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NTDB id 1323 RAOC RS07335 WP 004916218.1	.MLVKKVYGS ¹ AIHGVSAQT ² ITIEVNV ³ DQGV ⁴ .GYHLVGLPD ⁵ NAIK ⁶ ESSHR ⁷ ISAALKNVGY ⁸ KLP ⁹ GKKIT ¹⁰ INMAPADLRKEGSA	78
NTDB id 225178 B7P10 RS16000 WP 010926358.1	MTLAVLASRAIAGWQAPAVRVETHLGSGLPAFAIVGLPDVEVRESRERVRAAIQNSGFDFFPPGRITVNLSPADLPKASAR	80
NTDB id 1271 LPP RS03220 WP 011213198.1	MSLAFTTKRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETA ¹ AVKESKDRVRS ² AIINSQFEFPCRKITVNLGPANLPK ³ TGSG	80
NTDB id 1248 GC085 RS03150 WP 011213198.1	MSLAFTTKRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETA ¹ AVKESKDRVRS ² AIINSQFEFPCRKITVNLGPANLPK ³ TGSG	80
NTDB id 1397 DSB67 RS15690 WP 005535577.1	MGLAIIHSRASVGVQAPS ¹ VSVEVHISNGMPGFTLVGLPETTVKESKDRVRS ² AIVNSNFQFP ³ AKRITVNLAPADLPKEGGR	80
NTDB id 1153 A1552VC RS00115 WP 000521788.1	MGLAIIHSRASIGVQAPPVTV ¹ EVHISNGMPGFTLVGLPETTVKESRDRVRS ² AIINSRFEFPAKRITVNLAPADLPKEGGR	80
NTDB id 1387 A4U84 RS06900 WP 020457569.1	MSLAIIYSRASIGVEAPLV ¹ TVIEVHISGGSPGLTLVGLPEKSVKEAQDRVRSALMNANFDYPARRIT ² INLAPADLPKEGGR	80
NTDB id 1349 HI 1117 AAC22771.1	MSLAIVYSRASMGVQAPLV ¹ TVIEVHLSNGKPGFTLVGLPEKTVKEAQDRVRSALMNAQFKYPAKRITVNLAPADLPKEGGR	80
consensus	***!*** *****!*!* *****!*****!*****!!!!** *****!*****!*****!*****!*****!*****!*****	

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NTDB id 1323 RAOC RS07335 WP 004916218.1	YDLSIALGILAASGQIIAPE.....IERYLIMGELS ¹ LDGGLQPIKGVLP ² IAIRA ³ .REEGFKGITL ⁴ PKQNTREAAI ⁵ IVNDLE	152
NTDB id 225178 B7P10 RS16000 WP 010926358.1	FDLPIALGILLASGQVAASAAQTAALPDCVWAAELSLSGALVPLAAPLALALAVAREQP ¹ GATLVLPAGSAAVA ² AWVPGIR	160
NTDB id 1271 LPP RS03220 WP 011213198.1	FDLPIALGILAASEQIPLTN.....LANHEFIGELALS ¹ GELRGVSAIIPAVLAA ² ..HKDNQH ³ LIITANANAAEASLTGHQK	153
NTDB id 1248 GC085 RS03150 WP 011213198.1	FDLPIALGILAASEQIPLTN.....LANHEFIGELALS ¹ GELRGVSAIIPAVLAA ² ..HKDNQH ³ LIITANANAAEASLTGHQK	153
NTDB id 1397 DSB67 RS15690 WP 005535577.1	FDLPIALGILAASEQIATDK.....LKNYEFV ¹ GELALS ² GGLRTVKGVLPAALAA ³ ..NKKQRHLV ⁴ VPHANGDQAALVGKEQ	153
NTDB id 1153 A1552VC RS00115 WP 000521788.1	FDLPIALGILAASDQIARNK.....LESYEF ¹ IGELALS ² GELRGVKGVLPAALAA ³ ..NQVERCLV ⁴ VPHSNGDQAALVGVER	153
NTDB id 1387 A4U84 RS06900 WP 020457569.1	FDLPIALGILAASGQIDSDK.....LKRIE ¹ LLGELSLTGH ² LRGVHGAIPAVLAA ³ ..SKAKREI ⁴ IIVPQQNANEVSLVSNTQ	153
NTDB id 1349 HI 1117 AAC22771.1	FDLPIALGILAASDQIDASH.....LKQF ¹ EFV ² AELAL ³ TGQLRGVHGVIPAILAA ⁴ ..QKSKREL ⁵ ITAKQNANEASLVSDQN	153
consensus	***!***!***!***!***!* *****!***! ***** ***** **	

