

Resource Summary Report

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BLASTP

RRID:SCR_001010

Type: Tool

Proper Citation

BLASTP (RRID:SCR_001010)

Resource Information

URL:

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

Proper Citation: BLASTP (RRID:SCR_001010)

Description: Data analysis service whose programs search protein databases using a protein query. The algorithms used include blastp, psi-blast, phi-blast, and delta-blast.

Synonyms: blastp suite, Standard Protein BLAST

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

Keywords: blast, basic local alignment search tool, protein alignment, protein blast, data analysis service, protein

Availability: Freely available, Acknowledgement requested

Resource Name: BLASTP

Resource ID: SCR_001010

Alternate IDs: OMICS_00991

Record Creation Time: 20220129T080205+0000

Record Last Update: 20260801T190857+0000

Ratings and Alerts

No rating or validation information has been found for BLASTP.

No alerts have been found for BLASTP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 286 mentions in open access literature.

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

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

Mochales-Riaño G, et al. (2025) Chromosome-level reference genome for the medically important Arabian horned viper (*Cerastes gasperettii*). *GigaScience*, 14.

Bian C, et al. (2025) Chromosome-level genome assemblies of five *Sinocyclocheilus* species. *GigaByte* (Hong Kong, China), 2025, gigabyte155.

Mendel HC, et al. (2025) PeptideMiner-neuropeptide discovery across the animal kingdom. *GigaScience*, 14.

Froschauer K, et al. (2025) Complementary Ribo-seq approaches map the translome and provide a small protein census in the foodborne pathogen *Campylobacter jejuni*. *Nature communications*, 16(1), 3078.

Bharti S, et al. (2025) Single-cell transcriptome atlas of adult male and female human hookworm *Ancylostoma ceylanicum*. *iScience*, 28(11), 113846.

Han B, et al. (2025) Evolutionarily diverse caveolins share a common structural framework built around amphipathic disks. *The Journal of cell biology*, 224(9).

Nath R, et al. (2025) Lineage-Specific Class-A GPCR Dynamics Reflect Diverse Chemosensory Adaptations in Lophotrochozoa. *Molecular biology and evolution*, 42(3).

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

Zhang G, et al. (2025) Genomic and transcriptomic analyses of *Heteropoda venatoria* reveal the expansion of P450 family for starvation resistance in spiders. *GigaScience*, 14.

Yuan J, et al. (2025) A telomere-to-telomere genome assembly of koi carp (*Cyprinus carpio*) using long reads and Hi-C technology. *GigaScience*, 14.

Turner LA, et al. (2025) Differences in gene expression between high and low tolerance rainbow trout (*Oncorhynchus mykiss*) to acute thermal stress. *PloS one*, 20(1), e0312694.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant *Stylosanthes angustifolia*: insights into genome evolution and drought adaptation. *GigaScience*, 14.

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

Sivakumar P, et al. (2025) Sporophyte-directed gametogenesis in *Arabidopsis*. *Nature plants*, 11(3), 398.

Chen M, et al. (2025) The genome of *Hippophae salicifolia* provides new insights into the sexual differentiation of sea buckthorn. *GigaScience*, 14.

Bian C, et al. (2025) Telomere-to-telomere chromosome-scale genome assemblies of black and golden koi carp variants support construction of an ancient karyotype of Cypriniformes. *GigaScience*, 14.

Yuan S, et al. (2025) Multiomic Analyses Reveal the Molecular Mechanisms of Arid Adaptation in a Desert Rodent Species. *Molecular biology and evolution*, 42(10).

Basharat Z, et al. (2025) Proteome mining of *Yersinia Enterocolitica* for drug targets and computational inhibitor identification with ADMET, anti-inflammation potential and formulation characteristics. *BioData mining*, 18(1), 68.

Farag A, et al. (2025) Repurposing rupatadine as topical treatment against methicillin-resistant *Staphylococcus aureus*. *AMB Express*, 15(1), 132.