

logo

NTDB id 42742 HJ37 RS00145 WP 001883436.1
NTDB id 1143 A1552VC RS01965 WP 001883436.1
consensus



80
80

logo

NTDB id 42742 HJ37 RS00145 WP 001883436.1
NTDB id 1143 A1552VC RS01965 WP 001883436.1
consensus



160
160

logo

NTDB id 42742 HJ37 RS00145 WP 001883436.1
NTDB id 1143 A1552VC RS01965 WP 001883436.1
consensus



240
240

logo

NTDB id 42742 HJ37 RS00145 WP 001883436.1
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consensus



320
320

logo

NTDB id 42742 HJ37 RS00145 WP 001883436.1
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consensus



400
400

logo

NTDB id 42742 HJ37 RS00145 WP 001883436.1
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consensus



480
480

logo

NTDB id 42742 HJ37 RS00145 WP 001883436.1
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consensus



560
560

logo

NTDB id 42742 HJ37 RS00145 WP 001883436.1
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consensus

TLVDDLLDYHKMRYGALDIQRCAVDLSSATRLVLELSHLLGKKTLRINQVSEQPVVVSADPQRLEQVLYNLIGNAIKY
TLVDDLLDYHKMRYGALDIQRCAVDLSSATRLVLELSHLLGKKTLRINQVSEQPVVVSADPQRLEQVLYNLIGNAIKY
!!

640
640

logo

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consensus

TSEGKIVISATYIDDKVRVQVDTGGGIPAEQLEHIFEPLIQAGHDASRYRQGAGLGLSISRQLIELMHGTLVSSQPMV
TSEGKIVISATYIDDKVRVQVDTGGGIPAEQLEHIFEPLIQAGHDASRYRQGAGLGLSISRQLIELMHGTLVSSQPMV
!!

720
720

logo

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consensus

GTTFSFTLPLASEEEIAQARLTELPHFQAPEVLDSELPEQSNLPENEHGPIIIIVADDEPVNLRVLDSEFLRLEGYRVHTAQ
GTTFSFTLPLASEEEIAQARLTELPHFQAPEVLDSELPEQSNLPENEHGPIIIIVADDEPVNLRVLDSEFLRLEGYRVHTAQ
!!

800
800

logo

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DGHQVLEAIKREKPELVLLDIMPPGMSGYQVCEKLRQTYDHAELPIIMLTALNQSDDRVRGFEAGANDYLSKPFNKQELA
DGHQVLEAIKREKPELVLLDIMPPGMSGYQVCEKLRQTYDHAELPIIMLTALNQSDDRVRGFEAGANDYLSKPFNKQELA
!!

880
880

logo

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ARIVAHLTASKAELRRIENAQLQKELKHRAMVEASLLETQGRILLEQLESAPAEILCVKEGKRVFANEAAARLFRRTPEQ
ARIVAHLTASKAELRRIENAQLQKELKHRAMVEASLLETQGRILLEQLESAPAEILCVKEGKRVFANEAAARLFRRTPEQ
!!

960
960

logo

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LKRSNAEELIAPKFLNIEQEHCYGNIDVYVDDVRQHLSADVLRLPQGSGLQAMYIFNVGGSVNAARIHNLLETAVEALSSY
LKRSNAEELIAPKFLNIEQEHCYGNIDVYVDDVRQHLSADVLRLPQGSGLQAMYIFNVGGSVNAARIHNLLETAVEALSSY
!!

1040
1040

logo

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AFEGDKDKLQKLKELGGEFTRLADKASGEYQSKQDLMRAVLVEAMTSALNYWERSVSGSKFTFAEQSGLWRVYLDLDRSTLQ
AFEGDKDKLQKLKELGGEFTRLADKASGEYQSKQDLMRAVLVEAMTSALNYWERSVSGSKFTFAEQSGLWRVYLDLDRSTLQ
!!

1120
1120

logo

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TRTLDKYLRIETLPKTPRWRTVLNSLDYILEHCKEAGPERTHIEMQRDKLQKLLTSE
TRTLDKYLRIETLPKTPRWRTVLNSLDYILEHCKEAGPERTHIEMQRDKLQKLLTSE
TRTLDKYLRIETLPKTPRWRTVLNSLDYILEHCKEAGPERTHIEMQRDKLQKLLTSE
!!

1177
1177

- non conserved
- similar
- ≥ 50% conserved