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NTDB id 1323 RAOC RS07335 WP 004916218.1	MSLAIVYSRASIGVQAPLVTVIEVHLSNGKPGFTLVGLPETTVKESKDRVRSALVNSQFEFPARRITVNLAPADLPKEGGR	78
NTDB id 259907 PMC2000 RS02585 WP 004530962.1	.MLVKKVYGSATIHGVSAQTTITIEVNVDQGV.GYHLVGLPDNATIKESSHRTISAALKNVGYKLPGKKITINMAPADLRKEGSA	80
NTDB id 1271 LPP RS03220 WP 011213198.1	MSLAVVRSRAPAAGRAPEVTVEVHLANGLPFSFIVGLPDLEVRESRERVRAALQNCGFEPFVRRITVNLAPADLPKESGR	80
NTDB id 1248 GC085 RS03150 WP 011213198.1	MSLAFTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETA VKESKDRVRSALINSQFEFPCRKITVNLGPANLPKGTSG	80
NTDB id 1397 DSB67 RS15690 WP 005535577.1	MSLAFTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETA VKESKDRVRSALINSQFEFPCRKITVNLGPANLPKGTSG	80
NTDB id 1153 A1552VC RS00115 WP 000521788.1	MGLAIIHSRASVGVQAPSVSVEVHISNGMPGFTLVGLPETTVKESKDRVRSALVNSNFQFPKRITVNLAPADLPKEGGR	80
NTDB id 1387 A4U84 RS06900 WP 020457569.1	MGLAIIHSRASIGVQAPPVTVIEVHISNGMPGFTLVGLPETTVKESRDRVRSALINSRFEFPAKRITVNLAPADLPKEGGR	80
NTDB id 1349 HI 1117 AAC22771.1	MSLAIIYSRASIGVEAPLVTVIEVHISGGSPGLTLVGLPEKSVKEAQDRVRSALMNAFQFYPARRITINLAPADLPKEGGR	80
consensus	MSLAIVYSRASMGVQAPLVTVIEVHLSNGKPGFTLVGLPEKTVKEAQDRVRSALMNAQFKYPAKRITVNLAPADLPKEGGR	80

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NTDB id 1323 RAOC RS07335 WP 004916218.1	FDLPIALGILAASGQIIAPETIERYLIMGELSLDGGQLPIKGVLPPIAIRAR.....EEGFGKGTII	136
NTDB id 259907 PMC2000 RS02585 WP 004530962.1	FDLPIALGILAASGQLPAGALDGRFAGELSLTGALRPMRGAFAMACGTARGQQADDDGSPAQAESPPARATAPNAEELY	160
NTDB id 1271 LPP RS03220 WP 011213198.1	FDLPIALGILAASEQIPLTNLANHEFIGELALSGELRGVSAIIPAVLAA.....HKDNQHLLI	137
NTDB id 1248 GC085 RS03150 WP 011213198.1	FDLPIALGILAASEQIPLTNLANHEFIGELALSGELRGVSAIIPAVLAA.....HKDNQHLLI	137
NTDB id 1397 DSB67 RS15690 WP 005535577.1	FDLPIALGILAASEQIATDKLNKNEFVGLALSGGLRTVKGVLPAALAA.....NKKQRHLV	137
NTDB id 1153 A1552VC RS00115 WP 000521788.1	FDLPIALGILAASDQIARNKLESYEFIGELALSGEIRGVKGVLPALAA.....NQVERCLV	137
NTDB id 1387 A4U84 RS06900 WP 020457569.1	FDLPIALGILAASGQIDSDKLRKRIELLGELSLTGHLRGVHGAIIPAVLAA.....SKAKREII	137
NTDB id 1349 HI 1117 AAC22771.1	FDLPIALGILAASDQIDASHLKKQFEFVAELALTGQLRGVHGVIPIALAA.....QKSKRELI	137
consensus	FDLPIALGILAASDQIDASHLKKQFEFVAELALTGQLRGVHGVIPIALAA.....QKSKRELI	137

