Jalview 2005

File Tools Help Window

Load Alignments and Projects

Input Alignment ▶ from File
Save Project   from URL
Load Project   from Textbox
Quit

Alignment File Menu
Save in a different format or export as an image, web page or lineart 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.

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   ▶

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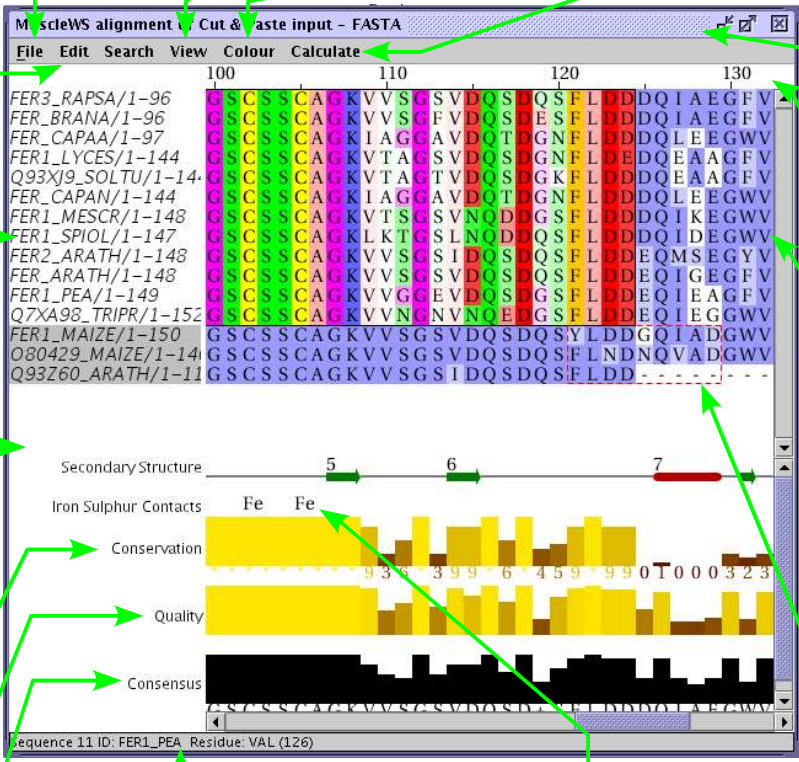Undo and Redo. Copy, cut and paste sequences. Remove groups, gaps, residues and sequence homologs.

Undo   Ctrl-Z
Redo
Cut   Ctrl-X
Copy   Ctrl-C
Paste   ▶
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

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

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.

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.

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
☑ Boxes   ○ Clustalx colours
☑ Text   ● BLOSUM62
☐ Colour Text   ○ Percentage Identity
Border colour   ○ 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.

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.

Helix
Sheet
Label
Colour
Remove Annotation

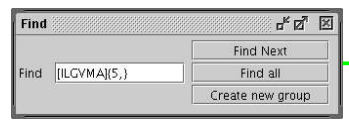**Residue information bar**
Gives sequence number, residue name and position in sequence for nearest residue to mouse pointer.

MuscleWS alignment of Cut & Paste input - FASTA

File Edit Search View Colour Calculate

100   110   120   130

FER3_RAPSA/1-96
FER_BRANA/1-96
FER_CAPAA/1-97
FER1_LYCES/1-144
Q93XJ9_SOLTU/1-144
FER_CAPAN/1-144
FER1_MESCR/1-148
FER1_SPIOL/1-147
FER2_ARATH/1-148
FER_ARATH/1-148
FER1_PEA/1-149
Q7XA98_TRIPR/1-152
FER1_MAIZE/1-150
O80429_MAIZE/1-14
Q93Z60_ARATH/1-11

Secondary Structure   5   6   7

Iron Sulphur Contacts   Fe Fe

Conservation   9 3 7   3 9 9   6 4 5 9   9 9 0 T 0 0 0 3 2 3

Quality

Consensus

Sequence 11 ID: FER1_PEA Residue: VAL (126)

Jalview Ⓡⓔⓕⓔⓡⓔⓝⓒⓔ
Version 2.0 www.jalview.org

Find
Enter regular expressions to search sequences and their Ids.

