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NTDB id 1323 RAOC RS07335 WP 004916218.1	MSLALYSRAAGYAPVTVVHLSNGPGFTLVGLPEAVKESDRVRSALNSFEFPARRITVNLAPADLPKEGGR	78
NTDB id 1271 LPP RS03220 WP 011213198.1	.MLVKKVYGSAGIHGVSAQTTITIEVNVDDGV.GYHLVGLPDNAIKESSHRISAALKNVGYKLPKGGKITINMAPADLRKEGSA	80
NTDB id 1248 GC085 RS03150 WP 011213198.1	MSLAFTTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETA VKESKDRVRSALINSQFEFPCKRITVNLGPANLPKGTGSG	80
NTDB id 1096437 ACMXYS RS01050 WP 415897343.1	MSLAFTTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETA VKESKDRVRSALINSQFEFPCKRITVNLGPANLPKGTGSG	80
NTDB id 1397 DSB67 RS15690 WP 005535577.1	MSLATAYTRAQVGIDAPAVTVEVHLSGGLPSFSIVGLPEAAVKESRERVRSALINSQFEFPQRRITVNLAPADLPKEGGR	80
NTDB id 1153 A1552VC RS00115 WP 000521788.1	MGLAIITHSRASVGVQAPSVSVEVHISNGMPGFTLVGLPETTVKESKDRVRSALVNSNFQFPKRITVNLAPADLPKEGGR	80
NTDB id 1349 HI 1117 AAC22771.1	MGLAIITHSRASIGVQAPPVTVVEVHISNGMPGFTLVGLPETTVKESRDRVRSALINSRFEFPKRITVNLAPADLPKEGGR	80
NTDB id 1387 A4U84 RS06900 WP 020457569.1	MSLAIVYSRASMGVQAPLVTIEVHLSNGKPGFTLVGLPEKTVKEAQDRVRSALMNAQFKYPAKRITVNLAPADLPKEGGR	80
consensus	MSLAIIYSRASIGVEAPLVTIEVHISGGSPGLTLVGLPEKS VKEAQDRVRSALMNANFDYPARRITINLAPADLPKEGGR	80

