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logo
NTDB id 1111 NGFG RS09220 WP 003689814.1          ...MSDLSVLSPFA.VPLAAVLGLLVGSFLNVVIYRVPVMMERGWTVFAKEHLNLPLTDDESRTFNLMKPDSCCP   71
NTDB id 1080 FDQ49 RS18305 WP 022575844.1         MQDIIAYFIQNLTALYIAVALVSLCIGSFLNVVIYRTPRMMEQDWQQECQMLLNPEQPIIDHEKLTLSKPASSCP   75
NTDB id 1061 ABD1 RS18470 WP 001152280.1          MQDIIAYFIQNLTALYIAVALVSLCIGSFLNVVIYRTPKMMEQDWQQECQMLLNPEQPIIDHERLTLNKPASSCP   75
NTDB id 1145263 PHAGEPCYII10 RS23995 WP 003141356.1 .MELLDYLASHPLAFVLCAILLGLLVGSFLNVVVHRLPKMMERNWKAEAREALG.LEPEPKQATYNLVLPNSACP   73
NTDB id 1403 DSB67 RS12675 WP 010643256.1         ....MEVFQYYPWLFVVFATIFGLIVGSFLNVVIYRLPKIMELEWRRECAESFPEYKIEPPKETLTLSVPRSSCQ   71
NTDB id 1170 A1552VC RS11080 WP 000418747.1       ....MELFYFYPWLFPVLATLFGLIVGSFLNVVIYRLPKIMEREWRAECAASFPEYGITPPEGKLTLSLPRSTCP   71
consensus                                            *** *   * *  * * ***!**!!!!!!!**!*!**!! *!  **   *            **!  ! !*!*

logo
NTDB id 1111 NGFG RS09220 WP 003689814.1          KCRVPIRAWQNIPIVSYLLLRGKCASCQTKISIRYPLIELLTGVLFGLVAWQYGWSWITLGGLILTAFLISLTFI   146
NTDB id 1080 FDQ49 RS18305 WP 022575844.1         ACHQPIRWYQNIPLISWLVLRGKCGHCQHPISIRYPAIELLTMLCSLVVVMVFGPTIQMLFGLVLTWVLIALTFI   150
NTDB id 1061 ABD1 RS18470 WP 001152280.1          ACQQPIRWYQNIPVISWLVLRGKCGHCQHPISIRYPAIELLTMLCSLVVVMVFGPTIQMLFGLVLTWVLIALTFI   150
NTDB id 1145263 PHAGEPCYII10 RS23995 WP 003141356.1 RCGHEIRPWENIPLVSYLALGGKCSSCKAAIGKRYPLVELATALLSGYVAWHFGFTWQAGAMLLLTWGLLAMSLI   148
NTDB id 1403 DSB67 RS12675 WP 010643256.1         QCGTQIRIRDNIPVISWLLLRGKCHNCQAPINARYPLIELLTAFCSGFIAFHFGFSYFTVALVFFTFVLIAATFI   146
NTDB id 1170 A1552VC RS11080 WP 000418747.1       HCQTPIRVIDNIPLLSWLALRGQCSHCKAPISARYPLIELLTALMSLVIATHFPFGVFAVALLFFSYVLIAATFI   146
consensus                                          !  *!! * !!!**!*!*!*!*!  !* *!* !!!**!!*!** * ***  ****   ** ******!*****!

logo
NTDB id 1111 NGFG RS09220 WP 003689814.1          DADTQYLPDSMTLPLIWLGLIFNLDGGF.VPLQSAVLGAVAGYSSLWLLCAVYKLLTGKTGMGNGDFKLIAALGA   220
NTDB id 1080 FDQ49 RS18305 WP 022575844.1         DFDTQLLPDRFTLPLAALGLGINTFNIY.TSPNSAIWGYLIGFLCLWIVYYLFKVITGKEGMGYGDFKLLAALGA   224
NTDB id 1061 ABD1 RS18470 WP 001152280.1          DFDTQLLPDRFTLPLAALGLGINTFNIY.TSPNSAIWGYLIGFLCLWIVYYLFKVITGKEGMGYGDFKLLAALGA   224
NTDB id 1145263 PHAGEPCYII10 RS23995 WP 003141356.1 DADHQLLPDVLVLPLLWLGLIANHFGLF.ASLGDALFGAVFGYLSLWSVFWLFKLVTGKEGMGYGDFKLLAMLGA   222
NTDB id 1403 DSB67 RS12675 WP 010643256.1         DLDTMLLPDQLTLPLMWTGIALALAGISPVSLQDSIIGAMAGYLCLWSVYWLFKLLTGKEGMGYGDFKLLAALGA   221
NTDB id 1170 A1552VC RS11080 WP 000418747.1       DFDTLLLPDQLTLPLLWGGIALALLGFSPVSLSDAVIGAMAGYLSLWSIYWLFKLLTGKEGMGYGDFKLLAALGA   221
consensus                                         ! !*****!!! **!!!****!****  ***  *** ** !** !** !! *****!**!!!*!!!*!!!!!*!*!!!

logo
NTDB id 1111 NGFG RS09220 WP 003689814.1          WLGISALPVLIFVSSLIGLVAAIVMR....VAKGRHFAFGPALTVSGWIIFTANDSVWRAVNWWLTHPVR...   286
NTDB id 1080 FDQ49 RS18305 WP 022575844.1         WMGPLMLPLIVLLSSLLGAIIGIILLKLRND..NQPFAFGPYIAIAGWVAFLWGDQIM...KIYLGG......   286
NTDB id 1061 ABD1 RS18470 WP 001152280.1          WMGPLMLPLIVLLSSLLGAIIGIILLKLRND..NQPFAFGPYIAIAGWVAFLWGDQIM...KIYLGG......   286
NTDB id 1145263 PHAGEPCYII10 RS23995 WP 003141356.1 WGGWQILPLTILLSSLVGAILGVIMLRLRNAESGTPIPFGPYLAIAGWIALLWGDQIT...RTYLQF.AGFK.   290
NTDB id 1403 DSB67 RS12675 WP 010643256.1         WLGWQSLPMIILLSSVVGVIFGLIQLRLQKQGIEKAFPFGPYLAIAGWVSLIWGHQIL...NWYFTSILGV..   289
NTDB id 1170 A1552VC RS11080 WP 000418747.1       WLGWQQLPVIVLLSSVVGVIFGLIQLRQQKKGIDMAFPFGPYLAIAGWFALLWGDKVI...DWYFTTWVGQPL   291
consensus                                         !*!   !!*****!!**! * *******        * !!!*****!!** *******     **
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X non conserved

X similar

X ≥ 50% conserved