Find
Find [ILGVMA]{5,}
Find Next
Find all
Create new group

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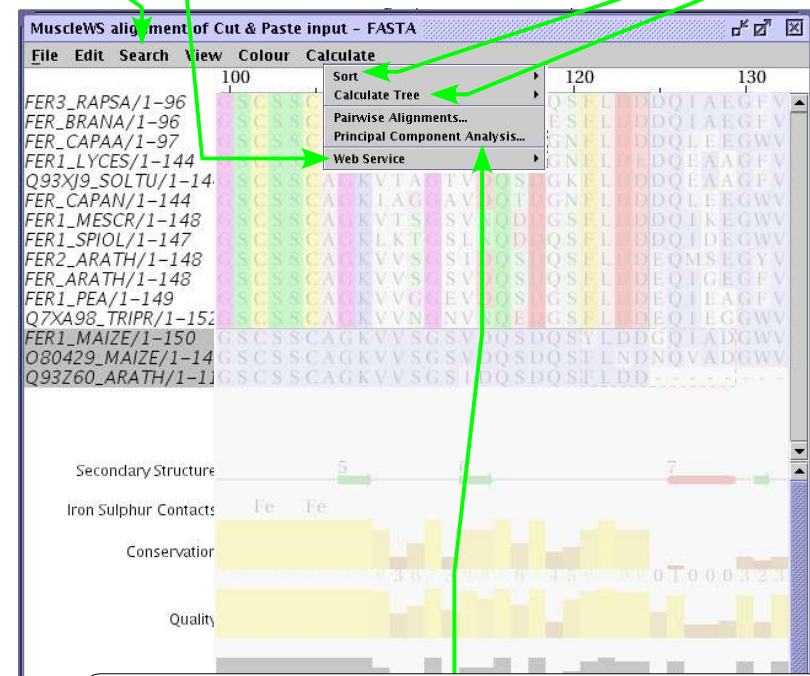Submit sequences and regions for alignment and realignment, or make a secondary structure prediction.

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...

MuscleWS alignment of Cut & Paste input – FASTA

File   Edit   Search   View   Colour   Calculate

100   120   130

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

FER3_RAPSA/1-96
FER_BRANA/1-96
FER_CAPAA/1-97
FER1_LYCES/1-144
Q93XJ9_SOLTU/1-14
FER_CAPAN/1-144
FER1_MESCR/1-148
FER1_SPIOL/1-147
FER2_ARATH/1-148
FER_ARATH/1-148
FER1_PEA/1-149
Q7XA98_TRIPR/1-152
FER1_MAIZE/1-150
O80429_MAIZE/1-14
Q93Z60_ARATH/1-11

Secondary Structure

Iron Sulphur Contacts   Fe   Fe
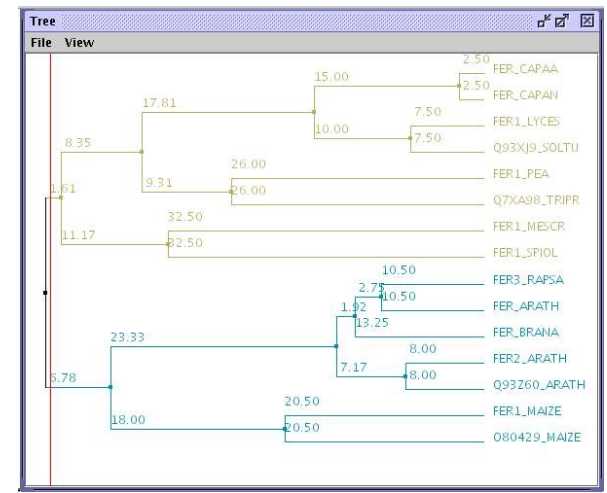
Conservation

Quality

Sequence

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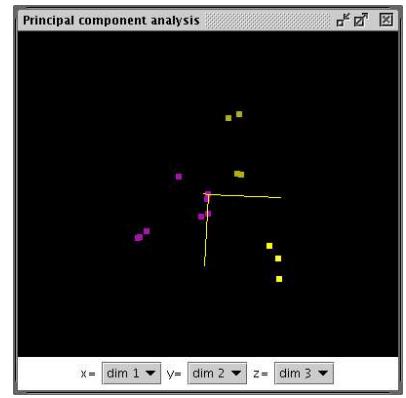Print or save your tree as an an image, postscript or newick tree file.

Save as   Newick Format
Output to Textbox...   EPS
Print   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

Muscle Alignment job

Muscle Alignment job – running   Cancel

Edgar, Robert C. (2004), MUSCLE: multiple sequence alignment with high accuracy and high throughput, Nucleic Acids Research 32(5), 1792–97.

Alignment of MuscleWS alignment of Cut & Paste input – FASTA
Job details

Running in transit between destination and queue

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.

Principal component analysis

x= dim 1 ▼ y= dim 2 ▼ z= dim 3 ▼

Tree
File   View

2.50   FER_CAPAA
15.00   2.50   FER_CAPAN
17.81   7.50   FER1_LYCES
8.35   10.00   7.50   Q93XJ9_SOLTU
         26.00   FER1_PEA
9.31   26.00   Q7XA98_TRIPR
1.61   32.50   FER1_MESCR
11.17   32.50   FER1_SPIOL
                  10.50   FER3_RAPSA
         2.75 10.50   FER_ARATH
1.92   13.25   FER_BRANA
23.33   8.00   FER2_ARATH
6.78   7.17 8.00   Q93Z60_ARATH
18.00   20.50   FER1_MAIZE
              20.50   O80429_MAIZE