

File Edit Select View Format Colour C

	100	110
FER_CAPAA/1-97	AGSCSSCAGKIAAGGA	
FER_CAPAN/1-144	AGSCSSCAGKIAAGGA	
FER1_SOLLC/1-144	AGSCSSCAGKVTAGS	
Q93XJ9_SOLTU/1-144	AGSCSSCAGKVTAGT	
FER1_PEA/1-149	AGSCSSCAGKVVGG	
Q7XA98_TRIPR/1-152	AGSCSSCAGKVVNGN	
FER1_MESCR/1-148	AGSCSSCAGKVTSGS	
FER1_SPIOL/1-147	AGSCSSCAGKLKTGS	
FER3_RAPSA/1-96	AGSCSSCAGKVVSGS	
FER1_ARATH/1-148	AGSCSSCAGKVVSGS	
FER_BRANA/1-96	AGSCSSCAGKVVSGF	
FER2_ARATH/1-148	AGSCSSCAGKVVSGS	
Q93Z60_ARATH/1-118	AGSCSSCAGKVVSGS	
FER1_MAIZE/1-150	AGSCSSCAGKVVSGS	
O80429_MAIZE/1-140	AGSCSSCAGKVVSGS	

Score = 5620
 Length of alignment = 150
 Sequence FER1_SPIOL : 1 - 147 (Sequence length = 147)
 Sequence FER1_MESCR : 1 - 148 (Sequence length = 148)

```

FER1_SPIOL MAATTTTMMG--MATTFVPKPQAPPMMALPSNTGRSLFGLKTGSRGGRMT-MAAYKVTLV
|||...| |.|.| |.||| |...| |.| |||...| |.| |||...|
FER1_MESCR MAATTAALSGATMSTAFAPK--TPPMTAALPTNVGRALFGLKSSASRGRVTAMAAKVTLV

FER1_SPIOL TPTGNVEFQCPDDVYILDAAEEEGIDLPYSCRAGSCSSCAGKLTGSLNQDDQSFLLDDQI
|| |. |..|||...| |...| |...| |...| |...| |...| |...| |...| |...| |...|
FER1_MESCR TPEGKQELECPDDVYILDAAEEAGIDLPYSCRAGSCSSCAGKVTSGSVNQDDGSLDDDDQI

FER1_SPIOL DEGWLVTCAAYPVSDVTIETHKEEELTA
|||...| |...| |...| |...| |...| |...| |...| |...| |...| |...| |...|
FER1_MESCR KEGWLTCVAYPTGDVTIETHKEEELTA
  
```

Percentage ID = 74.67

Score = 4170
 Length of alignment = 96
 Sequence FER3_RAPSA : 1 - 96 (Sequence length = 96)
 Sequence FER1_MESCR : 1 - 148 (Sequence length = 148)

```

FER3_RAPSA ATYKVKFITPEGEQEVECDVVLDAAEEAGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQ
|.||| ..||| |..| |...| |...| |...| |...| |...| |...| |...| |...| |...|
FER1_MESCR AAYKVTLVTPPEGKQELECPDDVYILDAAEEAGIDLPYSCRAGSCSSCAGKVTSGSVNQDDG

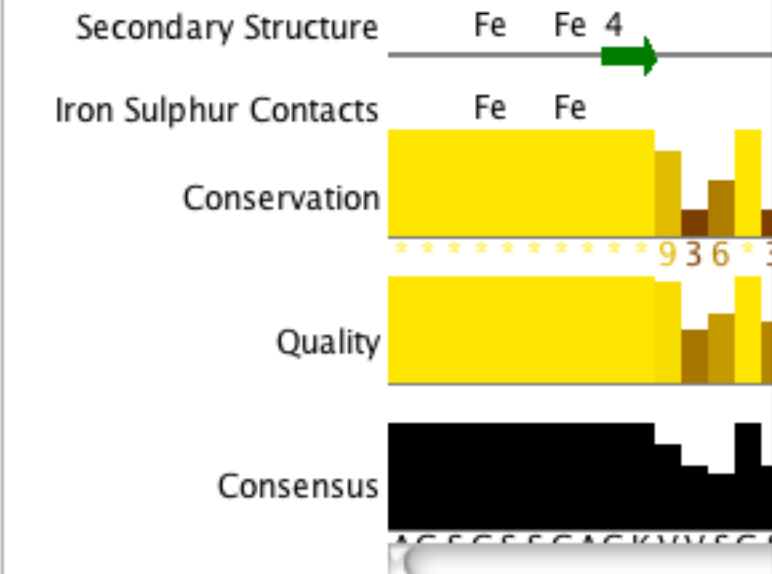
FER3_RAPSA SFLDDDQIAEGFVLTCAYPTSDVTIETHREEDMV
|||...| |...| |...| |...| |...| |...| |...| |...| |...| |...| |...|
FER1_MESCR SFLDDDQIKEGWLTCVAYPTGDVTIETHKEEELT
  
```

Percentage ID = 79.17

Score = 3910
 Length of alignment = 96
 Sequence FER3_RAPSA : 1 - 96 (Sequence length = 96)
 Sequence FER1_SPIOL : 1 - 147 (Sequence length = 147)

```

FER3_RAPSA ATYKVKFITPEGEQEVECDVVLDAAEEAGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQ
|.||| ..||| |. |. |...| |...| |...| |...| |...| |...| |...| |...|
FER1_SPIOL AAYKVTLVTPGNVEFQCPDDVYILDAAEEEGIDLPYSCRAGSCSSCAGKLTGSLNQDDQ
  
```



View in alignment editor