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NTDB id 1323 RAOC RS07335 WP 004916218.1	YPNQAAEASLVGQRYTQNTNLEVCDFCCQTSGLAQVKKLNNYTRDLSDIIGQQHAKRALEIAAAGGHN	216
NTDB id 259907 PMC2000 RS02585 WP 004530962.1	LPLPSAAEALVPGVTVYGAADLPALCAHLADTPDGR LAPVAAPR.LDALPAAATADLADVIGQAGAKRALEVAAAGGHH	239
NTDB id 1271 LPP RS03220 WP 011213198.1	IANANAAEASLTGHQKVFTANNLREVC DYLCQGTSLQSLPPKPD...LLNNYELDWS DIKQQHAKNAMVIAACGGHS	213
NTDB id 1248 GC085 RS03150 WP 011213198.1	IANANAAEASLTGHQKVFTANNLREVC DYLCQGTSLQSLPPKPD...LLNNYELDWS DIKQQHAKNAMVIAACGGHS	213
NTDB id 1397 DSB67 RS15690 WP 005535577.1	VPHANGDQAALVKGQEHKSAQSLLEVCAELCGQHQLNLYQTPKKK...ELKAHGRDLQDIIGQQQGKRALEIAAAGNHN	213
NTDB id 1153 A1552VC RS00115 WP 000521788.1	VPHSNGDQAALVGVVERHKSQSLLEVCAELCGQQTLSLFQSSPSV...QQVSQTRDLQDIIGQQQGKRALEIAAAGNHN	213
NTDB id 1387 A4U84 RS06900 WP 020457569.1	VPQQNANEVSLVSNQTQTYCASTLLQVVNFLNNRDQLPIAQQLSQNAIEN.RPLVSRDLTDIIGQQHAKRALIIAASGQHN	216
NTDB id 1349 HI 1117 AAC22771.1	IAKQNANEASLVSDQNTYFAQTLLDVVQFLNGQEKPLATEIVKESAVNFGSKNTLDTDIIGQQHAKRALTIAAAGQHN	217
consensus	IAKQNANEASLVSDQNTYFAQTLLDVVQFLNGQEKPLATEIVKESAVNFGSKNTLDTDIIGQQHAKRALTIAAAGQHN	217

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NTDB id 1323 RAOC RS07335 WP 004916218.1	ILFLGPPGSGKTM LAKRIPSILPPLTLKEALETTKIHSVAGKMGAE TSLMTIRPFRSPHHTISDVALVGGGSYPQPGEIS	296
NTDB id 259907 PMC2000 RS02585 WP 004530962.1	MLMGPPGAGKSM LAARLPALLPLTDDEALTSAAILSSSRAG.FSPAQRRRPFRAPHHSSSSAALVGGRNPPQGEIT	318
NTDB id 1271 LPP RS03220 WP 011213198.1	ILLSGAPGSGKTMMAKRFTSLLPPELSETQALECAAINSIRGKL.PDFREWRLPPFRAPHHTASPVALVGGGNPPKPGEIS	292
NTDB id 1248 GC085 RS03150 WP 011213198.1	ILLSGAPGSGKTMMAKRFTSLLPPELSETQALECAAINSIRGKL.PDFREWRLPPFRAPHHTASPVALVGGGNPPKPGEIS	292
NTDB id 1397 DSB67 RS15690 WP 005535577.1	LLFLGPPGTGKTMLASRLCDLLPEMSDEEAMETASVASTTQSE.INEHNNWKT RPFRA PHHSSSMAALVGGGSVPRPGEIS	292
NTDB id 1153 A1552VC RS00115 WP 000521788.1	LLFLGPPGTGKTMLASRLCDLLPEMSDEEAMETASVASTTQSE.INEHNNWKT RPFRA PHHSSSMAALVGGGSVPRPGEIS	292
NTDB id 1387 A4U84 RS06900 WP 020457569.1	LLFLGPPGTGKTMLASRLADLLPEMEDDEAIETASVTSVLVQNE.LNFQNNWKKRPFRSPHHSASMPALVGGGSIPKPGEIS	295
NTDB id 1349 HI 1117 AAC22771.1	LLFLGPPGTGKTMLASRLADLLPEMTDLEAIETASVTSVLVQNE.LNFHNNWKKRPFRAPHHSSASMPALVGGGTIPKPGEIS	296
consensus	LLFLGPPGTGKTMLASRLADLLPEMTDLEAIETASVTSVLVQNE.LNFHNNWKKRPFRAPHHSSASMPALVGGGTIPKPGEIS	296

