

Table Of Contents Search Jalview Documentation What's new Multiple Views New keystrokes and Me Reload and Save Creating Sequence Feat Amending or Deleting S Background Dependent Release History Editing Alignments Cursor Mode Key Strokes Input / Output Making figures Hidden Regions Viewing PDB Files Sequence Features Web Services Colour Schemes ClustalX Zappo Taylor Hydrophobicity Helix propensity Strand propensity Turn propensity Buried index Nucleotide colours Blosum62 by Percentage Identity

Jalview

a multiple alignment editor

Jalview Documentation

Jalview (2004) is a fast Java multiple alignment editor and analysis tool. It features many of the 1 of <u>AMAS</u>, for the analysis of sub-families and the prediction of functional sites, but is fully inter (View the <u>Jalview homepage</u>).

If you use Jalview in your work, please cite the bioinformatics paper:

Clamp, M., Cuff, J., Searle, S. M. and Barton, G. J. (2004), "The Jalview Java Alignment Editor", Bioinformatics, 20, 426-7.