

NCBI 2018 BLAST 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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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)	☐	☐	☐	☐	☐
Protein BLAST (blastp)	☐	☐	☐	☐	☐
Translated BLAST (blastx, tblastn, tblastx)	☐	☐	☐	☐	☐

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
- ☐ Verify identity of a query sequence
- ☐ Education/Instruction
- ☐ Other (please specify)

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.

- ☐ 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
- ☐ BLAST on a cloud provider, such as Amazon, Azure, Google, etc.
- ☐ 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+ applications?

- ☐ Daily
- ☐ Weekly
- ☐ Monthly
- ☐ Less often
- ☐ Never

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9. 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	☐	☐	☐	☐	☐	☐
Appropriate databases are easy to find and download	☐	☐	☐	☐	☐	☐
Available formatting options work well for me	☐	☐	☐	☐	☐	☐

10. What is your approach to managing BLAST+ software updates?

☐ I only update when it is absolutely necessary

☐ I have a script that regularly downloads the BLAST+ software

☐ I update when ever new versions are announced

☐ I use BLAST+ but someone else manages the installation and updates of the software

☐ I update yearly

☐ Other (please specify)

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

12. 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	☐	☐	☐	☐	☐	☐
Finding BLAST databases for a specific organism is easy	☐	☐	☐	☐	☐	☐
BLAST results return quickly	☐	☐	☐	☐	☐	☐
BLAST results are easy to read and understand	☐	☐	☐	☐	☐	☐
Downloading my results is easy and provides what I need	☐	☐	☐	☐	☐	☐
The Descriptions table has a clear and understandable layout	☐	☐	☐	☐	☐	☐
The Descriptions table has all the fields I need	☐	☐	☐	☐	☐	☐

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

14. Please indicate your level experience with the following technologies.

	Don't know about it	Know of it, but do not use it	Am planning to use it	Have used it	Use it regularly
Amazon Machine Image (AMI)	☐	☐	☐	☐	☐
Google Virtual Machine (VM)	☐	☐	☐	☐	☐
Docker	☐	☐	☐	☐	☐
Common Workflow Language (CWL)	☐	☐	☐	☐	☐
GitHub	☐	☐	☐	☐	☐
Python	☐	☐	☐	☐	☐
EDirect / E-Utilities	☐	☐	☐	☐	☐
BLAST+	☐	☐	☐	☐	☐
Kubernetes	☐	☐	☐	☐	☐
Bioconda	☐	☐	☐	☐	☐
Jupyter notebook	☐	☐	☐	☐	☐
Perl	☐	☐	☐	☐	☐
Building automated bioinformatics pipelines	☐	☐	☐	☐	☐
NCBI BLAST URL API	☐	☐	☐	☐	☐

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

☐ Yes ☐ No

16. Have you had any difficulty incorporating BLAST+ into this pipeline?

- ☐ Yes -- please give details below ☐ No

Please provide details of problems incorporating BLAST into your pipeline.

17. 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)
- ☐ Other NCBI databases
- ☐ Your own databases

18. 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)

19. How often do you use your pipeline?

Hours per day

Days per week

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

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