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2019 Survey Results Summary

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2019 Survey Results Summary

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

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

- Daily
 Less often than monthly
 Weekly
 Never
 Monthly

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.)
 Scripts that access the BLAST URL API
 BLAST website and upload files and/or paste sequences in the sequence field
 NCBI BLAST+ docket image from dockerhub
 Standalone BLAST+ with the **remote** option to submit BLAST searches to NCBI
 NCBI BLAST+ on a cloud provider, such as Amazon, Azure, Google, etc. Please specify the cloud provider in the comment field below.
 Standalone BLAST+ applications with my own/custom databases
 Through a third-party software. Please specify name of software in the comment field below.
 Standalone BLAST+ with downloaded BLAST databases/FASTA provided by NCBI

Name of third party software and/or cloud provider

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

- Daily
 Less often
 Weekly
 Never
 Monthly

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

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