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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

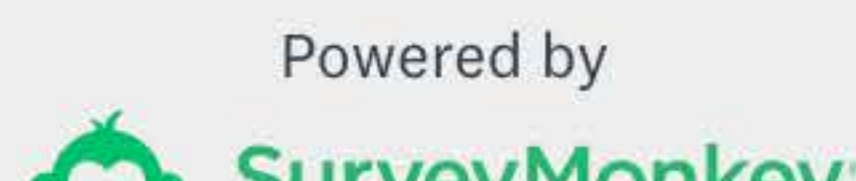
Extremely likely

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

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