

Jalview Reference

Version 2.0 www.jalview.org

Load Alignments and Projects

Input Alignment: from File, from URL, from Textbox

Save Project, Load Project, Quit

Alignment File Menu

Save in a different format or export as an image, web page or linear diagram. Import a newick tree with common sequence IDs.

Save As, Export, Output to Textbox, Print, Load Associated Tree, Close

View Menu

Options for alignment and annotation rendering that affect display and print/export. Controls display of overview window and uniprot annotation.

Font...
 Wrap
 Show Full Sequence ID
 Boxes
 Text
 Colour Text
 Show Gaps
 Show Annotations
 Sequence Features
 Overview Window...

Alignment Color Menu

Define and change residue colour scheme for alignment and defined regions. Apply residue conservation shading to residue colour.

Edit Menu

Undo and Redo. Copy, cut and paste sequences. Remove groups, gaps, residues and sequence homologs.

Undo (Ctrl-Z), Redo (Ctrl-Y), Cut (Ctrl-X), Copy (Ctrl-C), Paste (Ctrl-V), Delete, Select all (Ctrl-A), Deselect All (Escape), Invert Selection, Undefine groups, Remove Left, Remove Right, Remove Empty Columns, Remove All Gaps, Remove Redundancy..., Pad Gaps

Calculate Menu

Functions for reordering of sequences in the alignment. See over for calculating trees, spatial clusterings, alignments and predictions locally or via the web.

Sort, Calculate Tree, Pairwise Alignments..., Principal Component Analysis..., Web Service

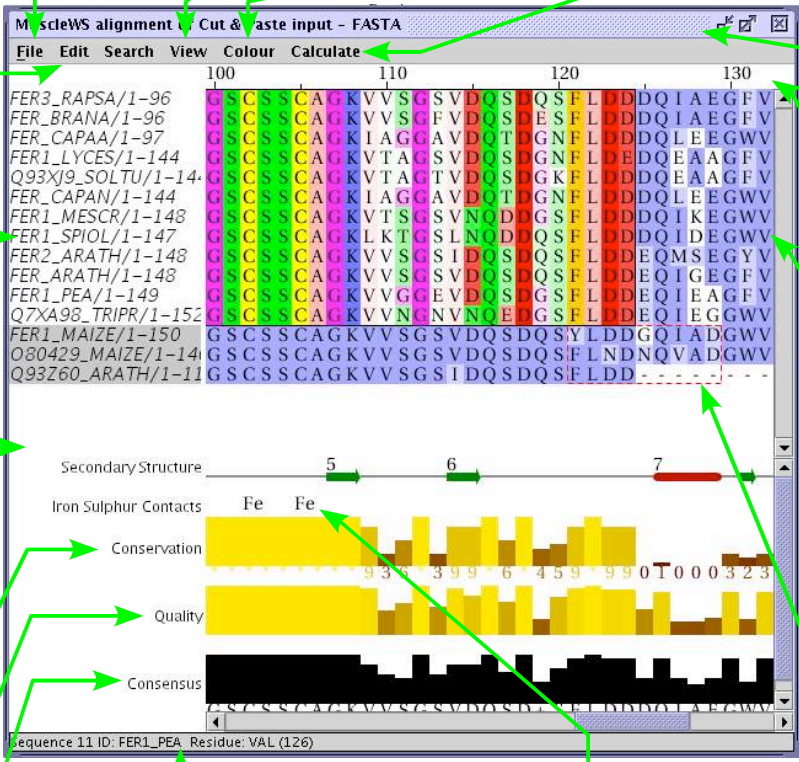
Sequence ID display

Displays sequence name, start and end positions. Right-click for sequence ID menu. Left-click: select sequences (shaded grey). Up and down arrow keys: reorder selection. Left-click+drag: change display width. Double left-click: view uniprot record.

Define: Sequence, Edit name, View PDB structure

The Alignment Window

Its title gives the name, original format and subsequent analysis steps for the alignment.



Alignment position bar

Click here to toggle position markers, and drag to select ranges of columns in the alignment.

Alignment display

Click and drag to define a region selection. Control+C copies selection to clipboard. Control+A to select all alignment. Escape to clear the current selection. Shift+left-click and drag: insert and delete gaps at pointer position.

Alignment Annotation label area

Right-click on row label to get annotation row menu. Left-click+drag to change height of area.

Add New Row, Hide This Row, Delete This Row, Show All Hidden Rows, Show Values In Textbox

Amino acid property conservation

Measurement of the conservation of physicochemical properties in a column.

Alignment Quality

BLOSUM62 score based on observed substitutions.

Residue Consensus

Gives the commonest residues and their percentage for each column of the alignment.

Residue information bar

Gives sequence number, residue name and position in sequence for nearest residue to mouse pointer.

