

logo

NTDB id 1062817 ACG4IX RS04165 WP 001911421.1  
NTDB id 1151 GTF74 RS04205 WP 001911421.1  
consensus



80  
80

logo

NTDB id 1062817 ACG4IX RS04165 WP 001911421.1  
NTDB id 1151 GTF74 RS04205 WP 001911421.1  
consensus



160  
160

logo

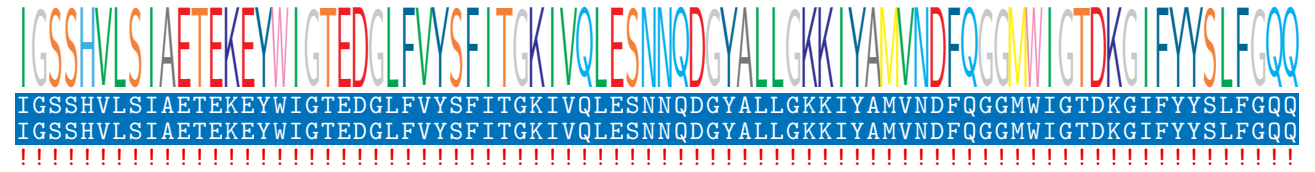
NTDB id 1062817 ACG4IX RS04165 WP 001911421.1  
NTDB id 1151 GTF74 RS04205 WP 001911421.1  
consensus



240  
240

logo

NTDB id 1062817 ACG4IX RS04165 WP 001911421.1  
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consensus



320  
320

logo

NTDB id 1062817 ACG4IX RS04165 WP 001911421.1  
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consensus



400  
400

logo

NTDB id 1062817 ACG4IX RS04165 WP 001911421.1  
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480  
480

logo

NTDB id 1062817 ACG4IX RS04165 WP 001911421.1  
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560  
560

logo

NTDB id 1062817 ACG4IX RS04165 WP 001911421.1  
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consensus

GISYYRNQELTKHFGAPYGLISNEFLSASCavgEEQDNSSLIIGSQFGVVKNTTEELAVSNLPNIQVTFSSQVSVNHHTTKL  
GISYYRNQELTKHFGAPYGLISNEFLSASCavgEEQDNSSLIIGSQFGVVKNTTEELAVSNLPNIQVTFSSQVSVNHHTTKL  
GISYYRNQELTKHFGAPYGLISNEFLSASCavgEEQDNSSLIIGSQFGVVKNTTEELAVSNLPNIQVTFSSQVSVNHHTTKL  
!!

640  
640

logo

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LGYRMSEPLKIAYGDSISFQFGALPSSRSQSLEYKLNDEQQWQRFDWALLNFDQLLPGKYRLKVRSANPTQRYRTEALFD  
LGYRMSEPLKIAYGDSISFQFGALPSSRSQSLEYKLNDEQQWQRFDWALLNFDQLLPGKYRLKVRSANPTQRYRTEALFD  
LGYRMSEPLKIAYGDSISFQFGALPSSRSQSLEYKLNDEQQWQRFDWALLNFDQLLPGKYRLKVRSANPTQRYRTEALFD  
!!

720  
720

logo

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FEVLQPWYMTSIALVGYVLSVLGLLALALWWRTRMILAANRKLKAQVELKTSQLRHQSKIVLSNNHQLRKQLQLHHTILG  
FEVLQPWYMTSIALVGYVLSVLGLLALALWWRTRMILAANRKLKAQVELKTSQLRHQSKIVLSNNHQLRKQLQLHHTILG  
FEVLQPWYMTSIALVGYVLSVLGLLALALWWRTRMILAANRKLKAQVELKTSQLRHQSKIVLSNNHQLRKQLQLHHTILG  
!!

800  
800

logo

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NVLDNIDASLRHLSSYAKVRAWSEFEAPFNKVKQELAQLHFMHRGDEDESKYHDLHLLIESALKSWQEEYSKALIKLTYS  
NVLDNIDASLRHLSSYAKVRAWSEFEAPFNKVKQELAQLHFMHRGDEDESKYHDLHLLIESALKSWQEEYSKALIKLTYS  
NVLDNIDASLRHLSSYAKVRAWSEFEAPFNKVKQELAQLHFMHRGDEDESKYHDLHLLIESALKSWQEEYSKALIKLTYS  
!!

880  
880

logo

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GEPRFVEVRQFNLDVLFNAVLTDIAIKRLYKHQELTIQLEVRNAQAVIVFSDFGAPIQNIIDKTMVTLGSSSYPLEELVIRS  
GEPRFVEVRQFNLDVLFNAVLTDIAIKRLYKHQELTIQLEVRNAQAVIVFSDFGAPIQNIIDKTMVTLGSSSYPLEELVIRS  
GEPRFVEVRQFNLDVLFNAVLTDIAIKRLYKHQELTIQLEVRNAQAVIVFSDFGAPIQNIIDKTMVTLGSSSYPLEELVIRS  
!!

960  
960

logo

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consensus

GGVLHVLALKERNVIELAWPLATLPELETIHKPEEGEQAQKVGIDEVEKEWLSKVEKLI ELHYSDPNFTTSTAAQALYVS  
GGVLHVLALKERNVIELAWPLATLPELETIHKPEEGEQAQKVGIDEVEKEWLSKVEKLI ELHYSDPNFTTSTAAQALYVS  
GGVLHVLALKERNVIELAWPLATLPELETIHKPEEGEQAQKVGIDEVEKEWLSKVEKLI ELHYSDPNFTTSTAAQALYVS  
!!

1040  
1040

logo

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consensus

ERSLQRRFKAATGKTFKESLNEVRLEKACQSLLSGAKIAQVAFDCGFNDPSYFSQRFKHHFGLSPSQFI EDQEN  
ERSLQRRFKAATGKTFKESLNEVRLEKACQSLLSGAKIAQVAFDCGFNDPSYFSQRFKHHFGLSPSQFI EDQEN  
ERSLQRRFKAATGKTFKESLNEVRLEKACQSLLSGAKIAQVAFDCGFNDPSYFSQRFKHHFGLSPSQFI EDQEN  
!!

1114  
1114

 non conserved  
 similar  
  $\geq 50\%$  conserved