

# BLAST 2023 Survey (NDB-406)

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Start of Block: Default Question Block

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All questions are optional, and you may exit the survey at any time.

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Which professional categories best describe you? Select all that apply.

- Bioinformatics professional
  - Educator
  - Healthcare professional
  - Librarian / Information Specialist
  - Life Science Researcher
  - Student
  - Technician
  - Computer Scientist / Software Developer
  - Other (please specify)
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Which of the following categories best describe your organization? Select all that apply.

- College or University
  - Commercial / Industry
  - Non-profit Organization
  - Research Institute
  - Government
  - Hospital/health organization
  - Other (please specify)
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How frequently do you use each of the following BLAST services on the web (<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"/> |
| SmartBLAST   | <input type="radio"/> | <input type="radio"/> | <input type="radio"/> | <input type="radio"/> | <input type="radio"/> |
| Global Align (align two or more sequence)          | <input type="radio"/> | <input type="radio"/> | <input type="radio"/> | <input type="radio"/> | <input type="radio"/> |
| PrimerBLAST  | <input type="radio"/> | <input type="radio"/> | <input type="radio"/> | <input type="radio"/> | <input type="radio"/> |
| COBALT (Constrained-based Multiple Alignment tool) | <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"/> |
| MOLE-BLAST   | <input type="radio"/> | <input type="radio"/> | <input type="radio"/> | <input type="radio"/> | <input type="radio"/> |

Why do you use BLAST? Select all that apply.

- Searching unknown mRNA transcripts for functional identification
  - Searching unknown mRNA transcripts for taxonomic identification
  - Searching unknown proteins for functional identification
  - Searching unknown proteins for taxonomic identification
  - Annotating genes on genomic sequence
  - Search with known sequences to find homologs in other organisms
  - Identify organisms (taxa) in environmental/metagenomic samples
  - Screening sequences for contamination
  - Designing/Screening Primers
  - Assembling genome fragments
  - Education/Instruction
  - Other (please specify)
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How frequently do you search with multiple of sequences? Select all that apply.

- Daily
  - Weekly
  - Monthly
  - Less than monthly
  - Never
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Which BLAST services do you use? Select all that apply.

- Use the BLAST+ applications on the command line remotely to submit BLAST searches to NCBI
  - Use the BLAST+ applications on the command line with my own/custom databases
  - Use the BLAST+ applications on the command line with BLAST databases/FASTA provided by NCBI
  - Submit BLAST searches using scripts that access the BLAST URL API
  - Use NCBI BLAST+ docker image from docker hub
  - Use BLAST on the cloud with a vendor (e.g AWS, GCP, etc).
  - Use BLAST through third-party software (please specify software used)
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- N/A (I do not use any of these services)
  - Other (please specify)
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How frequently do you use the standalone BLAST+ (command line) applications? Select all that apply.

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

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Why do you use the BLAST+ instead the BLAST web application?

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Please indicate how strongly you agree or disagree with the following statements about using BLAST+.

|   | Strongly Disagree     | Somewhat disagree     | Neither agree nor disagree | Somewhat agree        | Strongly agree        |
|---|-----------------------|-----------------------|----------------------------|-----------------------|-----------------------|
| I am satisfied with the performance of BLAST+.  | <input type="radio"/> | <input type="radio"/> | <input type="radio"/>      | <input type="radio"/> | <input type="radio"/> |
| I frequently look at the databases available to see if there is a better one for me to use. | <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"/> |
| I have an automated task that downloads the latest databases.                               | <input type="radio"/> | <input type="radio"/> | <input type="radio"/>      | <input type="radio"/> | <input type="radio"/> |

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What is one thing you would like to change in BLAST+?

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Please indicate how strongly you agree or disagree with the following statements about the BLAST web application.

|   | Strongly Disagree     | Somewhat disagree     | Neither agree nor disagree | Somewhat agree        | Strongly agree        |
|---|-----------------------|-----------------------|----------------------------|-----------------------|-----------------------|
| Knowing which BLAST databases to choose is easy.              | <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"/> |
| Finding BLAST databases for a specific genome is easy.        | <input type="radio"/> | <input type="radio"/> | <input type="radio"/>      | <input type="radio"/> | <input type="radio"/> |
| BLAST results are returned quickly.                           | <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"/> |
| 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"/> |
| The Descriptions table has a clear and understandable layout. | <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"/> |

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What is one thing you would like to change about the BLAST web application?

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What is the biggest challenge for you when you use BLAST?

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Please enter your email below if you would like us to contact you for a BLAST user interview.

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If you would like to provide more feedback, please contact us at [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)

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How likely are you to recommend BLAST to a friend or colleague?

- 0
- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10

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End of Block: Default Question Block

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