```
logo
NTDB id 1103 NMB RS07590 WP 002212976.1      ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1131 NGFG RS05740 WP 003695064.1     ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1390 A4U84 RS00055 WP 021115958.1    ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
NTDB id 230255 CBP31 RS09540 WP 087036725.1 MANRGINKVILIGHLGQDPEIRYMPNGNAVANITLATSETWRDKQSGEQKERTEWHRVVFFGKLAEIVGEYLRKGSQVYV   80
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                     **!!!!**! !!*!!**!*!!*!*!!*****!!!!*!*!* *!***!*!!!!********!!**!*!!*!!* !!*

logo
NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAP...YEEGYGQSQEA.....................   128
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAP...YDEGYGQSQEA.....................   128
NTDB id 1390 A4U84 RS00055 WP 021115958.1    EGKLKTRKWQDQNGQDRYTTEIQ....GDVLQMLDSRSSGGDF..GGNQGSGWNQAPAQTNYNQGGYSDNYA........   144
NTDB id 230255 CBP31 RS09540 WP 087036725.1 EGRLQTRKWQGQDGQDKYTTEIVV.DIGGTMQMLGGRPQGGGGQGGGGQGGGWGGQGGQGQQQQQGGGQSYGGQGGSPQQ   159
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQGGM...........................NVP   132
consensus                                   !!****!!*!***!*********    *  **!!**!  ****   *    **** * *

logo
NTDB id 1103 NMB RS07590 WP 002212976.1      .....YQ...RPAQQSRQPASDAPSHPQEAPAAPRRQPVP...AAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1     .....YQ...RPAQQSRQPAPDAPSHPQEAPAAPRRQPVP...AAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1    .QNNNFNG....................GNATRPQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 230255 CBP31 RS09540 WP 087036725.1  GGQGNWGGQQGSPQQSAPQGQPAYGQQQNKPAAPQSQPAPAPTYNEPPMDFDDDIPF   216
NTDB id 1166 A1552VC RS00795 WP 000168289.1  AQQGSWGQPQQPAKQHQPMQ...........QSAPQQYSQPQYNEPPMDFDDDIPF   177
consensus                                      *  **    *****   *  *    *  ****  ** *   *  !****!!!!!!
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X non conserved

X similar

X ≥ 50% conserved