Visualizing Multiple Sequence Alignment Results with Jalview
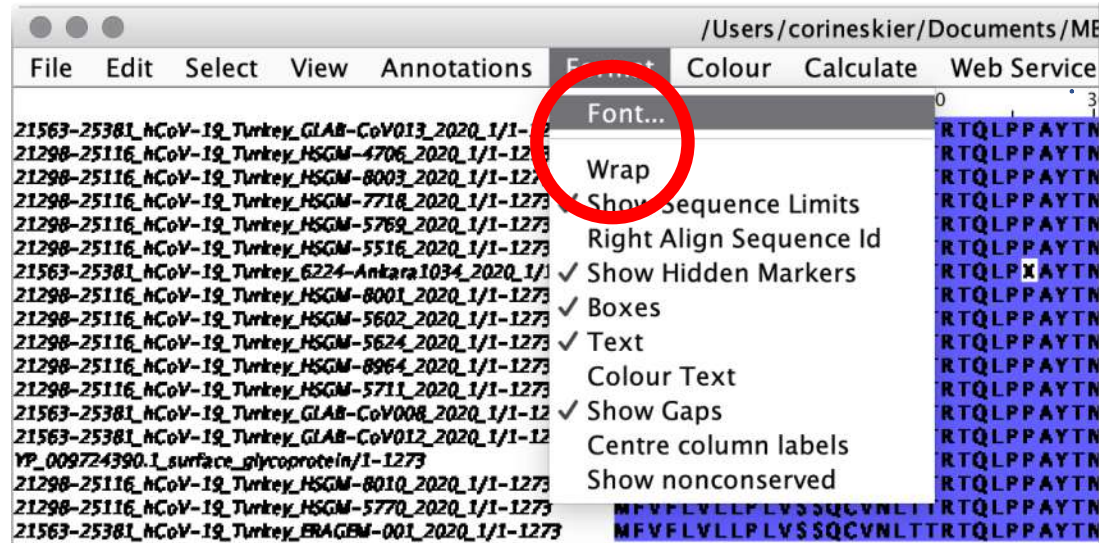
- Install Jalview

- http://www.jalview.org/getdown/release/

- Launch Jalview

- Input alignment from file, URL, or textbox
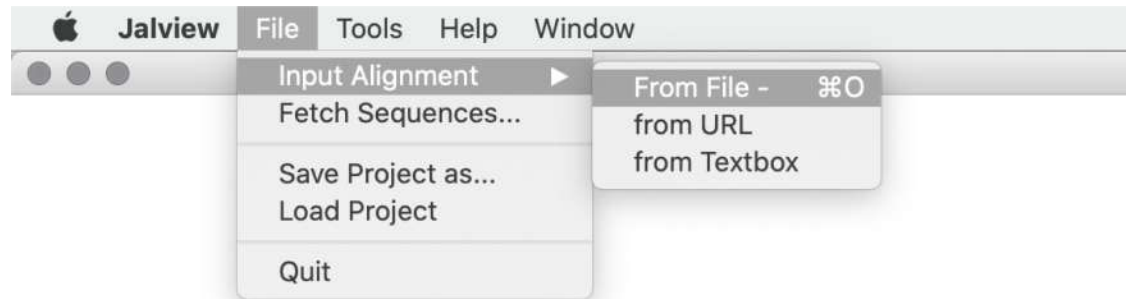
- Jalview accepts MSA results in multiple formats, including FASTA, FASTQ, MSF, and Clustal (.aln)
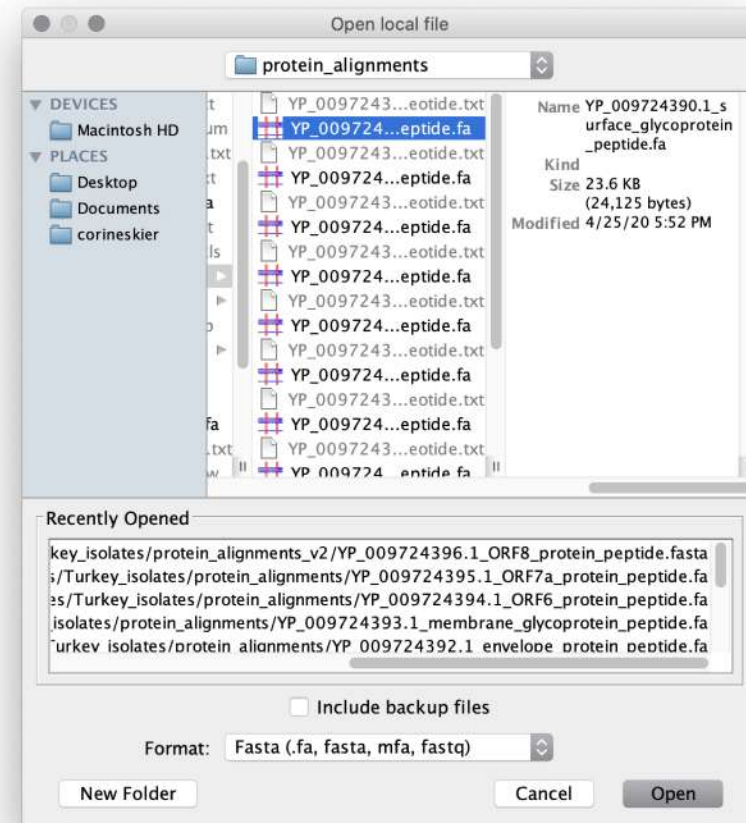
- Format menu options will affect final image
- For smaller alignments, choosing Wrap will help see the bigger picture
- Font options shown on the right

