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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 1114537 CCOS191 RS24370 WP 023629920.1 .MARGVNKVILVGTCGQDPEVRYLPNGNAVTNLSLATSEQWTDKQSGQKVERTEWHRVSLFGKVAEIAGEYLRKGSQCYI   79
NTDB id 1166 A1552VC RS00795 WP 000168289.1    MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI   80
consensus                                          **!!!!**! *!*!!**!**!*!*!! ****!!!!*!*!* *!***!*!!!!********!!*!!*!!*!!* *!*

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1        EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPY.DEGYG...........QSQEAY.QRPAQQSRQP   139
NTDB id 1103 NMB RS07590 WP 002212976.1         EGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENSGGAPY.EEGYG...........QSQEAY.QRPAQQSRQP   139
NTDB id 1390 A4U84 RS00055 WP 021115958.1       EGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGDFGGNQGSGWNQAPAQTNYNQGGYSDNYAQNNN....FN   150
NTDB id 1114537 CCOS191 RS24370 WP 023629920.1 EGKLQTREWEKD.GIKRYTTEIIV.DINGTMQLLGGRPQGQQGGGDQY....NQGGGNNYNQGGQQQQYNQAPRQQAQRP   153
NTDB id 1166 A1552VC RS00795 WP 000168289.1    EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGG....MP....AQGGMNVPAQQGS...WGQ.PQQPAKQH   148
consensus                                      !!****!***   !**!******      ***!**!  * ***     **    *     * ****  * ! * ** ***

logo

NTDB id 1131 NGFG RS05740 WP 003695064.1        APDAPSHPQEAPAAPRRQP.VPAAAPVEDIDDDIPF   174
NTDB id 1103 NMB RS07590 WP 002212976.1         ASDAPSHPQEAPAAPRRQP.VPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1       .....GGNATRP.QPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 1114537 CCOS191 RS24370 WP 023629920.1 .....QQAPQRP.AP.QQPAPQPAADFDSFDDDIPF   182
NTDB id 1166 A1552VC RS00795 WP 000168289.1    ......QPMQQS.APQQYSQPQYNEPPMDFDDDIPF   177
consensus                                            *    * *! ***  *************!!!!!!
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X non conserved

X similar

X ≥ 50% conserved