025 2:50 AM
49	no	11/12/2025 2:03 AM
50	Temporarily unavailable.	11/12/2025 2:00 AM
51	stick to	11/12/2025 1:34 AM
52	Not yet	11/11/2025 11:59 PM
53	No	11/11/2025 9:26 AM
54	No	11/11/2025 8:15 AM
55	No	11/10/2025 10:56 PM
56	N/A	11/10/2025 3:11 PM
57	Not applicable.	11/10/2025 2:12 PM
58	N/a	11/10/2025 1:43 PM
59	No	11/10/2025 11:43 AM
60	I have not integrated Pombase data with my own tools yet.	11/10/2025 10:25 AM
61	N/A	11/10/2025 10:04 AM
62	Didn't do such integration	11/10/2025 9:37 AM
63	NA	11/10/2025 9:31 AM
64	n/a	11/10/2025 9:18 AM
65	I previously attempted to transfer the product description of <i>S. pombe</i> to other fission yeast species based on orthologous gene relationships and submitted the annotated genomes to NCBI GenBank. I found that a significant number of gene product descriptions failed NCBI's	11/8/2025 1:47 PM

inspection because they contained words that NCBI deems inappropriate, such as "XX homolog" or "XX ortholog." Could you provide a set of gene product descriptions that pass inspection? I assume PomBase regularly updates its version to GenBank.

66	no	11/8/2025 11:59 AM
67	..	11/7/2025 11:27 PM
68	No	11/7/2025 3:03 PM
69	No	11/7/2025 10:46 AM
70	no	11/7/2025 9:02 AM
71	n/a	11/5/2025 11:45 AM
72	N/A	11/5/2025 11:45 AM
73	No	11/5/2025 8:44 AM
74	n/a	11/4/2025 7:50 PM
75	Links to papers that the specific information came from.	11/4/2025 6:39 PM
76	no	11/4/2025 12:46 PM
77	Cant think of anything right now.	11/4/2025 12:00 PM
78	Not applicable	11/3/2025 3:18 PM
79	N/A	11/3/2025 12:48 PM
80	No suggestions	11/3/2025 8:53 AM
81	NA	11/3/2025 4:51 AM
82	Not found yet!	11/3/2025 4:20 AM
83	No	11/3/2025 3:49 AM
84	no	11/3/2025 12:50 AM
85	Official account news.	11/2/2025 11:36 AM
86	No.	11/2/2025 8:47 AM
87	No	11/2/2025 4:00 AM
88	N/A	11/1/2025 4:03 PM
89	nothing	11/1/2025 5:56 AM
90	NA	10/31/2025 9:27 PM
91	Not right now	10/31/2025 8:46 PM
92	I don't have such data.	10/31/2025 6:40 PM
93	No, it is good	10/31/2025 3:18 PM
94	NO	10/31/2025 3:13 PM
95	N/A	10/31/2025 3:12 PM
96	no	10/31/2025 1:38 PM
97	No	10/31/2025 1:26 PM
98	No	10/31/2025 12:57 PM
99	-	10/31/2025 11:51 AM
100	N/A	10/31/2025 11:24 AM
101	--	10/31/2025 11:19 AM

PomBase User Survey 2025		SurveyMonkey
102	NA	10/31/2025 11:15 AM
103	N/A	10/31/2025 11:11 AM
104	nothing	10/31/2025 12:11 AM
105	N/A	10/30/2025 9:07 PM
106	N/A	10/30/2025 6:17 PM
107	No	10/30/2025 2:15 PM
108	No	10/30/2025 1:37 PM
109	Uniprot IDs as well as Pombase names	10/30/2025 12:11 PM
110	I, computational scientist, use my own program, so I need easier downloading of whole data, somehow raw ones.	10/30/2025 12:06 PM
111	No	10/30/2025 11:49 AM
112	N/A	10/30/2025 11:46 AM
113	Na	10/28/2025 11:17 AM
114	No	10/28/2025 10:59 AM
115	N/A	10/28/2025 10:42 AM
116	No	10/28/2025 9:44 AM
117	na	10/27/2025 9:04 AM
118	No	10/27/2025 8:29 AM
119	-	10/25/2025 1:38 PM
120	N/A	10/24/2025 1:12 PM
121	N/A	10/24/2025 11:14 AM
122	make GO analysis tool specific for pombe, as using stringdb/shinyGO sometimes gives redundant processes	10/24/2025 5:35 AM
123	No	10/24/2025 4:39 AM
124	none	10/24/2025 3:19 AM
125	no	10/24/2025 2:13 AM
126	Our group has a dataset regarding single-cell-based expression profile upon germination from dormancy. I hope let the data included (or linked?) in the pombase. I have asked once when we published the dataset, but it did not come true.	10/24/2025 1:24 AM
127	I have not participated in the PomBase data integration.	10/23/2025 11:41 PM
128	Others in my lab may use this. I don't.	10/23/2025 9:33 PM
129	N/A just download datasets I need	10/23/2025 8:44 PM
130	More streamlined gene page. Clear separation between High Throughput data (which have a significant error rate) and actual focused data. Essentiality should never be annotated from HT data. There has been instance when an essential gene, annotated as such, had its annotation wrongly changed to viable on the basis of HT data. This kind of over-reliance on HT data has made pombase riddled with inaccurate annotation and much less useful than even a few years ago.	10/23/2025 7:58 PM
131	n/a	10/23/2025 6:22 PM
132	No	10/23/2025 3:49 PM
133	No	10/23/2025 3:43 PM
134	Not currently	10/23/2025 2:59 PM

135	-I've been trying to use genome data (i.e. ChIP-seq) with an in-house algorithm, but having issues	10/23/2025 2:57 PM
136	-	10/23/2025 2:42 PM
137	No, it's fairly simply.	10/23/2025 2:30 PM
138	n/a	10/23/2025 1:46 PM
139	We're very satisfied with the current database — it meets all our needs.	10/23/2025 1:12 PM
140	No	10/23/2025 12:24 PM
141	No suggestions	10/23/2025 11:59 AM
142	No	10/23/2025 11:49 AM
143	no	10/23/2025 11:29 AM
144	In	10/23/2025 11:21 AM
145	I did not have the opportunity to do this.	10/23/2025 11:15 AM
146	No.	10/23/2025 11:11 AM
147	No	10/23/2025 10:58 AM
148	I have no idea but it can be adjust to Mobile Applications.	10/23/2025 10:50 AM
149	N/A	10/23/2025 10:48 AM
150	I have not	10/23/2025 10:24 AM
151	(I have not made my own pipelines.)	10/23/2025 10:22 AM
152	N/A	10/23/2025 10:20 AM
153	n/a	10/23/2025 10:19 AM
154	N/A	10/23/2025 10:11 AM
155	NA	10/23/2025 9:51 AM
156	I don't have	10/22/2025 2:12 PM
157	n/a	10/21/2025 5:42 PM
158	No	10/21/2025 5:30 PM
159	It's actually really good and useful with students because of the interface!	10/21/2025 3:15 PM
160	All good as is at the moment	10/21/2025 12:05 AM
161	No suggestions.	10/20/2025 6:36 PM
162	It is good enough now for me.	10/17/2025 4:37 AM
163	I have never tried to integrate PmBase with other tools.	10/17/2025 4:35 AM
164	None	10/17/2025 1:56 AM
165	N/A	10/16/2025 10:20 PM
166	no	10/16/2025 9:36 PM
167	N/A	10/16/2025 6:39 PM
168	No, I have not done; but other members of my lab have done it.	10/16/2025 4:16 PM
169	NA	10/16/2025 3:44 PM
170	no	10/16/2025 2:49 PM
171	NA	10/16/2025 1:07 PM
172	Sorry, I've no idea	10/16/2025 12:50 PM

173	no	10/16/2025 12:44 PM
174	na	10/12/2025 5:48 PM

Q11 Is there a genome browser dataset that you would like to see added to JBrowse? Please specify the source publication (DOI or PubMed ID)

Answered: 163 Skipped: 487

#	RESPONSES	DATE
1	replication origin data	11/19/2025 12:18 PM
2	Punned iD	11/18/2025 2:53 PM
3	N/A	11/18/2025 3:04 AM
4	No	11/17/2025 5:07 PM
5	nope	11/17/2025 4:40 PM
6	No	11/17/2025 4:15 PM
7	no	11/17/2025 4:12 PM
8	yes	11/17/2025 6:34 AM
9	no	11/17/2025 2:39 AM
10	miRNA/siRNA database	11/16/2025 4:08 PM
11	No	11/16/2025 1:08 AM
12	NA	11/15/2025 1:34 PM
13	not at the moment.	11/15/2025 1:15 AM
14	pubmed ID	11/14/2025 7:42 PM
15	pubmed	11/14/2025 2:34 PM
16	No	11/14/2025 4:41 AM
17	No	11/13/2025 5:34 PM
18	Looks good now.	11/13/2025 4:56 PM
19	Plant	11/13/2025 1:06 PM
20	No	11/13/2025 8:54 AM
21	-	11/13/2025 8:11 AM
22	N/A	11/13/2025 7:01 AM
23	No	11/13/2025 5:12 AM
24	none	11/13/2025 3:51 AM
25	yes	11/13/2025 3:09 AM
26	no	11/13/2025 12:11 AM
27	n/a	11/12/2025 10:14 PM
28	more datasets would be good in general	11/12/2025 8:15 PM
29	NA	11/12/2025 8:07 PM
30	I cannot think of any at this time.	11/12/2025 7:41 PM
31	NA.	11/12/2025 9:01 AM

32	NA	11/12/2025 8:45 AM
33	no	11/12/2025 8:40 AM
34	NO	11/12/2025 7:53 AM
35	No	11/12/2025 7:48 AM
36	no	11/12/2025 7:27 AM
37	no	11/12/2025 6:38 AM
38	no	11/12/2025 6:38 AM
39	no	11/12/2025 6:35 AM
40	no	11/12/2025 6:17 AM
41	Nothing	11/12/2025 6:03 AM
42	No	11/12/2025 4:35 AM
43	no	11/12/2025 3:04 AM
44	No.	11/12/2025 3:00 AM
45	No	11/12/2025 2:50 AM
46	no	11/12/2025 2:03 AM
47	yes	11/12/2025 2:00 AM
48	yes	11/12/2025 1:34 AM
49	PubMed ID	11/11/2025 11:59 PM
50	No	11/11/2025 9:26 AM
51	No	11/11/2025 8:15 AM
52	in general more variable datasets would be good.	11/11/2025 8:00 AM
53	No	11/10/2025 10:56 PM
54	Pubmed	11/10/2025 3:11 PM
55	No.	11/10/2025 2:12 PM
56	https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1010462	11/10/2025 1:43 PM
57	No	11/10/2025 11:43 AM
58	Not any I can think of	11/10/2025 10:25 AM
59	N/A	11/10/2025 10:04 AM
60	no	11/10/2025 9:31 AM
61	n/a	11/10/2025 9:18 AM
62	NA	11/8/2025 1:47 PM
63	human	11/8/2025 12:40 PM
64	no	11/8/2025 11:59 AM
65	.	11/7/2025 11:27 PM
66	No	11/7/2025 3:03 PM
67	No	11/7/2025 10:46 AM
68	Both DOI and PubMed ID	11/7/2025 9:05 AM
69	no	11/7/2025 9:02 AM

