

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

NCBI BLAST

RRID:SCR_004870

Type: Tool

Proper Citation

NCBI BLAST (RRID:SCR_004870)

Resource Information

URL: <http://blast.ncbi.nlm.nih.gov/Blast.cgi>

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Description: Web search tool to find regions of similarity between biological sequences. Program compares nucleotide or protein sequences to sequence databases and calculates statistical significance. Used for identifying homologous sequences.

Abbreviations: BLAST

Synonyms: NCBI Basic Local Alignment Search Tool, NCBI BLAST, Basic Local Alignment Search Tool, BLAST

Resource Type: data access protocol, data analysis software, data processing software, sequence analysis software, software application, software resource, web service

Defining Citation: [PMID:16845079](#), [PMID:18440982](#)

Keywords: genome, similarity, sequence, nucleotide, protein, gene, data, bio.tools

Funding: National Library of Medicine

Availability: Free, Freely available, Tutorial available

Resource Name: NCBI BLAST

Resource ID: SCR_004870

Alternate IDs: OMICS_01436, nlx_84530, biotools:blast

Alternate URLs: <http://blast.ncbi.nlm.nih.gov>, <https://bio.tools/blast>, <https://sources.debian.org/src/ncbi-blast/>

Record Creation Time: 20220129T080227+0000

Ratings and Alerts

No rating or validation information has been found for NCBI BLAST.

No alerts have been found for NCBI BLAST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17718 mentions in open access literature.

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

Campbell AS, et al. (2026) Molecular insights into electroreceptor ribbon synapses from differential gene expression in sturgeon lateral line organs. *Journal of anatomy*, 248(5), 784.

Daniel K, et al. (2026) Pre-existing neutralizing antibodies against cattle-transmitted influenza A virus H5N1 are detectable in unexposed individuals. *Immunity*, 59(2), 494.

Robinson E, et al. (2026) STK11 mutations and deletions define a distinct subtype of cervical adenocarcinoma. *medRxiv : the preprint server for health sciences*.

Plasil M, et al. (2026) A chromosome-level genome assembly of the snow leopard, *Panthera uncia*. *The Journal of heredity*, 117(2), 272.

Delgado-Suarez EJ, et al. (2026) Emergence of multidrug-resistant blaCTX-M-65/gyrA_D87Y clones among the circulating *Salmonella* Infantis population in Mexico. *Microbial genomics*, 12(2).

Begnel ER, et al. (2026) Comparison of gut virome in Kenyan infants born to women with and without HIV. *iScience*, 29(3), 114900.

Kohabir KAV, et al. (2026) Toward point-of-care and amplification-free detection of human cytomegalovirus using CRISPR-Cas12a. *iScience*, 29(7), 116494.

Zhang C, et al. (2026) Molecular investigation of the progenitors, origin and domestication patterns of diploid Chinese old garden roses. *Annals of botany*, 137(3), 655.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Gulla S, et al. (2026) MECOM Function Is Critical for AR-Driven Treatment-Resistant Prostate Cancer. *Cancer research*, 86(9), 2143.

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

van de Grift YBC, et al. (2026) GRHL and PGR control WNT4 expression via 3D looping of conserved and species-specific enhancers. *Cell reports*, 45(7), 117575.

Nail AN, et al. (2026) Deficient arsenic methylation and global proteomic reprogramming in human keratinocytes during arsenic-induced skin carcinogenesis. *Archives of toxicology*.

Modlin SJ, et al. (2026) Pervasive genome structure heterogeneity in *Mycobacterium tuberculosis* constitutively generates subpopulations with distinct clinical phenotypes. *iScience*, 29(5), 115045.

Yasuma-Mitobe K, et al. (2026) Intracellular acidification by microbiota-derived valeric acid facilitates trans-kingdom ecology limiting *Candida parapsilosis* colonization. *Cell host & microbe*, 34(7), 1320.

Francette AM, et al. (2026) Evolutionary analysis of transcription elongation factors reveals conserved and lineage-specific regulatory domains. *PLoS biology*, 24(6), e3003855.

Liu D, et al. (2026) Predominant Merkel Cell Polyomavirus DNA Detection in Essential Thrombocythemia within Myeloproliferative Neoplasms. *Cancer research communications*, 6(4), 742.

Cho A, et al. (2026) Aerobic sister lineage of breviate has gene-rich mitochondrial genomes. *Current biology : CB*, 36(6), 1481.

Zheng W, et al. (2026) Mutation elevation and functional alterations in *Escherichia coli* are pertinent to the onset of gestational diabetes mellitus. *Cell reports*, 45(4), 117143.

Rizk NM, et al. (2026) Microbial community assembly and pathogen signatures in groundwater and tap water systems in greater Cairo, Egypt. *The Journal of the Egyptian Public Health Association*, 101(1).