

Resource Summary Report

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BLASTX

RRID:SCR_001653

Type: Tool

Proper Citation

BLASTX (RRID:SCR_001653)

Resource Information

URL:

http://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastx&BLAST_PROGRAMS=blastx&PAGE_TYPE=blastx

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Description: Web application to search protein databases using a translated nucleotide query. Translated BLAST services are useful when trying to find homologous proteins to a nucleotide coding region. Blastx compares translational products of the nucleotide query sequence to a protein database. Because blastx translates the query sequence in all six reading frames and provides combined significance statistics for hits to different frames, it is particularly useful when the reading frame of the query sequence is unknown or it contains errors that may lead to frame shifts or other coding errors. Thus blastx is often the first analysis performed with a newly determined nucleotide sequence and is used extensively in analyzing EST sequences. This search is more sensitive than nucleotide blast since the comparison is performed at the protein level.

Abbreviations: BLASTX

Synonyms: Translated BLAST, Translated BLAST: blastx

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

Defining Citation: [PMID:28902395](#), [PMID:8485583](#)

Keywords: protein, translated nucleotide, blast, nucleotide, expressed sequence tag, sequence, genome, wgs, peptide, alignment, dna

Availability: Free, Freely Available

Resource Name: BLASTX

Resource ID: SCR_001653

Alternate IDs: nlx_153933, OMICS_00992

Alternate URLs:

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

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260821T193633+0000

Ratings and Alerts

No rating or validation information has been found for BLASTX.

No alerts have been found for BLASTX.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10411 mentions in open access literature.

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

Vaidya SP, et al. (2026) Chronic alcohol consumption and abstinence disrupt cholinergic gene expression in the mesopontine tegmentum of alcohol-preferring iP rats. Neuroscience letters, 875, 138539.

Choi NY, et al. (2026) Elucidating the Genetic Basis of Columnar Upright Architecture in Populus Through CRISPR Disruption of TILLER ANGLE CONTROL1. Plant biotechnology journal, 24(3), 1377.

Yang F, et al. (2026) A signature-protein-based approach for accurate and efficient profiling of the human gut virome. Cell reports methods, 6(1), 101250.

Li JL, et al. (2026) Molecular cloning and characterization of a GH10 thermophilic xylanase from hot spring and its potential application in promoting probiotic growth. BMC biotechnology, 26(1), 16.

Haywood LMB, et al. (2026) A novel kirkovirus may be associated with equine gastrointestinal disease. Equine veterinary journal, 58(2), 414.

Zhao Y, et al. (2026) Chromosome-level genome assembly and annotation of the Rhinogobio ventralis, an endangered endemic fish from the Yangtze River. Scientific data, 13(1).

Han S, et al. (2026) Evidence of Relaxed Selection in the Mitochondrial Genomes of Phototrophic Paulinella Lineages. Genome biology and evolution, 18(3).

Shipova AA, et al. (2026) From Adam's rib: the Siberian moth's female W chromosome is derived from its Z counterpart. *Molecular biology and evolution*, 43(3).

Volk A, et al. (2026) Investigation of cyanobacteria-hosted antibiotic resistance genes in cyanoHAB-impacted drinking water sources. *Environmental science and pollution research international*, 33(13), 6140.

Puente A, et al. (2026) Occurrence and Antimicrobial Resistance of *Acinetobacter* spp. in Processing Environments of Slaughterhouses and Meat Processing Facilities. *Foods (Basel, Switzerland)*, 15(7).

S??ndreli KL, et al. (2026) Transcriptomic and functional analyses uncover a conserved effector driving genotype-dependent virulence in the *Sphaerulina musiva*-*Populus trichocarpa* interaction. *mBio*, 17(5), e0312025.

Wang B, et al. (2026) Global genomic diversity of the selfing nematode *Caenorhabditis tropicalis* correlates with geography. *bioRxiv : the preprint server for biology*.

Debernardis R, et al. (2026) Dynamic interplay of maternal and paternal contributions to offspring phenotype in Eurasian perch. *BMC biology*, 24(1).

Wauters M, et al. (2026) Identification of DksA as a novel pro-inflammatory mediator of *Pseudomonas aeruginosa* under conditions mimicking chronic cystic fibrosis lung infection. *Virulence*, 17(1), 2670050.

Duque M, et al. (2026) Genome-Wide In Silico Analysis of the Type VI Secretion System (T6SS) Within the *Morganella* Genus. *MicrobiologyOpen*, 15(3), e70304.

Hagenbeek A, et al. (2026) Genome-resolved metagenomics reveals unexpected diversity and host range of *Candidatus Lariskella* (Rickettsiales: Midichloriaceae). *BMC genomics*, 27(1).

Zhu D, et al. (2026) The hidden role of rhizospheric viruses in promoting nitrogen fixation in soils. *Nature communications*, 17(1).

Guo X, et al. (2026) Reactive oxygen species in the rhizosphere orchestrate the recruitment of beneficial bacteria. *The EMBO journal*, 45(4), 1245.

Bernier L, et al. (2026) An Ammonium Transporter Gene Contributes to the Aggressiveness of the Dutch Elm Disease Pathogen *Ophiostoma novo-ulmi*. *Journal of fungi (Basel, Switzerland)*, 12(2).

Zhang J, et al. (2026) Transcriptomic insights into the role of CmLec4 in infection and development of *Cordyceps militaris*. *AMB Express*, 16(1).