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NTDB id 1323 RAOC RS07335 WP 004916218.1	.MLVKKVYGS ¹ AIHGVSAQT ² ITIEVNV ³ DQGV ⁴ .GYHLVGLP ⁵ DNA ⁶ IKESSHR ⁷ ISAALKNVG ⁸ YKLP ⁹ GKKIT ¹⁰ INMAPAD ¹¹ LRKEGSA	78
NTDB id 225219 B7P05 RS13220 WP 010928622.1	MTLAV ¹ LASRA ² IAGWQAPAVRVETH ³ LGSGLP ⁴ AFATVGLPD ⁵ VEVRESR ⁶ ERVRAAIQNSGF ⁷ DFPPGRITVNLSPADLPKASAR	80
NTDB id 1271 LPP RS03220 WP 011213198.1	MSLAFTTK ¹ TRSTIG ² IVAQPVSV ³ EVHLSNGLPSFT ⁴ MGVLAETA ⁵ AVKESKDRVRS ⁶ AIINSQF ⁷ EFPCRKITVNLGPANLPK ⁸ TGSG	80
NTDB id 1248 GC085 RS03150 WP 011213198.1	MSLAFTTK ¹ TRSTIG ² IVAQPVSV ³ EVHLSNGLPSFT ⁴ MGVLAETA ⁵ AVKESKDRVRS ⁶ AIINSQF ⁷ EFPCRKITVNLGPANLPK ⁸ TGSG	80
NTDB id 1397 DSB67 RS15690 WP 005535577.1	MGLAII ¹ HSRASVGVQAPS ² VSVEVHISNGMPGFTLVGLPETTVKESKDRVRS ³ AIVNSNFQFPAKRITVNLAPADLPKEGGR	80
NTDB id 1153 A1552VC RS00115 WP 000521788.1	MGLAII ¹ HSRASIGVQAPPVTV ² EVHISNGMPGFTLVGLPETTVKESRDRVRS ³ AIINSRFEFPAKRITVNLAPADLPKEGGR	80
NTDB id 1387 A4U84 RS06900 WP 020457569.1	MSLAII ¹ YSRASIGVEAPLVTV ² IEVHISGGSPGLTLVGLPEKSVKEAQDRVRSALMNANFDYPARRITINLAPADLPKEGGR	80
NTDB id 1349 HI 1117 AAC22771.1	MSLAIV ¹ YSRASMGVQAPLVTV ² IEVHLSNGKPGFTLVGLPEKTVKEAQDRVRSALMNAQFKYPAKRITVNLAPADLPKEGGR	80
consensus	***!*** *****!*!* *****!*****!*****!!!!** *****!*****!*****!*****!*****!*****!*****	

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NTDB id 1323 RAOC RS07335 WP 004916218.1	YDLSIALGILAASGQIIAPE.....IERYLIMGELS ¹ LDGGLQPIKGVLP ² IAIRA ³ .REEGF ⁴ KGITL ⁵ PKQNTREAA ⁶ IVNDLE	152
NTDB id 225219 B7P05 RS13220 WP 010928622.1	FDLPIALGIL ¹ LASGQVAASAAQTAALPDCVWAAEL ² SLSGALVPLAAPLALALAVAREQP ³ GATLVLPAGSA ⁴ AAVA ⁵ AWVPGIR	160
NTDB id 1271 LPP RS03220 WP 011213198.1	FDLPIALGILAASEQIPLTN.....LANHEFIGELALS ¹ GELRGVSA ² IIPAVLAA...HKDNQHLITANANAAEASLTGHQK	153
NTDB id 1248 GC085 RS03150 WP 011213198.1	FDLPIALGILAASEQIPLTN.....LANHEFIGELALS ¹ GELRGVSA ² IIPAVLAA...HKDNQHLITANANAAEASLTGHQK	153
NTDB id 1397 DSB67 RS15690 WP 005535577.1	FDLPIALGILAASEQIATDK.....LKNYEFV ¹ GELALS ² GGLRTVKGVLPAALAA...NKKQRHLVVP ³ HANGDQAALVGKEQ	153
NTDB id 1153 A1552VC RS00115 WP 000521788.1	FDLPIALGILAASDQIARNK.....LESYEF ¹ IGELALS ² GELRGVKGVLPAALAA...NQVERCLVVP ³ PHSNGDQAALVGVER	153
NTDB id 1387 A4U84 RS06900 WP 020457569.1	FDLPIAIGILAASGQIDSDK.....LKRIE ¹ LLGELSLTGH ² LRGVHGAIPAVLAA...SKAKREIIVPQ ³ QANANEVSLVSNTQ	153
NTDB id 1349 HI 1117 AAC22771.1	FDLPIAIGILAASDQIDASH.....LKQF ¹ EFV ² AELAL ³ TGQLRGVHGVIPAILAA...QKSKRELITAKQ ⁴ NANEASLVSDQN	153
consensus	***!***!***!***!***!* *****!***!*** ***** ***** ***** ***** *	

