

Resource Summary Report

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BLASTN

RRID:SCR_001598

Type: Tool

Proper Citation

BLASTN (RRID:SCR_001598)

Resource Information

URL:

http://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&BLAST_PROGRAMS=megaBlast&PAGE=b

Proper Citation: BLASTN (RRID:SCR_001598)

Description: Web application to search nucleotide databases using a nucleotide query.
Algorithms: blastn, megablast, discontinuous megablast.

Abbreviations: BLASTn

Synonyms: NCBI BLASTN, Nucleotide Blast, Standard Nucleotide BLAST

Resource Type: data analysis service, analysis service resource, production service resource, service resource, database, data or information resource

Defining Citation: [PMID:17666756](#), [PMID:18567917](#)

Keywords: nucleotide, alignment, compare, sequence, genome, blast, transcript, dna sequence

Availability: Free, Freely available

Resource Name: BLASTN

Resource ID: SCR_001598

Alternate IDs: nlx_153932, OMICS_00990

Alternate URLs:

http://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=b

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260805T044025+0000

Ratings and Alerts

No rating or validation information has been found for BLASTN.

No alerts have been found for BLASTN.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19679 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

He T, et al. (2026) Thousands-years-old deep-sea DNA viruses reveal the evolution of human pathogenic viruses. *Journal of advanced research*, 79, 379.

Perfilyev A, et al. (2026) Large-scale analysis of bacterial genomes reveals thousands of lytic phages. *Nature microbiology*, 11(1), 42.

Bedoya-Urrego K, et al. (2026) Next-Gen intestinal parasite detection: Leveraging metataxonomics for improved diagnosis of intestinal protists and helminths. *PloS one*, 21(1), e0330312.

León-Cadena A, et al. (2026) Updating the description of *Rhizobium* diversity associated with common bean cultivars in the Ecuadorian Andes: A phylogenetic and functional perspective. *PloS one*, 21(1), e0339774.

Tagirdzhanova G, et al. (2026) Chromosome-level genome assembly of the photobiont microalga *Trebouxia* sp. 'A48' from the lichen *Xanthoria parietina*. *The New phytologist*, 249(2), 1036.

Akanbi TM, et al. (2026) Isolation and characterization of TayeBlu, a novel bacteriophage of *Azotobacter vinelandii*. *Microbiology spectrum*, 14(1), e0128625.

Kulikov N, et al. (2026) The Chromosome-Scale Genome Assembly of the Redlip Blenny, *Ophioblennius macclurei* (Blenniidae). *Genome biology and evolution*, 18(1).

Song LCT, et al. (2026) Identification of proteins influencing CRISPR-associated transposases for enhanced genome editing. *Science advances*, 12(1), eaea1429.

Wu J, et al. (2026) Emerging adaptation of BJ/94 lineage H9N2 viruses to waterfowl: insights into enhanced replication and immune activation in the host cells. *Poultry science*, 105(1), 106182.

Vaiana C, et al. (2026) An integrated phenotypic and genomic approach to characterize MBL-producing Enterobacterales strains circulating in a Sicilian transplant center. *Microbiology spectrum*, 14(1), e0207725.

Lima Cunha W, et al. (2026) Molecular mechanisms associated with rootstock-scion interactions in rubber trees. *The plant genome*, 19(1), e70147.

Garg P, et al. (2026) Emerging genetic diversity and molecular epidemiology of *Entamoeba moshkovskii* among patients with acute diarrhoea in Northern India. *Tropical medicine and health*, 54(1), 3.

Figueroa Y, et al. (2026) STEC in the natural environment of Uruguay: genomic surveillance and environmental circulation in the framework of One Health. *Microbiology spectrum*, 14(1), e0315325.

Ji Y, et al. (2026) Patulin Biodegradation by *Rhodosporidiobolus ruineniae* and *Meyerozyma guilliermondii* Isolated From Fruits. *MicrobiologyOpen*, 15(1), e70198.

Yeki S, et al. (2026) Sex-Specific doublesex Regulation Targeting the Color-Patterning Gene *h* Underlies the Evolution of Wing Sexual Dimorphism in the Harlequin Ladybug *Harmonia axyridis*. *Evolution & development*, 28(1), e70028.

Zhou Z, et al. (2026) Chromosome-level genome provides novel insights into the starch metabolism regulation and evolutionary history of *Tetraselmis helgolandica*. *Journal of advanced research*, 79, 251.

Luo Z, et al. (2026) Host adaptation and genome evolution of the broad host range fungal rust pathogen, *Austropuccinia psidii*. *G3 (Bethesda, Md.)*, 16(1).

Sá-Guimarães TDE, et al. (2026) ZIKV Phylogenetic Characterization Reveals Evolutionary Diversity, Regional Dissemination, and Emergence of African Lineages in Brazil. *Journal of basic microbiology*, 66(1), e70122.

Yoo D, et al. (2026) Epigenetic and evolutionary features of ape subterminal heterochromatin. *Genome research*, 36(1), 38.

Ganesh A, et al. (2026) The Karnataka Individual Genome Project expands the human reference landscape to include South Asia. *HGG advances*, 7(1), 100516.