



MuscleWS alignment of Uniref50 Sequences

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	80	90	100	110	120																	
<i>FER_CAPAA/1-97</i>	EFD	CPDD	VYIL	DQAEE	AAGHDL	YPYSCR	AGSCSS	SCAGK	IAGG	AVDQ	T	DGN	FL	DDD								
<i>FER_CAPAN/1-144</i>	EFD	CPDN	VYIL	DQAEE	AAGHDL	YPYSCR	AGSCSS	SCAGK	IAGG	AVDQ	T	DGN	FL	DDD								
<i>FER1_SOLLC/1-144</i>	EFE	CPDD	VYIL	DQAEE	EGHDL	YPYSCR	AGSCSS	SCAGK	VTAG	SVDQ	S	DGN	FL	DED								
<i>Q93XJ9_SOLTU/1-144</i>	EFE	CPDD	VYIL	DQAEE	EGHDL	YPYSCR	AGSCSS	SCAGK	VTAG	TVDQ	S	DGK	FL	DDD								
<i>FER1_PEA/1-149</i>	EFE	CPSD	VYIL	DHAE	EVGID	LPYSCR	AGSCSS	SCAGK	VVGG	EV	DQ	S	DGS	FL	DDE							
<i>Q7XA98_TRIPR/1-152</i>	EFD	CPDD	VYIL	DHAE	EVGIE	LPYSCR	AGSCSS	SCAGK	VVNG	NVNQ	E	DGS	FL	DDE								
<i>FER1_MESCR/1-148</i>	ELE	CPDD	VYIL	DAEE	AGID	LPYSCR	AGSCSS	SCAGK	VTSG	SVN	Q	D	DGS	FL	DDD							
<i>FER1_SPIOL/1-147</i>	EFE	CPDD	VYIL	DAEE	EGID	LPYSCR	AGSCSS	SCAGK	LKTG	SLN	Q	D	D	Q	S	FL	DDD					
<i>FER3_RAPSA/1-96</i>	EVE	CDD	DVYV	LDA	EE	AGID	LPYSCR	AGSCSS	SCAGK	VVSG	S	V	D	Q	S	D	Q	S	FL	DDD		
<i>FER2_ARATH/1-148</i>	EVE	CDD	DVYV	LDA	EE	AGID	LPYSCR	AGSCSS	SCAGK	VVSG	S	V	D	Q	S	D	Q	S	FL	DDE		
<i>FER_BRANA/1-96</i>	EVE	CDD	DVYV	LDA	EE	AGID	LPYSCR	AGSCSS	SCAGK	VVSG	F	V	D	Q	S	D	E	S	FL	DDD		
<i>FER1_ARATH/1-148</i>	EVE	CEE	DVYV	LDA	EE	AGLD	LPYSCR	AGSCSS	SCAGK	VVSG	S	I	D	Q	S	D	Q	S	FL	DDE		
<i>Q93Z60_ARATH/1-118</i>	EVE	CEE	DVYV	LDA	EE	AGLD	LPYSCR	AGSCSS	SCAGK	VVSG	S	I	D	Q	S	D	Q	S	FL	DD-		
<i>FER1_MAIZE/1-150</i>	ELQ	VP	DD	VYIL	DQA	E	DGID	LPYSCR	AGSCSS	SCAGK	VVSG	S	V	D	Q	S	D	Q	S	Y	L	DDG
<i>O80429_MAIZE/1-140</i>	ELQ	VP	DD	VYIL	DFA	EE	EGID	LPF	SCR	AGSCSS	SCAGK	VVSG	S	V	D	Q	S	D	Q	S	FL	NDN