

Resource Summary Report

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Jalview

RRID:SCR_006459

Type: Tool

Proper Citation

Jalview (RRID:SCR_006459)

Resource Information

URL: <http://www.jalview.org/>

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Description: A free program for multiple sequence alignment editing, visualisation and analysis that is available in two forms: a lightweight Java applet for use in web applications, and a powerful desktop application that employs web services for sequence alignment, secondary structure prediction and the retrieval of alignments, sequences, annotation and structures from public databases and any DAS 1.53 compliant sequence or annotation server. Use it to view and edit sequence alignments, analyse them with phylogenetic trees and principal components analysis (PCA) plots and explore molecular structures and annotation. Jalview has built in DNA, RNA and protein sequence and structure visualisation and analysis capabilities. It uses Jmol to view 3D structures, and VARNA to display RNA secondary structure.

Abbreviations: Jalview

Resource Type: software resource

Defining Citation: [PMID:19151095](#), [DOI:10.1093/bioinformatics/btp033](#)

Keywords: edit, analysis, annotation, multiple sequence alignment, wysiwyg, bio.tools, FASEB list

Funding: BBSRC BBSB16542

Availability: GNU General Public License, v3, Acknowledgement requested

Resource Name: Jalview

Resource ID: SCR_006459

Alternate IDs: OMICS_00885, biotools:Jalview

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

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260725T190620+0000

Ratings and Alerts

No rating or validation information has been found for Jalview.

No alerts have been found for Jalview.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3769 mentions in open access literature.

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

Sebastian PJ, et al. (2026) Apparent expansion of virulent *Vibrio parahaemolyticus* in humans and sea otters. *Virulence*, 17(1), 2603698.

Tominaga T, et al. (2026) OmpA_C-Like Domain of PorE Is Essential for PorE Function in the Type IX Secretion System (T9SS) of *Porphyromonas gingivalis* and Some T9SS Cargo Proteins Are Secreted in a PorE-Independent Manner. *Microbiology and immunology*, 70(1), 15.

Juanpere-Borras M, et al. (2026) Genome-wide Identification of conditionally essential genes supporting *Streptococcus suis* growth in serum and cerebrospinal fluid. *Virulence*, 17(1), 2600145.

Wang M, et al. (2026) Development and preliminary application of a multiplex qPCR assay for the detection of avian leukosis virus subgroup J, reticuloendotheliosis virus, and chicken infectious anemia virus. *Poultry science*, 105(1), 106122.

Jolly JT, et al. (2025) Phosphatase activity is dispensable for PRL-3-mediated oncogenesis and tumor progression. *bioRxiv : the preprint server for biology*.

Han B, et al. (2025) Evolutionarily diverse caveolins share a common structural framework built around amphipathic disks. *The Journal of cell biology*, 224(9).

Le Bas A, et al. (2025) Structure of WzxE the lipid III flippase for Enterobacterial Common Antigen polysaccharide. *Open biology*, 15(1), 240310.

Huang A, et al. (2025) A genetic circuit that extends the useful range of a BMP morphogen arose alongside insect wing evolution. *Current biology : CB*, 35(23), 5840.

Maghsoodi N, et al. (2025) Computational design of a multi-epitope mRNA vaccine against orthopoxviruses: A path toward comprehensive poxvirus protection. *Computers in biology and medicine*, 196(Pt A), 110764.

Nath VR, et al. (2025) Ca²⁺ binding to Esyt modulates membrane contact site density in *Drosophila* photoreceptors. *The Journal of cell biology*, 224(5).

Batzenschlager M, et al. (2025) Competence for transcellular infection in the root cortex involves a post-replicative, cell-cycle exit decision in *Medicago truncatula*. *eLife*, 12.

Ellegaard KM, et al. (2025) SARS-CoV-2 sequencing artifacts associated with targeted PCR enrichment and read mapping. *PloS one*, 20(10), e0334009.

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

Bernasconi-Bisio F, et al. (2025) Discovery and preclinical development of a SdAb-based CAR-T technology for targeting CD33 in AML. *Molecular therapy. Oncology*, 33(1), 200949.

Lucaciu SA, et al. (2025) Skin disease-associated GJB4 variants differentially influence connexin stability, cell viability and channel function. *The Journal of physiology*, 603(15), 4383.

van Hooff JJE, et al. (2025) Repeated duplications and losses shaped SMC complex evolution from archaeal ancestors to modern eukaryotes. *Cell reports*, 44(7), 115855.

Fernández-Fernández R, et al. (2025) Genomic Analysis of Bacteriocin-Producing *Staphylococci*: High Prevalence of Lanthipeptides and the Micrococцин P1 Biosynthetic Gene Clusters. *Probiotics and antimicrobial proteins*, 17(1), 159.

van Wijk SW, et al. (2025) Lamin variants cause cardiac arrhythmogenicity in *Drosophila*. *Disease models & mechanisms*, 18(7).

Li T, et al. (2025) EzrA promotes Z-ring formation through interaction of its QNR motif with FtsA. *Journal of bacteriology*, 207(7), e0012525.

Chen D, et al. (2025) The cys-loop ligand-gated ion channel gene superfamily of the Colorado potato beetle, *Leptinotarsa decemlineata*. *BMC genomics*, 26(1), 702.