Resource Summary Report

Generated by NIF on Aug 30, 2026

TBLASTN

RRID:SCR_011822
Type: Tool

Proper Citation

TBLASTN (RRID:SCR_011822)

Resource Information

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

Proper Citation: TBLASTN (RRID:SCR_011822)

Description: Tool to search translated nucleotide databases using a protein query.

Abbreviations: TBLASTN

Synonyms: Translated BLAST: tblastn

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Keywords: protein

Resource Name: TBLASTN

Resource ID: SCR_011822

Alternate IDs: OMICS_00999

Record Creation Time: 20220129T080306+0000

Record Last Update: 20260829T183038+0000

Ratings and Alerts

No rating or validation information has been found for TBLASTN.

No alerts have been found for TBLASTN.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5696 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect Cryptophyllium westwoodii provide insights into the evolution of leaf-like masquerade. GigaScience, 15.

Chen G, et al. (2026) Draft assemblies for 177 bird species enhance genus-level coverage. GigaScience, 15.

Ortiz-Eriamiatoe J, et al. (2026) Genome-wide evolutionary characterization and expression analysis of the AT-HOOK MOTIF CONTAINING NUCLEAR LOCALIZED gene family in Brachypodium distachyon. G3 (Bethesda, Md.), 16(3).

Xiang X, et al. (2026) A mammalian-like piRNA pathway in Axolotl reveals the origins of piRNA-directed DNA methylation. The EMBO journal, 45(6), 1933.

Zhang D, et al. (2026) Assembling a chromosome-level genome for the Microtus fortis using PacBio HiFi and Hi-C technologies. Scientific data, 13(1).

Leal K, et al. (2026) Exploration of inactive metabolic pathways in Antarctic Pseudogymnoascus australis through elicitation: a genomic and metabolomic approach to investigate its biotechnological potential. IMA fungus, 17, e156018.

Huang X, et al. (2026) An Improved Chromosome-Level Genome Assembly and Comprehensive Annotation of the Model Ascidian Ciona savignyi. Scientific data, 13(1).

Hammond M, et al. (2026) Subcellular proteomics reveals a blueprint for endosymbiont integration in trypanosomatid Angomonas deanei. Nature communications, 17(1).

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

Huang C, et al. (2026) Convergent evolutionary shifts in AGT targeting between mitochondria and peroxisomes across mammal transitions to herbivory. Nature communications, 17(1).

Naranjo-Robayo N, et al. (2026) Updated taxonomy of the family Rhizobiaceae with proposals for 8 novel genera and 32 novel combinations. International journal of systematic and evolutionary microbiology, 76(4).

Villarreal DA, et al. (2026) Screening metatranscriptomes for ultrastable RNA secondary structures reveals hidden bacteriophages and novel capsid nanomaterials. bioRxiv : the preprint server for biology.

Wang J, et al. (2026) A chromosomal-level genome assembly of Phoxinus grumi (Cypriniformes: Leuciscidae). Scientific data, 13(1).

Tóth V, et al. (2026) Improved serological testing for bovine schistosomiasis in Eastern Africa. Parasites & vectors, 19(1).

Chary S, et al. (2026) Conserved but mechanistically diverse piRNA defence against endogenous retroviruses in insects. EMBO reports, 27(9), 2243.

Padyab S, et al. (2026) Genome-wide analysis of the MYB gene family and its stress-responsive expression under salinity and drought in sesame. Scientific reports, 16(1), 6203.

Bai S, et al. (2026) Decoding color variation: genome-wide characterization and expression analysis of pigment pathways in Neocaridina denticulata. BMC genomics, 27(1).

Royer M, et al. (2026) The mecillinam resistome in Klebsiella pneumoniae: how resistance to a one-target ?-lactam triggers a diversity of responses. Antimicrobial agents and chemotherapy, 70(3), e0120725.

Tsai YC, et al. (2026) Birth and death evolution of polyphenol oxidase (PPO) gene family in Oryza species. Botanical studies, 67(1), 4.

Cappella C, et al. (2026) Development of a Tool for High-Efficiency, Markerless and Iterative Genome Editing in Shouchella clausii. Microbial biotechnology, 19(2), e70287.