

logo

NTDB id 1046 HON27 RS03130 WP 168726941.1
NTDB id 374 SMU RS06885 WP 002262930.1
NTDB id 197482 AXX03 RS02120 WP 096834138.1
NTDB id 1047 HON27 RS03110 WP 000389061.1
consensus

MKEILKTLTEAMTLPEDSYSEQDAEFLEIFIEEIEEIFVDLQPLINKWMQSENIATLTEIRRHFTLKGSGRMIGAKSSA 80
MKEILKTLTEAMTLPEDSYSEQDAEFLEIFIEEIEEIFVDLQPLINKWMQSENIATLTEIRRHFTLKGSGRMIGAKSSA 0
..... 0
..... 0

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consensus

ELAWTVEDTLNRVINQSLQLTPTIQSYVQLVFKFYFLKLVDNFKQKRAHTLDFRPLILLGQQLQQQSLEPALEELLQLS 160
ELAWTVEDTLNRVINQSLQLTPTIQSYVQLVFKFYFLKLVDNFKQKRAHTLDFRPLILLGQQLQQQSLEPALEELLQLS 0
..... 0
..... 0

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consensus

HTLMAETVTGLELDYIEQDSLAEPIIQATHTEIEINLDETTLTFMEEAEEHLATIHQFLDQELHQYDSYNALIRALHTLR 240
HTLMAETVTGLELDYIEQDSLAEPIIQATHTEIEINLDETTLTFMEEAEEHLATIHQFLDQELHQYDSYNALIRALHTLR 0
..... 0
..... 0

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consensus

GSSAMAQVETIFEASTKVEHLFKILLQEELSSHSEEILLQEYREFVRDSLELLSRYSSSEQLEARLLQFNQSWDAYVEQ 320
GSSAMAQVETIFEASTKVEHLFKILLQEELSSHSEEILLQEYREFVRDSLELLSRYSSSEQLEARLLQFNQSWDAYVEQ 0
..... 0
..... 0

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consensus

HGDRTDPLMPSHGLVSQQLQLDVSELDAELDFEKGIRNEFPDYLERLSEQADLLLQHTHSQAMGLHEYTSQLKESYEV 400
HGDRTDPLMPSHGLVSQQLQLDVSELDAELDFEKGIRNEFPDYLERLSEQADLLLQHTHSQAMGLHEYTSQLKESYEV 0
..... 0
..... 0

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consensus

LLDKPALLQSDYIFEIYQKAHQQLIQLFDALAAGQRVGVVKQHQSI EELKLYTQYTPDISNDLPQQDSTSFEP IYNI EP 480
LLDKPALLQSDYIFEIYQKAHQQLIQLFDALAAGQRVGVVKQHQSI EELKLYTQYTPDISNDLPQQDSTSFEP IYNI EP 0
..... 0
..... 0

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consensus

EPEWATVENFSDSADWAVLGQSVQQDRQYISSTQVNRNFDADLLDIFLEEAEEELLEGLDIDLNIWVGEQENFAALNNLM 560
EPEVVATVENFSDSADWAVLGQSVQQDRQYISSTQVNRNFDADLLDIFLEEAEEELLEGLDIDLNIWVGEQENFAALNNLM 0
..... 0
..... 0

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consensus

RYLHTLKGGANMVQATYLGIIAHELESIIYERLIQKQLVWTSDDLIDFIRLVQDDLADRLQIMREQQLDYAAPYTINALKRA 640
RYLHTLKGGANMVQATYLGIIAHELESIIYERLIQKQLVWTSDDLIDFIRLVQDDLADRLQIMREQQLDYAAPYTINALKRA 0
..... 0
..... 0

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consensus

GQNSNFQPLPVVEAFDAESEVFSEQKVISEIIIDEIPVELEPALAELETHHDQVFDTAATELATPVEMITTVTSQENEVA 720
GQNSNFQPLPVVEAFDAESEVFSEQKVISEIIIDEIPVELEPALAELETHHDQVFDTAATELATPVEMITTVTSQENEVA 0
..... 0
..... 0

