

Resource Summary Report

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MEGA

RRID:SCR_000667

Type: Tool

Proper Citation

MEGA (RRID:SCR_000667)

Resource Information

URL: <http://megasoftware.net/>

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Description: Software integrated tool for conducting automatic and manual sequence alignment, inferring phylogenetic trees, mining web based databases, estimating rates of molecular evolution, and testing evolutionary hypotheses. Used for comparative analysis of DNA and protein sequences to infer molecular evolutionary patterns of genes, genomes, and species over time. MEGA version 4 expands on existing facilities for editing DNA sequence data from autosequencers, mining Web-databases, performing automatic and manual sequence alignment, analyzing sequence alignments to estimate evolutionary distances, inferring phylogenetic trees, and testing evolutionary hypotheses. MEGA version 6 enables inference of timetrees, as it implements RelTime method for estimating divergence times for all branching points in phylogeny.

Abbreviations: MEGA, MEGA6, MEGA4, MEGA 4, MEGA 11

Synonyms: MEGA11, Molecular Evolutionary Genetics Analysis, Molecular Evolutionary Genetics Analysis 6, Molecular Evolutionary Genetics Analysis 4

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

Defining Citation: [DOI:10.1093/molbev/msab120](https://doi.org/10.1093/molbev/msab120), [PMID:24132122](https://pubmed.ncbi.nlm.nih.gov/24132122/), [PMID:31904846](https://pubmed.ncbi.nlm.nih.gov/31904846/), [PMID:22923298](https://pubmed.ncbi.nlm.nih.gov/22923298/), [PMID:21546353](https://pubmed.ncbi.nlm.nih.gov/21546353/), [PMID:17488738](https://pubmed.ncbi.nlm.nih.gov/17488738/), [PMID:15260895](https://pubmed.ncbi.nlm.nih.gov/15260895/), [PMID:11751241](https://pubmed.ncbi.nlm.nih.gov/11751241/), [PMID:8019868](https://pubmed.ncbi.nlm.nih.gov/8019868/)

Keywords: comparative, analysis, DNA, protein, sequence, molecular, evolution, pattern, gene, genome, evolution, FASEB list

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NSF ABI 1661218;
NIGMS R35GM139504

Availability: Free, Available for download, Freely available

Resource Name: MEGA

Resource ID: SCR_000667

Alternate IDs: SCR_023017, nlx_156838

Alternate URLs: <https://www.megasoftware.net/mega4/>

Record Creation Time: 20220129T080202+0000

Record Last Update: 20260812T044011+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 2774 mentions in open access literature.

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

Liu J, et al. (2026) FERONIA kinase and PP2A antagonistically regulate salt tolerance in Arabidopsis. Current biology : CB, 36(2), 370.

Fu C, et al. (2026) AVP1-mediated pyrophosphate homeostasis coordinates calcium-dependent cellulose synthesis and autoimmunity during leaf growth. Developmental cell, 61(4), 820.

Dong Z, et al. (2026) Piezo3 is a novel mechanosensitive Piezo ion channel in vertebrates. bioRxiv : the preprint server for biology.

Lu Q, et al. (2026) Genomic characterization and pathogenicity validation of Mycoplasma ovipneumoniae strains from diseased sheep: insights into potential pathogenic mechanisms of GSWW364. Veterinary research, 57(1).

Chen S, et al. (2026) Diversity-triggered 2-naphthoic acid exudation recruits keystone microbial taxa to promote soybean drought tolerance. Cell host & microbe, 34(5), 844.

Francette AM, et al. (2026) Evolutionary analysis of transcription elongation factors reveals conserved and lineage-specific regulatory domains. *PLoS biology*, 24(6), e3003855.

Ijaz M, et al. (2026) Comparative insights into molecular characterization and resistance profiling of methicillin-resistant *Staphylococcus aureus* across dairy livestock in Pakistan. *Veterinary research communications*, 50(2), 130.

Takahashi J, et al. (2026) Spatial Multiomic Analyses Reveal Carcinogenic Pathways in End-Stage Renal Disease. *Cancer discovery*, 16(3), 478.

Li Q, et al. (2026) A Degron-Like Regulatory Region in the ASXL1 C-Terminal Domain Mediates HCF-1-Dependent Regulation of Protein Stability. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 40(8), e71770.

Chen L, et al. (2026) Mycobacterial metallophosphatase MmpE acts as a nucleomodulin to regulate host gene expression and promote intracellular survival. *eLife*, 14.

Yan L, et al. (2026) A NACHT domain-containing protein Ncp is required for appendage-associated unconventional protein secretion in the fungus *Penicillium herquei*. *iScience*, 29(7), 116464.

Shen F, et al. (2026) Capsule modulation enhances immunity and delays resistance in MDR *Acinetobacter baumannii*. *iScience*, 29(6), 115761.

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Javier MCF, et al. (2025) Draft genome of the endangered visayan spotted deer (*Rusa alfredi*), a Philippine endemic species. *GigaByte (Hong Kong, China)*, 2025, gigabyte150.

Chen PY, et al. (2025) Previously unrecognized diversity of far-red light-using terrestrial green algae and cyanobacteria. *iScience*, 28(10), 113486.

Zhuang X, et al. (2025) Rice stripe virus NS3 uses the host signaling pathways to control pathogenicity. *Developmental cell*, 60(17), 2363.

Deézsi-Magyar N, et al. (2025) Evaluating enterovirus diversity among symptomatic patients in Hungary during and after easing the COVID-19 lockdown. *Virology journal*, 22(1), 204.

Ito K, et al. (2025) Characterization of the NRPS operon homolog for surfactin A and surfactin C synthesis in *Bacillus* spp. *Archives of microbiology*, 207(7), 161.

Galvis-Marín JC, et al. (2025) Characterisation of Antifungal Resistance to Azoles in Colombian Isolates of *Malassezia* spp. *Mycoses*, 68(9), e70112.

José O, et al. (2025) Different populations of mouse egg cortical vesicles are responsible for post-fertilization zinc sparks and proteolysis of the zona pellucida. *iScience*, 28(6), 112606.