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NTDB id 1323 RAOC RS07335 WP 004916218.1	MSLAIIYSRASIGVAPLVTVIEVHLSNGKPGFTLVGLPETTVKESDRVRSALNFEFPARRITVNLAPADLPKEGGR	78
NTDB id 1271 LPP RS03220 WP 011213198.1	.MLVKKVYGSAIHGVSAQTITIEVNVDDGV.GYHLVGLPDNAIKESSHRISAALKNVGYKLPKGGKITINMAPADLRKEGSA	80
NTDB id 1248 GC085 RS03150 WP 011213198.1	MSLAFTTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETA VKESKDRVRSAIINSQFEFPCKRITVNLGPANLPKGTGSG	80
NTDB id 1029383 ABUK12 RS17920 WP 410013113.1	MSLAFTTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETA VKESKDRVRSAIINSQFEFPCKRITVNLGPANLPKGTGSG	80
NTDB id 1397 DSB67 RS15690 WP 005535577.1	MSLALIYTRASIGVQAPLISVEAHISKGLPGFTLVGLPDATIKGARDRVRSALLNNGDFDPARRITVSLAPADLPKEGGR	80
NTDB id 1153 A1552VC RS00115 WP 000521788.1	MGLAIIHSRASVGVQAPSVSVEVHISNGMPGFTLVGLPETTVKESKDRVRSAIIVNSNFQFPAKRITVNLAPADLPKEGGR	80
NTDB id 1349 HI 1117 AAC22771.1	MGLAIIHSRASIGVQAPPVTVEVHISNGMPGFTLVGLPETTVKESRDRVRSAIINSRFEFPAKRITVNLAPADLPKEGGR	80
NTDB id 1387 A4U84 RS06900 WP 020457569.1	MSLAIVYSRASMGVQAPLVTTIEVHLSNGKPGFTLVGLPEKTVKEAQDRVRSALMNAQFKYPAKRITVNLAPADLPKEGGR	80
consensus	MSLAIIYSRASIGVEAPLVTTIEVHISGGSPGLTTLVGLPEKSVKEAQDRVRSALMNANFDYPARRITINLAPADLPKEGGR	80

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NTDB id 1271 LPP RS03220 WP 011213198.1	YDLSTALGILAASGQIIAPEIERYLIMGELSLDGGQLPIKGVLPPIARAREEGFGKGIILPKQNTREAAIVNDLEVYGVEN	159
NTDB id 1248 GC085 RS03150 WP 011213198.1	FDLPIALGILAASEQIPLTNLANHEFIGELALSGELRGVSAIIPAVLAAHKD.NQHLLIIANANAAEASLTGHQKVFTANN	159
NTDB id 1029383 ABUK12 RS17920 WP 410013113.1	FDLPIALGILAASEQIPLTNLANHEFIGELALSGELRGVSAIIPAVLAAHKD.NQHLLIIANANAAEASLTGHQKVFTANN	159
NTDB id 1397 DSB67 RS15690 WP 005535577.1	YDLPIALAILAASEQIAADKLACHEFLGELALSGELRPVQGAIPAALAAQQA.GRRLLILSSHNSGEAALIPDSRVLVAGH	159
NTDB id 1153 A1552VC RS00115 WP 000521788.1	FDLPIALGILAASEQIATDKLKNYEFVGLALSGGLRTVKGVLPAALAAANKK.QRHLVVPHANGDQAALVGKEQHKSQAS	159
NTDB id 1349 HI 1117 AAC22771.1	FDLPIALGILAASDQIARNKLESYEFIGELALSGELTRGVKGVLPAALAAANQV.ERCLVVPHSNGDQAALVGVERHKSQAS	159
NTDB id 1387 A4U84 RS06900 WP 020457569.1	FDLPIAIGILAASDQLDASHLKQFEFVAELALTGQLRGVHGVIPAILAAQKS.KRELIIAKQNANEASLVSDQNTYFAQT	159
consensus	FDLPIAIGILAASGQIDSDKLKRIFELGELSLTGHLRGVHGAIPAVLAASKA.KRETIIVPQQNANEVSLVSNQTQTYCAST	159

