

Resource Summary Report

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SeaView

RRID:SCR_015059

Type: Tool

Proper Citation

SeaView (RRID:SCR_015059)

Resource Information

URL: <http://www.mybiosoftware.com/seaview-4-2-12-sequence-alignment-phylogenetic-tree-building.html>

Proper Citation: SeaView (RRID:SCR_015059)

Description: Graphical user interface for multiple sequence alignment and molecular phylogeny. SeaView also generates phylogenetic trees.

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

Defining Citation: [PMID:19854763](#), [DOI:10.1093/molbev/msp259](#)

Keywords: sequence alignment, molecular phylogeny, phylogenetic tree, bio.tools

Availability: Free, Available for download

Resource Name: SeaView

Resource ID: SCR_015059

Alternate IDs: OMICS_08908, biotools:seaview

Alternate URLs: <https://bio.tools/seaview>, <https://sources.debian.org/src/seaview/>

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260801T042746+0000

Ratings and Alerts

No rating or validation information has been found for SeaView.

No alerts have been found for SeaView.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1777 mentions in open access literature.

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

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

Penot-Raquin M, et al. (2025) Prevalence and environmental abundance of the TSET complex in cosmopolitan algal groups. *iScience*, 28(6), 112679.

Mata-Marcano C, et al. (2025) Morphological and molecular assessment of muscle metacercariae infecting tench *Tinca tinca* from fish farms and wild populations in Germany. *Scientific reports*, 15(1), 23700.

Crittenden J, et al. (2025) Isolation, characterization, and mycostimulation of fungi for the degradation of polycyclic aromatic hydrocarbons at a superfund site. *Biodegradation*, 36(1), 15.

Coskun ÖK, et al. (2025) Identifying the active microbes driving organosulfur cycling from taurine and methionine in marine sediment. *ISME communications*, 5(1), ycaf033.

Borowicz M, et al. (2025) Tailocin-Mediated Interactions Among Soft Rot *Pectobacteriaceae*. *Molecular ecology*, 34(8), e17728.

More KD, et al. (2025) Validating a Target-Enrichment Design for Capturing Uniparental Haplotypes in Ancient Domesticated Animals. *Molecular ecology resources*, 25(7), e14112.

Magero VO, et al. (2025) Distribution of the schistosome intermediate snail host *Biomphalaria pfeifferi* in East Africa's river systems and the prevalence of *Schistosoma mansoni* infection. *Transactions of the Royal Society of Tropical Medicine and Hygiene*, 119(3), 253.

Li W, et al. (2025) Functional variability of Nef in antagonizing SERINC5 during acute to chronic HIV-1 infection. *AIDS* (London, England), 39(3), 229.

Goremykin V, et al. (2025) ?High-level phylogenetic relationships within *Pezizomycotina* revisited. *IMA fungus*, 16, e153279.

Tonetti T, et al. (2025) Intercellular compartmentation of trehalose 6-phosphate metabolism in *Setaria viridis* leaves. *Journal of experimental botany*, 76(20), 5946.

Perez RL, et al. (2025) Transmission dynamics of *Escherichia coli* sequence type 131 in households-a one health prospective cohort study. *Nature communications*, 16(1), 8455.

Jiang HW, et al. (2025) Structure and evolution of photosystem I in the early-branching cyanobacterium *Anthocerotibacter panamensis*. *Proceedings of the National Academy of Sciences of the United States of America*, 122(20), e2427090122.

Suthaus A, et al. (2025) *Vampyrella crystallifera* sp. nov., an Amoeba That Dissolves Entire Algal Cells at a Remarkable Speed. *Ecology and evolution*, 15(3), e71089.

Karimi F, et al. (2025) Multiplex PCR-based identification of two sympatric stem borer species, *Sesamia cretica* and *Sesamia nonagrioides* (Lepidoptera: Noctuidae). *Journal of insect science* (Online), 25(6).

Arantes I, et al. (2025) Rapid spread of the SARS-CoV-2 Omicron XDR lineage derived from recombination between XBB and BA.2.86 subvariants circulating in Brazil in late 2023. *Microbiology spectrum*, 13(1), e0119324.

Czachura P, et al. (2025) ?Resin outpourings on conifers are inhabited by more members of Nectriaceae (Hypocreales, Sordariomycetes) than previously thought. *MycKeys*, 113, 337.

Picelli AM, et al. (2025) Phylogenetic assessment of *Plasmodium* (Saurocytozoon) *tupinambi* comb. nov. (Haemosporida, Plasmodiidae) in golden tegu lizards: shedding light on a long-standing Haemosporida taxonomic puzzle. *Parasitology*, 152(6), 583.

Mozzi A, et al. (2025) Population Genetic Structure and Human Adaptation of Kaposi Sarcoma-Associated Herpesvirus. *Open forum infectious diseases*, 12(3), ofaf111.

Planells-Cárcel A, et al. (2025) IAT4, a New Indolamine N-Acetyltransferase in *Saccharomyces cerevisiae* Involved in Melatonin Biosynthesis. *Journal of pineal research*, 77(3), e70053.