```
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 1170921 ACOMDH RS16300 WP 420332300.1 .MAGSVNKVILVGNLGADPEIRRTQDGRPIANLRIATSESWRDRNSGERREKTEWHRVVIFNEGLCKVAEQYLRKGSKVY   79
NTDB id 1166 A1552VC RS00795 WP 000168289.1   MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYG.KLAEVAGEYLRKGSQVY   79
consensus                                         **!!!!**!*!! !!**!****!*******!!!!*!*!***!***!*!!!!******* *****!**!!*!!* !!

logo
NTDB id 1103 NMB RS07590 WP 002212976.1        LEGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENS..GGAPYEEGYGQS........QEAYQRPAQQSRQPA.   140
NTDB id 1131 NGFG RS05740 WP 003695064.1       LEGRIQSRKYQGKDGIERTAYDIVA....NEMKMLGGRNENS..GGAPYDEGYGQS........QEAYQRPAQQSRQPA.   140
NTDB id 1390 A4U84 RS00055 WP 021115958.1      VEGKLKTRKWQDQNGQDRYTTEIQG....DVLQMLDSRSSGGDFGGN................QGSGWNQAPAQTNYNQG   137
NTDB id 1170921 ACOMDH RS16300 WP 420332300.1 LEGQLQTRKWQDQSGQDRYSTEVVLQGFNSNLTMLDGRGEGGQTGGLPDYGNDSQGGGGFGGGGGGGYGGGSGGG.....   154
NTDB id 1166 A1552VC RS00795 WP 000168289.1   IEGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQG...GMPAQGGMNVP......AQQGSWGQPQQPAKQHQ.   149
consensus                                     *!!****!!*!** !**!*******       * !!**! ***  *! *   *  *         * *** * *****

logo
NTDB id 1103 NMB RS07590 WP 002212976.1        ..SD..APSHPQEA....PAAPRR.QPVPAAAPVEDIDDDIPF   174
NTDB id 1131 NGFG RS05740 WP 003695064.1       ..PD..APSHPQEA....PAAPRR.QPVPAAAPVEDIDDDIPF   174
NTDB id 1390 A4U84 RS00055 WP 021115958.1      GYSDNYAQNNNFNGGNATRPQPAQKPAAQAEPPMDNFDDDIPF   180
NTDB id 1170921 ACOMDH RS16300 WP 420332300.1 ...................GSQGGGFGGPSGGGG..PMDDEIPF   177
NTDB id 1166 A1552VC RS00795 WP 000168289.1   ..........P.....MQQSAPQQYSQPQYNEPPMDFDDDIPF   177
consensus                                        *  *   *  *       **        ********!!*!!!
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X non conserved

X similar

X ≥ 50% conserved