

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: analysis service resource, data analysis service, data or information resource, database, production service resource, service 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: 20260905T132436+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 21160 mentions in open access literature.

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

Wu X, et al. (2026) Locus-Specific Human Endogenous Retrovirus ERVK18 Expression Indicates an Inflamed Microenvironment and Favorable Immunotherapy Outcome in Small Cell Lung Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(11), 2214.

Li SY, et al. (2026) TGF β 1 Activates Lnc-APUE to Promote Tumor Metastasis via the Alu Element-Driven STAU1-Mediated Decay of CDH1 mRNA. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(20), e18731.

Sinha A, et al. (2026) Prophage induction contributes to alterations in the gut phageome during intestinal inflammation. *Cell reports*, 45(7), 117491.

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.

Rangachar Srinivasa V, et al. (2026) Genomic epidemiology of healthcare-associated respiratory virus infections in Pittsburgh, Pennsylvania, 2018-2020. *Infection control and hospital epidemiology*, 47(1), 53.

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.

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

Serafim de Castro EM, et al. (2026) Ectoparasite-borne *Bartonella* and *Rickettsia* in Chilean populations of *Rattus rattus*: prevalence, genetic diversity and environmental associations. *Parasitology*, 153(2), 230.

De Filippo E, et al. (2026) Stepwise recombination suppression around the mating-type locus associated with a diploid-like life cycle in *Schizothecium* fungi. *Molecular biology and evolution*, 43(1).

Antochevis LC, et al. (2026) Molecular Epidemiology of Methicillin-Resistant *Staphylococcus aureus* Causing Healthcare-Associated Bloodstream Infections in Brazil: Results from A Prospective Countrywide Multicenter Study. *Infectious diseases and therapy*, 15(2), 507.

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.

Mungunkhuyag K, et al. (2026) Isolation and characterization of heavy metal tolerant microalgae from old mining areas of Saxony. *Scientific reports*, 16(1), 1337.

Zhang S, et al. (2026) Assembly and comparative analysis of the complete mitochondrial genome of the *Maclura tricuspidata*. *BMC genomics*, 27(1), 129.

Fan M, et al. (2026) Phylogenetic diversification and fitness trade-offs of TetA variants in mediating eravacycline resistance in *Klebsiella pneumoniae*. *Antimicrobial agents and chemotherapy*, 70(2), e0067125.

Biessy A, et al. (2026) Single-strain and consortium inoculations with plant-beneficial *Pseudomonas* spp. promote lettuce growth under field conditions. *Microbiology spectrum*, 14(2), e0350925.

Mizanur R, et al. (2026) Reported circulation of Zika and re-circulation of Chikungunya in Dengue-endemic Dhaka, Bangladesh in 2024. *PloS one*, 21(2), e0340119.

Wang M, et al. (2026) Temporal dynamics of the fecal microbiome in wintering seagulls: a One Health perspective. *BMC genomics*, 27(1), 191.

Fernández-Fernández R, et al. (2026) Structured Promoter Variability in Epigenetically Regulated Operons Contributes to Surface Adaptation in *Salmonella*. *Microbial biotechnology*, 19(2), e70312.

Cai L, et al. (2026) Recombination and Retroprocessing in Broomrapes Reveal RNA-Mediated Gene Transfer Mechanism and a Generalizable Model for Mitochondrial Evolution in Heterotrophic Plants. *Genome biology and evolution*, 18(2).