

logo

NTDB id 374 SMU RS06885 WP 002262930.1  
NTDB id 413 AAK55817.1 141..845( )  
NTDB id 1046 HON27 RS03130 WP 168726941.1  
NTDB id 235606 XM38 RS05420 WP 080806180.1  
NTDB id 1417 SGL RS04200 WP 014407071.1  
consensus

MKEILKTLTEAMTLPEDSYSEQDAEFLEIFIEEIEEFVDLQPLINKWQSENIATLTEIRRHFTLKGSGRMIGAKSSAELAWT  
.....  
MKEILKTLTEAMTLPEDSYSEQDAEFLEIFIEEIEEIEFVDLQPLINKWQSENIATLTEIRRHFTLKGSGRMIGAKSSAELAWT  
.....

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85  
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logo

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consensus

VEDTLNRVINQSLQLTPTIQSYVQLVFKFYFLKLVDFNKQKRAHTLDFRPLILLGQQLQQQSLEPALEELLQLSHTLMAETVTG  
.....  
VEDTLNRVINQSLQLTPTIQSYVQLVFKFYFLKLVDFNKQKRAHTLDFRPLILLGQQLQQQSLEPALEELLQLSHTLMAETVTG  
.....

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logo

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consensus

LELDYIEQDSLAEPIIQATHTEIEINLDETTLTFMEEAEEHLATIHQFLDQELHQYDSYNALIRALHTLRGSSAMAQVETIFEAS  
.....  
LELDYIEQDSLAEPIIQATHTEIEINLDETTLTFMEEAEEHLATIHQFLDQELHQYDSYNALIRALHTLRGSSAMAQVETIFEAS  
.....

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logo

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consensus

TKVEHLFKILLQEELSSHSEEILLQEYREFVRDSLELLSRYSSSEQLERALLQFNQSWDAYVEQHGDRTDPLMPHGLVSQLLQ  
.....  
TKVEHLFKILLQEELSSHSEEILLQEYREFVRDSLELLSRYSSSEQLERALLQFNQSWDAYVEQHGDRTDPLMPHGLVSQLLQ  
.....

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consensus

LDVSELLDAELDFEKGIRNEFPDYLERLSEQADLLLQHTHSQAMLGLHEYTSQLKESYEVLLDKPALLQSDYIFEIYQKAHQQLI  
.....  
LDVSELLDAELDFEKGIRNEFPDYLERLSEQADLLLQHTHSQAMLGLHEYTSQLKESYEVLLDKPALLQSDYIFEIYQKAHQQLI  
.....

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consensus

QLFDALAAGQRVGVVKQHS ILEELKLYTQYTPDISNDLPQQDSTSFEP IYNI EPEPEVWATVENFSDSADWAVLGQSVQQDRQY  
.....  
QLFDALAAGQRVGVVKQHS ILEELKLYTQYTPDISNDLPQQDSTSFEP IYNI EPEPEVWATVENFSDSADWAVLGQSVQQDRQY  
.....

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consensus

I SSTQVNRNFDADLLDIFLEEAELLEGLDITDLNIWVGEQENFAALNNLMRYLHTLKGGANMVQATYLG LIAHELES IYERLIQK  
.....  
ISSTQVNRNFDADLLDIFLEEAELLEGLDITDLNIWVGEQENFAALNNLMRYLHTLKGGANMVQATYLG LIAHELES IYERLIQK  
.....

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consensus

QLVVTSDLIDFIRLVQDDLADRLQIMREQQLDYAAPYTINALKRAGQNSNFQPLPVVEAFDAESEVFSEQKVI SEI IIDEIPVEL  
.....  
QLVVTSDLIDFIRLVQDDLADRLQIMREQQLDYAAPYTINALKRAGQNSNFQPLPVVEAFDAESEVFSEQKVI SEI IIDEIPVEL  
.....

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logo

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consensus

EPALAELETHHDQVFDTA VTELATPVEMITTVTSQENEVAANEQDIEAVVEQTFLEEATELLEMAESLLKQWFEQRTNRS ILLQL  
.....  
EPALAELETHHDQVFDTA VTELATPVEMITTVTSQENEVAANEQDIEAVVEQTFLEEATELLEMAESLLKQWFEQRTNRS ILLQL  
.....

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765  
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consensus

QRAVHSLKGGARMVGL EAVQAIAYQLENAFEQFALHNFNSNIYDHLL ESAIAWLKDAIFNHNYQHFDGLQQSLENIQFFETTIQI  
.....  
QRAVHSLKGGARMVGL EAVQAIAYQLENAFEQFALHNFNSNIYDHLL ESAIAWLKDAIFNHNYQHFDGLQQSLENIQFFETTIQI  
.....

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consensus

PTKLTRADLFSSEPVMTFIQGDGTEPPPMGAWEQTERLDQNNEMIRVSADLIEK MIDLSGENSINRSRIEMDLSQFSHTLVEME
.....
PTKLTRADLFSSEPVMTFIQGDGTEPPPMGAWEQTERLDQNNEMIRVSADLIEK MIDLSGENSINRSRIEMDLSQFSHTLVEME
.....

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935
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consensus

LAIQRLADQLRRMEGELETQIIAKHGI EHSRYTDFDPLEMDQYSSLNQLSKSLAESASDLVDFKNTLSDKIRDTESELLLQQSRIQ
.....
LAIQRLADQLRRMEGELETQIIAKHGI EHSRYTDFDPLEMDQYSSLNQLSKSLAESASDLVDFKNTLSDKIRDTESELLLQQSRIQ
.....

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1020
0
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consensus

AEIQEGLMRTRLVPPFSRLLPRLQRIVRQTSTALNRP AELFVNNT EGELDRNILERLVTPLEHMLRNAIDHGLEDRAQRQQANKPE
.....
AEIQEGLMRTRLVPPFSRLLPRLQRIVRQTSTALNRP AELFVNNT EGELDRNILERLVTPLEHMLRNAIDHGLEDRAQRQQANKPE
.....

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1105
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consensus

TGRIELNIQRQGTDVVVVFSDDGQGDVEKVRQKALLAGLIKPEQDLEQQDILQLIFHPGLSTAEQVTQISGRGVGLD VVQSDIK
.....
TGRIELNIQRQGTDVVVVFSDDGQGDVEKVRQKALLAGLIKPEQDLEQQDILQLIFHPGLSTAEQVTQISGRGVGLD VVQSDIK
.....

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1190
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SLGGHVSVESVYGGTTFTIRVPTTVAVSDALMVKVADQQFAIPLAQIDRIIRVSPASLEQYFESPQELFEYENKRYPLRYLSEF
.....
SLGGHVSVESVYGGTTFTIRVPTTVAVSDALMVKVADQQFAIPLAQIDRIIRVSPASLEQYFESPQELFEYENKRYPLRYLSEF
.....

0
0
1275
0
0



non conserved  
 similar  
  $\geq 50\%$  conserved