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: 20250519T203438+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 3334 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Bandura J, et al. (2025) Distinct Proteomic Brain States Underlying Long-Term Memory Formation in Aversive Operant Conditioning. Journal of proteome research, 24(1), 27.

Xiao B, et al. (2025) Deep learning-based assessment of missense variants in the COG4 gene presented with bilateral congenital cataract. BMJ open ophthalmology, 10(1).

Wæver SL, et al. (2025) Differentially localizing isoforms of the migraine component calcitonin gene-related peptide (CGRP), in the mouse trigeminal ganglion: ?CGRP is translated but, unlike ?CGRP, not sorted into axons. The journal of headache and pain, 26(1), 11.

Rhein-Knudsen N, et al. (2025) Identification and Characterization of a New Thermophilic ?-Carrageenan Sulfatase. Journal of agricultural and food chemistry, 73(3), 2044.

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

Sabari V L D, et al. (2025) Improving the binding affinity of plastic degrading cutinase with polyethylene terephthalate (PET) and polyurethane (PU); an in-silico study. Heliyon, 11(2), e41640.

Charlebois A, et al. (2025) Immunogenicity of Type IV Pilin Proteins from Clostridium perfringens in Chickens. Microorganisms, 13(1).

Lyu B, et al. (2025) G-quadruplex structures in 16S rRNA regions correlate with thermal adaptation in prokaryotes. Nucleic acids research, 53(3).

Stejskalova C, et al. (2025) A conserved acidic residue drives thyroxine synthesis within thyroglobulin and other protein precursors. The Journal of biological chemistry, 301(1), 108026.

Eadsforth TC, et al. (2025) Pharmacological and structural understanding of the Trypanosoma cruzi proteasome provides key insights for developing site-specific inhibitors. The Journal of biological chemistry, 301(1), 108049.

Koning HJ, et al. (2025) Structural plasticity of the coiled-coil interactions in human SFPQ. Nucleic acids research, 53(2).

Giese APJ, et al. (2025) Complexes of vertebrate TMC1/2 and CIB2/3 proteins form hair-cell mechanotransduction cation channels. eLife, 12.

Ding Y, et al. (2025) The ortholog of human DNAJC9 promotes histone H3-H4 degradation and is counteracted by Asf1 in fission yeast. Nucleic acids research, 53(3).

Callejas-Hernández F, et al. (2025) Redefining the spliceosomal introns of the sexually transmitted parasite Trichomonas vaginalis and its close relatives in columbid birds. bioRxiv : the preprint server for biology.

Zhegalova IV, et al. (2025) Convergent pairs of highly transcribed genes restrict chromatin looping in Dictyostelium discoideum. Nucleic acids research, 53(2).

Espinheira RP, et al. (2025) Discovery and Characterization of Mannan-Specialized GH5 Endo-1,4-?-mannanases: a Strategy for Açaí (Euterpe oleracea Mart.) Seeds Upgrading. Journal of agricultural and food chemistry, 73(1), 625.

Agnew A, et al. (2025) Structure and identification of the native PLP synthase complex from Methanosarcina acetivorans lysate. mBio, 16(1), e0309024.

Srivastav MK, et al. (2025) PhpCNF-Y transcription factor infiltrates heterochromatin to generate cryptic intron-containing transcripts crucial for small RNA production. Nature communications, 16(1), 268.

Varandas KC, et al. (2025) Glia detect and transiently protect against dendrite substructure disruption in C. elegans. Nature communications, 16(1), 79.

Ghosh Roy S, et al. (2025) Multiple mutations in polyketide synthase led to disruption of

Psittacofulvin production across diverse parrot species. Communications biology, 8(1), 69.