http://www.jalview.org/examples/uniref50.fa

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```
FER_CAPAA/1-97        1 ------------------------------------------------------------ASYK   4
FER_CAPAN/1-144       1 MA------SVSATMISTSFMPRKPAVTSL-KPIPNVGE--ALFGLKS-A--NGGKVTCMASYK  51
FER1_SOLLC/1-144      1 MA------SISGTMISTSFLPRKPAVTSL-KAISNVGE--ALFGLKS-G--RNGRITCMASYK  51
Q93XJ9_SOLTU/1-144    1 MA------SISGTMISTSFLPRKPVVTSL-KAISNVGE--ALFGLKS-G--RNGRITCMASYK  51
FER1_PEA/1-149        1 MATT---PALYGTAVSTSFLRTQPMPMSV-TTTKAFSN--GFLGLKT-SLKRGDLAVAMASYK  56
Q7XA98_TRIPR/1-152    1 MATT---PALYGTAVSTSFMRRQPVPMSV-ATTTTTKAFPSGFGLKSVSTKRGDLAVAMATYK  59
FER1_MESCR/1-148      1 MAAT--TAALSGATMSTAFAPK--TPPMTAALPTNVGR--ALFGLKS-SASR-GRVTAMAAYK  55
FER1_SPIOL/1-147      1 MAAT--TTTMMG--MATTFVPKPQAPPMMAALPSNTGR--SLFGLKT-GSR--GGRMTMAAYK  54
FER3_RAPSA/1-96       1 ------------------------------------------------------------ATYK   4
FER2_ARATH/1-148      1 MAST----ALSSAIVGTSFIRRSPAPISLRSLPSANTQ--SLFGLKS-GTARGGRVTAMATYK  56
FER_BRANA/1-96        1 ------------------------------------------------------------ATYK   4
FER1_ARATH/1-148      1 MAST----ALSSAIVSTSFLRRQQTPISLRSLPFANTQ--SLFGLKS-STARGGRVTAMATYK  56
Q93Z60_ARATH/1-118    1 MAST----ALSSAIVSTSFLRRQQTPISLRSLPFANTQ--SLFGLKS-STARGGRVTAMATYK  56
FER1_MAIZE/1-150      1 MATVLGSPRAPAFFSSSSLRAAPAPTAV--ALPAAKV--GIMGRSA-SSRR--RLRAQATYN  56
O80429_MAIZE/1-140    1 MAAT---------ALSMSILR---APPPCFSSPLRLRV--AVAKPLA-APMRRQLLRAQATYN  48

Conservation
                        13------------1201010---11001--0000000--2111001-2-----00020*7*6
Quality
Consensus
                        MA+TLGTPALSGT+VSTSFLRRQPAPTSLRSLPS+VG+FP+LFGLKSVSTARGGRVTAMATYK

FER_CAPAA/1-97        5 VKLITPDGPIEFDCPDDVYILDQAEEAGHDLPYSCRAGSCSSCAGKIAGGAVDQTDGNFLDDD  67
FER_CAPAN/1-144      52 VKLITPDGPIEFDCPDNVYILDQAEEAGHDLPYSCRAGSCSSCAGKIAGGAVDQTDGNFLDDD 114
FER1_SOLLC/1-144     52 VKLITPEGPIEFECPDDVYILDQAEEEGHDLPYSCRAGSCSSCAGKVTAGSVDQSDGNFLDED 114
Q93XJ9_SOLTU/1-144   52 VKLITPDGPIEFECPDDVYILDQAEEEGHDLPYSCRAGSCSSCAGKVTAGTVDQSDGKFLDDD 114
FER1_PEA/1-149       57 VKLVTPDGTQEFECPSDVYILDHAEEVGIDLPYSCRAGSCSSCAGKVVGGEVDQSDGSFLDDE 119
Q7XA98_TRIPR/1-152   60 VKLITPEGPQEFDCPDDVYILDHAEEVGIELPYSCRAGSCSSCAGKVVNGNVNQEDGSFLDDE 122
FER1_MESCR/1-148     56 VTLVTPEGKQELECPDDVYILDAAEEAGIDLPYSCRAGSCSSCAGKVTSGSVNQDDGSFLDDD 118
FER1_SPIOL/1-147     55 VTLVTPTGNVEFQCPDDVYILDAAEEEGIDLPYSCRAGSCSSCAGKLKTGSLNQDDQSFLDDD 117
FER3_RAPSA/1-96       5 VKFITPEGEQEVECDDDVYVLDAAEEAGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQSFLDDD  67
FER2_ARATH/1-148     57 VKFITPEGELEVECDDDVYVLDAAEEAGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQSFLDDE 119
FER_BRANA/1-96        5 VKFITPEGEQEVECDDDVYVLDAAEEAGIDLPYSCRAGSCSSCAGKVVSGFVDQSDESFLDDD  67
FER1_ARATH/1-148     57 VKFITPEGEQEVECEEDVYVLDAAEEAGLDLPYSCRAGSCSSCAGKVVSGSIDQSDQSFLDDE 119
Q93Z60_ARATH/1-118   57 VKFITPEGEQEVECEEDVYVLDAAEEAGLDLPYSCRAGSCSSCAGKVVSGSIDQSDQSFLDD- 118
FER1_MAIZE/1-150     57 VKLITPEGEVELQVPDDVYILDQAEEDGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQSYLDDG 119
O80429_MAIZE/1-140   49 VKLITPEGEVELQVPDDVYILDFAEEEGIDLPFSCRAGSCSSCAGKVVSGSVDQSDQSFLNDN 111

Conservation
                        *789**6*36*779568**9**3***3*59**9*************947*398*5*459*890
Quality
Consensus
```

Sequence 11 ID: FER_BRANA Residue: LYS (4)