

Resource Summary Report

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Geneious

RRID:SCR_010519

Type: Tool

Proper Citation

Geneious (RRID:SCR_010519)

Resource Information

URL: <http://www.geneious.com/>

Proper Citation: Geneious (RRID:SCR_010519)

Description: Software package for sequence alignment, assembly and analysis. Integrated and extendable desktop software platform for organization and analysis of sequence data. Bioinformatics software platform packed with molecular biology and sequence analysis tools.

Synonyms: Geneious Prime, Geneious 11.0, Geneious 11.1.2, Geneious 8.1, Geneious Basic

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

Defining Citation: [PMID:22543367](#)

Keywords: Sequence alignment software, data management software, analysis software, Geneious Biologics, bio.tools

Availability: Restricted

Resource Name: Geneious

Resource ID: SCR_010519

Alternate IDs: OMICS_00016, biotools:geneious

Alternate URLs: <http://nebc.nerc.ac.uk/news/geneiousonbl>, <https://bio.tools/geneious>

Record Creation Time: 20220129T080259+0000

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Ratings and Alerts

No rating or validation information has been found for Geneious.

No alerts have been found for Geneious.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12252 mentions in open access literature.

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

Frajman B, et al. (2026) Multiple long-distance dispersals accompanied by reduction of body size shaped the evolutionary history of four spurges (*Euphorbia*) endemic to Mediterranean islands. *Plant biology* (Stuttgart, Germany), 28(1), 178.

Wiatr M, et al. (2026) Memory B cell development in response to mRNA SARS-CoV-2 and nanoparticle immunization in mice. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2527869123.

Gergonne D, et al. (2026) Genomic Evidence for Dual Introductions, Limited Gene Flow and Niche Preferences in the Invasive Wasp *Vespula germanica* in South Africa. *Molecular ecology*, 35(1), e70217.

Jesus JG, et al. (2026) Do culturable seed endophyte communities differ between native and invasive Fabaceae sharing the same habitat? *Plant biology* (Stuttgart, Germany), 28(1), 249.

Jezkova I, et al. (2026) Local Maintenance and Genomic Diversity of Lymphocytic Choriomeningitis Virus in Natural Populations of House Mice in the Czech Republic Over a 24-Year Period. *Zoonoses and public health*, 73(1), 107.

Ford CE, et al. (2026) Detection of Novel Fish Viruses in Wisconsin Sportfish: Implications of Co-Infections for Disease Emergence. *Journal of fish diseases*, 49(1), e70010.

Figuerola Y, et al. (2026) STEC in the natural environment of Uruguay: genomic surveillance and environmental circulation in the framework of One Health. *Microbiology spectrum*, 14(1), e0315325.

Lawson LP, et al. (2026) Whole-genome sequence of the African Common Reed Frog (*Hyperolius viridiflavus viridiflavus*) from Ethiopia. *G3* (Bethesda, Md.), 16(1).

Nisa S, et al. (2026) Genotyping Reveals Potential Sources of Human Leptospirosis Outbreaks in Aotearoa New Zealand. *Zoonoses and public health*, 73(1), 54.

Voisin C, et al. (2026) Spatiotemporal Diversification of Forest Understorey Species Reveals the Existence of Multiple Pleistocene Forest Refugia in Central Europe. *Molecular ecology*, 35(1), e70200.

Malau-Aduli AEO, et al. (2026) Validation of stearyl-coA desaturase gene TaqMan probe-based SNP for genotyping Tattykeel Australian White MARGRA lamb for health-beneficial omega-3 long-chain fatty acids and intramuscular fat content. *PloS one*, 21(1), e0339573.

Fierro Morales JC, et al. (2025) Reduced cell-substrate adhesion formation promotes cell migration in Dictyostelium. *Molecular biology of the cell*, 36(8), ar98.

Erasmus A, et al. (2025) Redescription and Molecular Characterisation of *Gnathia tridens* Menzies & Barnard, 1959 (Isopoda: Gnathiidae), a Presumed Ubiquitous Nearshore Isopod from the Temperate Northern Pacific. *Acta parasitologica*, 70(2), 79.

Voigt O, et al. (2025) Genetic parallels in biomineralization of the calcareous sponge *Sycon ciliatum* and stony corals. *eLife*, 14.

Noble SAA, et al. (2025) Detection of invasive *Aedes vittatus* mosquitoes in Jamaica: molecular identification and surveillance implications. *Parasites & vectors*, 18(1), 469.

Guest SL, et al. (2025) Myosin 2 drives actin contractility in fast-crawling species outside of the amorphean lineage. *Current biology : CB*, 35(23), 5696.

Xin T, et al. (2025) Recessive epistasis of a synonymous mutation confers cucumber domestication through epitranscriptomic regulation. *Cell*, 188(17), 4517.

Graça AP, et al. (2025) MftG is crucial for ethanol metabolism of mycobacteria by linking mycofactocin oxidation to respiration. *eLife*, 13.

Ali RLMN, et al. (2025) Mitogenomes of mosquito species of Harris County in Texas. *Scientific reports*, 15(1), 22013.

Durán-Fuentes JA, et al. (2025) Repeatome diversity in sea anemone genomics (Cnidaria: Actiniaria) based on the Actiniaria-REPLib library. *BMC genomics*, 26(1), 473.