

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 2026

Jalview

RRID:SCR_006459

Type: Tool

Proper Citation

Jalview (RRID:SCR_006459)

Resource Information

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

Proper Citation: Jalview (RRID:SCR_006459)

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: 20260905T132554+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 4136 mentions in open access literature.

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

Ghoochani A, et al. (2026) Cell-type resolved protein atlas of brain lysosomes identifies SLC45A1-associated disease as a lysosomal disorder. *Cell*, 189(3), 765.

Zhao J, et al. (2026) Extracellular Vesicle-Mediated O-GlcNAcase Transfer Drives Neuronal Necroptosis to Facilitate Gallbladder Cancer Perineural Invasion. *Cancer research*, 86(6), 1392.

Squair DR, et al. (2026) ZNFX1 uses two-component ubiquitin circuitry to quarantine viral RNA. *Molecular cell*, 86(6), 1164.

Bjornson S, et al. (2026) Stepwise evolutionary transitions in Cladophorales plastid genomes reveal origins of hairpin chromosomes. *Current biology : CB*, 36(7), 1659.

Nakamoto JA, et al. (2026) Structural and functional diversity of toxin-antitoxin-chaperone systems. *Cell reports*, 45(3), 117024.

Medina E, et al. (2026) Structural basis for sialoglycan recognition by the immune inhibitory receptor Siglec-10. *Structure (London, England : 1993)*, 34(5), 768.

Mrkacek M, et al. (2026) ORMDL Proteins Turnover via Proteasome and Autophagy Is Cell-Type Dependent and Tied to Ceramide Homeostasis. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 40(6), e71655.

Dospinescu VM, et al. (2026) CO2-dependent opening of connexin 43 hemichannels. *eLife*, 14.

Li Q, et al. (2026) A Degron-Like Regulatory Region in the ASXL1 C-Terminal Domain Mediates HCF-1-Dependent Regulation of Protein Stability. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 40(8), e71770.

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

Sztanko KM, et al. (2026) A prophage-expressed type IV pilus component provides anti-phage defense. *Cell reports*, 45(1), 116759.

Yuan Z, et al. (2026) A direct role for a mitochondrial targeting sequence in signalling stress. *Nature*, 649(8099), 1302.

Riedelbauch S, et al. (2026) Recurrent innovation of protein-protein interactions in the *Drosophila* piRNA pathway. *The EMBO journal*, 45(6), 1909.

Fu L, et al. (2026) OsNAC10 negatively regulates salt tolerance by repressing OsHKT1;5 expression and reducing shoot-to-root Na⁺ recirculation in rice. *Plant communications*, 7(6), 101771.

Chosyang S, et al. (2026) Comparative analysis of the Aquaporin gene family in Cucurbitaceae: insights into evolutionary patterns and functional diversity. *BMC plant biology*, 26(1), 297.

Kapisheva M, et al. (2026) Protease-mediated maturation of M-PMV reverse transcriptase into a functional heterodimer. *Protein science : a publication of the Protein Society*, 35(2), e70469.

Lima LDP, et al. (2026) A Hanks-type bacterial kinase, PknS, directly phosphorylates the alternative sigma factor EcfK to promote resistance to protist predation. *The FEBS journal*, 293(9), 2772.

Matsumoto R, et al. (2026) A universal polyphosphate kinase powers in vitro transcription. *Nature communications*, 17(1), 1252.

Roth R, et al. (2026) PUFA modulation of ASIC3 involves both specific and lipid solvent-like interactions. *bioRxiv : the preprint server for biology*.

O'Shea CM, et al. (2026) Reliable repurposing of the antibody interactome inside the cell. *Nature communications*, 17(1).