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NTDB id 1323 RAOC RS07335 WP 004916218.1	MSLAIVYSRASIGVAPPVTVVHISNGPGETLVGLPETTVKESDRVRSALINSSEFPAPKRITYNLAPADLP	73
NTDB id 1271 LPP RS03220 WP 011213198.1	.MLVKKVYGSIAIHGVSAQTTITIEVNVDQGV.GYHLVGLPDNAIKESSHRTISAALKNVGVKLPKKITINMAPADLR	75
NTDB id 1248 GC085 RS03150 WP 011213198.1	MSLAFTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETAVKESKDRVRSAINSQFEFPCRKITVNLGPANLP	75
NTDB id 158956 SEETMRM9437 RS20590 WP 000050215.1	MSLAFTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETAVKESKDRVRSAINSQFEFPCRKITVNLGPANLP	75
NTDB id 1153 A1552VC RS00115 WP 000521788.1	MSLAIVHTRAALGVNAPPITIEVHISNGLPGLTMVGLPETTVKEARDRVRSAINSGYEFPAKKITINLAPADLP	75
NTDB id 1397 DSB67 RS15690 WP 005535577.1	MGLAIHHSRASIGVQAPPVTVEVHISNGMPGFTLVGLPETTVKESRDRVRSAINSRFEFPAKRITVNLAPADLP	75
NTDB id 1349 HI 1117 AAC22771.1	MGLAIHHSRASVGVQAPSVSVEVHISNGMPGFTLVGLPETTVKESKDRVRSAINSNFQFPAPKRITVNLAPADLP	75
NTDB id 1387 A4U84 RS06900 WP 020457569.1	MSLAIVYSRASMGVQAPLVTIEVHLSNGKPGFTLVGLPEKTVKEAQDRVRSALMNAQFKYPAKRITVNLAPADLP	75
consensus	MSLAIIYSRASIGVEAPLVTIEVHISGGSPGLTLVGLPEKSVKEAQDRVRSALMNAFDPARRITINLAPADLP	75

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NTDB id 1323 RAOC RS07335 WP 004916218.1	KEGGREDLPIALGILAASQIEKRNKNYEYELALSGLRGVGYIPAAALAAKRLIYPNAEASLV	148
NTDB id 1271 LPP RS03220 WP 011213198.1	KEGSAYDLSTIALGILAASQIIAPETIERYLIMGELSLDGGQLPIKGVLPPIAIRAREEGFKGITLPKQNTREAAITV	149
NTDB id 1248 GC085 RS03150 WP 011213198.1	KTGSGFDLPIALGILAASEQIPLTNLANHEFIFIGELALSSELGRVSAIIPAVLAAHKD.NQHLLIANANAAEASLT	149
NTDB id 158956 SEETMRM9437 RS20590 WP 000050215.1	KTGSGFDLPIALGILAASEQIPLTNLANHEFIFIGELALSSELGRVSAIIPAVLAAHKD.NQHLLIANANAAEASLT	149
NTDB id 1153 A1552VC RS00115 WP 000521788.1	KEGGRYDLPIAVALLAASEQLTASNLEAYELVGEALALTGALRGVPGAIISSATEAIRA.GRNTIIVATENAAEVGLT	149
NTDB id 1397 DSB67 RS15690 WP 005535577.1	KEGGRFDLPIALGILAASDQIARNKLESYEFIFIGELALSSEIRGVKGVLPAAALAAQV.ERCLVVPHSNGDQAALV	149
NTDB id 1349 HI 1117 AAC22771.1	KEGGRFDLPIALGILAASEQIATDKLKKNYEFVGEALALSGGLRITVKGVLPAALAAANKK.QRHLVVPHANGDQAALV	149
NTDB id 1387 A4U84 RS06900 WP 020457569.1	KEGGRFDLPIALGILAASDQLDASHLKQFEFVAELALTGQLRGVHGVIPAILAAQKS.KRELIIAKQNAMEASLV	149
consensus	KEGGRFDLPIALGILAASQIDSDKLEKRIELLGELSLTGHLRGVHGAIPAVLAASKA.KRETIIVPQQNAMEVSLV	149

