```
logo
                                                  ...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 297326 SM232103 RS21795 WP 000168322.1   MASRGVNKVILVGNLGQDPEVRYMPSGGAVANLTLATSESWRDKQTGEMKEQTEWHRVVMFGKLAEVAGEYLRKGSQVYI   80
NTDB id 1166 A1552VC RS00795 WP 000168289.1      MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                            **!!!!**!*!!*!!**!*!!*!*!!*****!!!!*!*!* *!***!*!!!!********!!*!!*!!*!!* !!*

logo

NTDB id 1103 NMB RS07590 WP 002212976.1          EGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAPYEEGY..GQSQEAYQRPAQQSR.....QPASDA..   143
NTDB id 1131 NGFG RS05740 WP 003695064.1          EGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAPYDEGY..GQSQEAYQRPAQQSR.....QPAPDA..   143
NTDB id 1390 A4U84 RS00055 WP 021115958.1         EGKLKTRKWQDQNGQDRYTTEIQ....GDVLQMLDSRSSGGD.FG.......GNQGSGWNQAPAQTNYNQGGYSDNYAQN   146
NTDB id 297326 SM232103 RS21795 WP 000168322.1   EGQLRTRKWTDQSGQERYTTEINVPQIGGVMQMLGGRQGG.G.APAG.....GQQQGGWGQPQ.........QPQQPQGG   144
NTDB id 1166 A1552VC RS00795 WP 000168289.1      EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGG.MPAQGGMNVPAQQGSWGQPQ.........QPAKQHQP   150
consensus                                        !!****!!**** !**!*****     * ***!!**!* * * **    *   **** *****  **       ***  *

logo

NTDB id 1103 NMB RS07590 WP 002212976.1          ...PSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1          ...PSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1         NNFNGGNATRPQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 297326 SM232103 RS21795 WP 000168322.1   NQFSGGAQSRPQQSAP.APSNEPP.MDFDDDIPF   176
NTDB id 1166 A1552VC RS00795 WP 000168289.1      .....MQQSAPQQYSQ.PQYNEPP.MDFDDDIPF   177
consensus                                              ***!*    * *  ***!****!!!!!!
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X non conserved

X similar

X ≥ 50% conserved