

## ASM Microbe Conference Survey

### We Welcome Your Feedback

We are collecting feedback to find out how you use NCBI's Microbial Genome resources, and what you'd like to see in the future. Thank you in advance for your time and interest.

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Public reporting burden for this collection of information is estimated to average 5 minutes per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. An agency may not conduct or sponsor, and a person is not required to respond to, a collection of information unless it displays a current valid OMB control number. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden, to NIH, Project clearance Branch, 6705 Rockledge Drive, MSC 7974, Bethesda, MD 20892-7974, ATTN: PRA (0925-0648). Do not return the completed form to this address.

1. What NCBI resources do you use the most?

2. Do you use bacterial (or other microbial) genome data from NCBI?

- Yes  
 No

3. Are you using GenBank or RefSeq data (choose all that apply)?

- GenBank  
 RefSeq  
 I'm not sure.

4. For the data you use, how do you find data of interest?

- NCBI Genome search
- NCBI BioProject search
- NCBI Nucleotide search
- BLAST

Other (please specify)

5. Do you want all bacterial genomes to be annotated (even thousands of sequenced isolates for the same species/strain)?

- Yes
- No

6. If yes, why?

7. Do you download RefSeq or GenBank genomes and/or proteins and/or gene data from NCBI?

- Yes
- No

8. If yes, what type, and how much, data do you download (e.g. a single genome, all for a species, all bacteria, all RefSeq, all GenBank)?

9. How do you download RefSeq or GenBank data (check all that apply)?

- NCBI Website
- FTP
- NCBI e-Utilities or APIs
- Other (please specify)

10. What do you want to do with bacterial genome sequence and/or annotation and/or metadata? What are your use cases?

11. What else do you need from NCBI for microbial genomes? Do you need more tools to facilitate submitting, downloading, visualizing, or interpreting the data? What types of tools or interpretations are most needed?

12. Any other comments?

13. Do you mind if we contact you for follow up? If not, please enter your email address below (optional).

14. How likely is it that you would recommend NCBI's microbial genome resources 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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