



MuscleWS alignment of Uniref50 Sequences

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	80	90	100	110	120	
<i>FER_CAPAA/1-97</i>	EFD	CPDDVYILDQAEEAGHDL	LPYSCRAGSCSSCAGKI	IAGGAVDQTDGN	FLDDD	
<i>FER_CAPAN/1-144</i>	EFD	CPDNVYILDQAEEAGHDL	LPYSCRAGSCSSCAGKI	IAGGAVDQTDGN	FLDDD	
<i>FER1_SOLLC/1-144</i>	EFE	CPDDVYILDQAEEEGHDL	LPYSCRAGSCSSCAGKVT	AGSV	DQSDGNFLDED	
<i>Q93XJ9_SOLTU/1-144</i>	EFE	CPDDVYILDQAEEEGHDL	LPYSCRAGSCSSCAGKVT	AGTVDQSDGK	FLDDD	
<i>FER1_PEA/1-149</i>	EFE	CPSDVYILDHAEVGI	DLPYSCRAGSCSSCAGKV	VGG	EV	DQSDGSFLDDE
<i>Q7XA98_TRIPR/1-152</i>	EFD	CPDDVYILDHAEVGI	ELPYSCRAGSCSSCAGKV	VNGNVN	QEDGSFLDDE	
<i>FER1_MESCR/1-148</i>	ELE	CPDDVYILDAAEEAGID	LPYSCRAGSCSSCAGKVT	SGSVN	QDDGSFLDDD	
<i>FER1_SPIOL/1-147</i>	EFE	QCPDDVYILDAAEEEGID	LPYSCRAGSCSSCAGKL	KTGSLN	QDDQSFLDDD	
<i>FER3_RAPSA/1-96</i>	EVE	CDDDVYVLDAAEEAGID	LPYSCRAGSCSSCAGKV	VSGSV	DQSDQSFLDDD	
<i>FER2_ARATH/1-148</i>	EVE	CDDDVYVLDAAEEAGID	LPYSCRAGSCSSCAGKV	VSGSV	DQSDQSFLDDE	
<i>FER_BRANA/1-96</i>	EVE	CDDDVYVLDAAEEAGID	LPYSCRAGSCSSCAGKV	VSGFV	DQSDQSFLDDD	
<i>FER1_ARATH/1-148</i>	EVE	CEEDVYVLDAAEEAGLD	LPYSCRAGSCSSCAGKV	VSGSID	QSDQSFLDDE	
<i>Q93Z60_ARATH/1-118</i>	EVE	CEEDVYVLDAAEEAGLD	LPYSCRAGSCSSCAGKV	VSGSID	QSDQSFLDD-	
<i>FER1_MAIZE/1-150</i>	ELQ	VPDDVYILDQAEEEDGID	LPYSCRAGSCSSCAGKV	VSGSV	DQSDQSYLDDG	
<i>O80429_MAIZE/1-140</i>	ELQ	VPDDVYILDFAEEEGID	LPFSCRAGSCSSCAGKV	VSGSV	DQSDQSFLNDN	