```
logo

NTDB id 1144429 C7S06 RS00320 WP 126317781.1  MNKTLKRRVFRHTALYTAILMFSHTGGGGGAMAQTHQYAIIMNERKQPEVKWKDQYNQSALKDKSRERTFSHTSQKNSLG   80
NTDB id 1090 CAA90909.1 1..3114( )            MNKTLKRQVFRHTALYAAILMFSHTGG.GGAMAQTHKYAIIMNERNQLEVKGNGQYST..IKDKDRERKFIYNKDRGG..   75
consensus                                     !!!!!!! !!!!!!!! !!!!!!!!!!*!!!!!!!! !!!!!!!! !*!!!    !!  ***!!! !!! ! *   *  **

logo

NTDB id 1144429 C7S06 RS00320 WP 126317781.1  ITSNFTSFNNNDELVSQQSGTAVFGTATYLPPYGKVSGFDTAELNKRGNAVNWIHTTRPGLAGYGYTGIRCGSTKDCPKL  160
NTDB id 1090 CAA90909.1 1..3114( )            ..GGSVFFDNTDTLVSQQRGTAVFGTATYLPPYGKVSGFDADGLQKRNNAVDWIHTTQAGLAGYAYTDVICRS.NQCPQL  152
consensus                                     **   * ! ! ! !!!!! !!!!!!!!!!!!!!!!!!!!    !*!! !!! !!!!! *!!!!!*!! * ! !*   !! !

logo

NTDB id 1144429 C7S06 RS00320 WP 126317781.1  TYKTRFSFDNPDLLKTRGGLDRHTEPSRENSPIYKLKDYPWLGVSFNLGGEGTAKDGRSSSKLVSSFDENNSNSNQNLVY  240
NTDB id 1090 CAA90909.1 1..3114( )            VYETKFSFDGIGLAKNAGSLDRHPDPSRENSPIYKLKDHPWLGVSFNLGSENTVKDGKSFNKLISSFSEGN..NNQTIVS  230
consensus                                      ! !*!!!! * ! !  ! !!!!**!!!!!!!!!!!!!*!!!!!!!!!! ! ! !!!*!  !!*!!! ! !** !! *!

logo

NTDB id 1144429 C7S06 RS00320 WP 126317781.1  TTEDHRISLSNWQQETTAMAYYLNAKLHLLDKKGIKDIT.GKTVRLGVLKPSIDVKTQNTGLSGILNFWSKWDIKDNGQI  319
NTDB id 1090 CAA90909.1 1..3114( )            TTRGHSISLSDWKREHTAMAYYLNAKLHLLDKKGIEDIAQGKTVDLGTLRPRVEATVR...RGELLNFWATWKIEDKGNI  307
consensus                                     !!  ! !!!! !  !*!!!!!!!!!!!!!!!!!!! !! *!!!! !! !*! **    ***   *!!!!  ! ! ! !*!

logo

NTDB id 1144429 C7S06 RS00320 WP 126317781.1  PVKLGLPEVKAGRCINEPNPNKNTQAPSPALTAPALWFGSVQNGKVQMYSASVSTYPGSSSSRIFLQELKTRTDPARPGR  399
NTDB id 1090 CAA90909.1 1..3114( )            TVRLGLPEVKAGRCVNKANPNPNAKAPSPALTAPALWFGPVKDGKAEMYSASVSTYPDSSSSRIYLQNLKRKTDPGKPGR  387
consensus                                     *!*!!!!!!!!!!!*! *!!!*!  !!!!!!!!!!!!!!*!  !!  !!!!!!!!!! !!!!!!*!! !!  *!!!**!!!

logo

NTDB id 1144429 C7S06 RS00320 WP 126317781.1  HSLAALDTQNIKSREPNFNSRQTVIRLPGGVYRIAPTR..DRIVGLNGNDGKNDTFGIYKDRLVTPEVDEWAKVLLPWTV  477
NTDB id 1090 CAA90909.1 1..3114( )            HSLETLTENDIKSREPNFTGRQTIIRLNGGVREIKLDRNNTEVVNFNGNDGNNDTFGIVKDLGVEPDTSEWKKVLLPWTV  467
consensus                                     !!!   !  * !!!!!!!!  !!!*!!!*!!!  ! * !**  *!  !!!!! !!!!!! !!  ! !*  !! !!!!!!!!

logo

NTDB id 1144429 C7S06 RS00320 WP 126317781.1  RYYGNDDIFKTFNQPNNKKQSDKKQYSQKYRIRTKEDDNDKPRDLGDIVNSPITAVGGYLATSANDGMVHIFKKTGTDQR  557
NTDB id 1090 CAA90909.1 1..3114( )            RGFADDNKFKAFNKEENN..DNKPKYSQKYRSR...DNNKGERNLGDIVNSPIVAVGEYLATSANDGMVHIFKQSGGDKR  542
consensus                                     ! ** !  !! !! * ! **  !* !!!!!! !***! !  *! !!!!!!!!! !!! !!!!!!!!!!!!!! *! ! !
```

```
logo

NTDB id 1144429 C7S06 RS00320 WP 126317781.1  GYELKLSYIPGTMERKDIEGNDSDLAKELRAFAEQGYVGDRYGVDGGFVLRRITDDQDKQKHFFMFGAMGLGGRGAYALD   637
NTDB id 1090 CAA90909.1 1..3114( )            SYNLKLSYIPGTMPRKDIQNTESTLAKDVRTFAEKGYVGDRYGVDGGFVLRKVDN.LNGQNRVFMFGAMGFGGRGAYALD   621
consensus                                      ! !!!!!!!!!!*!!!!    *! !!!**! !!! !!!!!!!!!!!!!!!!**  *    ! * !!!!!!! !!!!!!!!!

logo

NTDB id 1144429 C7S06 RS00320 WP 126317781.1  LTKID.SNPVGVSMFDVQNDKNNNKNDSNRVKLGYTVGTPQIGKTQNGKYAAFLASGYAAKDIVS.SDNTTALYVYDLKD   715
NTDB id 1090 CAA90909.1 1..3114( )            LTKADGSDPTAVSLFDVKDNG...NNGNNRVELGYTVGTPQIGKTHDGKYAAFLASGYATKEIITSGDNKTALYVYDLEG   698
consensus                                     !!! !*! ! *!!*!!!    *** !  !!! !!!!!!!!!!!!* !!!!!!!!!!!! !*!*** !! !!!!!!!!

logo

NTDB id 1144429 C7S06 RS00320 WP 126317781.1  TL.GTPIAKIEAPGGKGGLSSPTLVDKDLDGTVDIAYAGDRGGNMYRFDLSSDKPSEWAVRTIFEGTKPITSAPAVSRLA   794
NTDB id 1090 CAA90909.1 1..3114( )            NGTNNLIKKIEVPGGKGGLSSPTLVDKDLDGTVDIAYAGDRGGNMYRFDLSSQDPQQWSVRTIFEGTKPITSAPAISQLK   778
consensus                                       *  *! !!! !!!!!!!!!!!!!!!!
```

X non conserved
X similar
X $\geq$ 50% conserved