

logo

NTDB id 43543 V060002 RS16700 WP 001883436.1
NTDB id 1143 A1552VC RS01965 WP 001883436.1
consensus

MRLCPRFSLDLLVKVKKLVNFVTLGFSCLSPTHAWRSPQSFTESNTLIMFRFYRKQKFKRLQNTLMAAFALSIIPLTIT
MRLCPRFSLDLLVKVKKLVNFVTLGFSCLSPTHAWRSPQSFTESNTLIMFRFYRKQKFKRLQNTLMAAFALSIIPLTIT
MRLCPRFSLDLLVKVKKLVNFVTLGFSCLSPTHAWRSPQSFTESNTLIMFRFYRKQKFKRLQNTLMAAFALSIIPLTIT
!!

80
80

logo

NTDB id 43543 V060002 RS16700 WP 001883436.1
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consensus

ALFFLHSHSKDLEQQSTSYLVSVRDNKQQQVIDYMMAKESEVMGFVRSSELAYASGGRFYGLVNAFQRLDVSIEAAREHAQ
ALFFLHSHSKDLEQQSTSYLVSVRDNKQQQVIDYMMAKESEVMGFVRSSELAYASGGRFYGLVNAFQRLDVSIEAAREHAQ
ALFFLHSHSKDLEQQSTSYLVSVRDNKQQQVIDYMMAKESEVMGFVRSSELAYASGGRFYGLVNAFQRLDVSIEAAREHAQ
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160
160

logo

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consensus

QRYITGSGDQIKTSVLPQSSSYVGSERYRLLHKRYHWAYLELLKRSDFDDILLVDIDGNVVSIIYKYDNFGTNLLTGKYQ
QRYITGSGDQIKTSVLPQSSSYVGSERYRLLHKRYHWAYLELLKRSDFDDILLVDIDGNVVSIIYKYDNFGTNLLTGKYQ
QRYITGSGDQIKTSVLPQSSSYVGSERYRLLHKRYHWAYLELLKRSDFDDILLVDIDGNVVSIIYKYDNFGTNLLTGKYQ
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240
240

logo

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consensus

DTNLGHTFKRLEQTVNEQRKTNEFTPVVISDFVQEDGKQYAWLGAPIIQQGYLHSYAMFRLPSNAITKLI AEGSSNPSM
DTNLGHTFKRLEQTVNEQRKTNEFTPVVISDFVQEDGKQYAWLGAPIIQQGYLHSYAMFRLPSNAITKLI AEGSSNPSM
DTNLGHTFKRLEQTVNEQRKTNEFTPVVISDFVQEDGKQYAWLGAPIIQQGYLHSYAMFRLPSNAITKLI AEGSSNPSM
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320
320

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QTILVGGDHRSRRLTSAEIAVEKSKAVVDLALSGKRAVGTNTDGEQIIAAYAPINLKNIHVALVVELPEKEAFARVRQ
QTILVGGDHRSRRLTSAEIAVEKSKAVVDLALSGKRAVGTNTDGEQIIAAYAPINLKNIHVALVVELPEKEAFARVRQ
QTILVGGDHRSRRLTSAEIAVEKSKAVVDLALSGKRAVGTNTDGEQIIAAYAPINLKNIHVALVVELPEKEAFARVRQ
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400
400

logo

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LEKLFVFAMLTAVLVVIAASHYLSNFITSPLLKLTWAAERVSAGDLDEAMINTERKDEIGRLAVSFERMQRSIREKISLI
LEKLFVFAMLTAVLVVIAASHYLSNFITSPLLKLTWAAERVSAGDLDEAMINTERKDEIGRLAVSFERMQRSIREKISLI
LEKLFVFAMLTAVLVVIAASHYLSNFITSPLLKLTWAAERVSAGDLDEAMINTERKDEIGRLAVSFERMQRSIREKISLI
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480
480

logo

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KSQNKELESNLLIIRKQNDLQLANKLKDEFLATTSHLRTPLHGMIGIAEALISGANGPISAAHKYQLDIISSGQRLA
KSQNKELESNLLIIRKQNDLQLANKLKDEFLATTSHLRTPLHGMIGIAEALISGANGPISAAHKYQLDIISSGQRLA
KSQNKELESNLLIIRKQNDLQLANKLKDEFLATTSHLRTPLHGMIGIAEALISGANGPISAAHKYQLDIISSGQRLA
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560
560

