

logo

NTDB id 271169 C4E16 RS00145 WP 001883436.1  
NTDB id 1143 A1552VC RS01965 WP 001883436.1  
consensus

MRLCPRFSLDLLVKVKKLVNFVTLGFSCLSPTHAWRSPQSFTESNTLIMFRFYRKQKFKRLQNTLMAAFLALSIIPLTIT  
MRLCPRFSLDLLVKVKKLVNFVTLGFSCLSPTHAWRSPQSFTESNTLIMFRFYRKQKFKRLQNTLMAAFLALSIIPLTIT  
!!

80  
80

logo

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NTDB id 1143 A1552VC RS01965 WP 001883436.1  
consensus

ALFFLHSHSKDLEQQSTSYLVSVRDNKQQQVIDYMMAKESEVMGFVRSELAYASGGRFYGLVNAFQRLDVSIEAAREHAQ  
ALFFLHSHSKDLEQQSTSYLVSVRDNKQQQVIDYMMAKESEVMGFVRSELAYASGGRFYGLVNAFQRLDVSIEAAREHAQ  
ALFFLHSHSKDLEQQSTSYLVSVRDNKQQQVIDYMMAKESEVMGFVRSELAYASGGRFYGLVNAFQRLDVSIEAAREHAQ  
!!

160  
160

logo

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consensus

QRYITGSGDQIKTSVLPQSSSYVGSERYRLLHKRYHWAYLELLKRSDFDDILLVDIDGNVVSIIYKYDNFGTNLLTGKYQ  
QRYITGSGDQIKTSVLPQSSSYVGSERYRLLHKRYHWAYLELLKRSDFDDILLVDIDGNVVSIIYKYDNFGTNLLTGKYQ  
QRYITGSGDQIKTSVLPQSSSYVGSERYRLLHKRYHWAYLELLKRSDFDDILLVDIDGNVVSIIYKYDNFGTNLLTGKYQ  
!!

240  
240

logo

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consensus

DTNLGHTFKRLEQTVNEQRKTNEFTPVVISDFVQEDGKQYAWLGAPIIQGGYLHSYAMFRLPSNAITKLI AEGSSNPSM  
DTNLGHTFKRLEQTVNEQRKTNEFTPVVISDFVQEDGKQYAWLGAPIIQGGYLHSYAMFRLPSNAITKLI AEGSSNPSM  
DTNLGHTFKRLEQTVNEQRKTNEFTPVVISDFVQEDGKQYAWLGAPIIQGGYLHSYAMFRLPSNAITKLI AEGSSNPSM  
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320  
320

logo

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QTILVGQDHRSRRLTSAEIAVEKSKAVVDLALSGKRAVGTYTNTDGEQIIAAYAPINLKNIHWALVVELPEKEAFARVRQ  
QTILVGQDHRSRRLTSAEIAVEKSKAVVDLALSGKRAVGTYTNTDGEQIIAAYAPINLKNIHWALVVELPEKEAFARVRQ  
QTILVGQDHRSRRLTSAEIAVEKSKAVVDLALSGKRAVGTYTNTDGEQIIAAYAPINLKNIHWALVVELPEKEAFARVRQ  
!!

400  
400

logo

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LEKLFVFAMLTAVLWVIAASHYLSNFITSPLLLKTWAAERVSAGDLDEAMINTERKDEIGRLAVSFERMQRISIREKISLI  
LEKLFVFAMLTAVLWVIAASHYLSNFITSPLLLKTWAAERVSAGDLDEAMINTERKDEIGRLAVSFERMQRISIREKISLI  
LEKLFVFAMLTAVLWVIAASHYLSNFITSPLLLKTWAAERVSAGDLDEAMINTERKDEIGRLAVSFERMQRISIREKISLI  
!!

480  
480

logo

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KSQNKELESNLLIIRKQNDLQLANKLKDEFLATTSHLRTPLHGMIGIAEALISGANGPISAAHKYQLDIISSGQRLA  
KSQNKELESNLLIIRKQNDLQLANKLKDEFLATTSHLRTPLHGMIGIAEALISGANGPISAAHKYQLDIISSGQRLA  
KSQNKELESNLLIIRKQNDLQLANKLKDEFLATTSHLRTPLHGMIGIAEALISGANGPISAAHKYQLDIISSGQRLA  
!!

560  
560

logo

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consensus

TLVDDLLDYHKMRYGALDIQRCAVDLSSATRLVLELSHLLGKKTLRINQVSEQPVVWSADPQRLEQVLYNLIGNAIKY  
TLVDDLLDYHKMRYGALDIQRCAVDLSSATRLVLELSHLLGKKTLRINQVSEQPVVWSADPQRLEQVLYNLIGNAIKY  
!!

640  
640

logo

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consensus

TSEGKIVISATYIDDKVRVQVDTGGGIPAEQLEHIFEPLIQAGHDASRYRQGAGLGLSISRQLIELMHGTLVSSQPMV  
TSEGKIVISATYIDDKVRVQVDTGGGIPAEQLEHIFEPLIQAGHDASRYRQGAGLGLSISRQLIELMHGTLVSSQPMV  
!!

720  
720

logo

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consensus

GTTFSFTLPLASEEEIAQARLTELPHFQAPEVLDSELPEQSNLPENEHGPLLLVADDEPVNLRVLDSEFLRLEGYRVHTAQ  
GTTFSFTLPLASEEEIAQARLTELPHFQAPEVLDSELPEQSNLPENEHGPLLLVADDEPVNLRVLDSEFLRLEGYRVHTAQ  
!!

800  
800

logo

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consensus

DGHQVLEAIKREKPELVLLDIMPPGMSGYQVCEKLRQTYDHAELPIIMLTALNQSDDRVRGFEAGANDYLSKPFNKQELA  
DGHQVLEAIKREKPELVLLDIMPPGMSGYQVCEKLRQTYDHAELPIIMLTALNQSDDRVRGFEAGANDYLSKPFNKQELA  
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880  
880

logo

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consensus

ARIVAHLTASKAELRRIENAQLQKELKHRAMVEASLLETQGRILLEQLESAPAEILCVKEGKRVFANEAAARLFRRTPEQ  
ARIVAHLTASKAELRRIENAQLQKELKHRAMVEASLLETQGRILLEQLESAPAEILCVKEGKRVFANEAAARLFRRTPEQ  
!!

960  
960

logo

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consensus

LKRSNAEELIAPKFLNIEQEHCYGNIDVYVDDVRQHLSADVLRLPQGSGLQAMYIFNVGGSVNAARIHNLLETAVEALSSY  
LKRSNAEELIAPKFLNIEQEHCYGNIDVYVDDVRQHLSADVLRLPQGSGLQAMYIFNVGGSVNAARIHNLLETAVEALSSY  
!!

1040  
1040

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consensus

AFEGDKDKLQKLKELGGEFTRLADKASGEYQSKQDLMRVAVLVEAMTSALNYWERSVSGSKFTFAEQSGLWRVYLDLDRSTLQ  
AFEGDKDKLQKLKELGGEFTRLADKASGEYQSKQDLMRVAVLVEAMTSALNYWERSVSGSKFTFAEQSGLWRVYLDLDRSTLQ  
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1120  
1120

