```
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 140579 vpachn25 RS13830 WP 005466625.1  MASRGINKVILVGNLGNDPEIRYMPNGGAVANITIATSESWRDKATGEQREKTEWHRVVLFGKLAEVAGEYLRKGSQVYV   80
NTDB id 1166 A1552VC RS00795 WP 000168289.1     MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                           **!!!!**!*!!*!!**!*!!*!*!!*****!!!!*!*!* *!***!*!!!!********!!*!!*!!*!!* !!*

logo
NTDB id 1103 NMB RS07590 WP 002212976.1          EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYE........EGYGQSQEAYQRPAQQSRQPA...   140
NTDB id 1131 NGFG RS05740 WP 003695064.1         EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPYD........EGYGQSQEAYQRPAQQSRQPA...   140
NTDB id 1390 A4U84 RS00055 WP 021115958.1        EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGD.FGGN.......QGSGWNQA......PAQTNYNQGGYS   140
NTDB id 140579 vpachn25 RS13830 WP 005466625.1  EGQLQTRKWQDQSGQDRYSTEVVVQGFNGVMQMLGGRAQG.G.APAMGGQ..QQQQGGWGQPQQ....PAQQQYN.....   147
NTDB id 1166 A1552VC RS00795 WP 000168289.1     EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGG.MPAQGGMNVPAQQGSWGQPQQ....PAKQHQ......   149
consensus                                       !!****!!*!** !**!*******      ***!!**!  * * ***         *  ***! *     !!**  * *

logo
NTDB id 1103 NMB RS07590 WP 002212976.1          ......SDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1         ......PDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1        DNYAQNNNFNGGNATRPQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 140579 vpachn25 RS13830 WP 005466625.1  ...........APQQQQQAPQQPQQQYNEPPMDFDDDIPF   176
NTDB id 1166 A1552VC RS00795 WP 000168289.1     ............PMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
consensus                                                **  *******   **  !****!!!!!!
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X non conserved

X similar

X ≥ 50% conserved