```
logo
NTDB id 1131 NGFG RS05740 WP 003695064.1        ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1103 NMB RS07590 WP 002212976.1         ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL   76
NTDB id 1390 A4U84 RS00055 WP 021115958.1       ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV   78
NTDB id 1074833 ACI65L RS21470 WP 010295128.1  MASRGVNKVILVGNLGQDPEVRYMPNGGAVANITLATSESWRDKQTGEQKEKTEWHRVVLFGKLAEVAGEYLRKGSQVYI   80
NTDB id 1166 A1552VC RS00795 WP 000168289.1    MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                          **!!!!**!*!!*!!**!*!!*!*!!*****!!!!*!*!* *!***!*!!!!********!!*!!*!!*!!* !!*

logo
NTDB id 1131 NGFG RS05740 WP 003695064.1        EGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGA........PYDEGYGQSQEA.......YQRPAQQSR  137
NTDB id 1103 NMB RS07590 WP 002212976.1         EGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGA........PYEEGYGQSQEA.......YQRPAQQSR  137
NTDB id 1390 A4U84 RS00055 WP 021115958.1       EGKLKTRKWQDQNGQDRYTTEIQ....GDVLQMLDSRSSGGDFGG.......NQGSGWNQAPAQTNYNQGGYSDNYAQNN  147
NTDB id 1074833 ACI65L RS21470 WP 010295128.1  EGALQTRKWADQAGVERYTTEVVV.NVGGTMQMLGGRQGGGAPAGGGNAGGGQQQGGWGQPQQP............QGGN  147
NTDB id 1166 A1552VC RS00795 WP 000168289.1    EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQGGMNVPAQQGSWGQPQQP............AKQH  148
consensus                                      !!*****!!**** !**!******    *  **!!**!* *** **        *  ***! *          *    **

logo
NTDB id 1131 NGFG RS05740 WP 003695064.1        QPAPDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1         QPASDAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1       NF..NGGNATRPQPA..QKPAAQAEPPMDNFDDDIPF   180
NTDB id 1074833 ACI65L RS21470 WP 010295128.1  QF..SGGAQSQQRPAQNSAPAQSNEPP.MDFDDDIPF   181
NTDB id 1166 A1552VC RS00795 WP 000168289.1    QP..M.....QQSAPQQYSQPQYNEPP.MDFDDDIPF   177
consensus                                      **   *    *  **   ***  ***!****!!!!!!
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X non conserved

X similar

X ≥ 50% conserved