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1. Which professional category best describes you? Please select only one.

- Bioinformatics professional
 Life Science Researcher
 Educator
 Student
 Healthcare professional
 Technician
 Librarian / Information Specialist
 Computer Scientist / Software Developer
 Other (please specify)

2. Please pick one category that best describes your organization.

- College or University
 Research Institute
 Commercial / Industry
 Government
 Non-profit Organization
 Hospital/health care organization
 Other (please specify)

3. I am *primarily* interested in the genomes of _____. Please select the from the list below.

- Eukaryotes other than fungi
 Prokaryotes
 Viruses
 Fungi
 Metagenomes / microbiomes
 Organelles
 Plasmids
 Other (please specify)

4. Pick the scale of the number of genomes you typically include in your analyses.

- 1
 10
 100
 1,000
 >1,000

5. My primary reason for visiting the Genome site today is to ...

- Download the annotation or annotation report for a genome
 Download the sequence (FASTA) for the reference genome assembly
 Run a BLAST search against this organism/genome
 Find publications
 Review annotation statistics for the reference/representative genome
 Find all assemblies for this organism
 View a graphical sequence display for this genome
 Follow a link to an external (non-NCBI) resource
 Use the dendrogram (tree) to learn about sequence similarity based relationships of genomes for this organism (available for prokaryotic genomes only)
 Obtain general information about an organism (e.g. description, photo)
 Other (please specify)

6. How easy was it to accomplish the task you selected above?

- Very easy
 Easy
 Somewhat easy
 Neither easy nor difficult
 Somewhat difficult
 Difficult
 Very difficult

7. Considering your primary reason for visiting Genome today, will you also use the NCBI Assembly website to accomplish some part or all of this task?

- Yes
 No, Genome is sufficient
 I'm not familiar with NCBI Assembly

8. Which of the following reports provided by Genome have you used? Please check all that apply.

- Genome Assembly and Annotation Report
 Genome Tree report (prokaryotes only)
 Plasmid annotation report (prokaryotes only)
 Organelle annotation report

9. Have you ever used the Genome "Browse by organism" page to find genomes of interest?

- Yes
 No
 I am not aware of "Browse by organism."

10. In addition to the web pages, what other mechanisms do you use to obtain data from Genome?

- FTP
 E-Utilities / EDirect
 Other computational approaches (e.g. custom scripts)
 Only the website

11. How do you currently use the cloud for analysis of genome assembly sequences (FASTA)?

- Download (retrieve)
 Compute
 Both compute and download
 I don't use the cloud for analysis of genome assembly sequences
 I don't know what the cloud is

12. If genome assembly sequences were in the cloud, how would you want to work with them?

- Download (retrieve)
 Compute
 Both compute and download
 I would not want to use the cloud to work with genome assembly sequences

13. Please outline the workflow that you use with the data you are seeking today at NCBI, including other NCBI and non-NCBI resources used.

14. If there was one thing you could change about the Genome pages, what would it be?

15. What is your favorite feature on the Genome web pages?

16. How likely is it that you would recommend the Genome site to a friend or colleague?

Not at all likely

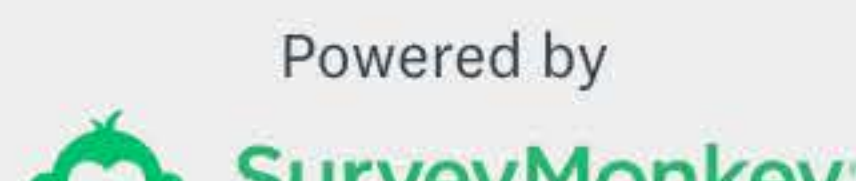
Extremely likely

0	1	2	3	4	5	6	7	8	9	10
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Prev

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We welcome your input! Please contact us at suggest@ncbi.nlm.nih.gov if you would like to provide additional feedback about NCBI Genome resources.

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