

logo

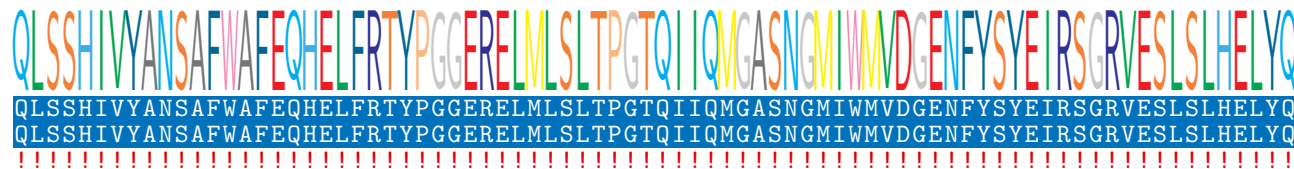
NTDB id 1066329 ACG4I1 RS10765 WP 001911421.1  
NTDB id 1151 GTF74 RS04205 WP 001911421.1  
consensus



80  
80

logo

NTDB id 1066329 ACG4I1 RS10765 WP 001911421.1  
NTDB id 1151 GTF74 RS04205 WP 001911421.1  
consensus



160  
160

logo

NTDB id 1066329 ACG4I1 RS10765 WP 001911421.1  
NTDB id 1151 GTF74 RS04205 WP 001911421.1  
consensus



240  
240

logo

NTDB id 1066329 ACG4I1 RS10765 WP 001911421.1  
NTDB id 1151 GTF74 RS04205 WP 001911421.1  
consensus



320  
320

logo

NTDB id 1066329 ACG4I1 RS10765 WP 001911421.1  
NTDB id 1151 GTF74 RS04205 WP 001911421.1  
consensus



400  
400

logo

NTDB id 1066329 ACG4I1 RS10765 WP 001911421.1  
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consensus



480  
480

logo

NTDB id 1066329 ACG4I1 RS10765 WP 001911421.1  
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consensus



560  
560

logo

NTDB id 1066329 ACG4I1 RS10765 WP 001911421.1  
NTDB id 1151 GTF74 RS04205 WP 001911421.1  
consensus

GISYYRNQELTKHFGAPYGLISNEFLSASCavgEEQDNSSLIIGSQFGVVKNTTEELAVSNLPNIQVTFSSQVSVNHHTTKL  
GISYYRNQELTKHFGAPYGLISNEFLSASCavgEEQDNSSLIIGSQFGVVKNTTEELAVSNLPNIQVTFSSQVSVNHHTTKL  
GISYYRNQELTKHFGAPYGLISNEFLSASCavgEEQDNSSLIIGSQFGVVKNTTEELAVSNLPNIQVTFSSQVSVNHHTTKL  
!!

640  
640

logo

NTDB id 1066329 ACG4I1 RS10765 WP 001911421.1  
NTDB id 1151 GTF74 RS04205 WP 001911421.1  
consensus

LGYRMSEPLKIAYGDSISFQFGALPSSRSQSLEYKLNDEQQWQRFDWALLNFDQLLPGKYRLKVRSANPTQRYRTEALFD  
LGYRMSEPLKIAYGDSISFQFGALPSSRSQSLEYKLNDEQQWQRFDWALLNFDQLLPGKYRLKVRSANPTQRYRTEALFD  
LGYRMSEPLKIAYGDSISFQFGALPSSRSQSLEYKLNDEQQWQRFDWALLNFDQLLPGKYRLKVRSANPTQRYRTEALFD  
!!

720  
720

logo

NTDB id 1066329 ACG4I1 RS10765 WP 001911421.1  
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consensus

FEVLQPWYMTSIALVGYVLSVLGLLALALWWRTRMILAANRKLKAQVELKTSQLRHQSKIVLSNNHQLRKQLQLHHTILG  
FEVLQPWYMTSIALVGYVLSVLGLLALALWWRTRMILAANRKLKAQVELKTSQLRHQSKIVLSNNHQLRKQLQLHHTILG  
FEVLQPWYMTSIALVGYVLSVLGLLALALWWRTRMILAANRKLKAQVELKTSQLRHQSKIVLSNNHQLRKQLQLHHTILG  
!!

800  
800

logo

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consensus

NVLDNIDASLRHLSSYAKVRAWSEFEAPFNKVKQELAQLFHMRGDEDESKYHDLHLLIESALKSWQEEYSKALIKLTYS  
NVLDNIDASLRHLSSYAKVRAWSEFEAPFNKVKQELAQLFHMRGDEDESKYHDLHLLIESALKSWQEEYSKALIKLTYS  
NVLDNIDASLRHLSSYAKVRAWSEFEAPFNKVKQELAQLFHMRGDEDESKYHDLHLLIESALKSWQEEYSKALIKLTYS  
!!

880  
880

logo

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consensus

GEPRFVEVRQFNLDVLFNAVLTDIAIKRLYKHQELTIQLEVRNAQAVIVFSDFGAPIQNIQDKTMVTLGSSSYPLEELVIRS  
GEPRFVEVRQFNLDVLFNAVLTDIAIKRLYKHQELTIQLEVRNAQAVIVFSDFGAPIQNIQDKTMVTLGSSSYPLEELVIRS  
GEPRFVEVRQFNLDVLFNAVLTDIAIKRLYKHQELTIQLEVRNAQAVIVFSDFGAPIQNIQDKTMVTLGSSSYPLEELVIRS  
!!

960  
960

logo

NTDB id 1066329 ACG4I1 RS10765 WP 001911421.1  
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consensus

GGVLHVLALKERNVIELAWPLATLPELETIHKPEEGEQAQKVGIDEVEKEWLSKVEKLI ELHYSDPNFTTSTAAQALYVS  
GGVLHVLALKERNVIELAWPLATLPELETIHKPEEGEQAQKVGIDEVEKEWLSKVEKLI ELHYSDPNFTTSTAAQALYVS  
GGVLHVLALKERNVIELAWPLATLPELETIHKPEEGEQAQKVGIDEVEKEWLSKVEKLI ELHYSDPNFTTSTAAQALYVS  
!!

1040  
1040

logo

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NTDB id 1151 GTF74 RS04205 WP 001911421.1  
consensus

ERSLQRRFKAATGKTFKESLNEVRLEKACQSLLSGAKIAQVAFDCGFNDPSYFSQRFKHHFGLSPSQFI EDQEN  
ERSLQRRFKAATGKTFKESLNEVRLEKACQSLLSGAKIAQVAFDCGFNDPSYFSQRFKHHFGLSPSQFI EDQEN  
ERSLQRRFKAATGKTFKESLNEVRLEKACQSLLSGAKIAQVAFDCGFNDPSYFSQRFKHHFGLSPSQFI EDQEN  
!!

1114  
1114

 non conserved  
 similar  
  $\geq 50\%$  conserved