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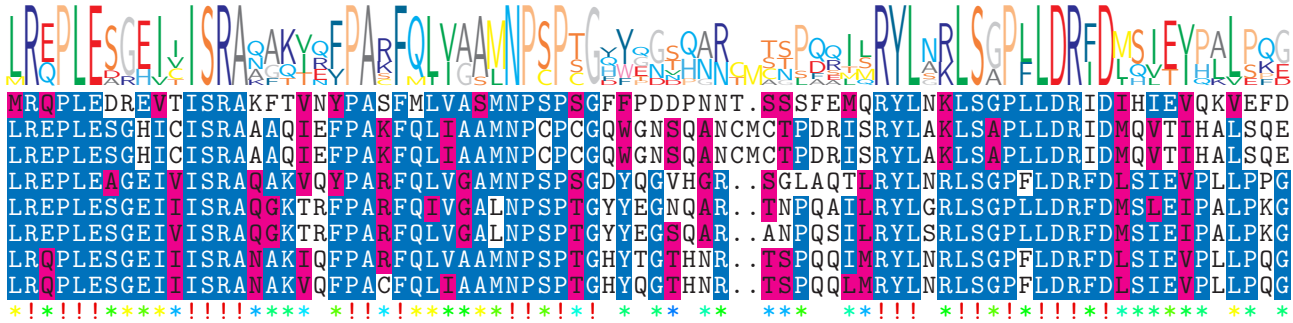
NTDB id 1323 RAOC RS07335 WP 004916218.1	LLEVCDELCGQTSLLSQPKPKLNNYTRDLSDIIGQQHAKRALEIAAGGHNLLFGPPGTGKTMLASRLSDP	238
NTDB id 1271 LPP RS03220 WP 011213198.1	IKVEIDFFNENCPLEPTKVNTREEFHKRVNLPFPDFSEVKGQETAKRAMEVAAAGGHNIIILIGPPGSGKTMLAKRIPSTIL	235
NTDB id 1248 GC085 RS03150 WP 011213198.1	LREVC DYLCQGTSLSQLPPKPDLLNNYELDWS DIKGQQHAKNAMVIAACGGHSILLSGAPGSGKTMMAKRFSTLL	235
NTDB id 1029383 ABUK12 RS17920 WP 410013113.1	LREVC DYLCQGTSLSQLPPKPDLLNNYELDWS DIKGQQHAKNAMVIAACGGHSILLSGAPGSGKTMMAKRFSTLL	235
NTDB id 1397 DSB67 RS15690 WP 005535577.1	LRDVCAFLQGGAE LNAVPGQDPT...PPAYDGADLSDITGQPQAKRALEIAAAGGHNLLILIGPPGTGKTMLASRLPGLM	235
NTDB id 1153 A1552VC RS00115 WP 000521788.1	LLEVCAELCGQHQLNLNYQTPKKK...ELKAHGRDLQDIIGQQQ GKRALEIAAAGNHNLLFLGPPGTGKTMLASRLCDLL	235
NTDB id 1349 HI 1117 AAC22771.1	LLEVCADLCGQQTLSLFQSSPSV...QQVSQTRDLQDIIGQQQ GKRALEIAAAGNHNLLFLGPPGTGKTMLASRLCDLL	239
NTDB id 1387 A4U84 RS06900 WP 020457569.1	LLQVVNF LNNRDQLPIAQQLSQNIAEN.RPLVSRDLTDIIGQQHAKRALIIAASGQHNLFLGPPGTGKTMLASRLADLL	238
consensus	LLEVCDELCGQTSLLSQPKPKLNNYTRDLSDIIGQQHAKRALEIAAGGHNLLFGPPGTGKTMLASRLSDP	238

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NTDB id 1323 RAOC RS07335 WP 004916218.1	PEMSDEAEETASITSLYQKEPNFRNWKRPFRAPHHSASMAALVGGGSLPRPGEISLAHNGVFLFDELPEFRRVLD	318
NTDB id 1271 LPP RS03220 WP 011213198.1	PPLTLKEALETTKIHSVAGKMGAETSLMTIRPFRSPHHTISDV ALVGGGSYPQPGGEISLAHNGVFLFDEMPFEKRTVLEV	314
NTDB id 1248 GC085 RS03150 WP 011213198.1	PELSETQALECAAINSIRGKLPD.FREWRLPPFRAPHHTASPV ALVGGGNPPKPGGEISLAHNGVFLFDELPEFNRQVLET	314
NTDB id 1029383 ABUK12 RS17920 WP 410013113.1	PELSETQALECAAINSIRGKLPD.FREWRLPPFRAPHHTASPV ALVGGGNPPKPGGEISLAHNGVFLFDELPEFNRQVLET	314
NTDB id 1397 DSB67 RS15690 WP 005535577.1	PPLSDAEAVETAALFSLMSAGAA.RRHWQRPFRAPHHSASMAALVGGGSLPRPGEISLAHNGVFLFDELPEFQRRLVDA	314
NTDB id 1153 A1552VC RS00115 WP 000521788.1	PEMSDEEAMETASVASLTQSEIN.EHNWKT RPFRAPHHSASSMAALVGGGSVPRPGEISLAHNGLLFLDEMPEFDRKVLDS	314
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NTDB id 1387 A4U84 RS06900 WP 020457569.1	PEMTDLEAIETASVTSLVQNELN.FHNWKKRPFRAPHHSASMPALVGGGTIPKPGGEISLATNGVFLFDELPEFERKVLDA	318
consensus	PEMTDLEAIETASVTSLVQNELN.FQNWKKRPFRSPHHSASMPALVGGGSIPKPGGEISLAHNGVFLFDELPEFERKVLDA	317

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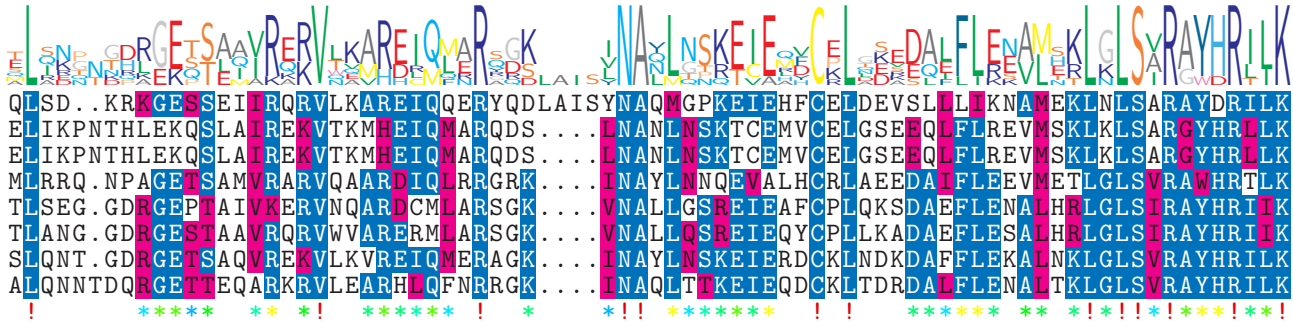
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consensus



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consensus



510
503
503
507
507
507
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510

X non conserved
X similar
X ≥ 50% conserved