

logo

NTDB id 1150183 DG247 RS11610 WP 001883436.1
NTDB id 1143 A1552VC RS01965 WP 001883436.1
consensus

MRLCPRFSLDLLVKVKKLVNFVTLGFSCLSPTHAWRSPQSFTESNTLIMFRFYRKQKFKRLQNTLMAAFALSIIPLTIT
MRLCPRFSLDLLVKVKKLVNFVTLGFSCLSPTHAWRSPQSFTESNTLIMFRFYRKQKFKRLQNTLMAAFALSIIPLTIT
MRLCPRFSLDLLVKVKKLVNFVTLGFSCLSPTHAWRSPQSFTESNTLIMFRFYRKQKFKRLQNTLMAAFALSIIPLTIT
!!

80
80

logo

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consensus

ALFFLHSHSKDLEQQSTSYLVSVRDNKQQQVIDYMMAKESEVMGFVRSSELAYASGGRFYGLVNAFQRDVSIEAAREHAQ
ALFFLHSHSKDLEQQSTSYLVSVRDNKQQQVIDYMMAKESEVMGFVRSSELAYASGGRFYGLVNAFQRDVSIEAAREHAQ
ALFFLHSHSKDLEQQSTSYLVSVRDNKQQQVIDYMMAKESEVMGFVRSSELAYASGGRFYGLVNAFQRDVSIEAAREHAQ
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160
160

logo

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consensus

QRYITGSGDQIKTSVLPQSSSYVGSERYRLLHKRYHWAYLELLKRSDFDDILLVDIDGNVVYSIYKYDNFGTNLLTGKYQ
QRYITGSGDQIKTSVLPQSSSYVGSERYRLLHKRYHWAYLELLKRSDFDDILLVDIDGNVVYSIYKYDNFGTNLLTGKYQ
QRYITGSGDQIKTSVLPQSSSYVGSERYRLLHKRYHWAYLELLKRSDFDDILLVDIDGNVVYSIYKYDNFGTNLLTGKYQ
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240
240

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DTNLGHTFKRLEQTVNEQRKTNEFTPVVISDFVQEDGKQYAWLGAPIIQQGYLHSYAMFRLPSNAITKLI AEGSSNPSM
DTNLGHTFKRLEQTVNEQRKTNEFTPVVISDFVQEDGKQYAWLGAPIIQQGYLHSYAMFRLPSNAITKLI AEGSSNPSM
DTNLGHTFKRLEQTVNEQRKTNEFTPVVISDFVQEDGKQYAWLGAPIIQQGYLHSYAMFRLPSNAITKLI AEGSSNPSM
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320
320

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QTILVGGDHRSRRLTSAEIAVEKSKAVVDLALSGKRAVGTYTNTDGEQIIAAYAPINLKNIHVALVVELPEKEAFARVRQ
QTILVGGDHRSRRLTSAEIAVEKSKAVVDLALSGKRAVGTYTNTDGEQIIAAYAPINLKNIHVALVVELPEKEAFARVRQ
QTILVGGDHRSRRLTSAEIAVEKSKAVVDLALSGKRAVGTYTNTDGEQIIAAYAPINLKNIHVALVVELPEKEAFARVRQ
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400
400

logo

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LEKLFVFAMLTAVLVVIAASHYLSNFITSPLLKLTWAAERVSAGDLDEAMINTERKDEIGRLAVSFERMQRSIREKISLI
LEKLFVFAMLTAVLVVIAASHYLSNFITSPLLKLTWAAERVSAGDLDEAMINTERKDEIGRLAVSFERMQRSIREKISLI
LEKLFVFAMLTAVLVVIAASHYLSNFITSPLLKLTWAAERVSAGDLDEAMINTERKDEIGRLAVSFERMQRSIREKISLI
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480
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logo

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KSQNKELESNLLIIRKQNDLQLANKLKDEFLATTSHLRTPPLHGMIGIAEALISGANGPISA AHKYQLDIISSGQRLA
KSQNKELESNLLIIRKQNDLQLANKLKDEFLATTSHLRTPPLHGMIGIAEALISGANGPISA AHKYQLDIISSGQRLA
KSQNKELESNLLIIRKQNDLQLANKLKDEFLATTSHLRTPPLHGMIGIAEALISGANGPISA AHKYQLDIISSGQRLA
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560
560

logo

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consensus

TLVDDLLDYHKMRYGALDIQRCAVDLSSATRLVLELSHHLLGKKTLRINQVSEQPVWVSADPQRLEQVLYNLIIGNAIKY
TLVDDLLDYHKMRYGALDIQRCAVDLSSATRLVLELSHHLLGKKTLRINQVSEQPVWVSADPQRLEQVLYNLIIGNAIKY
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640
640

logo

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TSEKIVISATYIDDKVRVQWDTGQGIPAEQLEHIFEPLIQAGHDASRYRQGAGLGLSISRQLIELMHGTLVSSQPMV
TSEKIVISATYIDDKVRVQWDTGQGIPAEQLEHIFEPLIQAGHDASRYRQGAGLGLSISRQLIELMHGTLVSSQPMV
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720
720

logo

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consensus

GTTFSFTLPLASEEEIAQARLTLPHFQAPEVLDSELPEQSNLPENEHGPLLVAADDEPVNLRVLDSEFLRLEGYRVHTAQ
GTTFSFTLPLASEEEIAQARLTLPHFQAPEVLDSELPEQSNLPENEHGPLLVAADDEPVNLRVLDSEFLRLEGYRVHTAQ
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800
800

logo

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DGHQVLEAIKREKPELVLLDIMPGMSGYQVCEKLRQTYDHAELPIIMLTALNQSDDRVRGFEAGANDYLSKPFNKQELA
DGHQVLEAIKREKPELVLLDIMPGMSGYQVCEKLRQTYDHAELPIIMLTALNQSDDRVRGFEAGANDYLSKPFNKQELA
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880
880

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ARIVAHLTASKAELRRINAQLQKELKHRAMVEASLLETQGRILLEQLESAPAEILCVKEGNKVRFANEAAARLFRRTPEQ
ARIVAHLTASKAELRRINAQLQKELKHRAMVEASLLETQGRILLEQLESAPAEILCVKEGNKVRFANEAAARLFRRTPEQ
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960
960

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LKRSNAEELIAPKFLNIEQEHCYGNIDVYVDDVRQHLSADVLRLPQGSGLQAMYIFNVGGSVNAARIHNLETAVEALSSY
LKRSNAEELIAPKFLNIEQEHCYGNIDVYVDDVRQHLSADVLRLPQGSGLQAMYIFNVGGSVNAARIHNLETAVEALSSY
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1040
1040

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AFEGDKDKLQKLKELGGEFTRLADKASGEYQSKQDLMRVAVLVEAMTSALNYWERVSGQSKFTFAEQSGLWRVYLDRLTQ
AFEGDKDKLQKLKELGGEFTRLADKASGEYQSKQDLMRVAVLVEAMTSALNYWERVSGQSKFTFAEQSGLWRVYLDRLTQ
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1120
1120

