

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: data analysis service, data or information resource, database, service resource, production service resource, analysis 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: 20260801T190158+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 10091 mentions in open access literature.

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

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

Jin S, et al. (2026) Microbial collagenase activity is linked to oral-gut translocation in advanced chronic liver disease. *Nature microbiology*, 11(1), 211.

Pronozin AY, et al. (2026) Diversity of lncRNAs in the pan-transcriptome of maize inbred lines. *BMC genomics*, 27(1), 1.

Vaidya SP, et al. (2025) Inhibition of HCN channels decreases motivation for alcohol and deprivation-induced drinking in alcohol preferring rats. *Neuropharmacology*, 270, 110371.

Han H, et al. (2025) A telomere-to-telomere phased genome of an octoploid strawberry reveals a receptor kinase conferring anthracnose resistance. *GigaScience*, 14.

Yen EC, et al. (2025) Chromosome-level genome assembly and methylome profile yield insights for the conservation of endangered loggerhead sea turtles. *GigaScience*, 14.

Schall PZ, et al. (2025) Integrative Genotyping and Analysis of Canine Structural Variation Using Long-read and Short-read Data. *Genome biology and evolution*, 17(10).

De Koch MD, et al. (2025) Novel lineage of anelloviruses with large genomes identified in dolphins. *Journal of virology*, 99(1), e0137024.

Ishizaka A, et al. (2025) Dysbiosis of gut microbiota in COVID-19 is associated with intestinal DNA phage dynamics of lysogenic and lytic infection. *Microbiology spectrum*,

13(1), e0099824.

Yoon SE, et al. (2025) Clinical Impact of Microbiome Characteristics in Treatment-Naïve Extranodal NK/T-Cell Lymphoma Patients. *Cancer research and treatment*, 57(2), 597.

Astaraki S, et al. (2025) High-throughput sequencing revealed the symptomatic common bean (*Phaseolus vulgaris* L.) virome in Iran. *Scientific reports*, 15(1), 1621.

Xian W, et al. (2025) TIPPO: A User-Friendly Tool for De Novo Assembly of Organellar Genomes with High-Fidelity Data. *Molecular biology and evolution*, 42(1).

Prigent L, et al. (2025) Sexual reproduction during diatom bloom. *ISME communications*, 5(1), ycae169.

Langley CA, et al. (2025) Antiviral Mx proteins have an ancient origin and widespread distribution among eukaryotes. *Proceedings of the National Academy of Sciences of the United States of America*, 122(4), e2416811122.

Agolino G, et al. (2025) Genome Mining and Characterization of Two Novel *Lactocaseibacillus rhamnosus* Probiotic Candidates with Bile Salt Hydrolase Activity. *Biomolecules*, 15(1).

Wang C, et al. (2025) Identifying Candidate Genes Related to Soybean (*Glycine max*) Seed Coat Color via RNA-Seq and Coexpression Network Analysis. *Genes*, 16(1).

Pourtois JD, et al. (2025) *Pseudomonas* superinfection drives Pf phage transmission within airway infections in patients with cystic fibrosis. *bioRxiv : the preprint server for biology*.

Krausfeldt LE, et al. (2025) Transcriptional profiles of *Microcystis* reveal gene expression shifts that promote bloom persistence in in situ mesocosms. *Microbiology spectrum*, 13(1), e0136924.

Wu F, et al. (2025) Comparative genomic analysis of ten *Elizabethkingia anophelis* isolated from clinical patients in China. *Microbiology spectrum*, 13(1), e0178024.

Campbell AS, et al. (2025) Opposing roles for Bmp signalling during the development of electrosensory lateral line organs. *eLife*, 14.