70	n/a	11/5/2025 11:45 AM
71	No	11/5/2025 11:45 AM
72	No	11/5/2025 8:44 AM
73	n/a	11/4/2025 7:50 PM
74	No	11/4/2025 6:39 PM
75	no	11/4/2025 12:46 PM
76	It would be good to be able to visualise where DNA binding/chromatin associated proteins are enriched in wild-type cells e.g. Telomeric proteins, Centromere Proteins Transcription factors.	11/4/2025 12:00 PM
77	Not particularly	11/3/2025 3:18 PM
78	N/A	11/3/2025 12:48 PM
79	Not found yet!	11/3/2025 4:20 AM
80	PubMed ID will be perfect	11/3/2025 3:49 AM
81	no	11/3/2025 12:50 AM
82	Species classification.	11/2/2025 11:36 AM
83	DOI	11/2/2025 9:09 AM
84	No.	11/2/2025 8:47 AM
85	No	11/2/2025 4:00 AM
86	No	11/1/2025 4:03 PM
87	nothing	11/1/2025 5:56 AM
88	NA	10/31/2025 9:27 PM
89	No	10/31/2025 8:46 PM
90	No	10/31/2025 6:40 PM
91	No	10/31/2025 3:18 PM
92	No	10/31/2025 3:13 PM
93	Right now, for my research, I'm fine with datasets added to the new genome browser.	10/31/2025 3:12 PM
94	no	10/31/2025 1:38 PM
95	No	10/31/2025 1:26 PM
96	DOI	10/31/2025 12:57 PM
97	-	10/31/2025 11:51 AM
98	N/A	10/31/2025 11:24 AM
99	--	10/31/2025 11:19 AM
100	NA	10/31/2025 11:15 AM
101	N/A	10/31/2025 11:11 AM
102	nothing	10/31/2025 12:11 AM
103	N/A	10/30/2025 9:07 PM
104	No	10/30/2025 6:17 PM
105	No	10/30/2025 2:15 PM
106	NO	10/30/2025 12:11 PM
107	No	10/30/2025 11:49 AM

108	N/A	10/30/2025 11:46 AM
109	No	10/28/2025 11:17 AM
110	Cannot think of one.	10/28/2025 10:59 AM
111	N/A	10/28/2025 10:42 AM
112	No	10/28/2025 9:44 AM
113	na	10/27/2025 9:04 AM
114	https://doi.org/10.1038/ng.3215	10/27/2025 8:29 AM
115	-	10/25/2025 1:38 PM
116	No	10/24/2025 1:12 PM
117	not yet	10/24/2025 5:35 AM
118	No	10/24/2025 4:39 AM
119	none	10/24/2025 3:19 AM
120	no	10/24/2025 2:13 AM
121	None	10/23/2025 11:41 PM
122	no	10/23/2025 9:33 PM
123	N/A	10/23/2025 8:44 PM
124	DOI	10/23/2025 6:22 PM
125	https://doi.org/10.1038/s41467-020-20595-1	10/23/2025 4:22 PM
126	PMID: 39747188; PMID: 25024163	10/23/2025 3:51 PM
127	No	10/23/2025 3:49 PM
128	No	10/23/2025 3:43 PM
129	Not currently	10/23/2025 2:59 PM
130	can't think of anything	10/23/2025 2:57 PM
131	-	10/23/2025 2:42 PM
132	No, I'm happy with what is available.	10/23/2025 2:30 PM
133	n/a	10/23/2025 1:46 PM
134	We're very satisfied with the current database — it meets all our needs.	10/23/2025 1:12 PM
135	No	10/23/2025 12:24 PM
136	Not really	10/23/2025 11:59 AM
137	No	10/23/2025 11:49 AM
138	no	10/23/2025 11:29 AM
139	Ideally, it would be nice to have Integrated tools for tagging/deletion/CRISPR etc, oligos design that can be found separately in other specific researchers websites that generously implement	10/23/2025 11:21 AM
140	No.	10/23/2025 11:15 AM
141	none	10/23/2025 11:11 AM
142	No	10/23/2025 10:58 AM
143	I have no information.	10/23/2025 10:50 AM
144	N/A	10/23/2025 10:48 AM
145	na	10/23/2025 10:24 AM

146	N/A	10/23/2025 10:20 AM
147	Can't think of one.	10/23/2025 10:19 AM
148	N/A	10/23/2025 10:11 AM
149	NA	10/22/2025 2:12 PM
150	n/a	10/21/2025 5:42 PM
151	no	10/21/2025 5:30 PM
152	Can't think of one right now - will send information	10/21/2025 12:05 AM
153	No suggestions.	10/20/2025 6:36 PM
154	It is good enough now for me.	10/17/2025 4:37 AM
155	Nothing in particular.	10/17/2025 4:35 AM
156	no	10/16/2025 9:36 PM
157	N/A	10/16/2025 6:39 PM
158	N/A	10/16/2025 4:16 PM
159	no	10/16/2025 3:44 PM
160	no	10/16/2025 2:49 PM
161	Yes, stop using the old reference and instead use li-Lin Du's T2T sequence; it is error free	10/16/2025 1:07 PM
162	Sorry, I've no idea	10/16/2025 12:50 PM
163	na	10/12/2025 5:48 PM

Q12 Is there a new feature or functionality that you would like to see in PomBase (new data type, tool or display, new advanced search option, etc.)?

Answered: 168 Skipped: 482

#	RESPONSES	DATE
1	protein PTMs	11/19/2025 12:18 PM
2	NIA	11/18/2025 3:04 AM
3	No	11/17/2025 5:07 PM
4	nope	11/17/2025 4:40 PM
5	No	11/17/2025 4:15 PM
6	no	11/17/2025 4:12 PM
7	If interactions are available, show interacting residues in physical interaction panel.	11/17/2025 1:16 PM
8	protein abundance	11/17/2025 6:34 AM
9	no	11/17/2025 2:39 AM
10	GO enrichment for S pombe specifically. Currently I upload my gene list in metascape which sometimes does not identify pombe genes.	11/16/2025 1:08 AM
11	NA	11/15/2025 1:34 PM
12	BLAST	11/15/2025 1:15 AM
13	No	11/14/2025 4:41 AM
14	No	11/13/2025 5:34 PM
15	chip-seq data	11/13/2025 5:28 PM
16	N/A	11/13/2025 4:56 PM
17	May be	11/13/2025 1:06 PM
18	A BLAST option on homologous proteins or a simpler way to get to protein/sequence alignment tools would be useful	11/13/2025 12:06 PM
19	RNA expression / whole genome sequence	11/13/2025 8:54 AM
20	No	11/13/2025 8:54 AM
21	-	11/13/2025 8:11 AM
22	I am not sure if this function exists already in pombase, but I like looking at co-expression networks. I use a different website for that currently called coxpres.jp but would use it in pombase if available.	11/13/2025 7:01 AM
23	No	11/13/2025 5:12 AM
24	Even if it remains in its current state, it will be of great help to research.	11/13/2025 3:51 AM
25	yes	11/13/2025 3:09 AM
26	no	11/13/2025 12:11 AM
27	n/a	11/12/2025 10:14 PM
28	NA	11/12/2025 8:07 PM

29	Strain database / catalog	11/12/2025 6:45 PM
30	go term relationship list	11/12/2025 9:06 AM
31	NA.	11/12/2025 9:01 AM
32	NA	11/12/2025 8:45 AM
33	I think new advanced search would be great	11/12/2025 8:40 AM
34	NO	11/12/2025 7:53 AM
35	No	11/12/2025 7:48 AM
36	yes	11/12/2025 7:27 AM
37	no	11/12/2025 6:38 AM
38	no	11/12/2025 6:38 AM
39	no	11/12/2025 6:35 AM
40	no	11/12/2025 6:17 AM
41	Nothing	11/12/2025 6:03 AM
42	No	11/12/2025 4:35 AM
43	yes	11/12/2025 3:04 AM
44	No.	11/12/2025 3:00 AM
45	Yes	11/12/2025 2:50 AM
46	It would be more useful to include ortholog information of other fission yeast species (besides <i>S. japonicas</i>) in the future.	11/12/2025 2:43 AM
47	no	11/12/2025 2:03 AM
48	I don't have any ideas for the moment	11/12/2025 2:00 AM
49	no	11/12/2025 1:34 AM
50	Not yet	11/11/2025 11:59 PM
51	Maybe integration with predicted motifs from The Encyclopedia of Domains (ted) which itself is integrated with CATH. Maybe links to curated trees for each protein in key model species as given by egglog (unless it already exists)	11/11/2025 9:26 AM
52	No	11/11/2025 8:15 AM
53	No	11/10/2025 10:56 PM
54	No	11/10/2025 11:43 AM
55	The current features work well for us.	11/10/2025 10:25 AM
56	N/A	11/10/2025 10:04 AM
57	...	11/10/2025 9:31 AM
58	none	11/10/2025 9:18 AM
59	I believe that the function of Pombase in locating gene orthology relationships should be enhanced. 1. I suggest adding species other than Human and <i>S. japonicus</i> (such as other fission yeasts and other common model organisms like mice and zebrafish). 2. I suggest refining the orthology relationships, clarifying whether they are 1-vs-1 correspondences or other different correspondences.	11/8/2025 1:47 PM
60	no	11/8/2025 11:59 AM
61	..	11/7/2025 11:27 PM
62	Not yet	11/7/2025 10:46 AM

63	no	11/7/2025 9:02 AM
64	n/a	11/5/2025 11:45 AM
65	No	11/5/2025 11:45 AM
66	No	11/5/2025 8:44 AM
67	No	11/4/2025 7:50 PM
68	No	11/4/2025 6:39 PM
69	Ask AI: A tab for asking question and get answers generated by artificial intelligence. For example, if i ask "tell me the role of Raf1 in heterochromatin". It should give me a quick summary based on literature and suggest relevant articles. Further, PomBase has massive data of RNA-seq, ChIP-seq and others. I should be able to ask question precise question based on it. For example, does Clr4 localise on mat region upon loss of Swi6?	11/4/2025 4:44 PM
70	no	11/4/2025 12:46 PM
71	Annotation of cen1, cen2, cen3, tel1L, tel1R, tel2L, tel2R, tel3L and tel3R would help. The annotation of centromere and telomere regions could be improved by adding the known complete repetitive structures. Likewise the entire h90 mat1-mat2-mat3 region should be included in the browser. They can be taken from available long nanopore sequence reads if needed.	11/4/2025 12:00 PM
72	Yes, new advanced search option.	11/3/2025 8:58 PM
73	Not particularly	11/3/2025 3:18 PM
74	A web tool for identifying causative mutations from whole-genome sequence data like Mudi (Iida et al. 2014)	11/3/2025 12:48 PM
75	A short summary of the role of the gene/protein, like there is at SGD - I often hover over the SGD definition on the cerevisiae homologous link or go to the homologs page on SGD to get a nice idea of what the gene/protein is doing.	11/3/2025 12:35 PM
76	Not found yet!	11/3/2025 4:20 AM
77	New tools or new advanced search	11/3/2025 3:49 AM
78	no	11/3/2025 12:50 AM
79	RNAseq reads mapping data.	11/2/2025 11:36 AM
80	No.	11/2/2025 8:47 AM
81	No	11/2/2025 4:00 AM
82	Not really	11/1/2025 4:03 PM
83	how protein-protein interactions and geentic interactions are actually conserved in other models or organisms with reference links	11/1/2025 1:02 PM
84	nothing	11/1/2025 5:56 AM
85	Maybe a feature for homolog searching.	10/31/2025 9:27 PM
86	No	10/31/2025 8:46 PM
87	If possible, linking to AlphaFold would be great to run predictive interactions/complexes	10/31/2025 8:23 PM
88	Search for similar protein structure.	10/31/2025 6:40 PM
89	It would be helpful if the citation were linked to the original paper	10/31/2025 3:18 PM
90	No	10/31/2025 3:13 PM
91	N/A	10/31/2025 3:12 PM
92	no	10/31/2025 1:38 PM
93	No	10/31/2025 1:26 PM

