

logo

NTDB id 76052 EN18 RS00145 WP 001883436.1
NTDB id 1143 A1552VC RS01965 WP 001883436.1
consensus



80
80

logo

NTDB id 76052 EN18 RS00145 WP 001883436.1
NTDB id 1143 A1552VC RS01965 WP 001883436.1
consensus



160
160

logo

NTDB id 76052 EN18 RS00145 WP 001883436.1
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consensus



240
240

logo

NTDB id 76052 EN18 RS00145 WP 001883436.1
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consensus



320
320

logo

NTDB id 76052 EN18 RS00145 WP 001883436.1
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consensus



400
400

logo

NTDB id 76052 EN18 RS00145 WP 001883436.1
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consensus



480
480

logo

NTDB id 76052 EN18 RS00145 WP 001883436.1
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consensus



560
560

logo

NTDB id 76052 EN18 RS00145 WP 001883436.1
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consensus

TLVDDLLDYHKMRYGALDIQRCVDLSSATRLVLELSHLLGKKTLRIINQVSEQPVVWSADPQRLEQVLYNLIGNAIKY
TLVDDLLDYHKMRYGALDIQRCVDLSSATRLVLELSHLLGKKTLRIINQVSEQPVVWSADPQRLEQVLYNLIGNAIKY
!!

640
640

logo

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consensus

TSEGKIVISATYIDDKVRVQVDTGQGI PAEQLEHIFEPLIQAGHDASRYRQGAGLGLSISRQLIELMHGTLVSSQPMV
TSEGKIVISATYIDDKVRVQVDTGQGI PAEQLEHIFEPLIQAGHDASRYRQGAGLGLSISRQLIELMHGTLVSSQPMV
TSEGKIVISATYIDDKVRVQVDTGQGI PAEQLEHIFEPLIQAGHDASRYRQGAGLGLSISRQLIELMHGTLVSSQPMV
!!

720
720

logo

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consensus

GTTFSFTLPLASEEEIAQARLTELPHFQAPEVLDSELPEQSNLPENEHGPIIIIVADDEPVNLRVLDSEFLRLEGYRVHTAQ
GTTFSFTLPLASEEEIAQARLTELPHFQAPEVLDSELPEQSNLPENEHGPIIIIVADDEPVNLRVLDSEFLRLEGYRVHTAQ
GTTFSFTLPLASEEEIAQARLTELPHFQAPEVLDSELPEQSNLPENEHGPIIIIVADDEPVNLRVLDSEFLRLEGYRVHTAQ
!!

800
800

logo

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DGHQVLEAIKREKPELVLLDIMPPGMSGYQVCEKLRQTYDHAELPIIMLTALNQSDDRVRGFEAGANDYLSKPFNKQELA
DGHQVLEAIKREKPELVLLDIMPPGMSGYQVCEKLRQTYDHAELPIIMLTALNQSDDRVRGFEAGANDYLSKPFNKQELA
DGHQVLEAIKREKPELVLLDIMPPGMSGYQVCEKLRQTYDHAELPIIMLTALNQSDDRVRGFEAGANDYLSKPFNKQELA
!!

880
880

logo

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ARIVAHLTASKAELRRIENAQLQKELKHRAMVEASLLETQGRILLEQLESAPAEILCVKEGKRVFANEAAARLFRRTPEQ
ARIVAHLTASKAELRRIENAQLQKELKHRAMVEASLLETQGRILLEQLESAPAEILCVKEGKRVFANEAAARLFRRTPEQ
ARIVAHLTASKAELRRIENAQLQKELKHRAMVEASLLETQGRILLEQLESAPAEILCVKEGKRVFANEAAARLFRRTPEQ
!!

960
960

logo

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LKRSNAEELIAPKFLNIEQEHCYGNIDVYVDDVRQHLSADVLRLPQGSGLQAMYIFNVGGSVNAARIHNLLETAVEALSSY
LKRSNAEELIAPKFLNIEQEHCYGNIDVYVDDVRQHLSADVLRLPQGSGLQAMYIFNVGGSVNAARIHNLLETAVEALSSY
LKRSNAEELIAPKFLNIEQEHCYGNIDVYVDDVRQHLSADVLRLPQGSGLQAMYIFNVGGSVNAARIHNLLETAVEALSSY
!!

1040
1040

logo

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AFEGDKDKLQKLKELGGEFTRLADKASGEYQSKQDLMRAVLVEAMTSALNYWERSVSGSKFTFAEQSGLWRVYLDLDRSTLQ
AFEGDKDKLQKLKELGGEFTRLADKASGEYQSKQDLMRAVLVEAMTSALNYWERSVSGSKFTFAEQSGLWRVYLDLDRSTLQ
AFEGDKDKLQKLKELGGEFTRLADKASGEYQSKQDLMRAVLVEAMTSALNYWERSVSGSKFTFAEQSGLWRVYLDLDRSTLQ
!!

1120
1120

logo

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consensus

TRTLDKYLRIETLPKTPRWRTVLNSLDYILEHCKEAGPERTHIEMQRDKLQKLLTSE
TRTLDKYLRIETLPKTPRWRTVLNSLDYILEHCKEAGPERTHIEMQRDKLQKLLTSE
TRTLDKYLRIETLPKTPRWRTVLNSLDYILEHCKEAGPERTHIEMQRDKLQKLLTSE
!!

1177
1177

- non conserved
- similar
- ≥ 50% conserved