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NTDB id 1323 RAOC RS07335 WP 004916218.1	FDLPIALGILAAASQILKPAKKNYEFELALSGELRGVGVPAALAAKRLHLYPNAEASLVGQVYVY	158
NTDB id 1271 LPP RS03220 WP 011213198.1	YDLSTALGILAASGQIIAPEIERYLIMGELSLDGGQLPIKGVLPPIAIRAREEGFGKTIILPKQNTREAAIVNDLEVYGVEN	159
NTDB id 1248 GC085 RS03150 WP 011213198.1	FDLPIALGILAASEQIPLTNLANHEFIGELALSGELRGVSAIIPAVLAAHKD.NQHLLIIANANAAEASLTGHQKVFTANN	159
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NTDB id 1153 A1552VC RS00115 WP 000521788.1	FDLPIALGILAASEQIATDKLKNYEFVGEALALSGGLRTVKGVLPAALAAANKK.QRHLVVPHANGDQAALVGKEQHKSQAS	159
NTDB id 1349 HI 1117 AAC22771.1	FDLPIALGILAASDQIARNKLESYEFIGELALSGELTRGVKGVLPAALAAANQV.ERCLVVPHSNGDQAALVGVERHKSQAS	159
NTDB id 1387 A4U84 RS06900 WP 020457569.1	FDLPIAIGILAASDQLDASHLKQFEFVAELALTGQLRGVHGVIPAILAAQKS.KRELIIAKQNANEASLVSDQNTYFAQT	159
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NTDB id 1271 LPP RS03220 WP 011213198.1	IKKEVIDFFNENCPLEPTKVNTREEFHKRVNLPFPDFSEVKGQETAKRAMEVAAAGGHNILLIGPPGSGKTMLAKRIPSTIL	235
NTDB id 1248 GC085 RS03150 WP 011213198.1	LREVCDFLCQGTSLQSLPPKPDLL...LLNNYELDWS DIKGQQAHRANAMVIAACGGHSILLSGAPGSGKTMMAKRFSTLL	235
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NTDB id 1397 DSB67 RS15690 WP 005535577.1	LLQVCAHLQGSSELISVAQAQVQPLS...TDAFGPDLGDVKGQAQAKRALEVAAAGGHNILLVGPPGSGKSM LANRLPGLL	235
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NTDB id 1349 HI 1117 AAC22771.1	LLEVCADLCGQQTLSLFQSSPSV...QQVSTRDLQDIIGQQQ GKRALEIAAAGNHNLLFLGPPGTGKTMLASRLCDLL	239
NTDB id 1387 A4U84 RS06900 WP 020457569.1	LLQVVNFNNRDQLPIAQQLSQNIAEN.RPLVSRDLTDIIGQQHAKRALIIAASGQHNNLLFLGPPGTGKTMLASRLADLL	238
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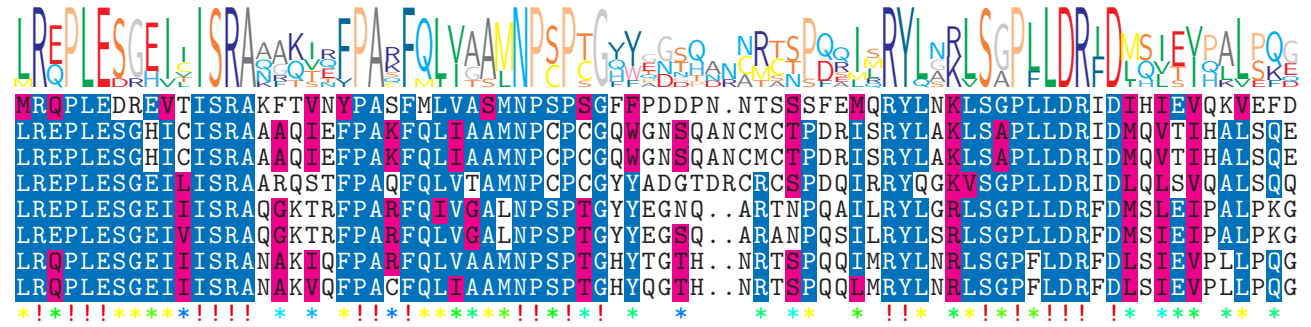
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NTDB id 1271 LPP RS03220 WP 011213198.1	PPLTLKEALETTKIHSVAGKMGAETSLMTIRPFRSPHHTISDVALVGGGSIYPQPGEISLAHNGVFLDELPEFKRTVLEV	314
NTDB id 1248 GC085 RS03150 WP 011213198.1	PELSETQALECAAINSIRGKLP.DFREWRLLPFRAPHHTASPVALVGGGNPPKPGEISLAHNGVFLDELPEFNRQVLET	314
NTDB id 1096437 ACMXYS RS01050 WP 415897343.1	PELSETQALECAAINSIRGKLP.DFREWRLLPFRAPHHTASPVALVGGGNPPKPGEISLAHNGVFLDELPEFNRQVLET	315
NTDB id 1397 DSB67 RS15690 WP 005535577.1	PQMTQEAELEVAAYVSIQSSS.ETRLPRKRPFRAHHTASSVALVGGGNPPKPGEISLAHQITFLDELPEFSRKVLEV	314
NTDB id 1153 A1552VC RS00115 WP 000521788.1	PEMSDEEAMETASVASLTQSEI.NEHNWKT RPFRAPHHSSSMAALVGGGSI PRPGEISLAHNGLLFLDEMPEFDRKVLDS	314
NTDB id 1349 HI 1117 AAC22771.1	PEMSDEEAMETASIASLTQKEI.NQHNWKL RPFRAPHHSSSMAALVGGGSI PRPGEISLAHNGLLFLDEMPEFERKVLDS	314
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consensus	PEMEDAEIETASVTSLVQNEL.NFQNWKKRPFRSPHHSASMPALVGGGSI PKPGEISLAHNGVFLDELPEFERKVLDA	317

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NTDB id 1248 GC085 RS03150 WP 011213198.1
NTDB id 1096437 ACMXYS RS01050 WP 415897343.1
NTDB id 1397 DSB67 RS15690 WP 005535577.1
NTDB id 1153 A1552VC RS00115 WP 000521788.1
NTDB id 1349 HI 1117 AAC22771.1
NTDB id 1387 A4U84 RS06900 WP 020457569.1
consensus

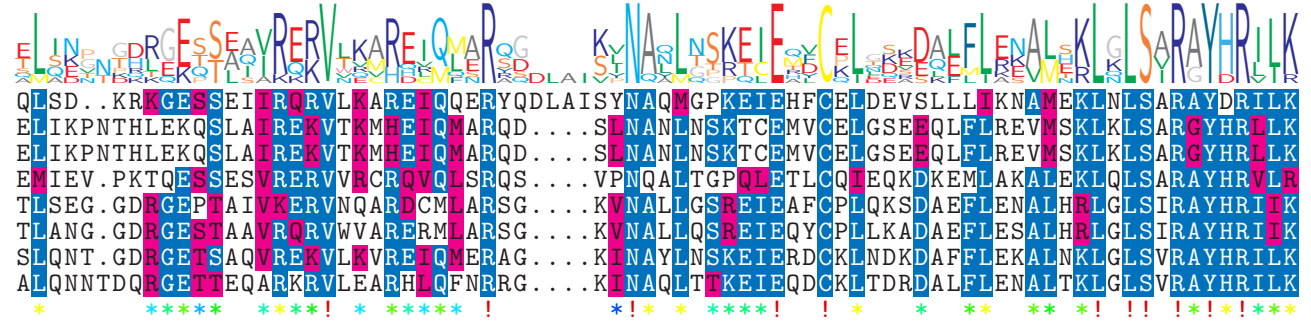
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consensus

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NTDB id 1349 HI 1117 AAC22771.1
NTDB id 1387 A4U84 RS06900 WP 020457569.1
consensus

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- X non conserved
- X similar
- X $\geq 50\%$ conserved