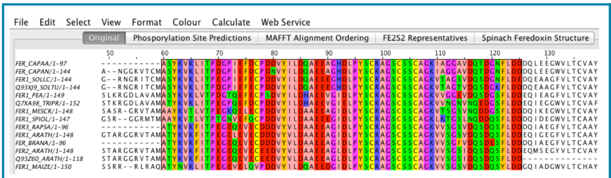
ACCESS PROTEIN AND RNA DATABASES

ALIGNMENT, EDITING AND ANNOTATION

Jalview

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

www.jalview.org



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FER_CAPAA/1-97      -----------ASYKVKLITPDGPIEFDCPDDVYILDQAEEAGHDLPYSCRAGSCSSCAGKIAGGAVDQTDGNFLDDDQLEEGWVLTCVAY
FER_CAPAN/1-144     A--NGGKVTCMASYKVKLITPDGPIEFDCPDNVYILDQAEEAGHDLPYSCRAGSCSSCAGKIAGGAVDQTDGNFLDDDQLEEGWVLTCVAY
FER1_SOLLC/1-144    G--RNGRITCMASYKVKLITPEGPIEFECPDDVYILDQAEEEGHDLPYSCRAGSCSSCAGKVTAGSVDQSDGNFLDEDQEAAGFVLTCVAY
Q93XJ9_SOLTU/1-144  G--RNGRITCMASYKVKLITPDGPIEFECPDDVYILDQAEEEGHDLPYSCRAGSCSSCAGKVTAGTVDQSDGKFLDDDQEAAGFVLTCVAY
FER1_PEA/1-149      SLKRGDLAVAMASYKVKLVTPDGTQEFECPSDVYILDHAEEVGIDLPYSCRAGSCSSCAGKVVGGEVDQSDGSFLDDEQIEAGFVLTCVAY
Q7XA98_TRIPR/1-152  STKRGDLAVAMATYKVKLITPEGPQEFDCPDDVYILDHAEEVGIELPYSCRAGSCSSCAGKVVNGNVNQEDGSFLDDEQIEGGWVLTCVAF
FER1_MESCR/1-148    SASR-GRVTAMAAYKVTLVTPEGKQELECPDDVYILDAAEEAGIDLPYSCRAGSCSSCAGKVTSGSVNQDDGSFLDDDQIKEGWVLTCVAY
FER1_SPIOL/1-147    GSR--GGRMTMAAYKVTLVTPTGNVEFQCPDDVYILDAAEEEGIDLPYSCRAGSCSSCAGKLKTGSLNQDDQSFLDDDQIDEGWVLTCAAY
FER3_RAPSA/1-96     -----------ATYKVKFITPEGEQEVECDDDVYVLDAAEEAGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQSFLDDDQIAEGFVLTCAAY
FER1_ARATH/1-148    GTARGGRVTAMATYKVKFITPEGELEVECDDDVYVLDAAEEAGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQSFLDDEQIGEGFVLTCAAY
FER_BRANA/1-96      -----------ATYKVKFITPEGEQEVECDDDVYVLDAAEEAGIDLPYSCRAGSCSSCAGKVVSGFVDQSDESFLDDDQIAEGFVLTCAAY
FER2_ARATH/1-148    STARGGRVTAMATYKVKFITPEGEQEVECEEDVYVLDAAEEAGLDLPYSCRAGSCSSCAGKVVSGSIDQSDQSFLDDEQMSEGYVLTCVAY
Q93Z60_ARATH/1-118  STARGGRVTAMATYKVKFITPEGEQEVECEEDVYVLDAAEEAGLDLPYSCRAGSCSSCAGKVVSGSIDQSDQSFLDD--------------
FER1_MAIZE/1-150    SSRR--RLRAQATYNVKLITPEGEVELQVPDDVYILDQAEEDGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQSYLDDGQIADGWVLTCHAY
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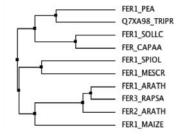
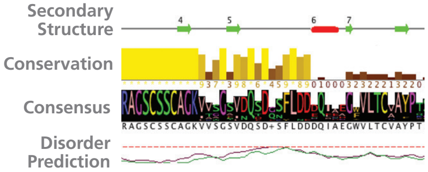
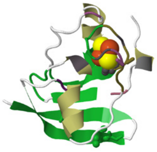
SEQUENCE ALIGNMENTS



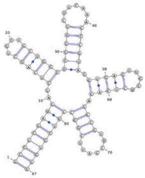
PHYLOGENETIC TREES



ANNOTATIONS



3D STRUCTURES



RNA

FUNCTIONAL AND STRUCTURAL ANALYSIS

FIGURE GENERATION

DOWNLOAD THE APPLICATION OR RUN IT IN A WEB BROWSER

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