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NTDB id 1323 RAOC RS07335 WP 004916218.1	VYGVENI ¹ KEVID ² FFNENC ³ PLEPTKVNTREEFHKRVNLP ⁴ FPDFSEVKGQETAKRAMEVAAAGGHN ⁵ ITILGPPGSGKTM ⁶ LAQ	232
NTDB id 225219 B7P05 RS13220 WP 010928622.1	VLAH ¹ ITLGEAAAYLAGHAELAPAERRSWP.....EVEPGPCLSDVRGQPAARRALEVAAAGGHSLLMCGPPGAGK ² SMLAQ	235
NTDB id 1271 LPP RS03220 WP 011213198.1	VFTANNLREVCDYLCQGTS ¹ LQSLPPKPD ² L...LLNNYELD ³ WDIKGQ ⁴ QHAKNAMVIAACGGHS ⁵ ILLSCAPGS ⁶ GKTMMAK	229
NTDB id 1248 GC085 RS03150 WP 011213198.1	VFTANNLREVCDYLCQGTS ¹ LQSLPPKPD ² L...LLNNYELD ³ WDIKGQ ⁴ QHAKNAMVIAACGGHS ⁵ ILLSCAPGS ⁶ GKTMMAK	229
NTDB id 1397 DSB67 RS15690 WP 005535577.1	HKSAQSLLEVCAELCGQHQLNLYQTPKKK...ELKAHGRDLQDIIGQQQ ¹ GKRALEIAAAGNHNLLFLGPPGTGKTM ² LAS	229
NTDB id 1153 A1552VC RS00115 WP 000521788.1	HKSAQSLLEVCA ¹ DLCGQTLSLFQSSPSV...QQVSQTRDLQDIIGQQQ ² GKRALEIAAAGNHNLLFLGPPGTGKTM ³ LAS	229
NTDB id 1387 A4U84 RS06900 WP 020457569.1	TYCASTLLQVVNF ¹ LNNRDQLPIAQQLSQNIAEN.RPLVSRDLTDIIGQQHAKRALIIAASGQHNNLLFLGPPGTGKTM ² LAS	232
NTDB id 1349 HI 1117 AAC22771.1	TYFAQTLLDVVQFLNGQEK ¹ LPLATEIVKESAVNFSGKNTL ² DLTDIIGQQHAKRALTIAAAGQHNNLLFLGPPGTGKTM ³ LAS	233
consensus	* ***** ** ** ! ***** !!* ***** *!!!! !***** !!!!!!!*****!	

