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# Jalview

## Welcome to Jalview's built in documentation.

Here are some good places to start:

- [What's New](#) summarises the new features in this release of Jalview.
- Learn how to [edit alignments](#) with Jalview.
- [Import and display sequence features on your alignment](#)
- Use [Jmol to view and superpose 3D structures](#) associated with sequences in the alignment

For more information, you might also want to take a look at the documentation section of the Jalview website (<http://www.jalview.org/about/documentation>).

If you are using the Jalview Desktop application and are looking for something specific, then try the search box (next to the print icon). If you're already viewing this in your web browser, then google the online version of these pages. If you don't find what you are looking for, or want to report a bug or make a feature request, then get in contact over at <http://www.jalview.org/community>

## Citing Jalview

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