```
logo      MNKTLKRRVFRHTALYAAILMFSHTGGGGRRRQTITYLLSMNERNQLEVKGNGQYSTIKDKDRERKFIYNKDRGGGGSVF
                      Q                  AMAKPHKTATTM

NTDB id 231762 CCD83 RS13235 WP 307875761.1   MNKTLKRRVFRHTALYAAILMFSHTGGGGRRRKPITTLLS................................    40
NTDB id 1090 CAA90909.1 1..3114( )            MNKTLKRQVFRHTALYAAILMFSHTGGGGAMAQTHKYAIMNERNQLEVKGNGQYSTIKDKDRERKFIYNKDRGGGGSVF    80
consensus                                     !!!!!!! !!!!!!!!!!!!!!!!!!!!!    **   *  ***************************************
```

```
logo      FDNTDTLVSQQRGTAVFGTATYLPPYGKVSGFDADGLQKRNNAVDWIHTTQAGLAGYAYTDVICRSNQCPQLVYETKFSF

NTDB id 231762 CCD83 RS13235 WP 307875761.1                                                                                   40
NTDB id 1090 CAA90909.1 1..3114( )            FDNTDTLVSQQRGTAVFGTATYLPPYGKVSGFDADGLQKRNNAVDWIHTTQAGLAGYAYTDVICRSNQCPQLVYETKFSF   160
consensus                                     ********************************************************************************
```

```
logo      DGIGLAKNAGSLDRHPDPSRENSPIYKLKDHPWLGVSFNLGSENTVKDGKSFNKLISSFSEGNNNQTIVSTTRGHSISLS

NTDB id 231762 CCD83 RS13235 WP 307875761.1                                                                                   40
NTDB id 1090 CAA90909.1 1..3114( )            DGIGLAKNAGSLDRHPDPSRENSPIYKLKDHPWLGVSFNLGSENTVKDGKSFNKLISSFSEGNNNQTIVSTTRGHSISLS   240
consensus                                     ********************************************************************************
```

```
logo      DWKREHTAMAYYLNAKLHLLDKKGIEDIAQGKTVDLGTLRPRVEATVRRGELLNFWATWKIEDKGNITVRLGLPEVKAGR

NTDB id 231762 CCD83 RS13235 WP 307875761.1                                                                                   40
NTDB id 1090 CAA90909.1 1..3114( )            DWKREHTAMAYYLNAKLHLLDKKGIEDIAQGKTVDLGTLRPRVEATVRRGELLNFWATWKIEDKGNITVRLGLPEVKAGR   320
consensus                                     ********************************************************************************
```

```
logo      CVNKANPNPNAKAPSPALTAPALWFGPVKDGKAEMYSASVSTYPDSSSSRIYLQNLKRKTDPGKPGRHSLETLTENDIKS

NTDB id 231762 CCD83 RS13235 WP 307875761.1                                                                                   40
NTDB id 1090 CAA90909.1 1..3114( )            CVNKANPNPNAKAPSPALTAPALWFGPVKDGKAEMYSASVSTYPDSSSSRIYLQNLKRKTDPGKPGRHSLETLTENDIKS   400
consensus                                     ********************************************************************************
```

```
logo      REPNFTGRQTIIRLNGGVREIKLDRNNTEVVNFNGNDGNNDTFGIVKDLGVEPDTSEWKKVLLPWTVRGFADDNKFKAFN

NTDB id 231762 CCD83 RS13235 WP 307875761.1                                                                                   40
NTDB id 1090 CAA90909.1 1..3114( )            REPNFTGRQTIIRLNGGVREIKLDRNNTEVVNFNGNDGNNDTFGIVKDLGVEPDTSEWKKVLLPWTVRGFADDNKFKAFN   480
consensus                                     ********************************************************************************
```

```
logo      KEENNDNKPKYSQKYRSRDNNKGERNLGDIVNSPIVAVGEYLATSANDGMVHIFKQSGGDKRSYNLKLSYIPGTMPRKDI

