

logo

NTDB id 1323 RAOC RS07335 WP 004916218.1	MSLAIVYSRASIGVAPLVTVVHLSNGPGFTLVGLPETTVKESDRVRSALINSFEFPAKRITVNLAPADLP	73
NTDB id 1271 LPP RS03220 WP 011213198.1	.MLVKKVYGSIAIHGVSAQTTITIEVNVDQGV.GYHLVGLPDNAIKESSHRTISAALKNVGVKLPKKITINMAPADLR	75
NTDB id 1248 GC085 RS03150 WP 011213198.1	MSLAFTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETAVKESKDRVRSAINSQFEFPCRKITVNLGPANLP	75
NTDB id 47973 NMBM01240149 RS09530 WP 002229025.1	MSLAFTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETAVKESKDRVRSAINSQFEFPCRKITVNLGPANLP	75
NTDB id 1153 A1552VC RS00115 WP 000521788.1	MSLALVYSRALSGMNAPLVEVEAHLANGLPHFNIVGLPDTEVKESRDRVRAAIIQSGFEFPAKKITVNLAPADLP	75
NTDB id 1397 DSB67 RS15690 WP 005535577.1	MGLAIIHSRASIGVQAPPVTVEVHISNGMPGFTLVGLPETTVKESRDRVRSAINSRFEFPAKRITVNLAPADLP	75
NTDB id 1349 HI 1117 AAC22771.1	MGLAIIHSRASVGVQAPSVSVEVHISNGMPGFTLVGLPETTVKESKDRVRSAINVSNFQFPAPKRITVNLAPADLP	75
NTDB id 1387 A4U84 RS06900 WP 020457569.1	MSLAIVYSRASMGVQAPLVITIEVHLSNGKPGFTLVGLPEKTVKEAQRDRVRSALMNAQFKYPAKRITVNLAPADLP	75
consensus	MSLAIIVYSRASIGVEAPLVITIEVHISGGSPGLTLVGLPEKSVKEAQRDRVRSALMNAFNDYPARRITINLAPADLP	75

logo

NTDB id 1323 RAOC RS07335 WP 004916218.1	KEGGRFDLPALGILAAASQIAKKNYEEGELALSGLRGVGYLPAALAAKSKRRLIYPNAEASLV	148
NTDB id 1271 LPP RS03220 WP 011213198.1	KEGSAYDLSTIALGILAASGQIIAPEIERYLIMGELSLDGGLQPIKGVLPPIAIRAREEGFKGITLPKQNTREAAITV	149
NTDB id 1248 GC085 RS03150 WP 011213198.1	KTGSGFDLPALGILAAASEQIPLTNLANHEFIFIGELALSGELRGVSAIIPAVLAAHK.DNQHLIIANANAAEASLT	149
NTDB id 47973 NMBM01240149 RS09530 WP 002229025.1	KTGSGFDLPALGILAAASEQIPLTNLANHEFIFIGELALSGELRGVSAIIPAVLAAHK.DNQHLIIANANAAEASLT	149
NTDB id 1153 A1552VC RS00115 WP 000521788.1	KESGRFDLPALGILAAASQVVAPEKLAEEYEFAGELALSGLLRPVIRGALAMAWQGMQ.AKRAFVLPPEENAGQAAMV	149
NTDB id 1397 DSB67 RS15690 WP 005535577.1	KEGGRFDLPALGILAAASQIARNKLESYEFIFIGELALSGEIRGVKGVLPAAALAAK.VERCLVVPHSNGDQAALV	149
NTDB id 1349 HI 1117 AAC22771.1	KEGGRFDLPALGILAAASEQIATDKLKNYEFVIGELALSGGLRTVKGVLPAALAAK.KQRHLVVPHANGDQAALV	149
NTDB id 1387 A4U84 RS06900 WP 020457569.1	KEGGRFDLPALGILAAASQIDSDKLEKRIELGELSLTGHLRGVHGAIIPAVLAASK.AKRETIIVPQQNANEVSLV	149
consensus	KEGGRFDLPALGILAAASQIDSDKLEKRIELGELSLTGHLRGVHGAIIPAVLAASK.AKRETIIVPQQNANEVSLV	149

