

ACCESS PROTEIN AND RNA DATABASES

ALIGNMENT, EDITING AND ANNOTATION



Jalview

FREE open source, multiple sequence alignment and structure analysis software for proteins and RNA

www.jalview.org

The screenshot displays the Jalview software interface with the following components:

- Menu Bar:** File, Edit, Select, View, Format, Colour, Calculate, Web Service.
- Toolbar:** Original, Phosphorylation Site Predictions, MAFFT Alignment Ordering, FE2S2 Representatives, Spinach Feredoxin Structure.
- Sequence Alignment:** A multiple sequence alignment of Feroxidase (FER) proteins from various species, including *FER1_CAPAA1-187*, *FER1_CAPAA1-144*, *FER1_SQLIC1-144*, *Q293B_SQLIC1-144*, *FER1_PEA1-189*, *Q293B_PEP1-152*, *FER1_MESR1-148*, *FER1_SPID1-147*, *FER1_MESR1-186*, *FER1_ARATH1-148*, *FER1_ARATH1-190*, *FER1_ARATH1-148*, *Q215D_ARATH1-118*, and *FER1_MAIZE1-150*. The alignment is color-coded by amino acid type.
- Phylogenetic Trees:** A tree diagram showing the evolutionary relationships between the different Feroxidase sequences.
- Annotations:** A section showing secondary structure elements (green arrows), conservation scores (yellow bars), consensus sequence (RAGSCSSCAGV...), and disorder prediction (red dashed line).
- 3D Structures:** A 3D ribbon diagram of a protein structure with a heme group (red and yellow spheres) and a prosthetic group (green and blue spheres).
- RNA:** A 2D diagram of an RNA secondary structure, showing a complex fold with multiple stems and loops.

FUNCTIONAL AND STRUCTURAL ANALYSIS

FIGURE GENERATION