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NTDB id 1323 RAOC RS07335 WP 004916218.1	VYGVENI ¹ KEVIDIFFNENC ² PLEPTKVNTREEFHKRVNLPFDFSEVKGQETAKRAMEVAAAGGHN ³ ITILGPPGSGKTM ⁴ LAQ	232
NTDB id 225178 B7P10 RS16000 WP 010926358.1	VLAHITLGEAAAYLAGHAELAPAERRSWP.....EAEPGPCLSDVRGQPAARRALEVAAAGGHSLLMCGPPGAGK ¹ SMLAQ	235
NTDB id 1271 LPP RS03220 WP 011213198.1	VFTANNLREVCDYLCQGTS ¹ LQSLPPKPD ² L...LLNNYELD ³ WDIKGQQHAKNAMVIAACGGHS ⁴ ILLSCAPGS ⁵ GKTMMAK	229
NTDB id 1248 GC085 RS03150 WP 011213198.1	VFTANNLREVCDYLCQGTS ¹ LQSLPPKPD ² L...LLNNYELD ³ WDIKGQQHAKNAMVIAACGGHS ⁴ ILLSCAPGS ⁵ GKTMMAK	229
NTDB id 1397 DSB67 RS15690 WP 005535577.1	HKSAQSLLEVCAELCGQHQLNLYQT ¹ PKKK...ELKAHGRDLQDIIGQQQGKRALEIAAAGNHNLLFLGPPGTGKTM ² LAS	229
NTDB id 1153 A1552VC RS00115 WP 000521788.1	HKSAQSLLEVCA ¹ DLCGQTL ² SLFQSSPSV...QQVSQTRDLQDIIGQQQGKRALEIAAAGNHNLLFLGPPGTGKTM 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 LPLATEIVKESAVNFSGKNTLDLTDIIGQQHAKRALTIAAAGQHNNLLFLGPPGTGKTM ² LAS	233
consensus	* ***** ** ** ! ***** !* ***** *!!!! !***** !!!!!!!*!!!!	

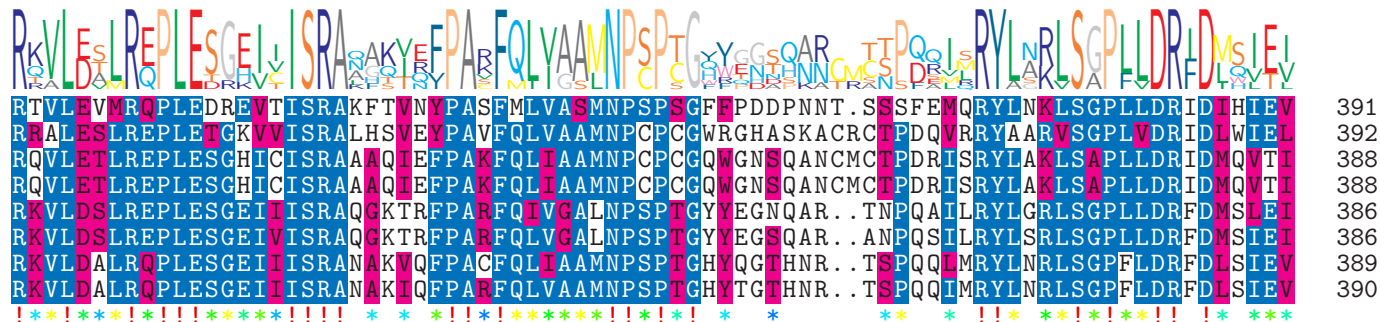
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NTDB id 1323 RAOC RS07335 WP 004916218.1	RIPSLPPLTLKEALET ¹ TKIHSVAGKMGAE ² SLMTIRPFRSPHHTISDVALVGGGSYPQPGEISLAHNGVFLD ³ EMPEFK	312
NTDB id 225178 B7P10 RS16000 WP 010926358.1	RLPGLLPLEQRQALEVAAIAGAGGAPEV...LRGQPPFRAPHHSASAAALVGGGARPPGEISLAHNGVFLD ¹ 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 PGEISLAHNGVFLD ⁶ ELPEFE	312
consensus	!* ***** *!!!!* ***** ** *****!*****!*****!*****!*****!*****!*****!*****	

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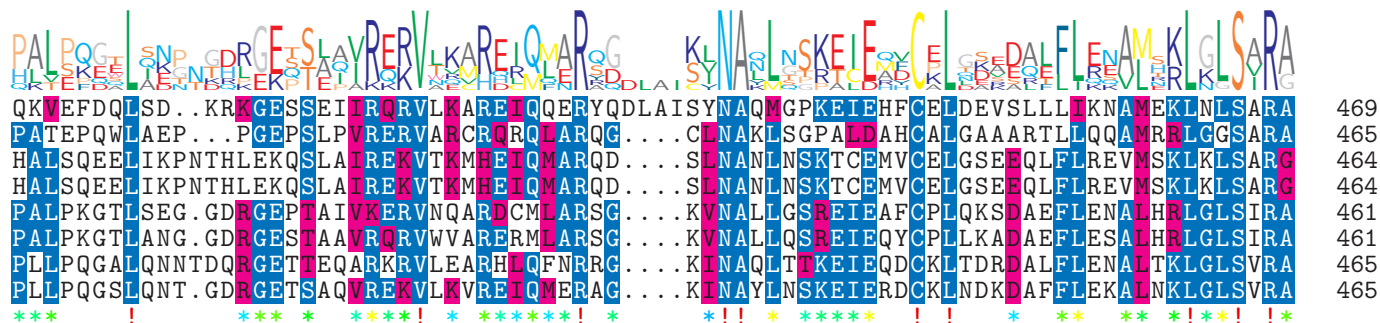
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consensus

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