## **Resource Summary Report**

Generated by FDI Lab - SciCrunch.org on May 3, 2025

# **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=

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:** production service resource, database, analysis service resource, data analysis service, service resource, data or information resource

Defining Citation: PMID:28902395, PMID:8485583

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

Funding:

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=blas

Record Creation Time: 20220129T080208+0000

Record Last Update: 20250503T055441+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: <u>SciCrunch Registry</u>

## **Usage and Citation Metrics**

We found 9579 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Xu Z, et al. (2025) An orphan viral genome with unclear evolutionary status sheds light on a distinct lineage of flavi-like viruses infecting plants. Virus evolution, 11(1), veaf001.

Li B, et al. (2025) Characteristics and phylogenetic analysis of the complete chloroplast genome of Rubus swinhoei Hance 1866 from the family Rosaceae. Mitochondrial DNA. Part B, Resources, 10(2), 119.

Prasad M, et al. (2025) De novo transcriptome profiling revealing genes involved in piperine biosynthetic pathway in Piper longum L. Scientific reports, 15(1), 2943.

Ren T, et al. (2025) Preparation of pH-Responsive Tanshinone IIA-Loaded Calcium Alginate Nanoparticles and Their Anticancer Mechanisms. Pharmaceutics, 17(1).

Debat H, et al. (2025) RNA Virus Discovery Sheds Light on the Virome of a Major Vineyard Pest, the European Grapevine Moth (Lobesia botrana). Viruses, 17(1).

Nichols RG, et al. (2025) Clade-specific long-read sequencing increases the accuracy and

specificity of the gyrB phylogenetic marker gene. mSystems, 10(1), e0148024.

Záhonová K, et al. (2025) Comparative Analysis of Protist Communities in Oilsands Tailings Using Amplicon Sequencing and Metagenomics. Environmental microbiology, 27(1), e70029.

Castelli M, et al. (2025) Hepatincolaceae (Alphaproteobacteria) are Distinct From Holosporales and Independently Evolved to Associate With Ecdysozoa. Environmental microbiology, 27(1), e70028.

Zhao ZA, et al. (2025) PiERF1 regulates cold tolerance in Plumbago indica L. through ethylene signalling. Scientific reports, 15(1), 1735.

Shah K, et al. (2025) Gibberellin-3 induced dormancy and suppression of flower bud formation in pitaya (Hylocereus polyrhizus). BMC plant biology, 25(1), 47.

Choi J, et al. (2025) Sticky organisms create underwater biological adhesives driven by interactions between EGF- and GlcNAc- containing polysaccharides. Nature communications, 16(1), 233.

Liang A, et al. (2025) Usp7 contributes to the tail regeneration of planarians via Islet/Wnt1 axis. Journal of translational medicine, 23(1), 137.

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.

Ribeyre Z, et al. (2025) De novo transcriptome assembly and discovery of droughtresponsive genes in white spruce (Picea glauca). PloS one, 20(1), e0316661.

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.

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

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

Agolino G, et al. (2025) Genome Mining and Characterization of Two Novel Lacticaseibacillus 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).