

Resource Summary Report

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Mesquite

RRID:SCR_017994

Type: Tool

Proper Citation

Mesquite (RRID:SCR_017994)

Resource Information

URL: <https://www.mesquiteproject.org/>

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Description: Software tool as modular system for evolutionary analysis. Software for evolutionary biology, designed to organize and analyze comparative data about organisms. Its emphasis is on phylogenetic analysis, but some of its modules concern population genetics, while others do non-phylogenetic multivariate analysis. Analyses available depend on modules installed. Comes with many packages already installed.

Synonyms: Mesquite 3.04, Mesquite 3.61

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

Keywords: Modular, evolutionary, analysis, organize, comparative data, organism, phylogenetic, population genetic, non-pylogenetic

Funding: David and Lucile Packard Foundation ;
NSERC Discovery grant ;
NSF ;
NSF DEB 1258220

Availability: Free, Available for download, Freely available

Resource Name: Mesquite

Resource ID: SCR_017994

Alternate URLs: <https://sources.debian.org/src/mesquite/>

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260905T132828+0000

Ratings and Alerts

No rating or validation information has been found for Mesquite.

No alerts have been found for Mesquite.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 183 mentions in open access literature.

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

Lecuona A, et al. (2026) Hindlimb functional morphology and locomotor biomechanics of the small Late Triassic pseudosuchian reptile *Gracilisuchus stipanicorum* (Archosauria: Gracilisuchidae). *Journal of anatomy*, 248(6), 1026.

Verrico B, et al. (2026) Brachypodium HISTONE DEACETYLASE 19.1 promotes yield, flowering, and freezing tolerance at the expense of drought tolerance. *BMC plant biology*, 26(1).

Deng X, et al. (2026) Comparative plastome analyses reveal life-form-associated selection signatures in Orchidaceae. *BMC plant biology*, 26(1).

Xu Y, et al. (2026) *Streptomyces* produce a diphtheria toxin-like exotoxin that targets insects. *Nature microbiology*, 11(5), 1271.

Cao DL, et al. (2026) Plastome phylogenomics unveils an East Asian origin and climatic niche-driven radiation of the temperate tribe Polygoneae (Polygonaceae). *Frontiers in plant science*, 17, 1792990.

Delgado-Suarez EJ, et al. (2026) Emergence of multidrug-resistant blaCTX-M-65/gyrA_D87Y clones among the circulating *Salmonella* *Infantis* population in Mexico. *Microbial genomics*, 12(2).

Aleksandrovich VV, et al. (2026) Variability of organelle genomes in a collection of early maturing soybean varieties. *Vavilovskii zhurnal genetiki i selektsii*, 30(2), 205.

Freitas LWS, et al. (2026) Descriptions of Four New Species in Cunninghamellaceae (Mucoromycota) from the Brazilian Savanna Through Integrative Taxonomy. *Journal of fungi* (Basel, Switzerland), 12(5).

Anele EU, et al. (2026) Distributions of *Xenopus* species and their helminth parasites in ecological zones of Nigeria. *PloS one*, 21(5), e0348516.

Morales-Mora LA, et al. (2026) *Trichoderma* spp. Associated with Teosinte (*Zea mays* spp. mexicana) Rhizosphere Exhibit Potential Plant Growth-Promoting and Antagonistic

Functional Traits. *Journal of fungi* (Basel, Switzerland), 12(6).

D'Angelo D, et al. (2025) ?IMA GENOME - F20 A draft genome assembly of *Agroatheliarolfii*, *Ceratobasidium papillatum*, *Pyrenopeziza brassicae*, *Neopestalotiopsis macadamiae*, *Sphaerellopsis filum* and genomic resources for *Colletotrichum spaethianum* and *Colletotrichum fructicola*. *IMA fungus*, 16, e141732.

Pommery Y, et al. (2025) Prenatal growth patterns of the upper jaw complex with implications for laryngeal echolocation in bats. *Journal of anatomy*, 246(3), 345.

Li P, et al. (2025) Salinity Stress Induces Phase Separation of Plant BARENTSZ to Form Condensates. *Rice* (New York, N.Y.), 18(1), 75.

Chen X, et al. (2025) ?Systematics and floral micromorphology of core *Aster* and its related groups (Asteraceae, Astereae): Taxonomic significance and phylogenetic insights. *PhytoKeys*, 257, 135.

Bouwman T, et al. (2025) Biochemical and molecular characterization of fungal isolates from California annual grassland soil. *Biotechnology for biofuels and bioproducts*, 18(1), 56.

Tseng YH, et al. (2025) Comparative plastome analyses and phylogenetic insights of *Elatostema*. *BMC plant biology*, 25(1), 537.

Sandhu P, et al. (2025) Enhanced analysis of the genomic diversity of *Mycobacterium bovis* in Great Britain to aid control of bovine tuberculosis. *Frontiers in microbiology*, 16, 1515906.

Farrer EC, et al. (2025) Environmental and host plant effects on taxonomic and phylogenetic diversity of root fungal endophytes. *FEMS microbiology letters*, 372.

Dos Santos Paixão V, et al. (2025) Chromosomal rearrangements drive diversity in arboreal rodents of the genus *Oecomys*. *Scientific reports*, 15(1), 6111.

von Baczko MB, et al. (2025) Biomechanical modeling of musculoskeletal function related to the terrestrial locomotion of *Riojasuchus tenuisiceps* (Archosauria: Ornithosuchidae). *Anatomical record* (Hoboken, N.J. : 2007), 308(2), 369.