# **Resource Summary Report**

Generated by NIF on May 16, 2025

## **WU-BLAST**

RRID:SCR\_011824

Type: Tool

### **Proper Citation**

WU-BLAST (RRID:SCR\_011824)

#### **Resource Information**

URL: http://www.ebi.ac.uk/Tools/sss/wublast/

Proper Citation: WU-BLAST (RRID:SCR\_011824)

**Description:** Tool to find regions of sequence similarity within selected protein databases

quickly, with minimum loss of sensitivity.

Abbreviations: WU-BLAST

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

service, service resource

Keywords: protein, dna, rna

**Funding:** 

Resource Name: WU-BLAST

Resource ID: SCR\_011824

Alternate IDs: OMICS\_01001

**Record Creation Time:** 20220129T080306+0000

**Record Last Update:** 20250516T053957+0000

## Ratings and Alerts

No rating or validation information has been found for WU-BLAST.

#### Data and Source Information

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 133 mentions in open access literature.

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

Chen G, et al. (2023) The Jasmine (Jasminum sambac) Genome Provides Insight into the Biosynthesis of Flower Fragrances and Jasmonates. Genomics, proteomics & bioinformatics, 21(1), 127.

Leung W, et al. (2023) Long-read genome assemblies for the study of chromosome expansion: Drosophila kikkawai, Drosophila takahashii, Drosophila bipectinata, and Drosophila ananassae. bioRxiv: the preprint server for biology.

Leung W, et al. (2023) Long-read genome assemblies for the study of chromosome expansion: Drosophila kikkawai, Drosophila takahashii, Drosophila bipectinata, and Drosophila ananassae. G3 (Bethesda, Md.), 13(10).

Li X, et al. (2022) Diverse function of the PISTILLATA, APETALA 3, and AGAMOUS-like MADS-box genes involved in the floral development in Alpinia hainanensis (Zingiberaceae). Gene, 839, 146732.

Vassallo CN, et al. (2022) A functional selection reveals previously undetected anti-phage defence systems in the E. coli pangenome. Nature microbiology, 7(10), 1568.

Yang Y, et al. (2020) Whole-genome sequencing of leopard coral grouper (Plectropomus leopardus) and exploration of regulation mechanism of skin color and adaptive evolution. Zoological research, 41(3), 328.

Sánchez-Jiménez MM, et al. (2020) Diagnosis of human and canine Brucella canis infection: development and evaluation of indirect enzyme-linked immunosorbent assays using recombinant Brucella proteins. Heliyon, 6(7), e04393.

Rosa BA, et al. (2020) Comparative genomics and transcriptomics of 4 Paragonimus species provide insights into lung fluke parasitism and pathogenesis. GigaScience, 9(7).

Liu T, et al. (2019) Evolution of Complex Thallus Alga: Genome Sequencing of Saccharina japonica. Frontiers in genetics, 10, 378.

Almadanim MC, et al. (2018) The rice cold-responsive calcium-dependent protein kinase

OsCPK17 is regulated by alternative splicing and post-translational modifications. Biochimica et biophysica acta. Molecular cell research, 1865(2), 231.

Oftedal BE, et al. (2017) T cell receptor assessment in autoimmune disease requires access to the most adjacent immunologically active organ. Journal of autoimmunity, 81, 24.

Chao LF, et al. (2017) An SMC-like protein binds and regulates Caenorhabditis elegans condensins. PLoS genetics, 13(3), e1006614.

Bensch S, et al. (2016) The Genome of Haemoproteus tartakovskyi and Its Relationship to Human Malaria Parasites. Genome biology and evolution, 8(5), 1361.

Mahadevan P, et al. (2016) An Analysis of Adenovirus Genomes Using Whole Genome Software Tools. Bioinformation, 12(6), 301.

McNulty SN, et al. (2016) Dictyocaulus viviparus genome, variome and transcriptome elucidate lungworm biology and support future intervention. Scientific reports, 6, 20316.

Nyasa RB, et al. (2016) An evolutionary approach to identify potentially protective B cell epitopes involved in naturally acquired immunity to malaria and the role of EBA-175 in protection amongst denizens of Bolifamba, Cameroon. Malaria journal, 15(1), 281.

Walter S, et al. (2015) A wheat ABC transporter contributes to both grain formation and mycotoxin tolerance. Journal of experimental botany, 66(9), 2583.

Lobato-Márquez D, et al. (2015) Distinct type I and type II toxin-antitoxin modules control Salmonella lifestyle inside eukaryotic cells. Scientific reports, 5, 9374.

Hobley L, et al. (2015) Giving structure to the biofilm matrix: an overview of individual strategies and emerging common themes. FEMS microbiology reviews, 39(5), 649.

Huang R, et al. (2015) The amino acid variation within the binding pocket 7 and 9 of HLA-DRB1 molecules are associated with primary Sjögren's syndrome. Journal of autoimmunity, 57, 53.