

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 analysis software, data processing software, data visualization software, sequence analysis software, software application, software resource

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: 20260821T194033+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 1817 mentions in open access literature.

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

Takahashi G, et al. (2026) Initiation of asexual reproduction by the AP2/ERF gene GEMMIFER in *Marchantia polymorpha*. *Current biology* : CB, 36(9), 2413.

Rajaonarivelo JA, et al. (2026) *Leptospira* prevalence and lineages vary across land-use types due to shifts in small mammal communities. *Applied and environmental microbiology*, 92(2), e0206125.

Haase MAB, et al. (2026) Ancient co-option of LTR retrotransposons as yeast centromeres. *Nature*, 651(8107), 1004.

Wang C, et al. (2026) New contributions to the taxonomy and phylogeny of Ciliophoria ciliates (Alveolata, Ciliophora, Phyllopharyngea) from China, with description of *Dysteria bella* sp. nov. and two rare species. *BMC microbiology*, 26(1).

Gans M, et al. (2026) Range Expansion of Obligate Antagonists but Not Mutualists in a Desert Fig (*Ficus petiolaris*). *Plants (Basel, Switzerland)*, 15(7).

Dirnberger M, et al. (2026) Total-evidence phylogeny reveals recent crown group radiation and biogeographical history of hamsters. *BMC biology*, 24(1).

Virieux-Petit M, et al. (2026) Adaptive evolution of *Pseudomonas aeruginosa* ST299 population colonizing a hospital copper water network over a 2.5-year period. *Microbial genomics*, 12(1).

Yuan Y, et al. (2026) Phosphorothioate DNA modification by BREX type 4 systems in the human gut microbiome. *Nature communications*, 17(1), 1717.

Johnson E, et al. (2026) Ancient environmental genome reveals a migratory brown bear individual in Early Holocene Scandinavia. *Proceedings of the National Academy of Sciences of the United States of America*, 123(16), e2527944123.

Hernández-Vázquez A, et al. (2026) Study of Microbial Communities in the Soda Lake of Isabel Island: Identification of Polyhydroxybutyrate (PHB) Degrading Enzymes. *Environmental microbiology reports*, 18(1), e70279.

Tomihara K, et al. (2026) Cis-regulatory evolution of Wnt family genes contributes to a morphological difference between silkworm species. *PLoS biology*, 24(3), e3003605.

Bourke BP, et al. (2026) Diverse novel and avian-associated viruses in the ileal viromes of Northern Mockingbird (*Mimus polyglottos*). *Archives of virology*, 171(4).

Horáček N, et al. (2026) Expansion of the geranylgeranyl pyrophosphate synthase gene family underlies the evolution of terpenoid biosynthesis in termites. *PLoS biology*, 24(4), e3003648.

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

Cieminska K, et al. (2026) Residue-level determinants of the thermal stability of the extremophilic Ts2631 endolysin. *Scientific reports*, 16(1).

Dos Santos MJM, et al. (2026) In Silico Analysis and Expression Profiling of Adhesin-Like Flocculins in *Trichosporon asahii*. *Mycopathologia*, 191(1), 28.

Okertchiri EA, et al. (2026) Full length TECPR1 displays 'cis' Dysferlin domain architecture. *bioRxiv : the preprint server for biology*.

Degré G, et al. (2026) Demonstration of the Role of Both a Ttr and a Psr Homologue Enzymes in the Respiration of Tetrathionate by an Environmental Bacterium *Shewanella* sp. ANA-3. *Environmental microbiology*, 28(3), e70258.

Zakry? B, et al. (2026) A unique sessile loricate euglenid, *Lepocinclis loricata* sp. nov. (Euglenophyta, Phacaceae), from South Africa: Evolutionary implications. *Journal of phycology*, 62(3), 846.

Motta EVS, et al. (2026) Divergent microbiome signatures between managed and wild honey bee (*Apis mellifera*) populations in South Texas. *Microbiology spectrum*, 14(3), e0339425.