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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](mailto:blast-help@ncbi.nlm.nih.gov) if you would like to provide additional feedback about NCBI BLAST.**

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Done