94	No	10/31/2025 12:57 PM
95	-	10/31/2025 11:51 AM
96	As I work in microscopy, a collation of microscopy data with examples would be incredibly useful although would require a lot of work. ORFeome images are useful but often not representative of localisation patterns under native promoter	10/31/2025 11:24 AM
97	--	10/31/2025 11:19 AM
98	AI assistant, just to facilitate moving accross different tools, but of course it is much to ask.	10/31/2025 11:15 AM
99	N/A	10/31/2025 11:11 AM
100	nothing	10/31/2025 12:11 AM
101	N/A	10/30/2025 9:07 PM
102	No	10/30/2025 6:17 PM
103	No	10/30/2025 2:15 PM
104	I would love to a tools similar to Pattern-Matching on SGD - https://www.yeastgenome.org/nph-patmatch	10/30/2025 1:37 PM
105	NO	10/30/2025 12:11 PM
106	No	10/30/2025 11:49 AM
107	An advanced search option that allows you to look for non coding genomic regions like low complexity regions	10/30/2025 11:46 AM
108	This may also be a feature that exists that I didn't know about (or maybe this has been incorporated into the new genome browser), but it would be useful to be able to make your own custom track libraries (multiple tracks from different conditions or experiments). For example, you're interested in transposon integration data (only WT conditions from Grech and Lee studies) and promoters. It would be nice to be able to set all of those tracks into one click and that way you could just pull that up more easily than having to individually find and click those tracks.	10/28/2025 8:33 PM
109	No	10/28/2025 11:17 AM
110	Cannot think of one	10/28/2025 10:59 AM
111	N/A	10/28/2025 10:42 AM
112	No	10/28/2025 9:44 AM
113	no	10/27/2025 9:04 AM
114	Related to my answer to question 11, it would be great to have access to polymorphic variations for each gene, as done in SGD here for my favorite gene: https://www.yeastgenome.org/strainAlignment?locus=YHR099W Given the gene, you might have guessed who answered that ;-)	10/27/2025 8:29 AM
115	-	10/25/2025 1:38 PM
116	no	10/24/2025 1:12 PM
117	It would be very helpful if a small summary of 2-3 sentences to describe the gene function was added at the top of each gene's page, similar to the yeast genome.org for budding yeast.	10/24/2025 11:14 AM
118	GO analysis	10/24/2025 5:35 AM
119	No	10/24/2025 4:39 AM
120	none	10/24/2025 3:19 AM
121	It's not a big deal, but I'd like the paper pages to open in new tabs.	10/24/2025 2:49 AM
122	no	10/24/2025 2:13 AM
123	None	10/23/2025 11:41 PM

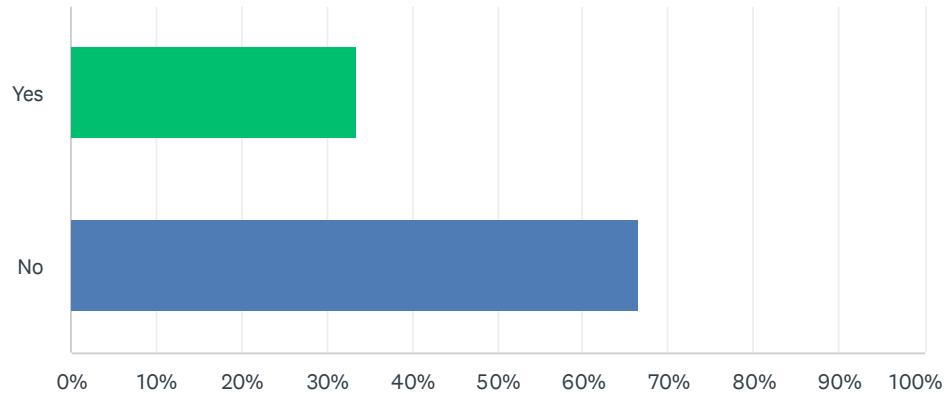
124	Can't think of one	10/23/2025 8:44 PM
125	it would be helpful to have easy access to sequence alignment tools from pombase	10/23/2025 6:22 PM
126	No	10/23/2025 3:49 PM
127	No	10/23/2025 3:43 PM
128	It would be really useful to link recent publications to to each gene/protein, especially for preparing grants/literature review	10/23/2025 3:39 PM
129	Not currently	10/23/2025 2:59 PM
130	not at present	10/23/2025 2:57 PM
131	-	10/23/2025 2:42 PM
132	No	10/23/2025 2:30 PM
133	n/a	10/23/2025 1:46 PM
134	We routinely take protein data from pombase and load them into alphafold. I wonder if there could be a faster way to communicate between the two services.	10/23/2025 1:21 PM
135	No	10/23/2025 12:24 PM
136	Maybe, it might be a good idea to include a small microscopy image or a section showing the normal location of the protein in question in a wildtype cell.	10/23/2025 11:59 AM
137	No	10/23/2025 11:49 AM
138	no -although MS-identified cysteine modifications are widely reported in other organisms (e.g.Oxymouse, cerevisiae) so for our research it would be good to identify which conserved cysteines are modified/oxidised in other organisms	10/23/2025 11:29 AM
139	Maybe chemical profiling dataset for specific genes / conditions and to be able to cross them with your chemical profiling dataset generated in your lab.	10/23/2025 11:15 AM
140	Maybe a possibility to compare two or more genes in the same window. Like when you are comparing technical parameters for some appliances...	10/23/2025 11:11 AM
141	Download expression data for a single given gene. In the pombeTV versions, the possibility to download expression data for a single given gene in a particular condition will be very useful to generate graphs. This is possible in the Bähler Expression viewer but not in pombeTV viewers.	10/23/2025 10:58 AM
142	I have mentioned in Q8 and Q10.	10/23/2025 10:50 AM
143	No	10/23/2025 10:48 AM
144	cf my answer at question 9. Another idea would be to have a streamlined tool to provide a ready to use pipeline for DNA/RNA sequencing ? A bit like galaxy but for Pombe. It would be great to feed the raw fasta.gz from illumina and get the vcf files output (from various tools ideally) in a few clicks. Same with salmon quantifications.	10/23/2025 10:24 AM
145	In PomBase, I would like to see how the information was obtained (namely Methods). Also, I would like to see the similarity (percentages) of a pombe protein with orthologous proteins as well as alignment details.	10/23/2025 10:22 AM
146	Metabolic data	10/23/2025 10:20 AM
147	Can't think of one.	10/23/2025 10:19 AM
148	N/A	10/23/2025 10:11 AM
149	Strain/plasmid availability from repositories	10/23/2025 9:51 AM
150	NA	10/22/2025 2:12 PM
151	n/a	10/21/2025 5:42 PM
152	no	10/21/2025 5:30 PM
153	Link to homologous gene for a few more species beyond human, japonicus and cerevisiae; for	10/21/2025 12:05 AM

example *Neurospora crassa*, FungiDB, and/or JGI taphrinomycotina genomes?

154	No suggestions.	10/20/2025 6:36 PM
155	being able to search by old (now-replaced) gene name. At least for some of them it does not work (e.g. <i>ade4</i>)	10/17/2025 3:02 PM
156	It is good enough now for me.	10/17/2025 4:37 AM
157	I am satisfied with the current toolset.	10/17/2025 4:35 AM
158	It would be nice if endogenously tagged protein localization images could be included in addition to the "GO cellular component", but I understand there are not databases from which to pull this. However, if in community curation individual scientists could supply an image it would great!	10/16/2025 10:20 PM
159	no	10/16/2025 9:36 PM
160	N/A	10/16/2025 6:39 PM
161	N/A	10/16/2025 4:16 PM
162	no	10/16/2025 3:44 PM
163	no	10/16/2025 2:49 PM
164	A detail I noticed is that the SNP from Jeffares are listed on Uniprot but - to my knowledge - not on Pombase, it might be useful to add them if possible.	10/16/2025 1:47 PM
165	Sorry, I've no idea	10/16/2025 12:50 PM
166	no	10/16/2025 12:44 PM
167	I love Advanced Search. I'd like it to be possible to easily count from the right end of the chromosome (eg the last 200 kb)	10/16/2025 11:52 AM
168	na	10/12/2025 5:48 PM

Q13 Have you curated any of your papers in Canto (the PomBase community curation tool)?

