Resource Summary Report

Generated by NIF on Aug 10, 2026

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_TYP

Proper Citation: BLASTX (RRID:SCR_001653)

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: database, data or information resource, service resource, data analysis service, analysis service resource, production 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: 20260810T040318+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 NIF .

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.

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

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.

Shen G, et al. (2026) Integrated transcriptomic and metabolomic analysis reveals the regulatory role of lignin biosynthesis in raspberry (Rubus niveus) prickle development. BMC plant biology, 26(1), 275.

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

She Q, et al. (2026) Rapid dissemination of Staphylococcus aureus in the neonatal intensive care unit is associated with invasive infection. Nature communications, 17(1).

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.

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

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).

Placide A, et al. (2026) The de novo transcriptome of the freshwater copepod Cyclops abyssorum tatricus reveals high-elevation adaptation. Scientific reports, 16(1).

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.

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).

Molina-Montenegro MA, et al. (2026) The endomicrobiome and weed invasiveness in Mediterranean ecosystems worldwide. Nature communications, 17(1).

Becerril M, et al. (2026) Temperature changes reveal different transcriptional responses in the larvae of the bark beetle Dendroctonus rhizophagus during the cold season. Scientific reports, 16(1).

Begnel ER, et al. (2026) Comparison of gut virome in Kenyan infants born to women with and without HIV. iScience, 29(3), 114900.

Yang S, et al. (2026) Trade-off between accumulation potential and transmission efficiency in hypovirus variants infecting phytopathogenic fungi. mBio, 17(2), e0292225.

Wang C, et al. (2026) Multi-Tissue Omics Analysis Uncovers Translational Regulation Underlying Complex Traits in Pigs. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(20), e74200.

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