

Resource Summary Report

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Mega BLAST

RRID:SCR_011920

Type: Tool

Proper Citation

Mega BLAST (RRID:SCR_011920)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/blast/html/megablast.html>

Proper Citation: Mega BLAST (RRID:SCR_011920)

Description: Software that uses the greedy algorithm for nucleotide sequence alignment search.

Abbreviations: Mega BLAST

Resource Type: software resource

Resource Name: Mega BLAST

Resource ID: SCR_011920

Alternate IDs: OMICS_01435

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260801T190425+0000

Ratings and Alerts

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

No alerts have been found for Mega BLAST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 280 mentions in open access literature.

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

Wu Y, et al. (2025) Fusobacterium lineage profiling facilitates the clarification of the associations between non-nucleatum Fusobacterium and colorectal cancer. NPJ biofilms and microbiomes, 11(1), 197.

Xu Q, et al. (2025) Biocontrol Potential of Bacillus stercoris Strain DXQ-1 Against Rice Blast Fungus Guy11. Microorganisms, 13(7).

Shen W, et al. (2024) Characterization of a broad-spectrum antifungal strain, Streptomyces gramineus STR-1, against Magnaporthe oryzae. Frontiers in microbiology, 15, 1298781.

Ze M, et al. (2024) Beneficial effects of Bacillus mojavensis strain MTC-8 on plant growth, immunity and disease resistance against Magnaporthe oryzae. Frontiers in microbiology, 15, 1422476.

Ahn M, et al. (2023) Bat ASC2 suppresses inflammasomes and ameliorates inflammatory diseases. Cell, 186(10), 2144.

Ramos LS, et al. (2023) SARS-CoV-2 Post-Infection and Sepsis by Saccharomyces cerevisiae: A Fatal Case Report-Focus on Fungal Susceptibility and Potential Virulence Attributes. Tropical medicine and infectious disease, 8(2).

Andreou A, et al. (2023) Is the Association of the Rare rs35667974 IFIH1 Gene Polymorphism With Autoimmune Diseases a Case of RNA Epigenetics? Journal of molecular evolution, 91(2), 204.

Zhou Y, et al. (2023) Exploiting a conjugative endogenous CRISPR-Cas3 system to tackle multidrug-resistant Klebsiella pneumoniae. EBioMedicine, 88, 104445.

Shao W, et al. (2022) Function of the Mitochondrial Transport Protein BcMtp1 in Regulating Vegetative Development, Asexual Reproduction, Stress Response, Fungicide Sensitivity, and Virulence of Botrytis cinerea. Journal of fungi (Basel, Switzerland), 9(1).

Martínez-Murcia A, et al. (2022) SARS-CoV-2 Variants Identification; A Fast and Affordable Strategy Based on Partial S-Gene Targeted PCR Sequencing. Viruses, 14(11).

Zhu M, et al. (2022) Two NF- κ B subunits are associated with antimicrobial immunity in Hyriopsis cumingii. Developmental and comparative immunology, 129, 104336.

Behnezhad F, et al. (2022) Molecular detection and genotyping of Human Cytomegalovirus in kidney transplant recipients under ganciclovir prophylaxis in Iran. Intervirology, 66(1), 1.

Kalimuthu AK, et al. (2022) Cytotoxic Potential of Bioactive Compounds from Aspergillus flavus, an Endophytic Fungus Isolated from Cynodon dactylon, against Breast Cancer: Experimental and Computational Approach. Molecules (Basel, Switzerland), 27(24).

Al-Busaidi A, et al. (2022) The Effect of Date Palm Genotypes on Rhizobacterial Community Structures under Saline Environments. *Biology*, 11(11).

Laake I, et al. (2022) Concurrent Infection With Multiple Human Papillomavirus Types Among Unvaccinated and Vaccinated 17-Year-Old Norwegian Girls. *The Journal of infectious diseases*, 226(4), 625.

Angosto-Bazarra D, et al. (2022) Evolutionary analyses of the gasdermin family suggest conserved roles in infection response despite loss of pore-forming functionality. *BMC biology*, 20(1), 9.

Jin H, et al. (2022) Anaerobic Biohydrogenation of Isoprene by *Acetobacterium wieringae* Strain Y. *mBio*, 13(6), e0208622.

Zhang F, et al. (2022) Phosphate limitation intensifies negative effects of ocean acidification on globally important nitrogen fixing cyanobacterium. *Nature communications*, 13(1), 6730.

Nkemngo FN, et al. (2022) Xeno-monitoring of molecular drivers of artemisinin and partner drug resistance in *P. falciparum* populations in malaria vectors across Cameroon. *Gene*, 821, 146339.

Hosseini N, et al. (2021) Lineage analysis of human papillomavirus type 39 in cervical samples of Iranian women. *Virology journal*, 18(1), 152.