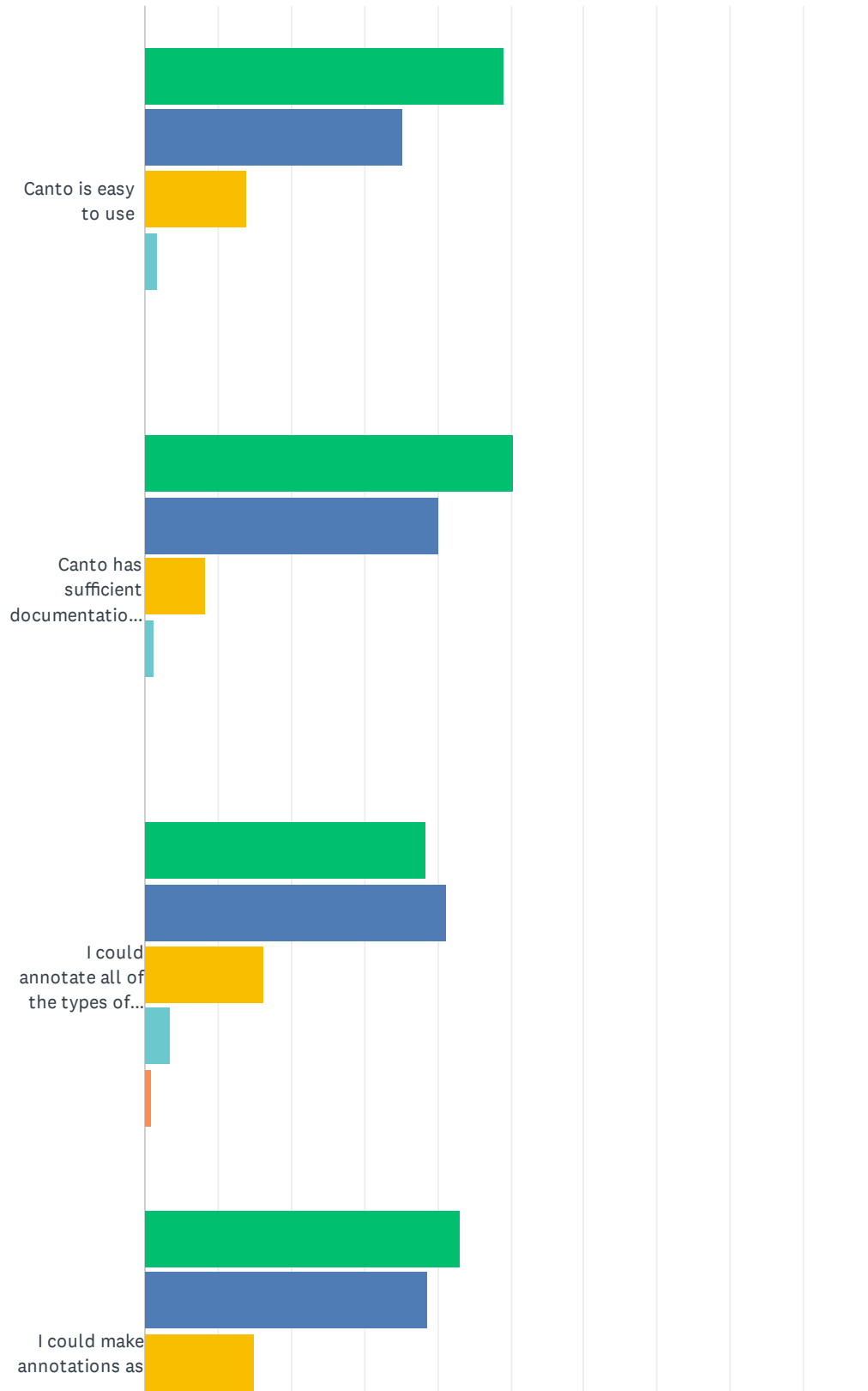
Answered: 626 Skipped: 24

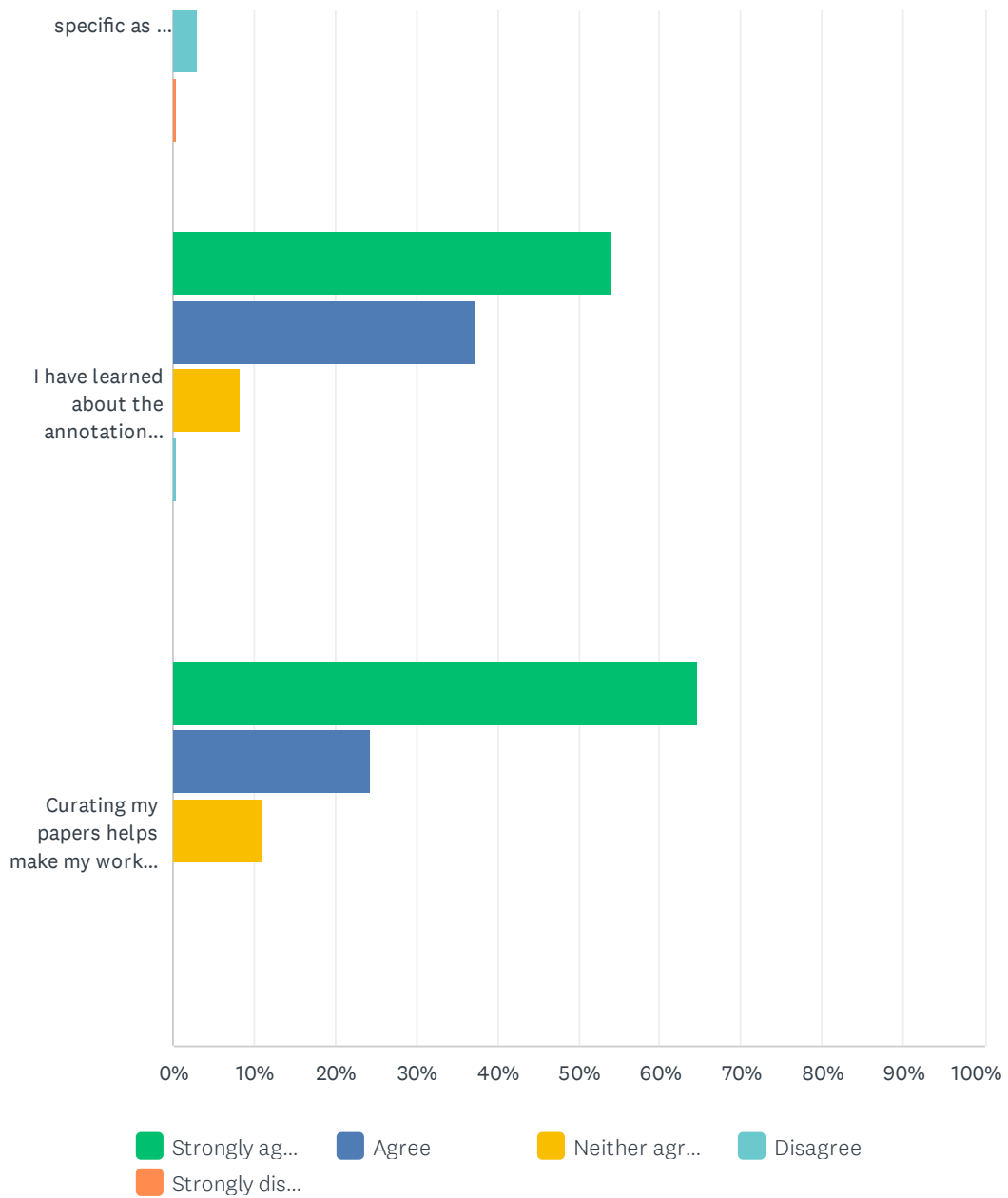


ANSWER CHOICES	RESPONSES	
Yes	33.55%	210
No	66.45%	416
TOTAL		626

Q14 If you answered "Yes" to Question 13, do you agree or disagree with each of these statements?

Answered: 231 Skipped: 419

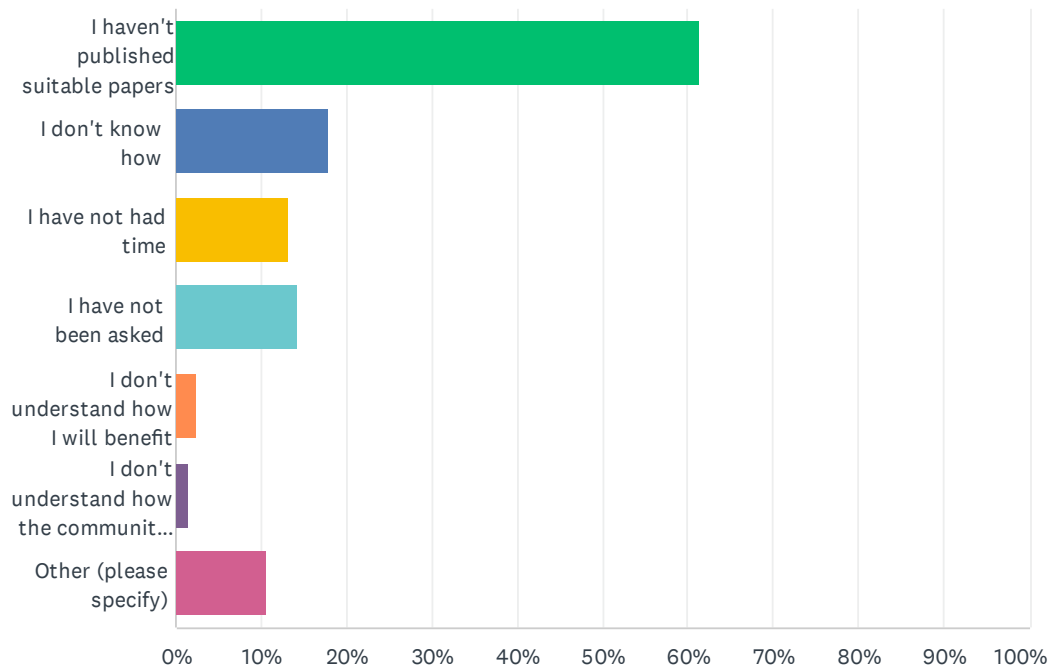




	STRONGLY AGREE	AGREE	NEITHER AGREE NOR DISAGREE	DISAGREE	STRONGLY DISAGREE	TOTAL	WEIGHTED AVERAGE
Canto is easy to use	49.13% 113	35.22% 81	13.91% 32	1.74% 4	0.00% 0	230	1.68
Canto has sufficient documentation and help	50.22% 114	40.09% 91	8.37% 19	1.32% 3	0.00% 0	227	1.61
I could annotate all of the types of data I wanted to (breadth)	38.43% 88	41.05% 94	16.16% 37	3.49% 8	0.87% 2	229	1.87
I could make annotations as specific as I wanted to (depth)	42.98% 98	38.60% 88	14.91% 34	3.07% 7	0.44% 1	228	1.79
I have learned about the annotation process by curating my papers	53.95% 123	37.28% 85	8.33% 19	0.44% 1	0.00% 0	228	1.55
Curating my papers helps make my work more visible	64.60% 146	24.34% 55	11.06% 25	0.00% 0	0.00% 0	226	1.46

Q15 If you answered "No" to Question 13, why not? (select all that apply)

Answered: 422 Skipped: 228



ANSWER CHOICES	RESPONSES	
I haven't published suitable papers	61.37%	259
I don't know how	18.01%	76
I have not had time	13.27%	56
I have not been asked	14.22%	60
I don't understand how I will benefit	2.37%	10
I don't understand how the community will benefit	1.42%	6
Other (please specify)	10.66%	45
Total Respondents: 422		

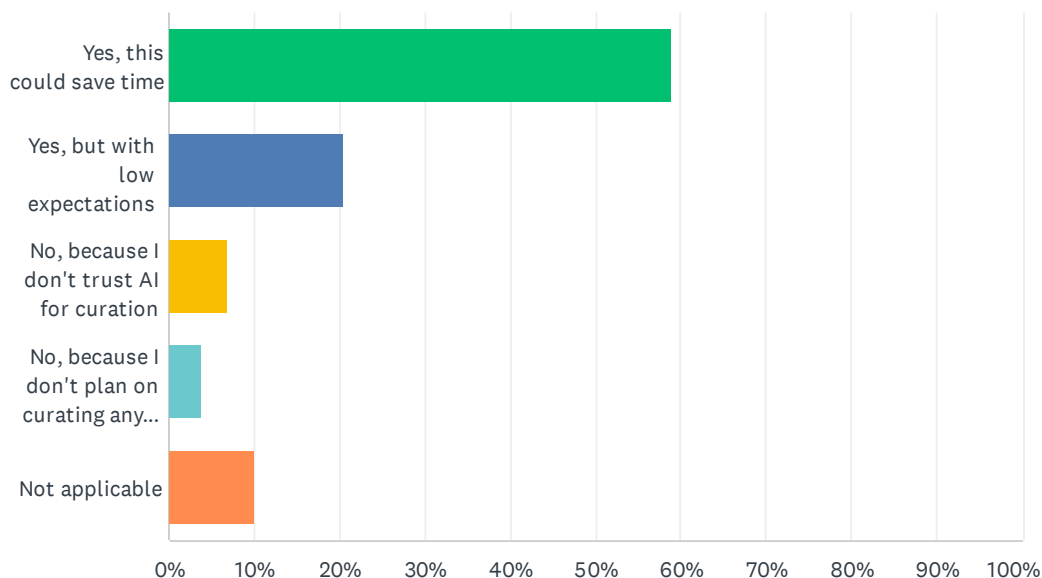
#	OTHER (PLEASE SPECIFY)	DATE
1	Other lab members have curated a paper I contributed to	11/17/2025 4:15 PM
2	I want to! And some lab members have done so.	11/13/2025 5:34 PM
3	my co-workers (students and post-docs) have done this instead of me	11/12/2025 9:06 PM
4	Another member of the lab did it for me	11/12/2025 9:00 PM
5	I wasn't aware of this possibility	11/12/2025 7:53 PM
6	I cannot get these GenZ workers to do anything extra like these annotations.	11/10/2025 2:12 PM
7	Will be doing this in the near future	11/7/2025 9:07 AM

8	I am a new PI, perhaps my postdoc advisor used Canto for my papers	11/6/2025 12:32 AM
9	People in my lab have done it; at the moment I don't have time.	11/5/2025 11:45 AM
10	I haven't think about it	11/4/2025 3:45 PM
11	I presume it should be my supervisor who does this?	11/3/2025 12:35 PM
12	I wasn't sure what it was	11/2/2025 2:09 AM
13	For non-native English speakers, there are aspects that present a high hurdle (though there's no good solution).	11/1/2025 1:44 AM
14	don't want my research to get scopped	10/31/2025 5:05 PM
15	I just didn't have a chance to use it	10/31/2025 3:49 PM
16	Currently I am not working on pombe.	10/31/2025 12:57 PM
17	Someone else took charge of this for my paper	10/31/2025 11:24 AM
18	I had never heard of this.	10/31/2025 11:21 AM
19	Still have not been in charge to do so.	10/31/2025 11:15 AM
20	Pombase has curated it.	10/31/2025 3:41 AM
21	Some of our work was using nmr1 to analyze a structural domain of a transcription factor. As this work was performed in vitro, it was not possible to add our in vitro findings to Canto	10/30/2025 1:37 PM
22	My supervisor did that for our paper	10/27/2025 11:56 AM
23	I'm not directly working on Spombe	10/27/2025 9:04 AM
24	Yet to be published	10/24/2025 5:35 AM
25	I answered yes, but it's been so long ago that I did this that I don't remember.	10/23/2025 9:33 PM
26	without proper curation from pombase, this will be superseded by inaccurate data from other sources (such as High Throughput data)	10/23/2025 7:58 PM
27	I make the people in the lab do it (first author)	10/23/2025 7:48 PM
28	difficulty in starting the process meant that the initiative was dropped	10/23/2025 2:57 PM
29	I'm not sufficiently motivated to highlight my own research	10/23/2025 2:12 PM
30	n/a	10/23/2025 1:46 PM
31	collaborators have done it	10/23/2025 1:30 PM
32	It's the first time I hear about Canto.	10/23/2025 1:21 PM
33	I have a technical paper with some phenotypic results, but I understand technical papers are not eligible	10/23/2025 12:30 PM
34	I think it was not available when asked to curate the paper.	10/23/2025 11:15 AM
35	I answered Yes to the previous question	10/23/2025 11:11 AM
36	I think my colleague have done.	10/23/2025 10:50 AM
37	I have not yet curated all my papers (main reason above)	10/21/2025 5:42 PM
38	Done by other members of the lab.	10/21/2025 3:15 PM
39	I'm a big intimidated by curating.	10/20/2025 6:36 PM
40	Haven't published before and never heard of Canto until right now	10/18/2025 1:48 AM
41	I have tried but it seems to complex and time consuming.	10/17/2025 1:00 AM
42	Can't get through this question without answering, should be skipped over	10/16/2025 6:39 PM
43	N/A	10/16/2025 4:16 PM

44	Yes	10/16/2025 12:44 PM
45	I'd like to do it, but never manage to make time for it.	10/16/2025 11:52 AM

Q16 Many funding calls now prioritise AI-driven projects. We plan to use advanced rule-based AI to extract genes, alleles, phenotypes, and GO annotations directly from manuscripts. After validating its accuracy, we'll use it to pre-populate Canto sessions for author review, reducing manual data input. Would you be willing to review AI-generated annotations for your papers?

