Genome Survey

We want to improve NCBI's products and services. We would like to learn more about how this site helps you with your work, and what we can do better. Please click "next" below to get started.

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Genome Survey

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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Genome Survey, Contact Us

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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