```
logo
NTDB id 1103 NMB RS07590 WP 002212976.1          ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDRN.GQRVERTEWHNITMYR.KLAEIAGQYLKKGGLVY   75
NTDB id 1131 NGFG RS05740 WP 003695064.1         ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDRN.GQRVERTEWHNITMYR.KLAEIAGQYLKKGGLVY   75
NTDB id 1390 A4U84 RS00055 WP 021115958.1        ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFR.RQAEVAGQYLRKGSKVY   77
NTDB id 139470 PhaeoP11 RS09755 WP 024097409.1  .MAGSVNKVILIGNLGRDPEVRSFQNGGKVCNLRIATSETWKDRNTGERREKTEWHSVAIFSEGLVRVAEQYLRKGSKVY   79
NTDB id 1166 A1552VC RS00795 WP 000168289.1     MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYG.KLAEVAGEYLRKGSQVY   79
consensus                                           **!!!!**!*!!*!!**!****!**!*****!!!!*!*!***!***!*!!!! ***** *****!**!!*!!* !!

logo
NTDB id 1103 NMB RS07590 WP 002212976.1          LEGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAP...YE....EGYGQSQE.......AYQR.PAQQS  136
NTDB id 1131 NGFG RS05740 WP 003695064.1         LEGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAP...YD....EGYGQSQE.......AYQR.PAQQS  136
NTDB id 1390 A4U84 RS00055 WP 021115958.1        VEGKLKTRKWQDQNGQDRYTTEIQ....GDVLQMLDSRSSGGDFGGN......QGSGWNQAPAQTNYNQGGYSDNYAQNN  147
NTDB id 139470 PhaeoP11 RS09755 WP 024097409.1  IEGQLQTRKWQDQSGQDRYSTEVVLQGIGGTLTMLDGRNDGGQGGGGGSYGGGSGGGYGGGGGGYDSGQGG....GNQGG  155
NTDB id 1166 A1552VC RS00795 WP 000168289.1     IEGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQGGMPAQGGMN...................V....PAQQG  136
consensus                                       *!!****!!*!** !**!******    *  * !!**!*******   *       ****          **   **!*

logo
NTDB id 1103 NMB RS07590 WP 002212976.1          R..QPASDAP.SHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1         R..QPAPDAP.SHPQEAPAAPRRQPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1        NFNGG....NATR....PQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 139470 PhaeoP11 RS09755 WP 024097409.1  GFGGGSQGGASH.....................NIDDDEIPF   176
NTDB id 1166 A1552VC RS00795 WP 000168289.1     SWGQPQQPAKQHQPMQQSAPQQYSQPQYNEPPMDFDDDIPF   177
consensus                                        * **    *  * *    **    *     *  **** !!*!!!
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X non conserved

X similar

X ≥ 50% conserved