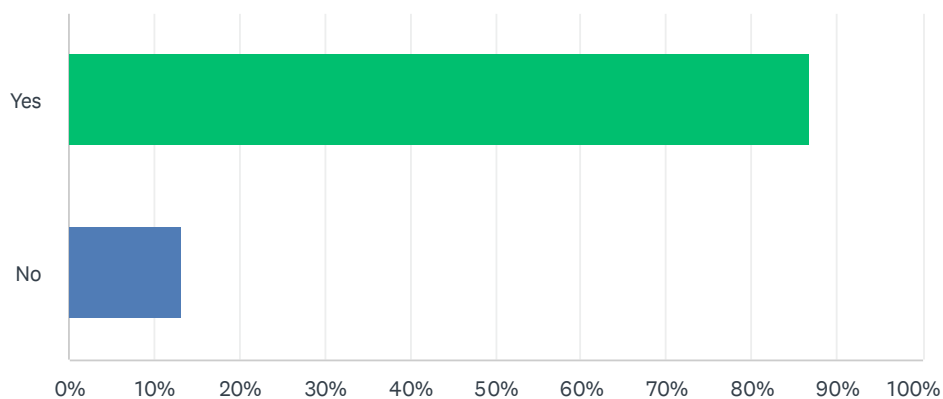
Answered: 623 Skipped: 27



ANSWER CHOICES	RESPONSES	
Yes, this could save time	58.75%	366
Yes, but with low expectations	20.39%	127
No, because I don't trust AI for curation	6.90%	43
No, because I don't plan on curating any papers	3.85%	24
Not applicable	10.11%	63
TOTAL		623

Q17 Is *S. pombe* your primary organism of research?

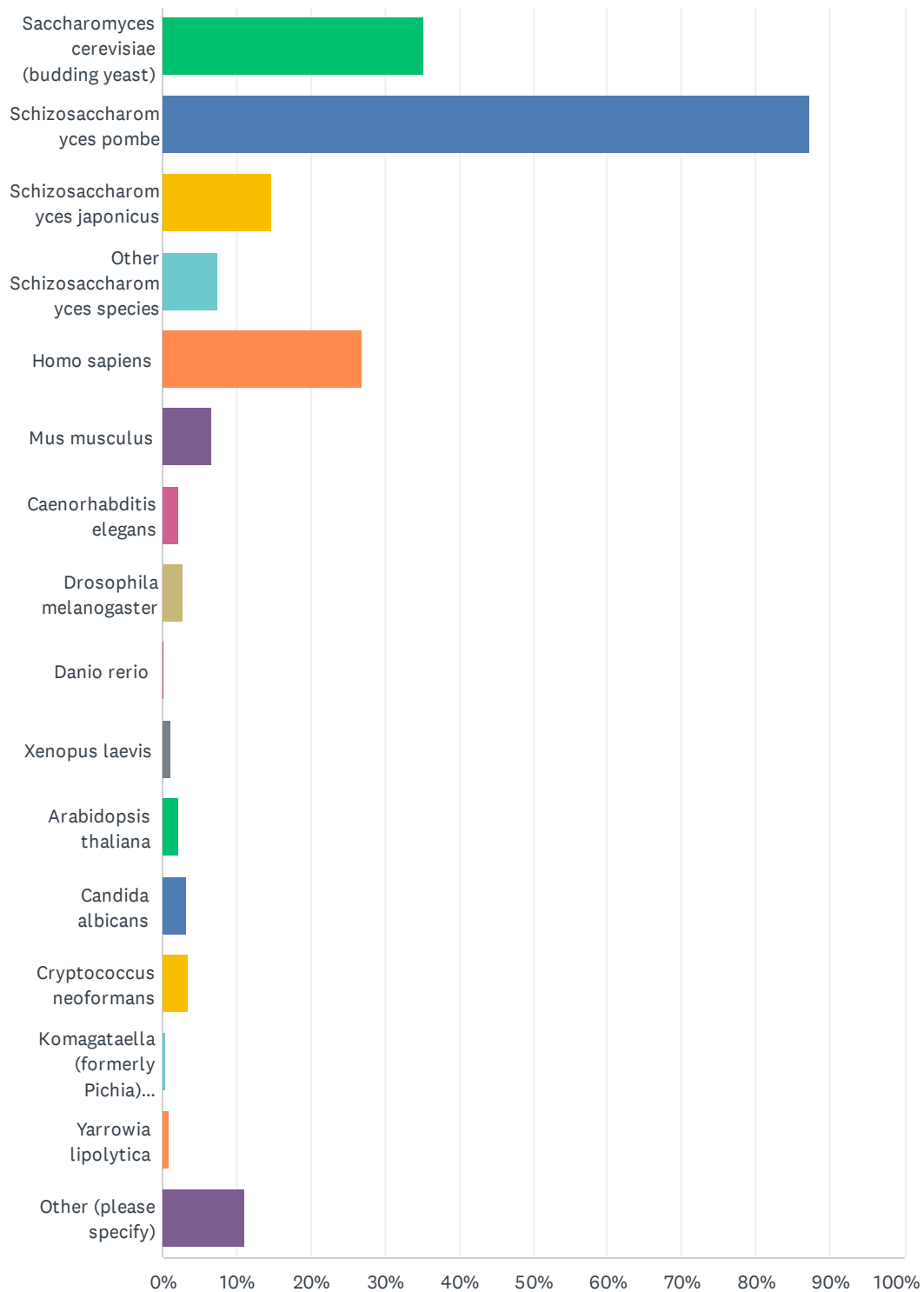
Answered: 633 Skipped: 17



ANSWER CHOICES	RESPONSES	
Yes	86.73%	549
No	13.27%	84
TOTAL		633

Q18 Which organisms does your lab work on? (select all that apply)

Answered: 627 Skipped: 23



ANSWER CHOICES	RESPONSES	
Saccharomyces cerevisiae (budding yeast)	35.25%	221
Schizosaccharomyces pombe	87.24%	547
Schizosaccharomyces japonicus	14.67%	92
Other Schizosaccharomyces species	7.50%	47
Homo sapiens	26.79%	168
Mus musculus	6.70%	42
Caenorhabditis elegans	2.23%	14
Drosophila melanogaster	2.71%	17
Danio rerio	0.32%	2
Xenopus laevis	1.12%	7
Arabidopsis thaliana	2.23%	14
Candida albicans	3.19%	20
Cryptococcus neoformans	3.35%	21
Komagataella (formerly Pichia) pastoris	0.48%	3
Yarrowia lipolytica	0.96%	6
Other (please specify)	11.00%	69
Total Respondents: 627		

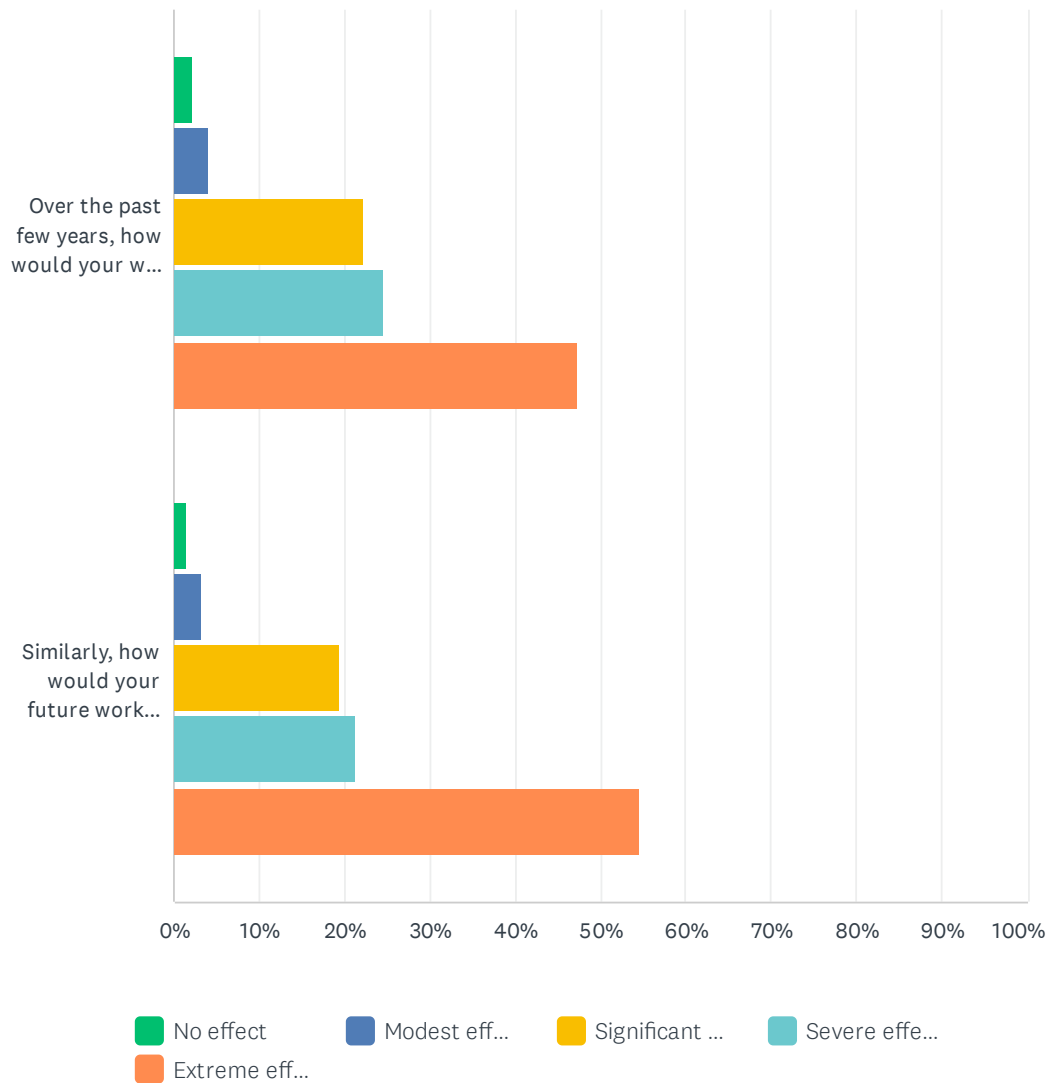
#	OTHER (PLEASE SPECIFY)	DATE
1	Chickpea	11/18/2025 3:04 AM
2	Ustilago maydis	11/17/2025 9:06 AM
3	A large number of microbial eukaryote model systems	11/17/2025 8:32 AM
4	c elegans	11/13/2025 5:28 PM
5	Aspergillus nidulans	11/13/2025 10:21 AM
6	DT40 (chicken cell line)	11/13/2025 8:54 AM
7	Neurospora crassa	11/13/2025 1:57 AM
8	Killifish	11/12/2025 7:08 PM
9	We are working on S. pombe but just getting going as we speak	11/12/2025 7:04 PM
10	All saccharomycotina yeast and also taphrinomycotina for bioinformatic analysis.	11/11/2025 9:26 AM
11	E. coli	11/10/2025 10:56 PM
12	Killifish	11/10/2025 3:11 PM
13	C. Lusitaniae	11/10/2025 1:43 PM
14	Neurospora crassa	11/10/2025 9:47 AM
15	Chimpanzee, Gorilla, Macaque	11/10/2025 9:41 AM
16	Killifish	11/10/2025 9:36 AM