- For better visibility, choosing anti-alias fonts is helpful, but will cause performance issues on slower computers with large alignments
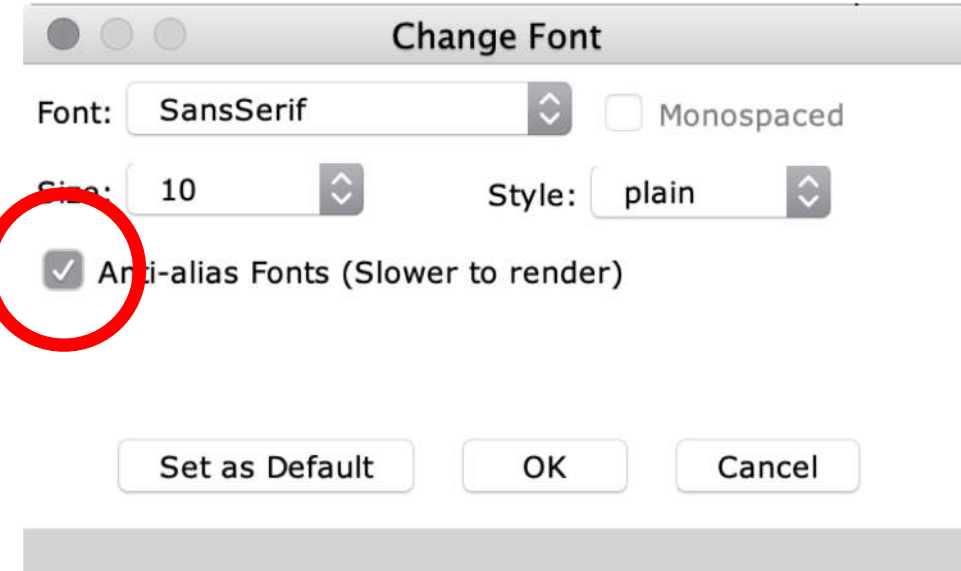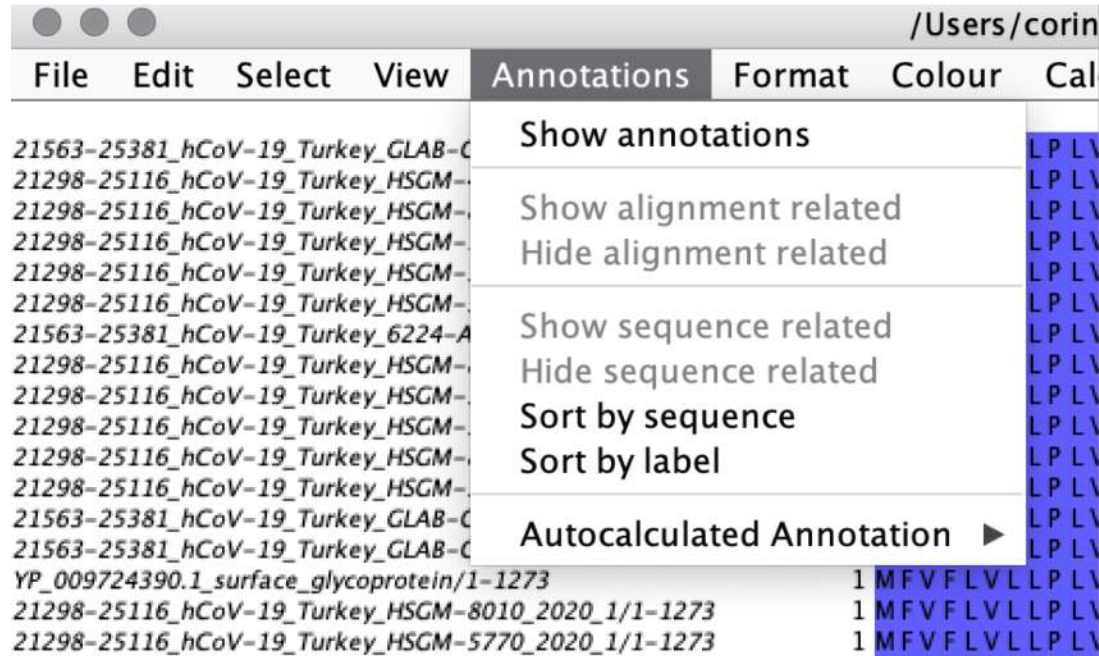
- Showing annotations will display consensus sequence, conservation level, and (if applicable) quality level

