

# Resource Summary Report

Generated by [dkNET](#) on Aug 30, 2026

## TBLASTN

RRID:SCR\_011822

Type: Tool

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### Proper Citation

TBLASTN (RRID:SCR\_011822)

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### Resource Information

**URL:**

[http://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=tblastn&PAGE\\_TYPE=BlastSearch&LINK\\_LOC=](http://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=tblastn&PAGE_TYPE=BlastSearch&LINK_LOC=BLAST_)

**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

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### Ratings and Alerts

No rating or validation information has been found for TBLASTN.

No alerts have been found for TBLASTN.

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### Data and Source Information

## Usage and Citation Metrics

We found 5696 mentions in open access literature.

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

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum 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-Eriamiatoc 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  $\beta$ -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.