17	E. coli, Shewanella	11/10/2025 9:18 AM
18	Nothobranchius furzerie	11/10/2025 9:17 AM
19	rat	11/8/2025 2:25 AM
20	Aspergillus spp.	11/7/2025 11:27 PM
21	Di not have a lab	11/7/2025 10:46 AM
22	Other non-conventional yeast species	11/7/2025 9:39 AM
23	Naganishia liquefaciens (Basidiomycetes yeast)	11/7/2025 9:05 AM
24	microbes in general	11/7/2025 9:03 AM
25	Aspergillus nidulans	11/5/2025 11:45 AM
26	chicken	11/5/2025 8:44 AM
27	Sea urchin	11/4/2025 3:45 PM
28	Zymoseptoria tritici	11/4/2025 12:00 PM
29	Magnaporthe oryzae	11/3/2025 1:05 PM
30	Chicken	11/2/2025 12:24 AM
31	Gallus gallus	11/1/2025 1:39 PM
32	E coli	11/1/2025 6:36 AM
33	E. coli	11/1/2025 4:13 AM
34	tetrahymena thermophila	10/31/2025 3:50 PM
35	physcomitrella patens	10/31/2025 2:37 PM
36	Paracentrotus lividus	10/31/2025 2:09 PM
37	rattus novegicus	10/31/2025 1:21 PM
38	(mammalian cell lines)	10/31/2025 12:57 PM
39	Zymoseptoria tritici	10/31/2025 12:45 PM
40	Zymoseptora tritici	10/31/2025 12:29 PM
41	Zymoseptoria tritici	10/31/2025 12:20 PM
42	Ustilago maydis	10/31/2025 12:00 PM
43	Bombyx mori	10/31/2025 11:57 AM
44	Zymoseptoria tritici	10/31/2025 11:24 AM
45	E. coli	10/30/2025 1:40 PM
46	Rattus norvegicus	10/24/2025 3:50 AM
47	E. coli	10/23/2025 9:33 PM
48	Zymoseptoria tritici	10/23/2025 6:22 PM
49	E. coli	10/23/2025 4:53 PM
50	Zymoseptoria tritici	10/23/2025 4:22 PM
51	Neurospora, Schizophyllum	10/23/2025 4:14 PM
52	Homo sapiens (human cell culture)	10/23/2025 2:30 PM
53	Nakaseomyces glabratus	10/23/2025 1:35 PM
54	bacteria	10/23/2025 1:29 PM

55	Immortalized and primary mammalian cultured cells from different sources	10/23/2025 1:21 PM
56	physcomitrium patens	10/23/2025 12:20 PM
57	Archaea - e.g. Thermococcus, Haloferax, Methanocauldococcus	10/23/2025 10:37 AM
58	chlamydiae	10/23/2025 10:19 AM
59	Candida auris	10/23/2025 10:19 AM
60	Zymoseptoria tritici	10/23/2025 10:03 AM
61	We plan to work with other Schizosaccharomyces pombe (like S.j.) in the future	10/21/2025 5:42 PM
62	Testing some early non-model Fungi (Saitoella, Spizellomyces)	10/21/2025 12:05 AM
63	Tetrahymena, Paramecium	10/17/2025 4:35 AM
64	Maize, duckweed, mammalian cell culture	10/17/2025 12:09 AM
65	Tetrahymena thermophila	10/16/2025 4:31 PM
66	Tetrahymena thermophila	10/16/2025 12:50 PM
67	Pombe	10/16/2025 12:44 PM
68	Zymoseptoria tritici	10/16/2025 11:52 AM
69	Nothobranchius furzeri	10/12/2025 5:48 PM

Q19 Overall, please think about what PomBase makes possible within the entire body of work you do, and consider what would be different without PomBase.

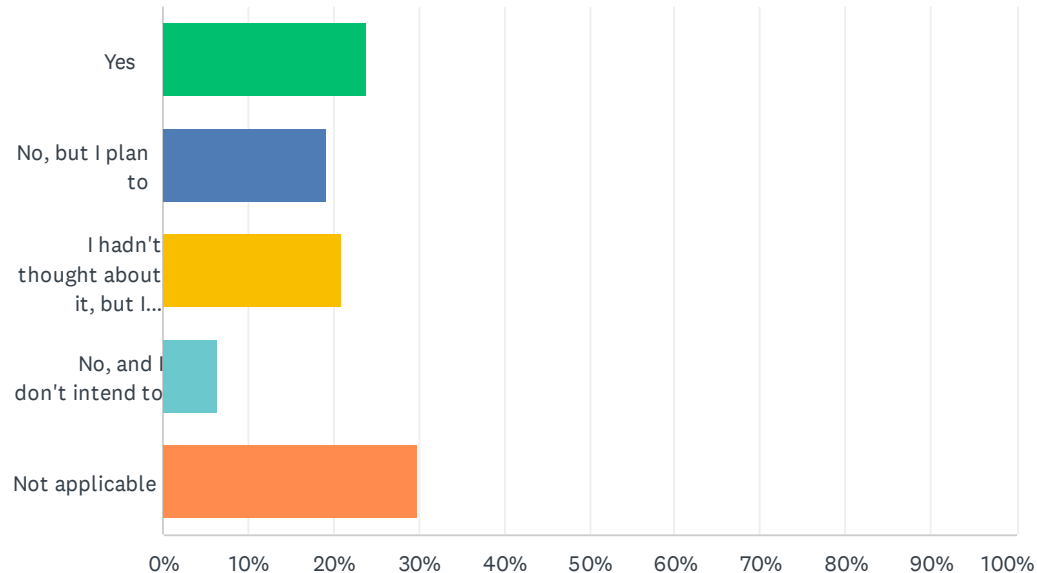
Answered: 632 Skipped: 18



	NO EFFECT	MODEST EFFECT, E.G. DELAYS BUT NO SUBSTANTIVE CHANGE IN WHAT COULD BE DONE	SIGNIFICANT EFFECT - E.G. PROJECTS WOULD REQUIRE ADDITIONAL PERSONNEL OR OTHER RESOURCES	SEVERE EFFECT - SOME PROJECTS WOULD NOT BE FEASIBLE	EXTREME EFFECT - ALL PROJECTS HINDERED; FAR LESS WORK WOULD BE POSSIBLE	TOTAL	WEIGHTED AVERAGE
Over the past few years, how would your work have been affected if PomBase had not existed (2012-present)?	2.06% 13	3.97% 25	22.22% 140	24.44% 154	47.30% 298	630	4.11
Similarly, how would your future work fare without PomBase?	1.46% 9	3.24% 20	19.45% 120	21.23% 131	54.62% 337	617	4.24

Q20 Have you previously used your contribution to community curation as part of data dissemination and management plans?

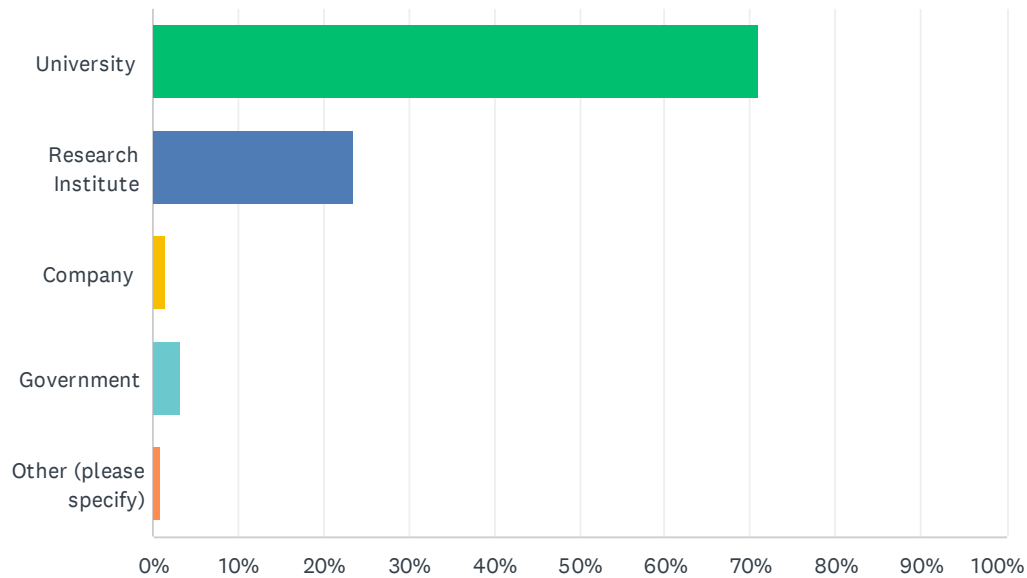
Answered: 618 Skipped: 32



ANSWER CHOICES	RESPONSES	
Yes	23.79%	147
No, but I plan to	19.09%	118
I hadn't thought about it, but I intend to	20.87%	129
No, and I don't intend to	6.31%	39
Not applicable	29.94%	185
TOTAL		618

Q21 What kind of institution do you work at?

Answered: 636 Skipped: 14

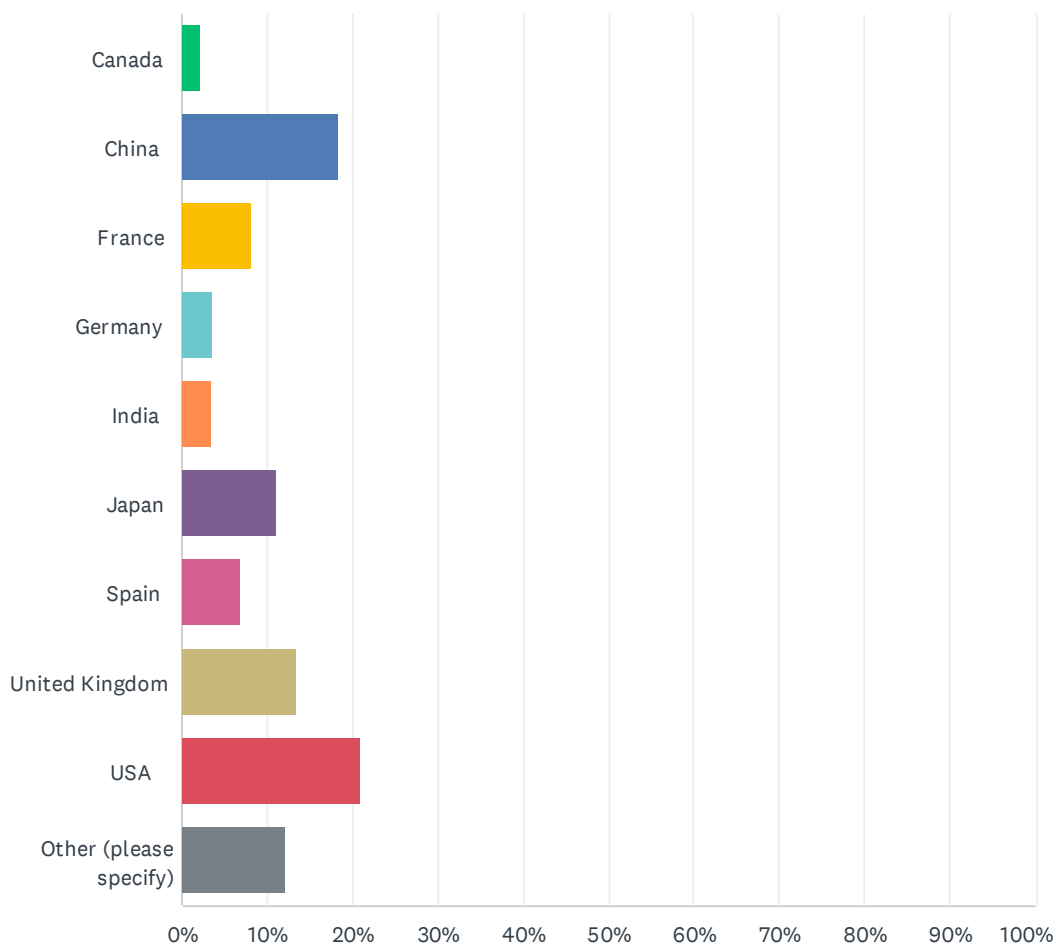


ANSWER CHOICES	RESPONSES	
University	70.91%	451
Research Institute	23.43%	149
Company	1.57%	10
Government	3.30%	21
Other (please specify)	0.79%	5
TOTAL		636

#	OTHER (PLEASE SPECIFY)	DATE
1	Academic medical center	11/17/2025 4:15 PM
2	Hospital	11/12/2025 9:01 AM
3	Medical school	11/10/2025 11:43 AM
4	Joint Center University/Research council	11/10/2025 9:31 AM
5	Unemployed	11/7/2025 10:46 AM

Q22 What is your geographical location?

