

## NCBI Submission 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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Next



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

- Bioinformatics professional
- Student
- Educator
- Computer Scientist / Software Developer
- Life Science Researcher
- Other (please specify)

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

- College or University
- Non-profit Organization
- Commercial / Industry
- Government
- Other (please specify)

**3. Have you ever submitted sequence data to NCBI?**

- Yes, completed successfully
- Started a submission but did not complete it
- No

Prev

Next

**4. What was your primary goal when you visited the site today?**

- Prepare in advance to make a new data submission
- Complete existing data submission & submit to NCBI
- Begin new data submission & submit to NCBI
- Assist a friend or colleague with their submission
- Other (please specify)

**5. What, if anything, is currently preventing you from submitting sequence data to NCBI? Please check all that apply.**

- Scientific research not yet complete
- Errors in my submission so far
- Not yet sure how to submit this data
- Need NCBI guidance
- Awaiting data or input from a colleague
- Nothing
- Other (please specify)

**6. How helpful would the following features be in submitting sequence data to NCBI or managing your submission?**

	Very helpful	Somewhat helpful	Not very helpful	Not at all helpful
Ability to upload a data file and have the required fields populated from the file	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Make it easier to select the appropriate NCBI BioSample type	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
More options for data management (add data, edit data) after submission	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
One webpage showing all submissions to GenBank or SRA, and status	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Updated user interface design (less text, more visuals)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Improved help documentation	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
New or improved 'Group' submission options	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

**7. What else do you think would help you submit sequence data to NCBI?**

**8. If you started, but did not finish, a sequence data submission, what was the primary reason?**

**9. Based on your understanding of sequence submission thus far, how well do you think the web submission options offered by NCBI will meet your needs as a submitter?**

- Very well – NCBI really understands what I need and makes the process very easy.
- Well – NCBI generally understands what I need but presents some things differently than what I'd expect.
- Neither well nor poorly – NCBI makes it possible but sometimes complicated to submit sequence data.
- Poorly – NCBI uses arbitrary rules, requirements and terminology.
- Very poorly – NCBI does not understand or meet my needs as a submitter.

**10. Why did you select the answer you gave in the previous question?**

**11. How likely is it that you would recommend the NCBI Submission Portal 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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**4. What types of data have you submitted? Please check all that apply.**

- Raw reads
- Assembled genome(s)
- Targeted sequences: Viral sequences, 16S ribosomal RNA, COX1, etc
- Assembled transcriptome(s)
- Targeted Locus Study
- Other (please specify)

**5. How easy was it to submit your sequence data using NCBI's web tools/website? If you have made multiple submissions, please evaluate your most recent submission.**

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

**6. Why did you select the answer you gave in the previous question?**

**7. How well do you think the web submission options offered by NCBI meet your needs as a submitter?**

- Very well – NCBI really understands what I need and makes the process very easy.
- Well – NCBI generally understands what I need but presents some things differently than what I'd expect.
- Neither well nor poorly – NCBI makes it possible but sometimes complicated to submit sequence data.
- Poorly – NCBI uses arbitrary rules, requirements and terminology.
- Very poorly – NCBI does not understand or meet my needs as a submitter.

**8. Why did you select the answer you gave in the previous question?**

**9. What changes have you seen NCBI make to sequence submission web tools that have helped you as a submitter?**

**10. How helpful would the following features be in submitting sequence data to NCBI or managing your submission?**

	Very helpful	Somewhat helpful	Not very helpful	Not at all helpful
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**11. How else can NCBI improve sequence submissions for you?**

**12. NCBI recently made options to manage and edit submission data for SRA (Sequence Read Archive) data submitters. Are you aware of that based on the options you see on this website?**

- Yes
- No

**13. What kind of edits to your sequence data would you like to be able to make, post-submission?**

**14. Which of the following have you used as part of submission to NCBI? Please check all that apply.**

- BankIt
- BioProject
- BioSample
- Submission Portal GenBank
- Genome (WGS)
- GEO
- Sequence Read Archive (SRA)
- Sequin
- Tbl2ASN
- Transcriptome Shotgun Assembly (TSA)

**15. How likely is it that you would recommend the NCBI Submission Portal 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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**The NCBI team values our users and welcomes all input! Please write to us at [suggest@ncbi.nlm.nih.gov](mailto:suggest@ncbi.nlm.nih.gov) if you'd like to share additional feedback or help us test new sequence submission features.**

Prev

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