Resource Summary Report

Generated by NIF on May 15, 2025

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

Funding:

Resource Name: Mega BLAST

Resource ID: SCR_011920

Alternate IDs: OMICS_01435

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250420T014602+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 278 mentions in open access literature.

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

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.

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

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-?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.

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

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).

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.

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.

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.

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.

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

Li N, et al. (2021) High-Throughput Metagenomics for Identification of Pathogens in the Clinical Settings. Small methods, 5(1), 2000792.

Santos CM, et al. (2021) Molecular and serological characterization of pathogenic Leptospira spp. isolated from symptomatic dogs in a highly endemic area, Brazil. BMC veterinary research, 17(1), 221.