Answered: 636 Skipped: 14



ANSWER CHOICES	RESPONSES
Canada	2.04% 13
China	18.40% 117
France	8.02% 51
Germany	3.62% 23
India	3.46% 22
Japan	11.01% 70
Spain	6.92% 44
United Kingdom	13.52% 86
USA	20.91% 133
Other (please specify)	12.11% 77
TOTAL	636

#	OTHER (PLEASE SPECIFY)	DATE
1	Australia	11/19/2025 11:28 AM
2	Poland	11/17/2025 4:12 PM
3	Czech Republic	11/14/2025 4:41 AM
4	Poland	11/13/2025 10:17 AM
5	Switzerland	11/13/2025 8:53 AM
6	turkey	11/13/2025 8:17 AM
7	Slovakia	11/13/2025 8:11 AM
8	Europe	11/13/2025 7:27 AM
9	Switzerland	11/13/2025 7:04 AM
10	Switzerland	11/13/2025 7:01 AM
11	Republic of Korea	11/13/2025 3:51 AM
12	South America	11/13/2025 1:57 AM
13	Singapore	11/13/2025 12:32 AM
14	Norway	11/12/2025 8:53 PM
15	Australia	11/12/2025 8:27 PM
16	Denmark	11/12/2025 8:15 PM
17	Sweden	11/12/2025 6:40 PM
18	Sweden	11/12/2025 6:39 PM
19	Slovakia, Europe	11/11/2025 12:42 PM
20	Türkey	11/11/2025 8:38 AM
21	Denmark	11/11/2025 8:15 AM
22	Finland	11/10/2025 9:47 AM
23	South Africa	11/10/2025 9:37 AM

24	Denmark	11/9/2025 7:56 AM
25	South Korea	11/7/2025 11:27 PM
26	Italy	11/7/2025 4:05 PM
27	Slovakia	11/7/2025 9:39 AM
28	Switzerland	11/7/2025 9:07 AM
29	Switzerland	11/7/2025 9:02 AM
30	Slovakia	11/7/2025 8:55 AM
31	spain	11/6/2025 12:24 PM
32	South Africa	11/5/2025 11:45 AM
33	Switzerland	11/3/2025 1:05 PM
34	South Korea	11/3/2025 12:15 AM
35	Australia	11/2/2025 10:27 PM
36	Switzerland	11/1/2025 4:53 PM
37	Sweden	11/1/2025 3:10 PM
38	South East Asia, Singapore	11/1/2025 12:41 PM
39	Singapore	10/31/2025 6:40 PM
40	Czechia	10/31/2025 2:37 PM
41	Switzerland	10/31/2025 1:41 PM
42	Switzerland	10/31/2025 1:38 PM
43	Taiwan	10/31/2025 12:46 PM
44	Singapore	10/31/2025 12:43 PM
45	Switzerland	10/31/2025 12:00 PM
46	Switzerland	10/31/2025 11:52 AM
47	Poland	10/31/2025 11:51 AM
48	South africa	10/31/2025 11:20 AM
49	Taiwan	10/31/2025 11:14 AM
50	Sweden	10/31/2025 11:10 AM
51	Singapore	10/31/2025 11:09 AM
52	Australia	10/30/2025 9:07 PM
53	Europe	10/30/2025 11:42 AM
54	Switzerland	10/29/2025 3:54 PM
55	Switzeland	10/28/2025 1:15 PM
56	Switzerland	10/28/2025 11:17 AM
57	EUROPE	10/27/2025 2:29 PM
58	Switzerland	10/24/2025 12:35 PM
59	México	10/23/2025 11:41 PM
60	Czechia	10/23/2025 12:20 PM
61	Turkey	10/23/2025 12:00 PM

62	UK	10/23/2025 11:15 AM
63	Czech Republic	10/23/2025 11:11 AM
64	Israel	10/23/2025 10:49 AM
65	Czech Republic	10/23/2025 10:17 AM
66	South Korea	10/23/2025 10:11 AM
67	Switzerland	10/23/2025 9:51 AM
68	Switzerland	10/23/2025 9:49 AM
69	Switzerland	10/22/2025 2:12 PM
70	Switzerland	10/21/2025 1:02 PM
71	switzerland	10/17/2025 7:03 PM
72	Taiwan	10/17/2025 8:32 AM
73	Austria	10/16/2025 9:36 PM
74	Switzerland	10/16/2025 1:47 PM
75	South Africa	10/16/2025 12:49 PM
76	Singapore	10/16/2025 12:33 PM
77	Switzerland	10/16/2025 12:33 PM

Q23 Is there anything else you would like to tell us that was not covered in the previous questions?

Answered: 171 Skipped: 479

#	RESPONSES	DATE
1	no	11/19/2025 12:18 PM
2	thanks for provide us the scientific information through, pomBase	11/18/2025 3:44 PM
3	I have transferred into a lab that doesn't work on pombe, but I still find the information on Pombase useful and visit it occasionally.	11/18/2025 9:14 AM
4	I have moved from Pombe into working in plants. I see a huge difference in the quality and ease of Pombase compared to plant databases. Pombase was absolutely critical for my work in pombe, and I only wish the same quality arabidopsis database was available. It's absolutely crucial that this database retains funding, as it's an incredible resource for fission yeast research.	11/17/2025 5:20 PM
5	No	11/17/2025 5:07 PM
6	nope	11/17/2025 4:40 PM
7	No	11/17/2025 4:15 PM
8	Pombase is extremely important database and very well accessible. Crucial for successful research!	11/17/2025 4:12 PM
9	Thanks all the time!	11/17/2025 9:43 AM
10	Keep up the good work - we are very grateful!	11/17/2025 8:32 AM
11	no	11/17/2025 2:39 AM
12	N/A	11/16/2025 1:08 AM
13	NA	11/15/2025 1:34 PM
14	I don't know how we would continue our S. pombe projects without the HUGE resource that Pombase has become for our lab.	11/14/2025 9:22 PM
15	No	11/14/2025 4:41 AM
16	We really need T2T genome for pombe.	11/13/2025 4:56 PM
17	Simply to say that PomBase is a high quality resource that benefits my research tremendously.	11/13/2025 4:01 PM
18	Nothing	11/13/2025 1:06 PM
19	The obvious: it is crucial that Pombase not only to continues to exist but also to expand its scope	11/13/2025 10:17 AM
20	Thanks for all the hard work!	11/13/2025 8:54 AM
21	-	11/13/2025 8:11 AM
22	Pombase has provided a learning tool and an aid which is irreplaceable. Research without Pombase would be impossible. It helps uncover minute details which in science are of great attention.	11/13/2025 5:12 AM
23	By taking the chance, I want to say that the fission yeast Schizosaccharomyces pombe provides an excellent experimental system for mechanistic studies, enabling elucidation of key processes relevant to fundamental biological events. Similarly, PomBase is an important online resource that substantially accelerates life science.	11/13/2025 5:11 AM

24	none.	11/13/2025 3:51 AM
25	thank you	11/13/2025 3:09 AM
26	We hope that the T2T pombe genome will be out ASAP.	11/13/2025 12:17 AM
27	no	11/13/2025 12:11 AM
28	NA	11/12/2025 8:07 PM
29	No everything seems excellent.	11/12/2025 7:41 PM
30	This is an awesome resource, extremely important for both the S. pombe and S. cerevisiae communities, super useful!	11/12/2025 7:04 PM
31	Strain database	11/12/2025 6:45 PM
32	no	11/12/2025 9:37 AM
33	NA.	11/12/2025 9:01 AM
34	NA	11/12/2025 8:45 AM
35	no	11/12/2025 8:40 AM
36	NO	11/12/2025 7:53 AM
37	I need pombase !	11/12/2025 7:48 AM
38	no	11/12/2025 6:38 AM
39	no	11/12/2025 6:38 AM
40	no	11/12/2025 6:35 AM
41	no	11/12/2025 6:34 AM
42	no	11/12/2025 6:34 AM
43	no	11/12/2025 6:17 AM
44	Nothing	11/12/2025 6:03 AM
45	no	11/12/2025 3:04 AM
46	No.	11/12/2025 3:00 AM
47	No, It's perfect!	11/12/2025 2:50 AM
48	i hope we are better	11/12/2025 2:03 AM
49	I don't have any ideas for the moment	11/12/2025 2:00 AM
50	The Pombase is the best website ever curated for researchers.	11/12/2025 1:55 AM
51	no	11/12/2025 1:34 AM
52	No	11/11/2025 11:59 PM
53	Thank you for carefully curating the scientific community's data for S pombe. It is an example for other model organisms databases. I love how you are pushing the boundaries integrating new datasets and engaging with GO Cams and I also appreciate the valuable work you do cleaning up inappropriate annotations.	11/11/2025 9:26 AM
54	It is great to find this unique site to find all related to an organism	11/10/2025 3:11 PM
55	In the absence of labor/graduate students in the lab, doing extra work is almost impossible as the administration is hostile to basic research that doesn't produce companies and the US government is anti-science.	11/10/2025 2:12 PM
56	Thank you for making the best database!	11/10/2025 1:43 PM
57	No	11/10/2025 11:43 AM
58	I just want to emphasise how highly we value Pombase. It has been instrumental in enabling	11/10/2025 10:25 AM

the progression of our project which would have been impossible to do otherwise, and we deeply appreciate all the work Valerie, Kim, and Pascal put into continued development and maintenance of the database.

59	No	11/10/2025 10:04 AM
60	I sincerely hope that PomBase will get continued funding. Thank you so much for all your efforts!	11/10/2025 9:37 AM
61	I will retire soon so no "future" work will be done	11/10/2025 9:31 AM
62	NA	11/8/2025 1:47 PM
63	PomBase is an indispensable resource for our research. We use it daily and have benefited greatly from its comprehensive and reliable data over the years. There is no equivalent alternative, making PomBase essential for our work and for the broader fission yeast community.	11/8/2025 11:59 AM
64	Strongly support Pombase and its major commitments to scientific excellence and collaboration.	11/8/2025 2:25 AM
65	..	11/7/2025 11:27 PM
66	no	11/7/2025 3:03 PM
67	No	11/7/2025 10:46 AM
68	PomBase is a key part of my research and makes doing research a lot simpler and quicker. There is a wide community of users and it's incredibly helpful to know you can always find what you need or reach out to someone if needed.	11/7/2025 9:57 AM
69	Thank you and keep up the good work	11/7/2025 9:07 AM
70	n/a	11/5/2025 11:45 AM
71	I think using rule-based AI to pre-populate Canto sessions for authors is a great idea. Also, I think that Pombase will remain important in the future, even now that individual researchers have access to AI tools. Pombase provides a one-stop shop for information, including in areas where a researcher might not even know enough to write a suitable AI prompt.	11/5/2025 11:45 AM
72	PomBase is an exceptional tool that I use everyday in my research.	11/4/2025 7:50 PM
73	No	11/4/2025 6:39 PM
74	Thank you! Great database	11/4/2025 12:46 PM
75	PomBase is an absolutely essential, irreplaceable resource that underpins every aspect of many research programmes in the UK. The scientific impact of PomBase-enabled research extends far beyond fission yeast biology. Approximately 70% of fission yeast genes have human orthologs, with over 350 genes conserved in <i>S. pombe</i> but absent from budding yeast. This makes fission yeast—and by extension, PomBase—particularly valuable for understanding human gene functions and disease mechanisms. PomBase serves a substantial UK research community. The database supports fission yeast researchers at Cambridge, UCL, Oxford, Sussex, Dundee, and numerous other UK institutions. The approximately 2,000-person global fission yeast community publishes 500 papers annually, with UK researchers contributing a disproportionately large fraction of this output. PomBase cannot be replaced or substituted. The database represents over a decade of expert curation, integrating knowledge from thousands of publications with sophisticated ontology-based annotation systems. The alternative—individual researchers attempting to maintain their own knowledge repositories—would be catastrophically inefficient, scientifically unreliable, and economically wasteful.	11/4/2025 12:00 PM
76	no	11/4/2025 6:18 AM
77	I think the question whether Pombase would impair my projects is not the right question. Pombase is a resource that allows us a clear, direct and easy access to a wealth of information. So of course, this information can be found, disseminated, elsewhere...but what Pombase does is making us save a huge amount of search time, and this is unique. The added value that Pombase brings is incredibly important.	11/3/2025 3:18 PM
78	I love your work. Thank you and good luck!	11/3/2025 10:30 AM