NTDB id 231762 CCD83 RS13235 WP 307875761.1                                                                                   40
NTDB id 1090 CAA90909.1 1..3114( )            KEENNDNKPKYSQKYRSRDNNKGERNLGDIVNSPIVAVGEYLATSANDGMVHIFKQSGGDKRSYNLKLSYIPGTMPRKDI   560
consensus                                     ********************************************************************************
```

```
logo            QNTESTLAKDVRTFAEKGYVGDRYGVDGGFVLRKVDNLNGQNRVFMFGAMGFGGRGAYALDLTKADGSDPTAVSLFDVKD
NTDB id 231762 CCD83 RS13235 WP 307875761.1   ..........................................................................   40
NTDB id 1090 CAA90909.1 1..3114( )            QNTESTLAKDVRTFAEKGYVGDRYGVDGGFVLRKVDNLNGQNRVFMFGAMGFGGRGAYALDLTKADGSDPTAVSLFDVKD   640
consensus       ********************************************************************************

logo            NGNNGNNRVELGYTVGTPQIGKTHDGKYAAFLASGYATKEIITSGDNKTALYVYDLEGNGTNNLIKKIEVPGGKGGLSSP
NTDB id 231762 CCD83 RS13235 WP 307875761.1   ..........................................................................   40
NTDB id 1090 CAA90909.1 1..3114( )            NGNNGNNRVELGYTVGTPQIGKTHDGKYAAFLASGYATKEIITSGDNKTALYVYDLEGNGTNNLIKKIEVPGGKGGLSSP   720
consensus       ********************************************************************************

logo            TLVDKDLDGTVDIAYAGDRGGNMYRFDLSSQDPQQWSVRTIFEGTKPITSAPAISQLKDKRVVIFGTGSDLSEEDVDNME
NTDB id 231762 CCD83 RS13235 WP 307875761.1   ..........................................................................   40
NTDB id 1090 CAA90909.1 1..3114( )            TLVDKDLDGTVDIAYAGDRGGNMYRFDLSSQDPQQWSVRTIFEGTKPITSAPAISQLKDKRVVIFGTGSDLSEEDVDNME   800
consensus       ********************************************************************************

logo            EQYIYGIFDDDTATTGTVNFSDSGGGLLEQVLRRDNDNKTLFLTDYKRSDGSGNKGWWKLKDGQRVTVKPTWLRTAFV
NTDB id 231762 CCD83 RS13235 WP 307875761.1   ..........................................................................   40
NTDB id 1090 CAA90909.1 1..3114( )            EQYIYGIFDDDTATTGTVNFSDSGGGLLEQVLRRDNDNKTLFLTDYKRSDGSGNKGWVVKLKDGQRVTVKPTVVLRTAFV   880
consensus       ********************************************************************************

logo            TIHKYTGTDKCGAETAILGINTADGGKLTKKSARPIVPEANTAVAQYSGHKKGTNGKSIPIGCMQKSNEIVCPNGYVYDK
NTDB id 231762 CCD83 RS13235 WP 307875761.1   ..........................................................................   40
NTDB id 1090 CAA90909.1 1..3114( )            TIHKYTGTDKCGAETAILGINTADGGKLTKKSARPIVPEANTAVAQYSGHKKGTNGKSIPIGCMQKSNEIVCPNGYVYDK   960
consensus       ********************************************************************************

   <0

logo            PVNVRYLDEKKTDGFSTTADGDAGGSGIDPAGKRSGKNNRCFSQKGVRTLLMNDLDSLDITGPTCGMKRISWREVFY
NTDB id 231762 CCD83 RS13235 WP 307875761.1   ..........................................................................   40
NTDB id 1090 CAA90909.1 1..3114( )            PVNVRYLDEKKTDGFSTTADGDAGGSGIDPAGKRSGKNNRCFSQKGVRTLLMNDLDSLDITGPTCGMKRISWREVFY*   1037
consensus       ********************************************************************************
```

X non conserved
X similar
X ≥ 50% conserved