

Resource Summary Report

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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: data analysis service, service resource, production service resource, analysis service resource

Keywords: protein, dna, rna

Resource Name: WU-BLAST

Resource ID: SCR_011824

Alternate IDs: OMICS_01001

Record Creation Time: 20220129T080306+0000

Record Last Update: 20260801T191018+0000

Ratings and Alerts

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

No alerts have been found for WU-BLAST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 134 mentions in open access literature.

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

Lu Y, et al. (2025) Intrahepatic Microbial Heterogeneity in Multifocal Hepatocellular Carcinoma and Its Association with Host Genomic and Transcriptomic Alterations. *Cancer discovery*, 15(8), 1630.

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*.

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*. *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. *Bioinformatics*, 12(6), 301.

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.

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

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.