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

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

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

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

3. How frequently do you use each of the following services on the BLAST web service (<https://blast.ncbi.nlm.nih.gov/>)?

	Daily	Weekly	Monthly	Less than monthly	Never
Nucleotide BLAST (blastn)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Protein BLAST (blastp)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Translated BLAST (blastx, tblastn, tblastx)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Align two or more sequences	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Primer-BLAST	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
IgBLAST	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

4. Why do you use BLAST? Please check all that apply.

- Identify unknown mRNA transcript
- Identify unknown proteins
- Annotate novel genomic sequences
- Search for homologs in other organisms
- Identify organisms (taxa) in environmental / metagenomic samples
- Screen for contamination
- Other (please specify)
- Designing/Screening Primers
- Verify the identity of the source organism for the query sequence
- Verify the corresponding gene for a query sequence
- Maps reads to a genome assembly
- Education/Instruction

5. How often do you search with multiple sequences in a single BLAST search?

- Daily
- Weekly
- Monthly
- Less often than monthly
- Never

6. Do you run BLAST searches for others in your organization, for example, as a service?

- Yes
- No

7. How do you run BLAST searches? Please check all that apply.

- Not applicable (I do not use any of the services listed.)
- BLAST website and upload files and/or paste sequences in the sequence field
- Standalone BLAST+ with the **remote** option to submit BLAST searches to NCBI
- Standalone BLAST+ applications with my own/custom databases
- Standalone BLAST+ with downloaded BLAST databases/FASTA provided by NCBI
- Scripts that access the BLAST URL API
- NCBI BLAST+ docket image from dockerhub
- NCBI BLAST+ on a cloud provider, such as Amazon, Azure, Google, etc. Please specify the cloud provider in the comment field below.
- Through a third-party software. Please specify name of software in the comment field below.

Name of third party software and/or cloud provider

8. How often do you use the standalone BLAST+ (command line) applications?

- Daily
- Weekly
- Monthly
- Less often
- Never

9. Why do you use BLAST+ instead of the BLAST web pages?

10. If you use the Docker image, why do you use BLAST+ Docker instead of installing BLAST+?

11. How strongly you agree or disagree with the following statements about the standalone BLAST+ applications?

	Strongly disagree	Disagree	Neither agree nor disagree	Agree	Strongly agree	N/A
The BLAST+ package is easy to download and install	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Appropriate databases are easy to find and download	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Available formatting options work well for me	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Limiting my search by organism is easy	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

12. If there was one thing you could change about BLAST+, what would it be?

13. Do you use BLAST+ as part of an automated pipeline?

- Yes
 No

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14. What databases do you use with BLAST in your pipeline? Please check all that apply.

- Pre-formatted BLAST database (nr, nt, others from BLAST FTP site)
- Pre-formatted BLAST database (nr, nt, others from cloud service provider such as Google or Amazon)
- Other NCBI databases
- My own databases

15. When running your pipeline which of the following technologies or services do you use?

- Python
- Amazon Machine Image (AMI)
- Google Virtual Machine (VM)
- Common Workflow Language (CWL)
- Docker
- GitHub
- NCBI EDirect or E-Utilities
- NCBI BLAST URL API
- Other (please specify)

16. What changes would you like us to make to BLAST to make it more compatible with your pipeline?

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17. How strongly do you agree or disagree with the following statements about the BLAST web service?

	Strongly disagree	Disagree	Neither agree nor disagree	Agree	Strongly agree	N/A
Knowing which BLAST databases to choose is easy	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Finding BLAST databases for a specific organism is easy	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
BLAST results return quickly	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
BLAST results are easy to read and understand	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Downloading my results is easy and provides what I need	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
The Descriptions table has a clear and understandable layout	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
The Descriptions table has all the fields I need	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

18. Please list any additional fields you would add to the Descriptions table.

19. Please provide any additional functionality you would like to add to the Descriptions table.

20. Please list any additional types of formats or images that you would want to save or print.

21. Would you be interested in sharing your database and/or using other researchers' similar databases?

Yes

No

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22. How likely is it that you would recommend NCBI BLAST 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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23. If there was one thing you could change about BLAST, what would it be?

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We welcome your input! Please contact us at blast-help@ncbi.nlm.nih.gov if you would like to provide additional feedback about NCBI BLAST.

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Done