

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: 20260903T234828+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 [kravitz2](#) .

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.

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

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

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.

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

Patraskaki M, et al. (2026) Unveiling Immune System Perturbations in Early Development Through Zebrafish Models of NADHX Repair Deficiency. *Journal of inherited metabolic disease*, 49(2), e70149.

Bologna NG, et al. (2026) Transcriptome-wide analysis of Arabidopsis DICER-LIKE1 RNA substrates. *Nucleic acids research*, 54(3).

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.

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.

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

Byun HR, et al. (2026) Bandavirus dabieense Isolated From a Wild Leopard Cat (*Prionailurus bengalensis euptilura*) in the Republic of Korea. *Transboundary and emerging diseases*, 2026, 4160320.

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.

Mackenzie ES, et al. (2026) An enzyme's metal preference evolves through redox modulation driven by the cofactor's secondary coordination sphere. *Molecular biology and evolution*, 43(3).

Chourir A, et al. (2026) Design of a multiepitope immunotherapy for fish allergy. *Scientific reports*, 16(1).

Kalamara M, et al. (2026) Regulatory rewiring drives intraspecies competition in *Bacillus subtilis*. *PLoS genetics*, 22(2), e1012050.