



logo

NTDB id 277738 AM462 RS16985 WP 000768943.1  
NTDB id 1063 ABD1 RS15730 WP 000768961.1  
consensus

SYANVPLPIAGQ<sup>R</sup>ETRDAEGNITKYYYAVQSKI<sup>R</sup>NLFTDVS<sup>A</sup>VAADGSLTKISTSGTNLLKIPAAPE<sup>E</sup>TNPFDTVANTA  
SYANVPLPIAGQPETRDAEGNITKYYYAVQSKIRNLFTDVS<sup>A</sup>VAADGSLTKISTSGTNLLKIPAAPEETNPFDTVANTA  
SYAKVPLPIAGQ<sup>R</sup>ETRDAEGNITKYYYAVQSKIRNLFTDVS<sup>A</sup>VAADGSLTKISTSGTNLLKIPAAPEGTNPFDTVANTA  
!!

634  
618

logo

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SYVLGKFD<sup>P</sup>STGQNILKAFPI<sup>S</sup>LK<sup>L</sup>K<sup>L</sup>L<sup>N</sup>YLGYSTDI<sup>S</sup>ATTLPSSLVTSNEPYLSMGGSIHSLPVQLTYNGTLDDNGNLT  
SYVLGKFD<sup>P</sup>STGQNILKAFPI<sup>S</sup>LK<sup>L</sup>K<sup>L</sup>K<sup>L</sup>L<sup>N</sup>YLGYSTDI<sup>S</sup>ATTLPSSLVTSNEPYLSMGGSIHSLPVQLTYNGTLDDNGNLT  
SYVLGKFD<sup>P</sup>STGQNILKAFPI<sup>S</sup>LK<sup>L</sup>K<sup>L</sup>K<sup>L</sup>L<sup>N</sup>YLGYSTDI<sup>S</sup>ATTLPSSLVTSNEPYLSMGGSIHSLPVQLTYNGTLDDNGNLT  
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714  
698

logo

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SAREQSILYGTMEGGLHIVDASSGIEQW<sup>F</sup>VPADILNDSVASKALVVGQSDASAPAHGMDGAWVSDPAYNITTVGSGSSA  
SAREQSILYGTMEGGLHIVDASSGIEQW<sup>F</sup>VPADILNDSVASKALVVGQSDASAPAHGMDGAWVSDPAYNITTVGSGSSA  
SAREQSILYGTMEGGLHIVDASSGIEQW<sup>F</sup>VPADILNDSVASKALVVGQSDASAPAHGMDGAWVSDPAYNITTVGSGSSA  
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794  
778

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VSKVTAKQ<sup>M</sup>NIYGGMRMGSSYYGLDVLSP<sup>T</sup>SPKLLFRIGADQ<sup>R</sup>TDYSRMGQSSWSKPVLANIRYNGSIRRVLIVGGGYDQC  
VSKVTAKQ<sup>M</sup>NIYGGMRMGSSYYGLDVLSP<sup>T</sup>SPKLLFRIGADQ<sup>R</sup>TDYSRMGQSSWSKPVLANIRYNGSIRRVLIVGGGYDQC  
VSKVTAKQ<sup>M</sup>NIYGGMRMGSSYYGLDVLSP<sup>T</sup>SPKLLFRIGADQ<sup>R</sup>TDYSRMGQSSWSKPVLANIRYNGSIRRVLIVGGGYDQC  
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874  
858

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YEKPNITLTDACFTNGKAKGNAVYIIDAKTGQRLW<sup>T</sup>SDTGSNTDNANMKHSIVSRISTLDRDADGLVDHLYFGDLGGQI  
YEKPNITLTDACFTNGKAKGNAVYIIDAKTGQRLW<sup>T</sup>SDTGSNTDNANMKHSIVSRISTLDRDADGLVDHLYFGDLGGQI  
YEKPNITLTDACFTNGKAKGNAVYIIDAKTGQRLW<sup>T</sup>SDTGSNTDNANMKHSIVSRISTLDRDADGLVDHLYFGDLGGQI  
!!

954  
938

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FRVDLNNNQTKTNSTYSSFGVRVRLANLATNDSTYDGTNDYTGGNAPRFYEPPTVTIHDYGIHTFITVGIASGDRSTPL  
FRVDLNNNQTKTNSTYSSFGVRVRLANLATNDSTYDGTNDYTGGNAPRFYEPPTVTIHDYGIHTFITVGIASGDRSTPL  
FRVDLNNNQTKTNSTYSSFGVRVRLANLATNDSTYDGTNDYTGGNAPRFYEPPTVTIHDYGIHTFITVGIASGDRSTPL  
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1034  
1018

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DVYPLTGREGMTP<sup>A</sup>SALSGRPVNNVYGIIDRDFVKKNLMSLTDNQL<sup>E</sup>TKDITRTGLRKNPQILRTGETRVAQIFFPTTGV  
DVYPLTGREGMTP<sup>A</sup>SALSGRPVNNVYGIIDRDFVKKNLMSLTDNQL<sup>E</sup>TKDITRTGLRKNPQILRTGETRVAQIFFPTTGV  
DVYPLTGREGMTP<sup>T</sup>SALSGRPVNNVYGIIDRDFVKKNLMSLTDNQL<sup>E</sup>TKDITRTGLRKNPQILRTGETRVAQIFFPTTGV  
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1114  
1098

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consensus



1194  
1178

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consensus



1274  
1258

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consensus



1284  
1268

- X non conserved
- X similar
- X ≥ 50% conserved