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consensus

ANEQDI EAVEQTFLEEATELLEMAESLLKQWFEQRTNRSILLQLQRAVHSLKGGARMVGLEAVQAIAYQLENAFEQFAL 800
ANEQDIEAVEQTFLEEATELLEMAESLLKQWFEQRTNRSILLQLQRAVHSLKGGARMVGLEAVQAIAYQLENAFEQFAL 0
..... 0
..... 0

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consensus

HHFNSNIYDHLLLESAIAWLKDAIFNHNYQHFDGLQQSLENIQFFETTIQIPTKLTRADLFSSEPVMFTIQGDGTEPPPM 880
HHFNSNIYDHLLLESAIAWLKDAIFNHNYQHFDGLQQSLENIQFFETTIQIPTKLTRADLFSSEPVMFTIQGDGTEPPPM 0
..... 0
..... 0

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consensus

GAWEQTERLDQNNEMIRVSADLIEKMIDLSGENSINRSRIEMDLSQFSHTLVEMELAIQRLADQLRRMEGELETQIIAKH 960
GAWEQTERLDQNNEMIRVSADLIEKMIDLSGENSINRSRIEMDLSQFSHTLVEMELAIQRLADQLRRMEGELETQIIAKH 0
..... 0
..... 0

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G I E H S R Y T D F D P L E M D Q Y S S L N Q L S K S L A E S A S D L V D F K N T L S D K I R D T E S L L L Q Q S R I Q A E I Q E G L M R T R L V P F S R L L P
G I E H S R Y T D F D P L E M D Q Y S S L N Q L S K S L A E S A S D L V D F K N T L S D K I R D T E S L L L Q Q S R I Q A E I Q E G L M R T R L V P F S R L L P 1040
. 0
. 0
. 0

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consensus
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RLQRIVRQTSTALNRP AELFVNNT EGELDRN I LERLVTPLEHMLRNAIDHGLEDR AQRQQANKPETGR I ELNIQRQGTDV 1120
 RLQRIVRQTSTALNRP AELFVNNT EGELDRN I LERLVTPLEHMLRNAIDHGLEDR AQRQQANKPETGR I ELNIQRQGTDV 0
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 0

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NTDB id 1047 HON27 RS03110 WP 000389061.1
consensus
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VVVFSDDGQGI DVEKVRQKALLAGLIKPEQDLEQQDILQLIFHPGLSTAEQVTQISGRGVGLDWQSDIKSLGGHVSVES
VVVFSDDGQGIDVEKVRQKALLAGLIKPEQDLEQQDILQLIFHPGLSTAEQVTQISGRGVGLDVVQSDIKSLGGHVSVES 1200
.....
.....
.....
.....

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consensus
```

YYGGTTFTIRVPTTVAVSDALMVKVADQQFAIPLAQIDRIIRVSPASLEQYFESPQELFEYENKRYPLRYLSEFVGNQP
 YYGGTTFTIRVPTTVAVSDALMVKVADQQFAIPLAQIDRIIRVSPASLEQYFESPQELFEYENKRYPLRYLSEFVGNQP 1280
 0
 0
 0
 0

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```

IPRLNGVMYSLPVLMIKANNGQTVALLVDQLIGSRAQIVVKPIGQQFSSIGAIAGATILG DGQVCLILDGQNIARQIQST 1360
IPRLNGVMYSLPVLMIKANNGQTVALLVDQLIGSRAQIVVKPIGQQFSSIGAIAGATILG DGQVCLILDGQNIARQIQST 0
..... 0
..... 0
..... 0

logo

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[illegible]

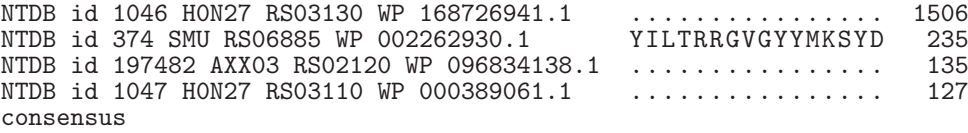
logo



logo



logo



X non conserved
X similar
X ≥ 50% conserved