



# MuscleWS alignment of Uniref50 Sequences - FASTA

File Edit Select View Format Colour Calculate Web Service

	110	120	130	140
FER_CAPAA/1-97	SCAGKLAGGAVD	DTDGNELDD	DDOLEFGWVLT	CVAYPQSDVTIETHKE
FER_CAPAN/1-144	SCAGKLAGGAVD	DTDGNELDD	DDOLEFGWVLT	CVAYPQSDVTIETHKE
FER1_SOLLC/1-144	SCAGKVTAGSV	LDNQLDD	DDOLEFGWVLT	CVAYPKGDVTIETHKE
Q93XJ9_SOLTU/1-144	SCAGKVTAGTV	LDNQLDD	DDOLEFGWVLT	CVAYPKCDVTIETHKE
FER1_PEA/1-149	SCAGKVVGGEV	LDNQLDD	DDOLEFGWVLT	CVAYPQSDVTIETHKE
Q7XA98_TRIPR/1-152	SCAGKVVNGNV	LDNQLDD	DDOLEFGWVLT	CVAYPQSDVTIETHKE
FER1_MESCR/1-148	SCAGKVTSGSVNQDDG	SFLDD	DDQIKEGWVLT	CVAYPQSDVTIETHKE
FER1_SPIOL/1-147	SCAGKLTGSLNQDDQ	SFLDD	DDQIDEGWVLT	CVAYPQSDVTIETHKE
FER3_RAPSA/1-96	SCAGKVVSGSVDQSDQ	SFLDD	DDQIAEGFVLT	CVAYPQSDVTIETHKE
FER1_ARATH/1-148	SCAGKVVSGSVDQSDQ	SFLDDE	EQIGEGFVLT	CVAYPQSDVTIETHKE
FER_BRANA/1-96	SCAGKVVSGFVDQSD	SFLDD	DDQIAEGFVLT	CVAYPQSDVTIETHKE
FER2_ARATH/1-148	SCAGKVVSGSIDQSDQ	SFLDDE	EQMSEGYVLT	CVAYPQSDVTIETHKE
Q93Z60_ARATH/1-118	SCAGKVVSGSIDQSDQ	SFLDD	-----	CVAYPQSDVTIETHKE

Selection ▶

- Edit
- Output to Textbox...
- Create Sequence Feature

Group ▶

- ferredoxin
- Remove Group

Group Colour ▶

- Text Colour
- None
- Clustalx colours
- BLOSUM62**
- Percentage Identity
- Zappo
- Taylor
- Hydrophobicity
- Helix propensity
- Strand propensity
- Turn propensity
- Buried Index
- Nucleotide
- User Defined...
- mostly blue
- Above % Identity
- Conservation



Sequence 4 ID: Q93XJ9\_SOLTU Residue: ALA (95)