79	I don't regularly use PomBase but I find it essential for comparative analyses between different models	11/3/2025 9:39 AM
80	Thanks for you help and hope better and better in the future!	11/3/2025 4:20 AM
81	No	11/3/2025 3:49 AM
82	Would it be feasible to establish documentation for the individual protocols or bioinformatic pipelines? This would allow for the standardized execution of experiments.	11/3/2025 1:49 AM
83	PomBase is great. Thank you for your contribution!	11/3/2025 12:59 AM
84	No.	11/2/2025 11:36 AM
85	This is to suggest the addition of a dedicated bioinformatics section to PomBase, justified by the surge in evolutionary and multi-omics research on <i>S. pombe</i> and other fungi. This new section would serve to highlight methodological approaches and document dry-lab experimental procedures. Many researchers, particularly those new to the field, may lack clear guidance on appropriate methodologies for bioinformatics analysis.	11/2/2025 10:19 AM
86	No.	11/2/2025 8:47 AM
87	No	11/2/2025 4:00 AM
88	No, but I'd like to mention that compared to other model organism databases (such as SGD), I find Pombase extremely user friendly and helpful. The interface is easy to navigate and its existence is essential for us to continue doing research in all areas of biology where <i>S. pombe</i> is used as a model.	11/1/2025 4:03 PM
89	I lead a project where <i>S. pombe</i> is now used to show protein function conservation but I am not anymore working on pombe biology itself. I also use pombe in teaching and practicals	11/1/2025 1:02 PM
90	Pombase is essential for my research.	11/1/2025 1:44 AM
91	No	10/31/2025 8:46 PM
92	No	10/31/2025 6:40 PM
93	Pombase is an essential asset to study not only pombe but also eukaryotic genetics/genomics. I cannot think of my study done well without it.	10/31/2025 3:49 PM
94	PomBase is an excellent resource, and I truly appreciate it	10/31/2025 3:18 PM
95	No	10/31/2025 3:13 PM
96	N/A	10/31/2025 3:12 PM
97	no	10/31/2025 1:38 PM
98	PomBase has grown to be indispensable for pombe/yeast researchers.	10/31/2025 12:57 PM
99	-	10/31/2025 11:51 AM
100	Pombase is very amazing.	10/31/2025 11:21 AM
101	#SavePombase, best database and definitely indispensable for basic research	10/31/2025 11:15 AM
102	Thanks!	10/30/2025 11:44 PM
103	N/A	10/30/2025 9:07 PM
104	No	10/30/2025 6:17 PM
105	I love pombase, its really improved over the past few years, very easy to use and a very valuable resource. Best of luck!	10/30/2025 12:58 PM
106	Thank you very much for your work!	10/30/2025 12:46 PM
107	PombeBase is very useful for my daily work, I really appreciate that it is available and it would be a big lost if it dissapears.	10/30/2025 12:26 PM
108	Pombase is amazing!	10/30/2025 12:11 PM

109	Pombase is an amazing working tool, and losing it would be a catastrophe for the scientific community.	10/30/2025 11:49 AM
110	Thank you for your work!	10/30/2025 11:46 AM
111	This is just a question, but there are a handful of introns that are marked at 1-2 bp long in the genome browser. Can these regions be spliced out? I will list the ones I found below. ## geneID region intron_length ## 1 SPAC1071.01c CDS 1 ## 2 SPAC23A1.20 CDS 2 ## 3 SPAC29E6.04 CDS 1 ## 4 SPBC18E5.15 CDS 1 ## 5 SPBC1A4.06c CDS 1 ## 6 SPBC1E8.04 CDS 2 ## 7 SPBC29A3.06 CDS 1 ## 8 SPBC32F12.08c CDS 1 ## 9 SPBC337.02c CDS 2 ## 10 SPBC577.14c CDS 1 ## 11 SPBCPT2R1.06c CDS 2 ## 12 SPCC1442.04c CDS 2 ## 13 SPCC1494.11c CDS 2 ## 14 SPCP20C8.03 CDS 2	10/28/2025 8:33 PM
112	No	10/28/2025 11:17 AM
113	Pombase is an essential research tool for my group. Details of this depth are difficult to find on platforms for other model organisms.	10/28/2025 10:59 AM
114	no	10/27/2025 9:04 AM
115	Keep the great work and good luck for the grant renewal!	10/27/2025 8:29 AM
116	Thanks for all your effort. Without Pombase I honestly would be lost. It would make planning experiments a lot harder and much more time consuming. And lots of projects would not have developed at all without the easy accessible and well presented information in pombase.	10/25/2025 1:38 PM
117	Thanking Pombase crew again for their continuous support !	10/24/2025 1:32 PM
118	No	10/24/2025 4:39 AM
119	I want to extract the list of GOterm and the genes included in the GOterm.	10/24/2025 3:44 AM
120	none	10/24/2025 3:19 AM
121	no	10/24/2025 2:13 AM
122	Pombase is essential for researchers. I hope it lasts forever with sufficient funding. Many many thanks for your great contribution to the society. I cannot thank you enough.	10/24/2025 1:24 AM
123	Nothing. Thank you very much.	10/23/2025 11:41 PM
124	I think PomBase is very useful to the community, but as lab head I don't use it much; hence, my limited responses here. But I strongly hope, and urge, that PomBase continues.	10/23/2025 9:33 PM
125	This is a great resource for students starting off in working on genetics in Pombe. Myself and other graduate students in my lab have used Pombase as a database for gene sequences, genome datasets, and genome annotations that we use for class work, and work on our own research. This database makes this work approachable for people who are not familiar with the literature and provides resources for students to begin doing exploratory work to develop their dissertation/research projects.	10/23/2025 8:44 PM
126	I have worked on pombe for a very long time. Pombase used to be very useful. It isn't anymore. I only use it to download gene sequence data and nothing else. There is an over focus on automated data annotation and high-throughput data, at the expense of a large literature that require a bit more curation. I feel that pombase only interact with a few group leader in the field, at the expense of others. A large number of fission yeast paper are absent. A large segment of the field is not represented. Each gene page is overloaded with informations from only a few paper and high-throughput (HT) data, which dilute the relevant data and makes, non-HT data difficult to find. There is also a number of serious errors in annotation as HT data (which are inherently less reliable for individual genes and are only reliable for statistical trends) have superseded the careful and focused work of previous investigators. That is the reason why I (and others) won't curate my own papers. The work I put in would just be thoughtlessly dismissed by the next HT dataset. This is a serious problem. I have communicated the problem with Top2 essentiality being wrongly converted to "viable" by a single HT dataset riddled with errors. This process dismisses the work of a number of passionate pombe researchers. I obtained correction for Top2 only but a number of other genes are still wrongfully annotated, and the seriousness of the issue was not understood. [REDACTED] This opinion is my own	10/23/2025 7:58 PM

127	Pombase is a crucial resource that has made my work in pombe possible, I would be absolutely lost without it	10/23/2025 7:40 PM
128	Thank you for consistently improving and updating PomBase!	10/23/2025 6:54 PM
129	keep up the great work.	10/23/2025 5:49 PM
130	PomBase is invaluable, keep up the great work!	10/23/2025 3:51 PM
131	No	10/23/2025 3:49 PM
132	No, but thank you so much all your work into building such a great resource for Pombe researchers!	10/23/2025 3:43 PM
133	this is amazing!!	10/23/2025 3:39 PM
134	PomBase is the best community resource there is! It is essential to my group's research productivity. With PomBase I welcome at least 10 undergraduates/year to work on bench-based projects. Without PomBase resources this number would drop to 1 or 2/yr. It is absolutely essential to graduate student and PDF research. Additionally, they become community members and care about their work within the greater context. Finally, PomBase is my tool of choice to check when I have a question about ANY cell biology question. Its resources and broad links facilitate deeper research questions and hypothesis generation. PomBase is ESSENTIAL and CRUCIAL for my lab's work and productivity	10/23/2025 2:57 PM
135	No	10/23/2025 2:30 PM
136	Pombase has been a go -to resource to investigate genetic interactions between genes of interest, but also is so useful in terms of general information. Simply put it is incredibly useful on a daily basis and has been since its inception.	10/23/2025 1:54 PM
137	n/a	10/23/2025 1:46 PM
138	Pombase is a critical tool that my entire lab uses daily. We cannot do the work we do without Pombase.	10/23/2025 1:21 PM
139	No	10/23/2025 1:12 PM
140	No	10/23/2025 11:49 AM
141	The support with the annotations I found more difficult to do in Canto was great. The standard of annotations in Pombase for papers I have read is superb.	10/23/2025 11:29 AM
142	Thank you for keeping PomBase alive and evolving!	10/23/2025 11:11 AM
143	No	10/23/2025 10:58 AM
144	There is nothing in particular.	10/23/2025 10:50 AM
145	Pombase is an extremely valuable tool. It should be allowed to continue for the benefit of the entire fission yeast community.	10/23/2025 10:48 AM
146	Well done Pombase team! Kind regards	10/23/2025 10:24 AM
147	I think that PomBase is the most sophisticated genome/functional database among those for model organisms.	10/23/2025 10:22 AM
148	Thank you!	10/23/2025 10:20 AM
149	Keep up the good work, hope you'll get the monies for doing this.	10/23/2025 10:19 AM
150	Our company has sold s.pombe deletion library. We'd like to help pombase to be reached out to diverse research field.	10/23/2025 10:11 AM
151	Beyond its value for research, PomBase is an essential resource in my teaching practice. I regularly use it in tutorials to introduce students to yeast as a model organism, guiding them through decades of curated research data with ease.	10/23/2025 10:07 AM
152	NA	10/23/2025 9:51 AM
153	We need "very much" the pombase for everyday work	10/23/2025 9:51 AM
154	No	10/22/2025 2:12 PM

155	no	10/21/2025 5:42 PM
156	no	10/21/2025 5:30 PM
157	Well done! You are a real asset to the Pombe community. Thank you very much for your involvement!	10/21/2025 3:15 PM
158	My project greatly relied on the curated data and carefully annotated genes and gene products. Without, it would have still been possible, but I would likely not have started it in the first place due to constraints in time and costs. Every step along the way, I always checked back in with PomBase, also fuelling smaller projects along the way because of how easy PomBase makes it to get a broad overview and also to extract specific information and related publications. I cannot stress enough how vital PomBase was for my PhD research and I am very grateful to the curators for their incredibly valuable work.	10/21/2025 1:02 PM
159	Thank you for all your work and assembling a very thoughtful survey!	10/21/2025 2:32 AM
160	Here's a niche suggestion for you to consider: I'm not sure this is really within the scope of pombase, but part of my work involves computational modeling of processes in pombe. I sometimes wonder whether the results of that part of our work could be incorporated in some way, but I'm not sure that makes sense - I can see the justification for keeping the focus on experimental results.	10/20/2025 6:36 PM
161	Thank you for all your work! Our research would not be possible without Pombase.	10/20/2025 3:29 PM
162	No	10/17/2025 4:37 AM
163	Just keep up the great work. Thanks.	10/17/2025 1:00 AM
164	I am new to Pombe and Pombase has been an indispensable resource for learning the intricacies of this system since day 1.	10/17/2025 12:09 AM
165	no	10/16/2025 9:36 PM
166	Keep working hard, pombe users really depend on your work. And thanks for all your help!!!	10/16/2025 4:16 PM
167	no	10/16/2025 3:44 PM
168	PomBase is essential for our research. It is the most complete, accessible and useful organism database I have ever used, and it should be the gold standard for other model organisms.	10/16/2025 2:44 PM
169	Thanks for your work! Congrats!	10/16/2025 2:03 PM
170	Change the reference genome, please	10/16/2025 1:07 PM
171	No	10/16/2025 12:50 PM