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NTDB id 1323 RAOC RS07335 WP 004916218.1	NDLEVYGVENIKEVIDFFENENCPLEPTKVNTREEFHKRVNLPFPDFSEVKGQETAKRAMEVAAAGGHNIIILIGPP	223
NTDB id 1271 LPP RS03220 WP 011213198.1	GHQKVFTANNLREVCDYLCQGTSLQSLPPKPDLLNNYELDWSDIKQQQHAKNAMVIAACGGHSILLSGAP	220
NTDB id 1248 GC085 RS03150 WP 011213198.1	GHQKVFTANNLREVCDYLCQGTSLQSLPPKPDLLNNYELDWSDIKQQQHAKNAMVIAACGGHSILLSGAP	220
NTDB id 158956 SEETMRM9437 RS20590 WP 000050215.1	SKEGCFIADHLQTVCAFLEGKHALERPLAQD.MASPTATADLRDVIGQEQCKRGLEITAAAGGHNLLLTIGPP	219
NTDB id 1153 A1552VC RS00115 WP 000521788.1	GVERHKSAQSLLEVCAIDLGGQTLTLFQSSPSV.QQVSQTRDLQDIIGQQQCKRALEIAAAGNHNLLFLGPP	220
NTDB id 1397 DSB67 RS15690 WP 005535577.1	GKEQHKSAAQSLLEVCAELCGQHQLNLQYTPKKK.ELKAHGRDLQDIIGQQQCKRALEIAAAGNHNLLFLGPP	220
NTDB id 1349 HI 1117 AAC22771.1	SDQNTYFAQTLLDVVQFLNGQEKPLATEIVKESAVNFGSKNTLDLTDIIGQQHAKRALTIAAAGQHNLLFLGPP	224
NTDB id 1387 A4U84 RS06900 WP 020457569.1	SNTQTYCASTLLQVVNFLNNRDQLPIAQQLSQNIAEN.RPLVSRDLTDIIGQQHAKRALIAAAGQHNLLFLGPP	223
consensus	NDLEVYGVENIKEVIDFFENENCPLEPTKVNTREEFHKRVNLPFPDFSEVKGQETAKRAMEVAAAGGHNIIILIGPP	223

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NTDB id 1323 RAOC RS07335 WP 004916218.1	GSGKTMLAKRIPSTILPPLTLKEALETTHSVAGKMGAEATSLMTIRPFRSPHHTISDVALVGGGSYPQPGEISLA	298
NTDB id 1271 LPP RS03220 WP 011213198.1	GSGKTMMAKRFSTLLPELSETQALECAAINSIRGKLPDF.REWRLPPFRAPHHTASPVALVGGGNPPKPGEISLA	294
NTDB id 1248 GC085 RS03150 WP 011213198.1	GSGKTMMAKRFSTLLPELSETQALECAAINSIRGKLPDF.REWRLPPFRAPHHTASPVALVGGGNPPKPGEISLA	294
NTDB id 158956 SEETMRM9437 RS20590 WP 000050215.1	GTGKTMLASRLSGTILPPLSNEEALESAAILSLVNADTVQ.KRWQQRPFSPHHSASLTAMVGGGATPAPGEISLA	293
NTDB id 1153 A1552VC RS00115 WP 000521788.1	GTGKTMLASRLCDLLPEMSDEEAMETASIASLTQQEINQ.HNWKLRPFRAPHHSSSMAALVGGGTIPRPGEISLA	294
NTDB id 1397 DSB67 RS15690 WP 005535577.1	GTGKTMLASRLCDLLPEMSDEEAMETASIASLTQSEINE.HNWKTRPFRAPHHSSSMAALVGGGSVPRPGEISLA	294
NTDB id 1349 HI 1117 AAC22771.1	GTGKTMLASRLTGLLPEMTDLEAIETASVTSLVQNELNF.HNWKRPFRAPHHSASMPALVGGGTIPKPGEISLA	298
NTDB id 1387 A4U84 RS06900 WP 020457569.1	GTGKTMLASRLADLLPEMEDLEAIETASVTSLVQNELNF.QNWKRPFRSPHHSASMPALVGGGTIPKPGEISLA	297
consensus	GSGKTMLAKRIPSTILPPLTLKEALETTHSVAGKMGAEATSLMTIRPFRSPHHTISDVALVGGGSYPQPGEISLA	298

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NTDB id 1387 A4U84 RS06900 WP 020457569.1
consensus



☒ non conserved
☒ similar
☒ ≥ 50% conserved