

Resource Summary Report

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MEGA

RRID:SCR_023017

Type: Tool

Proper Citation

MEGA (RRID:SCR_023017)

Resource Information

URL: <https://www.megasoftware.net/>

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Description: Software for molecular evolutionary genetics analysis. Enables comparative analysis of molecular sequences in phylogenetics and evolutionary medicine.

Abbreviations: MEGA

Synonyms: MEGA11, Molecular Evolutionary Genetics Analysis

Resource Type: data processing software, data analysis software, software resource, software application

Defining Citation: [DOI:10.1093/molbev/msab120](https://doi.org/10.1093/molbev/msab120), [PMID:31904846](https://pubmed.ncbi.nlm.nih.gov/31904846/)

Keywords: molecular evolutionary genetics analysis, molecular evolutionary, genetics analysis, comparative analysis, molecular sequences, phylogenetics, evolutionary medicine

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Availability: Free, Available for download, Freely available

Resource Name: MEGA

Resource ID: SCR_023017

Record Creation Time: 20221130T050154+0000

Ratings and Alerts

No rating or validation information has been found for MEGA.

No alerts have been found for MEGA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4087 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Ray R, et al. (2024) Eliciting a single amino acid change by vaccination generates antibody protection against group 1 and group 2 influenza A viruses. *Immunity*, 57(5), 1141.

Hiraki-Kajiyama T, et al. (2024) An atlas and database of neuropeptide gene expression in the adult zebrafish forebrain. *The Journal of comparative neurology*, 532(6), e25619.

Manzulli V, et al. (2024) *Psychrobacter raelei* sp. nov., isolated from a dog with peritonitis. *International journal of systematic and evolutionary microbiology*, 74(4).

Juteršek M, et al. (2024) Transcriptome-informed identification and characterization of *Planococcus citri* cis- and trans-isoprenyl diphosphate synthase genes. *iScience*, 27(4), 109441.

Wang T, et al. (2024) Isolation and identification of specific *Enterococcus faecalis* phage C-3 and G21-7 against Avian pathogenic *Escherichia coli* and its application to one-day-old geese. *Frontiers in microbiology*, 15, 1385860.

Tan X, et al. (2024) Large-scale genomic and transcriptomic analyses elucidate the genetic basis of high meat yield in chickens. *Journal of advanced research*, 55, 1.

Zhang A, et al. (2024) Identification and Genetic Diversity Analysis of the Pathogen of Anthracnose of Pepper in Guizhou. *Plants (Basel, Switzerland)*, 13(5).

Wu Y, et al. (2024) Diversity of species and geographic distribution of tick-borne viruses in China. *Frontiers in microbiology*, 15, 1309698.

Beaulieu-Jones BK, et al. (2024) Disease progression strikingly differs in research and real-world Parkinson's populations. *NPJ Parkinson's disease*, 10(1), 58.

Yuan W, et al. (2024) NIa-Pro of sugarcane mosaic virus targets Corn Cysteine Protease 1 (CCP1) to undermine salicylic acid-mediated defense in maize. *PLoS pathogens*, 20(3),

e1012086.

Cueva DF, et al. (2024) Evidence of population genetic structure in Ecuadorian Andean bears. *Scientific reports*, 14(1), 2834.

Al-Ardi MH, et al. (2024) G1 the common *Echinococcus granulosus* genotype infected domestic cat (*Felis catus*) in Iraq. *Journal of veterinary science*, 25(1), e7.

Fu PF, et al. (2024) First molecular detection and genetic characterization of porcine circovirus 4 in the Gansu Province of China. *PLoS one*, 19(2), e0293135.

Koofhethile CK, et al. (2024) The HIV-2 proviral landscape is dominated by defective proviruses. *AIDS (London, England)*, 38(3), 309.

Jian R, et al. (2024) Genetic diversity of vector-borne zoonotic pathogens in companion dogs and cats, Tianjin, China. *Frontiers in veterinary science*, 11, 1373178.

Cao M, et al. (2024) Investigation of porcine circovirus type 2 and porcine circovirus type 3 infections based on dual TaqMan fluorescent quantitative PCR method and genetic evolutionary analysis of these two viruses. *Frontiers in microbiology*, 15, 1385137.

Wang Z, et al. (2024) On-site detection and differentiation of African swine fever virus variants using an orthogonal CRISPR-Cas12b/Cas13a-based assay. *iScience*, 27(4), 109050.

Zhang F, et al. (2024) Epidemiological monitoring and genetic variation analysis of pathogens associated with porcine viral diarrhea in southern China from 2021 to 2023. *Frontiers in microbiology*, 15, 1303915.

Elmetwalli A, et al. (2024) Probiotic-derived silver nanoparticles target mTOR/MMP-9/BCL-2/dependent AMPK activation for hepatic cancer treatment. *Medical oncology (Northwood, London, England)*, 41(5), 106.

Schüler MA, et al. (2024) Novel insights into phage biology of the pathogen *Clostridioides difficile* based on the active virome. *Frontiers in microbiology*, 15, 1374708.