```
logo

NTDB id 301556 DRA77 RS00280 WP 101135504.1  MNKTLKRRVFRHTALYAAILMFSHTGGGGAQAETHNYAIVMNEQNQLKVKQKDSYSTLREKDRERKFIYNKGWQGGGSVL   80
NTDB id 1090 CAA90909.1 1..3114( )           MNKTLKRQVFRHTALYAAILMFSHTGGGGAMAQTHKYAIIMNERNQLEVKGNGQYSTIKDKDRERKFIYNKDRGGGGSVF   80
consensus                                    !!!!!!! !!!!!!!!!!!!!!!!!!!!! ! !! !!!*!!! !!! !!     !!!***!!!!!!!!!!!    !!!!!

logo

NTDB id 301556 DRA77 RS00280 WP 101135504.1  FDNTDTLVSRQSGTAVFGTATYLPPYGKVSGFDANALKERNNAVDWIHTTRAGLAGYAYTNVICRSHQCPQLVYKTRFSF  160
NTDB id 1090 CAA90909.1 1..3114( )           FDNTDTLVSQQRGTAVFGTATYLPPYGKVSGFDADGLQKRNNAVDWIHTTQAGLAGYAYTDVICRSNQCPQLVYETKFSF  160
consensus                                    !!!!!!!!! ! !!!!!!!!!!!!!!!!!!!!!!! *!  !!!!!!!!!!! !!!!!!!!! !!!!!*!!!!!!! !*!!!

logo

NTDB id 301556 DRA77 RS00280 WP 101135504.1  DNPDLAKRGGGLDRHTEPSRDNSLIYKLKDHPWLGVSFNLGSENTVKNSQSSSRLISSFSEDNNNQTIVSTTENHPISLG  240
NTDB id 1090 CAA90909.1 1..3114( )           DGIGLAKNAGSLDRHPDPSRENSPIYKLKDHPWLGVSFNLGSENTVKDGKSFNKLISSFSEGNNNQTIVSTTRGHSISLS  240
consensus                                    !  * !!!  *! !!!!**!!!*!!*!!!!!!!!!!!!!!!!!!!!!!!    !  *!!!!!!! !!!!!!!!!!!   !*!!!

logo

NTDB id 301556 DRA77 RS00280 WP 101135504.1  DGQREHTAVAYYLNAKLHLLDKKGIKDIT.GKTVRLGVLKPSIDVKTQRTGLGGLLGFHAKWDIKDTGQIPVELGLPQIK  319
NTDB id 1090 CAA90909.1 1..3114( )           DWKREHTAMAYYLNAKLHLLDKKGIEDIAQGKTVDLGTLRPRVEATVR...RGELLNFWATWKIEDKGNITVRLGLPEVK  317
consensus                                    !   !!!!!*!!!!!!!!!!!!!!!!! !! *!!!! !! !*! **    *** ! !! !*! ! ! ! !*!*! !!!! *!

logo

NTDB id 301556 DRA77 RS00280 WP 101135504.1  AGRCINKPNPNPKAQALSPALTAPALWFGPVQNGKVQMYSASVSTYPDSSSSQIFLQNLSRKDDTSKPGRYSLKPLSTSE  399
NTDB id 1090 CAA90909.1 1..3114( )           AGRCVNKANPNPNAKAPSPALTAPALWFGPVKDGKAEMYSASVSTYPDSSSSRIYLQNLKRKTDPGKPGRHSLETLTEND  397
consensus                                    !!!!*!!*!!!! ! !*!!!!!!!!!!!!!!! !!  !!!!!!!!!!!!!!! !*!!!! !! !* !!!!*!! *!*   *

logo

NTDB id 301556 DRA77 RS00280 WP 101135504.1  IKSKEPTFTGRQTVIRLDGGVQQIKLQGNEVT..SFNVNN.GNNTFGIVKDLGVDPDASEWKKVLLPWTVRASNDDNQFK  476
NTDB id 1090 CAA90909.1 1..3114( )           IKSREPNFTGRQTIIRLNGGVREIKLDRNNTEVVNFNGNDGNNDTFGIVKDLGVEPDTSEWKKVLLPWTVRGFADDNKFK  477
consensus                                    !!!*!! !!!!!!*!!! !!!   !!!   !    ** !! ! * ! !!!!!!!!!!*!! !!!!!!!!!!!!!*   !!! !!

logo

NTDB id 301556 DRA77 RS00280 WP 101135504.1  TINQQLN.QQKIQYSQRYRIRDN..GNRDLGDIVNSPIVAVGEYLATSANDGMVHIFKQSGGDKRSYNLKLSYIPGTMPR  553
NTDB id 1090 CAA90909.1 1..3114( )           AFNKEENNDNKPKYSQKYRSRDNNKGERNLGDIVNSPIVAVGEYLATSANDGMVHIFKQSGGDKRSYNLKLSYIPGTMPR  557
consensus                                      !   !* *!* !!!*!! !!!**! ! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
```

```
logo
NTDB id 301556 DRA77 RS00280 WP 101135504.1  QYFDNDTSALKDSTLAKELRTFAEKGYVGDRYGVDGGFVLRKVER.NGKDHVFMFGAMGFGGRGAYALDLTKADGSDPTA   632
NTDB id 1090 CAA90909.1 1..3114( )           KDIQNT.....ESTLAKDVRTFAEKGYVGDRYGVDGGFVLRKVDNLNGQNRVFMFGAMGFGGRGAYALDLTKADGSDPTA   632
consensus                                         ! ******!!!!!**!!!!!!!!!!!!!!!!!!!!!!!!* *!!   *!!!!!!!!!!!!!!!!!!!
```

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