logo

NTDB id 1323 RAOC RS07335 WP 004916218.1	NDLEVYGVENIKEVIDFFNENCIPLEPTKVNTREEFHKRNVLPFPDFSEVKGQETAKRAMEVAAAGGHNIIILIGPP	223
NTDB id 1271 LPP RS03220 WP 011213198.1	GHQKVFTANNLREVCDYLCQGTSLQSLPPKPDLLNNYELDWSDIKQQQHAKNAMVIAACGGHSSILLSGAP	220
NTDB id 1248 GC085 RS03150 WP 011213198.1	GHQKVFTANNLREVCDYLCQGTSLQSLPPKPDLLNNYELDWSDIKQQQHAKNAMVIAACGGHSSILLSGAP	220
NTDB id 47973 NMBM01240149 RS09530 WP 002229025.1	RGITVYGARSLGEVAAHLNGIEPLAQTECSVPQ.MPSEHGGQPDLCVKGQHTARLALALEIAAAGGHSLLMYGPP	222
NTDB id 1153 A1552VC RS00115 WP 000521788.1	GVERHKSAQSLLEVCAELCGQHQLNLYQTPKKK...ELKAHGRDLQDIIGQQQCKRALEIAAAGGHNLLFLGPP	220
NTDB id 1397 DSB67 RS15690 WP 005535577.1	GKEQHKSASLLLEVCAELCGQHQLNLYQTPKKK...ELKAHGRDLQDIIGQQQCKRALEIAAAGGHNLLFLGPP	220
NTDB id 1349 HI 1117 AAC22771.1	SDQNTYFAQTLLDVVQFLNGQEKPLATEIVKESAVNFGSKNTLDLTDIIGQQHAKRALTIAAAGGHNLLFLGPP	224
NTDB id 1387 A4U84 RS06900 WP 020457569.1	SNTQTYCASTLLQVVNFLNNRDQLPIAQQLSQNIAEN.RPLVSRDLTDIIGQQHAKRALTIAAAGGHNLLFLGPP	223
consensus	NDLEVYGVENIKEVIDFFNENCIPLEPTKVNTREEFHKRNVLPFPDFSEVKGQETAKRAMEVAAAGGHNIIILIGPP	223

logo

NTDB id 1323 RAOC RS07335 WP 004916218.1	GSGKTMlakRIPsILPPLTLKEALETtkIHSVAGKMGaETSLMTIRPFRSPHHTISDVALVGGGSYPQPGEISLA	298
NTDB id 1271 LPP RS03220 WP 011213198.1	GSGKTMMAKRfSTLLPELSEtQALECAAINsIRGKLpD.FREWRLPFRAPHHTASPVALVGGGNPPKPGEISLA	294
NTDB id 1248 GC085 RS03150 WP 011213198.1	GSGKTMMAKRfSTLLPELSEtQALECAAINsIRGKLpD.FREWRLPFRAPHHTASPVALVGGGNPPKPGEISLA	294
NTDB id 47973 NMBM01240149 RS09530 WP 002229025.1	GTGKSMLSQRlPGILPPLTEDELVEVWALRSLLPNHQ...QLDSHRPFRSPHHSASAAAMVGGGSDPRPGEISLA	295
NTDB id 1153 A1552VC RS00115 WP 000521788.1	GTGKTMLASRLCDLLPEMSDEEAMETASIASLTQQEIN.QHNWKLPRFRAPHHSSSMAALVGGGTIPRPGEISLA	294
NTDB id 1397 DSB67 RS15690 WP 005535577.1	GTGKTMLASRLCDLLPEMSDEEAMETASVASLTQSEIN.EHNWKLTRPFRAPHHSSSMAALVGGGSVPRPGEISLA	294
NTDB id 1349 HI 1117 AAC22771.1	GTGKTMLASRLTGLPEMTDLAETETASVTSLVQNELN.FHNWKLPRFRAPHHSSASMPALVGGGTIPKPGEISLA	298
NTDB id 1387 A4U84 RS06900 WP 020457569.1	GTGKTMLASRLADLLPEMEDDEAETETASVTSLVQNELN.FQNWKLPRFRPHHSASMPALVGGGSIPKPGEISLA	297
consensus	GSGKTMlakRIPsILPPLTLKEALETtkIHSVAGKMGaETSLMTIRPFRSPHHTISDVALVGGGSYPQPGEISLA	298

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consensus



☒ non conserved
☒ similar
☒ ≥ 50% conserved