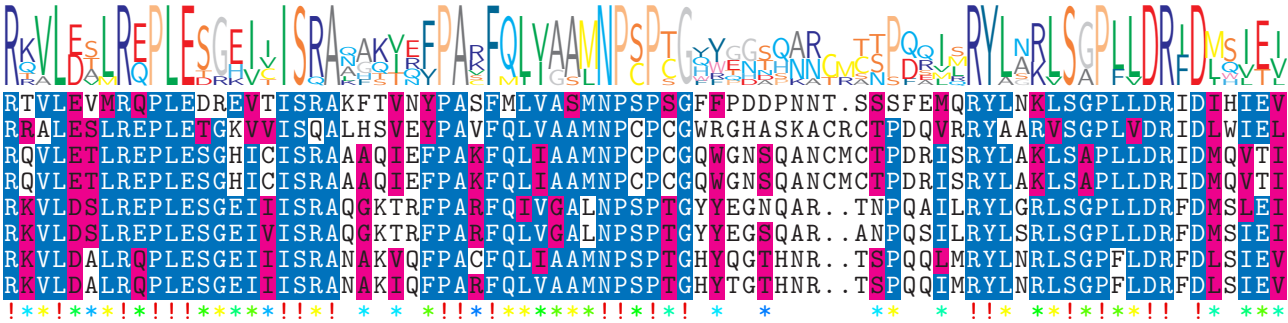
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NTDB id 1323 RAOC RS07335 WP 004916218.1	RIPSLP ¹ PLTLKEALET ² TKIHSVAGKMGAE ³ TSMTIRPFRSPHHTISDVALVGGGSYPQPGEISLAHNGVFLD ⁴ EMPEFK	312
NTDB id 225219 B7P05 RS13220 WP 010928622.1	RLPGLLPLEQRQALEVAAIAGAGGAPEV...LRGPPFRAPHHSASAAALVGGGARPPGEISLAHNGVFLD ² ELPEFE	312
NTDB id 1271 LPP RS03220 WP 011213198.1	RFSTLLPELSETQALECAA ¹ AINSIRGKLPD.FREWRLPPFRAPHHTASPV ² ALVGGGNPPK ³ PGEISLAHNGVFLD ⁴ ELPEFN	308
NTDB id 1248 GC085 RS03150 WP 011213198.1	RFSTLLPELSETQALECAA ¹ AINSIRGKLPD.FREWRLPPFRAPHHTASPV ² ALVGGGNPPK ³ PGEISLAHNGVFLD ⁴ ELPEFN	308
NTDB id 1397 DSB67 RS15690 WP 005535577.1	RLCDLLPEMSDEEAMETASV ¹ ASLTQSEIN.EHNWKT ² RPFRA ³ PHHSSSMAALVGGGSVPRPGEISLAHNGLLFLD ⁴ EMPEFD	308
NTDB id 1153 A1552VC RS00115 WP 000521788.1	RLCDLLPEMSDEEAMETASIASLTQ ¹ QEIN.QHNWKL ² RPFRA ³ PHHSSSMAALVGGGTIPR ⁴ PGEISLAHNGLLFLD ⁵ EMPEFE	308
NTDB id 1387 A4U84 RS06900 WP 020457569.1	RLADLLPEMEDDEAIETASV ¹ SLVQNELN.FQNWKK ² RPFRA ³ PHHSASMAALVGGGSIPK ⁴ PGEISLAHNGVFLD ⁵ ELPEFE	311
NTDB id 1349 HI 1117 AAC22771.1	RLTGLLPEMTDL ¹ EAIETASV ² SLVQNELN.FHNWKK ³ RPFRA ⁴ PHHSASMPALVGGGTIPK ⁵ PGEISLATNGVFLD ⁶ ELPEFE	312
consensus	!* ***** *!*!* * ***** *****!*****!*****!*****!*****!*****!*****!*****	

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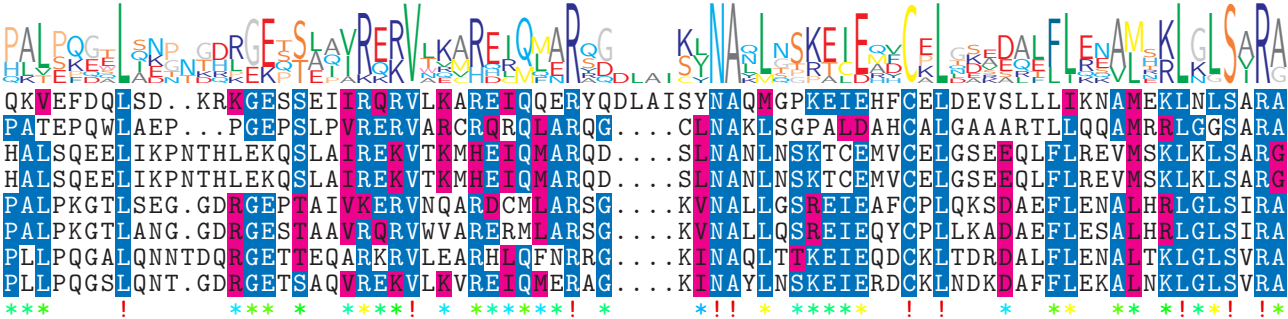


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consensus



510
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☒ non conserved
☒ similar
☒ ≥ 50% conserved