Helix Sheet Label Colour Remove Annotation

User Defined Annotation

Rows are first added through the annotation row menu. Left-click: select position for annotation. ctrl+left-click: add to selection. Right-click: menu to add secondary structure and/or label.

Region Selection

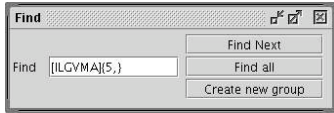
Right-click to get region menu to define a colour, view style, and name for selected area.

Define: feredoxin, Remove Group, Group Colour: None, Clustalx colours, BLOSUM62, Percentage Identity, Zappo, Taylor, Hydrophobicity, Helix propensity, Strand propensity, Turn propensity, Buried Index, Nucleotide, User Defined, Above % Identity, Conservation

Control or shift+click+drag: insert/delete gaps in selected sequences at pointer position. Use tree or web service calculation menu to analyse region.

Find

Enter regular expressions to search sequences and their IDs.



Regular Expression Element	Effect
.	Matches any single character
[]	Matches any one of the characters in the brackets
^	Matches at the start of an ID or sequence
\$	Matches at the end of an ID or sequence
*	Matches if the preceding element matches zero or more times
?	Matches if the preceding element matched once or not at all
+	Matches if the preceding element matched at least once
{count}	Matches if the preceding element matches a specified number of times
{min,}	Matches if the preceding element matched at least the specified number of times
{min,max}	Matches if the preceding element matches min or at most max number of times

Where to get help

About
Documentation

Web services Menu

Submit sequences and regions for alignment and realignment, or make a secondary structure prediction.

Clustal Alignment...
Muscle Alignment...
JNet...
Clustal Realign...

Sort Menu

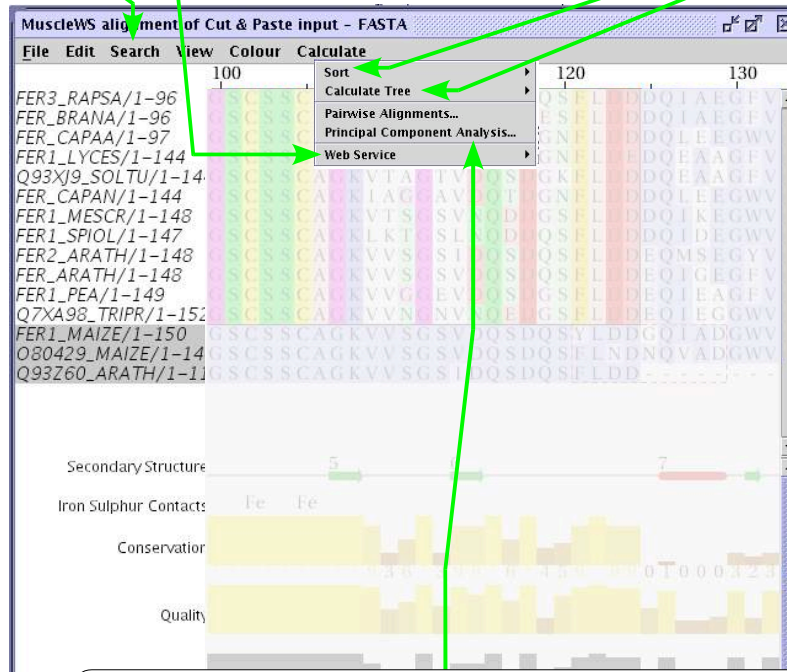
Options for reordering sequences.

by ID
by Group
by Pairwise Identity
By Tree Order

Tree Menu

Create trees for the whole alignment or just a selected region.

Average Distance Using % Identity...
Neighbour Joining Using % Identity...
Average Distance Using BLOSUM62...
Neighbour joining using BLOSUM62...



Tree Viewer

For browsing calculated or imported trees. Click on a node to swap the branch order. Click anywhere else to partition the tree and define sequence groups.

Tree File Menu

Print or save your tree as an image, postscript or newick tree file.

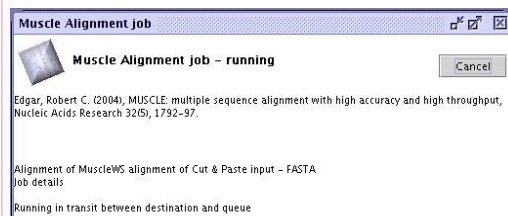
Save as
Output to Textbox...
Print

Newick Format
EPS
PNG

Tree View Menu

Change the appearance and scaling of the tree view.

Fit To Window
 Font Size - 12
 Show Distances
 Show Bootstrap Values
 Mark Unlinked Leaves



Web Service Dialog

Gives the name, method reference, current status and log information for a webservice calculation. The Cancel button stops the current job permanently.

Principal Component Analysis Viewer

Visualizes sequence clusters as a cloud of points in 3D. Move the mouse over a point to identify a sequence. Click and drag to change the view. Use the x,y and z menus to change the PCA dimensions.

