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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 334054 EPK90 RS04445 WP 128391813.1 MSARGVNKVILVGNLGQDPEVRYMPNGTAVTSLSLATSETWRDKQTGENREKTEWHRVVLFGKLAEIAGEYLRKGSQVYI   80
NTDB id 1166 A1552VC RS00795 WP 000168289.1 MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                     **!!!!**!*!!*!!**!*!!*!*!! ****!!!!*!*!* *!***!*!!!!********!!*!!*!!*!!* !!*

logo

NTDB id 1103 NMB RS07590 WP 002212976.1      EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGG........APYEEGYGQSQEAYQRPAQQSRQPASDA.   143
NTDB id 1131 NGFG RS05740 WP 003695064.1     EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGG........APYDEGYGQSQEAYQRPAQQSRQPAPDA.   143
NTDB id 1390 A4U84 RS00055 WP 021115958.1    EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGDF.......GGNQGSGWNQAPAQTN....YNQGGYSDNY   143
NTDB id 334054 EPK90 RS04445 WP 128391813.1 EGKLRTREWQDSEGTKRYTTEIVV.DVNGTMQMLGGAKNSTN..TSGNNKPSSQQDGWGKPQQPQP....S.........   144
NTDB id 1166 A1552VC RS00795 WP 000168289.1 EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQGGMNVPAQQGSWGQPQQPAK....Q.........   147
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    AQNNNFNGGNATRPQPAQKPAAQAEPPMDNFDDDIPF................   180
NTDB id 334054 EPK90 RS04445 WP 128391813.1  .......QA..Q....QSAPSNPANEPPMDFDDDIPFLGHGYGVCRKAIYAIS   184
NTDB id 1166 A1552VC RS00795 WP 000168289.1  .......HQPMQQSAPQQYSQPQYNEPPMDFDDDIPF................   177
consensus                                          *   **    *   **  !****!!!!!!
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X non conserved

X similar

X $\geq$ 50% conserved