Visualizing Multiple Sequence Alignment Results with Jalview

- Install Jalview
- http://www.jalview.org/getdown/release/
- Launch Jalview
- Input alignment from file, URL, or textbox

•••	Input Alignment 🔹 🕨	From File - #C
	Fetch Sequences	from URL
	Save Project as Load Project	from Textbox
	Quit	

 Jalview accepts MSA results in multiple formats, including FASTA, FASTQ, MSF, and Clustal (.aln)

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	Include backup files	
Form	at: Fasta (.fa, fasta, mfa, fastq)	0

- 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 antialias fonts is helpful, but will cause performance issues on slower computers with large alignments



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- 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



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- 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

