

	10	20	30	40	50	60	70	80	90	100
FER_CAPAA/1-97										
FER_CAPAN/1-144	MA	---	SVS	ATM	IST	SFMP	RKPA	VTSL	-KPI	PNVGE
FER1_SOLLC/1-144	MA	---	SIS	GTM	IST	SFLP	RKPA	VTSL	-KAI	SNVGE
Q93XJ9_SOLTU/1-144	MA	---	SIS	GTM	IST	SFLP	RKPA	VTSL	-KAI	SNVGE
FER1_PEA/1-149	MA	---	SIS	GTM	IST	SFLP	RKPA	VTSL	-KAI	SNVGE
Q7XA98_TRIPR/1-152	MATT	---	PAL	YGTA						
FER1_MESCR/1-148	MAAT	---	TAA	LSGAT						
FER1_SPIOL/1-147	MAAT	---	TTT	MMG						
FER3_RAPSA/1-96										
FER2_ARATH/1-148	MAST	---	ALS	SAI						
FER_BRANA/1-96										
FER1_ARATH/1-148	MAST	---	ALS	SAI						
Q93Z60_ARATH/1-118	MAST	---	ALS	SAI						
FER1_MAIZE/1-150	MAT	VL	GSP	RAP	AFF					
Q80429_MAIZE/1-140	MAAT	---								

Selection ▶

- Sequence Details
- Show annotations ▶
- Hide annotations ▶
- Add reference annotations
- Edit ▶
- Output to Textbox... ▶
- Create Sequence Feature...
- Remove Group
- Edit Group ▶

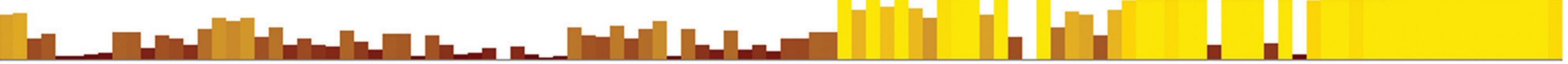
- Edit name and description of current group
- Group Colour ▶
- ✓ Boxes
- ✓ Text
- Colour Text
- Border colour
- Show nonconserved

- Text Colour
- ✓ None
- Clustalx colours
- BLOSUM62
- Percentage Identity
- Zappo
- Taylor
- Hydrophobicity
- Helix Propensity
- Strand Propensity
- Turn Propensity
- Buried Index
- Nucleotide
- User Defined...

Conservation



Quality



Consensus



MA+T LGTPALS GT+VST SFLRRQPAPTS LRS LPS+VG+FP+ LFGLKSVSTAR GGRVTAMATYKVKLITPEGEQEF ECPDDVY ILDA AEEAGIDL PYS CRAGSCSS CAGKV