



Table Of Contents Search

- Jalview Documentation
  - What's new
    - Graduated Feature Color
    - Sort by Features
    - Envision2 Service
    - Release History
  - Editing Alignments
  - Cursor Mode
  - Key Strokes
  - Input / Output
  - Making Figures
  - Hidden Regions
  - Multiple Views
  - Viewing Trees
  - Fetching Sequences
  - Sequence Features
  - Web Services
  - Colour Schemes
  - Calculations
  - Alignment Annotations
  - Viewing PDB Files
  - VAMSAS Data Exchange
  - Window Menus
  - Preferences
  - Memory Settings
  - Command Line
  - Privacy
  - Useful information
    - Amino Acid Table
    - Amino Acid Properties

# Jalview

a multiple alignment editor

## Jalview Documentation

Jalview (2009) is a fast Java multiple alignment editor and analysis tool. It features many of the features of [AMAS](#), for the analysis of sub-families and the prediction of functional sites, but is fully interactive. (View the [Jalview homepage](#)).

If you use Jalview in your work, please cite the Jalview 2 paper in Bioinformatics:

Waterhouse, A.M., Procter, J.B., Martin, D.M.A, Clamp, M., Barton, G.J (2009), "Jalview version 2: A Multiple Sequence Alignment and Analysis Workbench," *Bioinformatics* **25** (9) 1189-1191 doi: 10.1093/bioinformatics/btp033