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TLVDDLLDYHKMRYGALDIQRCAVDLSSATRLVLELSHHLLGKKTLRINQVSEQPVVWSADPQRLEQVLYNLIIGNAIKY
TLVDDLLDYHKMRYGALDIQRCAVDLSSATRLVLELSHHLLGKKTLRINQVSEQPVVWSADPQRLEQVLYNLIIGNAIKY
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640
640

logo

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TSEKIVISATYIDDKVRVQWDTGQGIPAEQLEHIFEPLIQAGHDASRYRQGAGLGLSISRQLIELMHGTLVSSQPMV
TSEKIVISATYIDDKVRVQWDTGQGIPAEQLEHIFEPLIQAGHDASRYRQGAGLGLSISRQLIELMHGTLVSSQPMV
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720
720

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consensus

GTTFSFTLPLASEEEEIAQARLTLPHFQAPEVLDSELPEQSNLPENEHGPELLLVADDEPVNLRVLDSEFLRLEGYRVHTAQ
GTTFSFTLPLASEEEEIAQARLTLPHFQAPEVLDSELPEQSNLPENEHGPELLLVADDEPVNLRVLDSEFLRLEGYRVHTAQ
GTTFSFTLPLASEEEEIAQARLTLPHFQAPEVLDSELPEQSNLPENEHGPELLLVADDEPVNLRVLDSEFLRLEGYRVHTAQ
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800
800

logo

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DGHQVLEAIKREKPELVLLDIMPGMSGYQVCEKLRQTYDHAELPIIMLTALNQSDDRVRGFEAGANDYLSKPFNKQELA
DGHQVLEAIKREKPELVLLDIMPGMSGYQVCEKLRQTYDHAELPIIMLTALNQSDDRVRGFEAGANDYLSKPFNKQELA
DGHQVLEAIKREKPELVLLDIMPGMSGYQVCEKLRQTYDHAELPIIMLTALNQSDDRVRGFEAGANDYLSKPFNKQELA
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880
880

logo

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ARIVAHLTASKAELRRINAQLQKELKHRAMVEASLLETQGRILLEQLESAPAEILCVKEGNKVRFANEAAARLFRRTPEQ
ARIVAHLTASKAELRRINAQLQKELKHRAMVEASLLETQGRILLEQLESAPAEILCVKEGNKVRFANEAAARLFRRTPEQ
ARIVAHLTASKAELRRINAQLQKELKHRAMVEASLLETQGRILLEQLESAPAEILCVKEGNKVRFANEAAARLFRRTPEQ
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960
960

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LKRSNAEELIAPKFLNIEQEHCYGNIDVYVDDVRQHLSADVLRLPQGSGLQAMYIFNVGGSVNAARIHNLETAVEALSSY
LKRSNAEELIAPKFLNIEQEHCYGNIDVYVDDVRQHLSADVLRLPQGSGLQAMYIFNVGGSVNAARIHNLETAVEALSSY
LKRSNAEELIAPKFLNIEQEHCYGNIDVYVDDVRQHLSADVLRLPQGSGLQAMYIFNVGGSVNAARIHNLETAVEALSSY
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1040
1040

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AFEGDKDKLQKLKELGGEFTRLADKASGEYQSKQDLMRAVLVEAMTSALNYWERVSGQSKFTFAEQSGLWRVYLDRLTLQ
AFEGDKDKLQKLKELGGEFTRLADKASGEYQSKQDLMRAVLVEAMTSALNYWERVSGQSKFTFAEQSGLWRVYLDRLTLQ
AFEGDKDKLQKLKELGGEFTRLADKASGEYQSKQDLMRAVLVEAMTSALNYWERVSGQSKFTFAEQSGLWRVYLDRLTLQ
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1120
1120

