

logo

NTDB id 412321 GTF73 RS04010 WP 001911421.1
NTDB id 1151 GTF74 RS04205 WP 001911421.1
consensus



80
80

logo

NTDB id 412321 GTF73 RS04010 WP 001911421.1
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consensus



160
160

logo

NTDB id 412321 GTF73 RS04010 WP 001911421.1
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consensus



240
240

logo

NTDB id 412321 GTF73 RS04010 WP 001911421.1
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consensus



320
320

logo

NTDB id 412321 GTF73 RS04010 WP 001911421.1
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consensus



400
400

logo

NTDB id 412321 GTF73 RS04010 WP 001911421.1
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consensus



480
480

logo

NTDB id 412321 GTF73 RS04010 WP 001911421.1
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consensus



560
560

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G I S Y Y R N Q E L T K H F G A P Y G L I S N E F L S A S C A V G E E Q D N S S L I I G S Q F G W K T N T E E L A V S N L P N I Q V T F S Q V S V N H T T K L
 G I S Y Y R N Q E L T K H F G A P Y G L I S N E F L S A S C A V G E E Q D N S S L I I G S Q F G V V K T N T E E L A V S N L P N I Q V T F S Q V S V N H T T K L
 G I S Y Y R N Q E L T K H F G A P Y G L I S N E F L S A S C A V G E E Q D N S S L I I G S Q F G V V K T N T E E L A V S N L P N I Q V T F S Q V S V N H T T K L

640
640

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LGYRMSEPLKIAYGDSISFQFGALPSSRSQSLEYKLNDEQQWQRFDWALLNFDQLLPQKYRLKVRSANPTQRYRTEALFD
 LGYRMSEPLKIAYGDSISFQFGALPSSRSQSLEYKLNDEQQWQRFDWALLNFDQLLPQKYRLKVRSANPTQRYRTEALFD
 LGYRMSEPLKIAYGDSISFQFGALPSSRSQSLEYKLNDEQQWQRFDWALLNFDQLLPQKYRLKVRSANPTQRYRTEALFD

720
720

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FEVLQPMYMTSIALVGYVLSVLGLLALALWWRTRMILAANRKLKAQVELKTSQLRHQSKIVLSNNHQLRKQLQLHHTILG
FEVLQPMYMTSIALVGYVLSVLGLLALALWWRTRMILAANRKLKAQVELKTSQLRHQSKIVLSNNHQLRKQLQLHHTILG
FEVLQPMYMTSIALVGYVLSVLGLLALALWWRTRMILAANRKLKAQVELKTSQLRHQSKIVLSNNHQLRKQLQLHHTILG

800
800

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NVLDNIDASLRHLSSYAKVRAWSEFEAPFNKVQELAQLHFMHRGDEDESKYHDLHLLESALKSWQEEYSKALIKLTYS
 NVLDNIDASLRHLSSYAKVRAWSEFEAPFNKVQELAQLHFMHRGDEDESKYHDLHLLESALKSWQEEYSKALIKLTYS
 NVLDNIDASLRHLSSYAKVRAWSEFEAPFNKVQELAQLHFMHRGDEDESKYHDLHLLESALKSWQEEYSKALIKLTYS

880
880

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GEPRFVEVRQFNLDVLFNAVLTDAIKRLYKHQELTIQLEVRNAQAVIVFSDFGAPIQNI DKTMTVLSGSSYPLEELVIRS
GEPRFVEVRQFNLDVLFNAVLTDAIKRLYKHQELTIQLEVRNAQAVIVFSDFGAPIQNI DKTMTVLSGSSYPLEELVIRS
GEPRFVEVRQFNLDVLFNAVLTDAIKRLYKHQELTIQLEVRNAQAVIVFSDFGAPIQNI DKTMTVLSGSSYPLEELVIRS

960
960

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GGVLHVLALKERNVIELAWPLATLPELETIHKPEEGEQAAKVGIDEVEKEWLSKVEKLIELHYSDPNFTTSTAAQALYS
GGVLHVLALKERNVIELAWPLATLPELETIHKPEEGEQAAKVGIDEVEKEWLSKVEKLIELHYSDPNFTTSTAAQALYS
GGVLHVLALKERNVIELAWPLATLPELETIHKPEEGEQAAKVGIDEVEKEWLSKVEKLIELHYSDPNFTTSTAAQALYS

1040
1040

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ERSLQRRFKAATGKTFKESLNEVRLEKACQSLLSGAKIAQVAFDCGFNDPSYFSQRFKHHFGLSPSQFIEDQEN
ERSLQRRFKAATGKTFKESLNEVRLEKACQSLLSGAKIAQVAFDCGFNDPSYFSQRFKHHFGLSPSQFIEDQEN 1114
ERSLQRRFKAATGKTFKESLNEVRLEKACQSLLSGAKIAQVAFDCGFNDPSYFSQRFKHHFGLSPSQFIEDQEN 1114

1114
1114

 non conserved
 similar
 $\geq 50\%$ conserved