- Annotations clutter up image when exported, especially in Wrap mode, and "Show annotations" should be deselected before exporting image

- Choosing the two color options circled below will create a stark image of mutation heavy sites
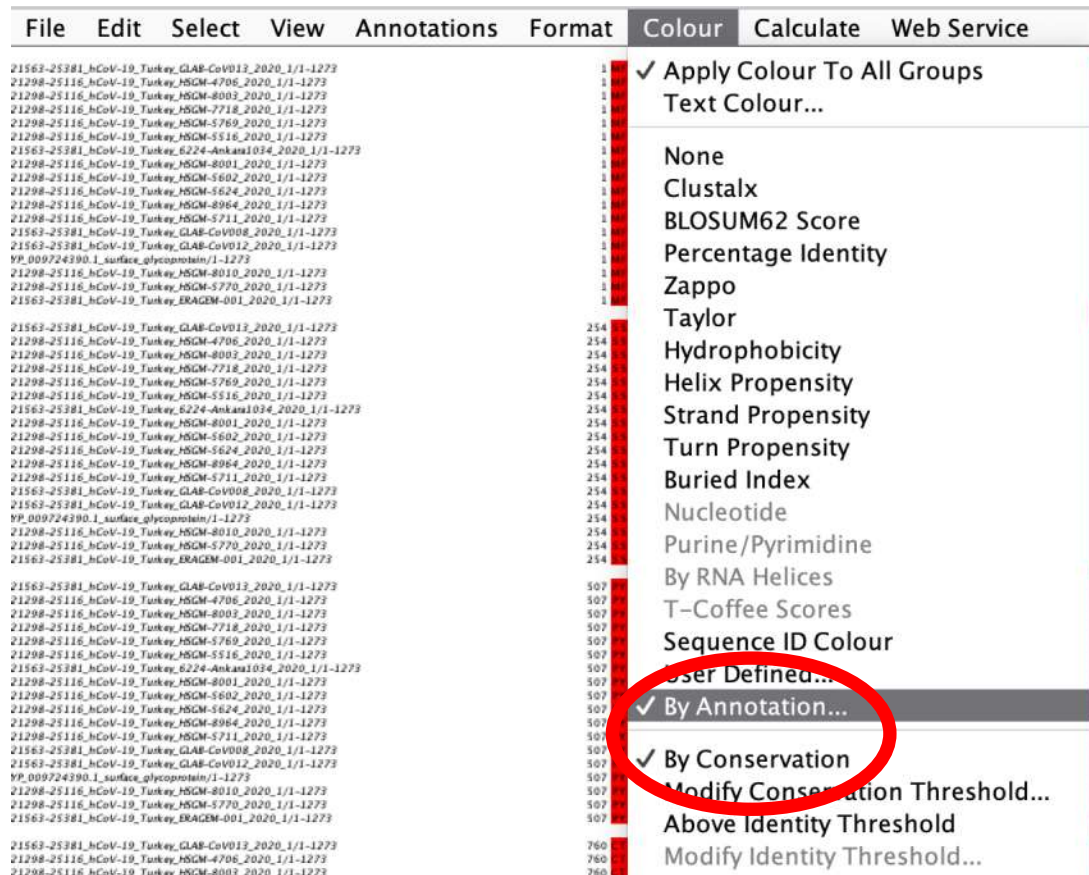
- Choose one color for minimum score, and one color for maximum score
- Choosing "Conservation" and "Above Threshold" lowlights mutated sites (i.e. reduces their color compared to conserved sites)
- Choose "Below Threshold" to highlight mutations

The fewer samples, the lower this number should be
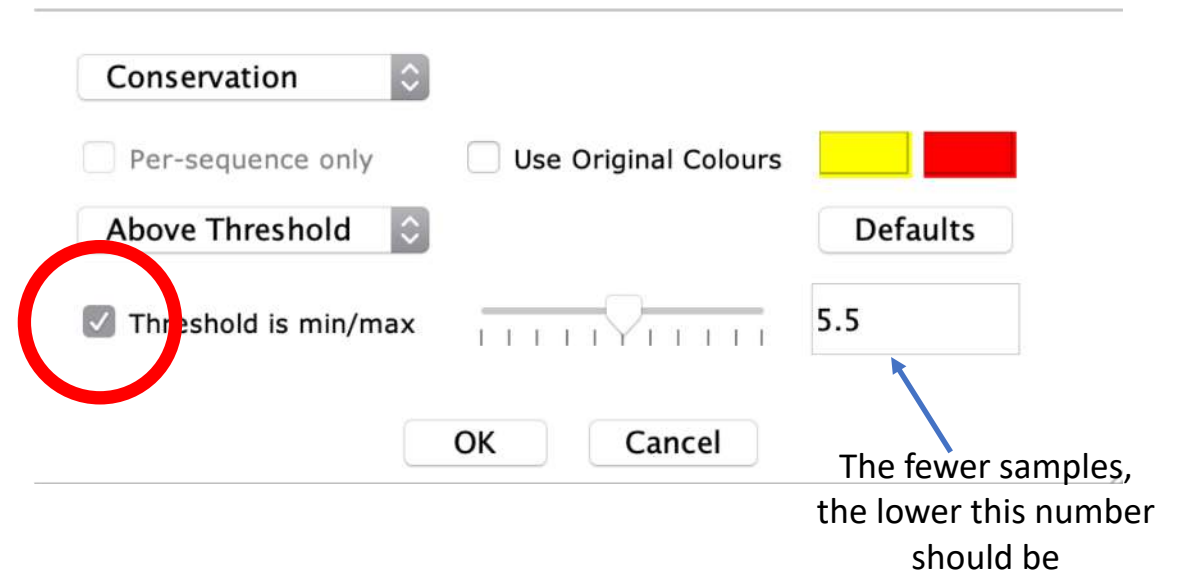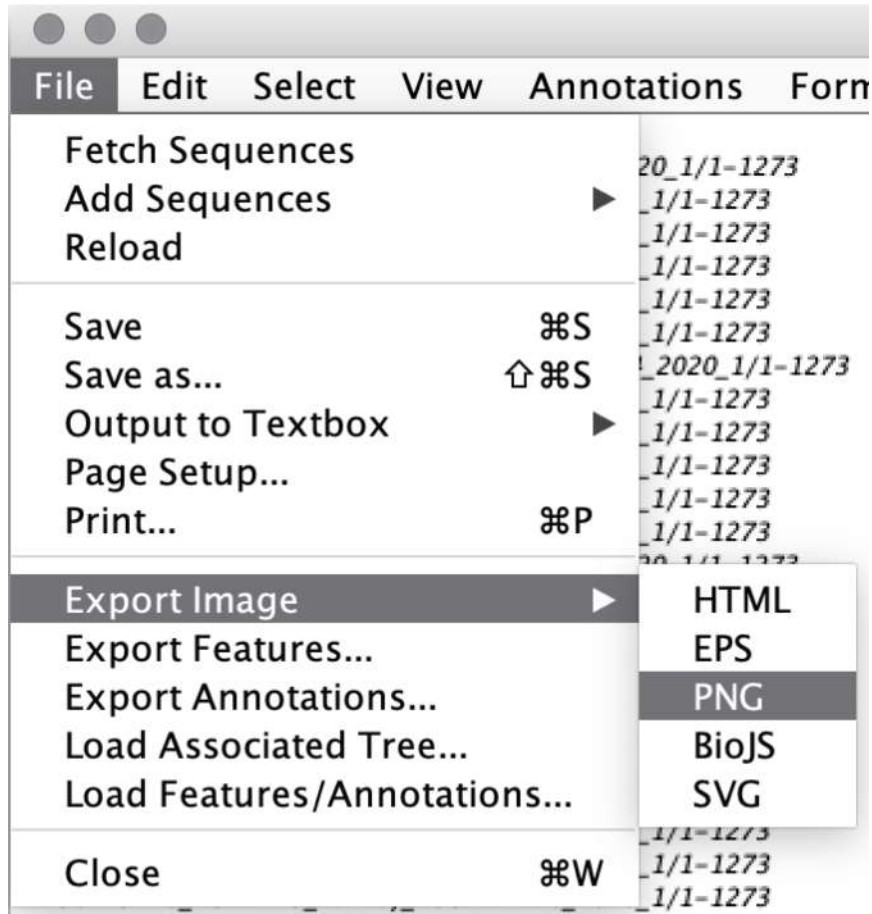
- Image can be exported in multiple formats
- HTML allows direct selection of text
- SVG can be modified with vector graphics software
- PNG generates flat image for publication

Final Image