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NTDB id 1323 RAOC RS07335 WP 004916218.1	MSLAIVYSRASIGVAPLVTVVHLSNGPGETLVGLPETTVKESDRVRSALINSFEPAKRITVNLAPADLPKEGGR	78
NTDB id 1271 LPP RS03220 WP 011213198.1	.MLVKKVYGSAIHGVSAQTTITIEVNVDDGV.GYHLVGLPDNAIKESSHRISAAIKNVGYKLPKGGKITINMAPADLRKEGSA	80
NTDB id 1248 GC085 RS03150 WP 011213198.1	MSLAFTTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETAVKESKDRVRSAINSQFEFPCRKITVNLGPANLPKGTGSG	80
NTDB id 1009342 ABNK32 RS30255 WP 032693771.1	MSLAFTTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETAVKESKDRVRSAINSQFEFPCRKITVNLGPANLPKGTGSG	80
NTDB id 1397 DSB67 RS15690 WP 005535577.1	MSLAIVYTRAALGIGAPLITVEVHISNGLPGLTMVGLPETTVREARDRVRSAINSGYAYPAKKITINLAPADLPKEGGR	80
NTDB id 1153 A1552VC RS00115 WP 000521788.1	MGLAIIHSRASVGVQAPSVSVEVHISNMGPGFTLVGLPETTVKESKDRVRSAINVSNFQFPAKRITVNLAPADLPKEGGR	80
NTDB id 1349 HI 1117 AAC22771.1	MGLAIIHSRASIGVQAPPVTVVEVHISNMGPGFTLVGLPETTVKESRDRVRSAINSRFEFPAKRITVNLAPADLPKEGGR	80
NTDB id 1387 A4U84 RS06900 WP 020457569.1	MSLAIVYSRASMGVQAPLVTIEVHLSNGKPGFTLVGLPEKTVKEAQDRVRSALMNAQFKYPAKRITVNLAPADLPKEGGR	80
consensus	MSLAIIYSRASIGVEAPLVTIEVHISGGSPGLTLVGLPEKSVKEAQDRVRSALMNAFDPARRITINLAPADLPKEGGR	80



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NTDB id 1323 RAOC RS07335 WP 004916218.1	FDLPIALGILAASQQLKATKEDLNKNYEFYGEALGGLRGVKGYPALAAKKNRLLIPNQNAEASLVGLGQVYA	158
NTDB id 1271 LPP RS03220 WP 011213198.1	YDLSTALGILAASGQIIAPETIERYLIMGELSLDGGQLPIKGVLPPIARAREEGFGKGIILPKQNTREAAIVNDLEVYGVEN	159
NTDB id 1248 GC085 RS03150 WP 011213198.1	FDLPIALGILAASEQIPLTNLANHEFIGELALSGELRGVSAIIPAVLAAHKDN.QHLIIANANAAEASLTGHQKVFTANN	159
NTDB id 1009342 ABNK32 RS30255 WP 032693771.1	FDLPIALGILAASEQIPLTNLANHEFIGELALSGELRGVSAIIPAVLAAHKDN.QHLIIANANAAEASLTGHQKVFTANN	159
NTDB id 1397 DSB67 RS15690 WP 005535577.1	YDLPIALALLVASEQLKAPRLNQYEFVGELALTGALRGVPGAISAMEAIKAG.RKIVISNENSPVEGLTGGSDCLIATD	159
NTDB id 1153 A1552VC RS00115 WP 000521788.1	FDLPIALGILAASEQIATDKLNQYEFVGELALSGGLRTVKGVLPAALAAANKKQ.RHLVVPHANGDQAALVGKEQHKSAQS	159
NTDB id 1349 HI 1117 AAC22771.1	FDLPIALGILAASDQIARNKLESYEFIGELALSGEIRGVKGVLPAALAAANQVE.RCLVVPHSNGDQAALVGVERHKSQS	159
NTDB id 1387 A4U84 RS06900 WP 020457569.1	FDLPIAIGILAASDQLDASHLKQFEFVAELALTGQLRGVHGVIPAILAAQKSK.RELIIAKQNANEASLVSDQNTYFAQT	159
consensus	FDLPIAIGILAASGQIDSDKLKRIFELGELSLTGHLRGVHGAIPAVLAASKAK.RETIIVPQQNANEVSLVSNQTQYCAST	159



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NTDB id 1323 RAOC RS07335 WP 004916218.1	LLEVCDELCCGQTSLLIQDCKPKLLANSTLNNTIRDLSDIIGQQHAKRALEIAAGGHNLLFLGPPGTGKTMLASRLSD	238
NTDB id 1271 LPP RS03220 WP 011213198.1	IKVEIDFFNENCPLEPTKVNTREEFHKRNVLPFPDFSEVKGQETAKRAMEVAAAGGHNIIILGPPGSGKTMLAKRIPSTIL	235
NTDB id 1248 GC085 RS03150 WP 011213198.1	LREVC DYLCQGTSLQSLPPKPDLL...LNNYELDWS DIKGQQHAKNAMVIAACGGHSILLSGAPGSGKTMMAKRFSTLL	235
NTDB id 1009342 ABNK32 RS30255 WP 032693771.1	LREVC DYLCQGTSLQSLPPKPDLL...LNNYELDWS DIKGQQHAKNAMVIAACGGHSILLSGAPGSGKTMMAKRFSTLL	234
NTDB id 1397 DSB67 RS15690 WP 005535577.1	LQEVCAFLGRRHALANPLPE....GEYTDETSVDLRDLVIGQRQ GKRALEIIAAGGHNLLMIGPPGTGKTMLASRLPGLL	235
NTDB id 1153 A1552VC RS00115 WP 000521788.1	LLEVCAELCGQHQLNLNYQTPKKK...ELKAHGRDLQDIIGQQQGKRALEIAAAGNHNLLFLGPPGTGKTMLASRLCDLL	235
NTDB id 1349 HI 1117 AAC22771.1	LLEVCADLCGQQTLSLFQSSPSV...QQVSRDLQDIIGQQQGKRALEIAAAGNHNLLFLGPPGTGKTMLASRLCDLL	235
NTDB id 1387 A4U84 RS06900 WP 020457569.1	LLDVVQFLNGQEKPLATEIVKESAVNFSGKNTLLDLDIIGQQHAKRALTIAAAGQHNLLFLGPPGTGKTMLASRLTGLL	239
consensus	LLQVVNFLNNRDQLPIAQQLSQNIAEN.RPLVSRDLTDIIGQQHAKRALIIAASGQHLLFLGPPGTGKTMLASRLADLL	238



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NTDB id 1323 RAOC RS07335 WP 004916218.1	PEMSDEALEETASISLVQKEPNEHNWKRPFRAPHHSASMAALVGGGSIIPGGEISLAHNGVFLDELPEFERKVLDA	318
NTDB id 1271 LPP RS03220 WP 011213198.1	PPPLTLKEALETTKIHSVAGKMGAETSLMTIRPFRSPHHTISDV ALVGGGSYPQPGGEISLAHNGVFLDEMPFEKRTVLEV	314
NTDB id 1248 GC085 RS03150 WP 011213198.1	PELSETQALECAAINSIRGKLPDF.REWRLLPFRAPHHTASPV ALVGGGNPPKPGGEISLAHNGVFLDELPEFNRQVLET	314
NTDB id 1009342 ABNK32 RS30255 WP 032693771.1	PELSETQALECAAINSIRGKLPDF.REWRLLPFRAPHHTASPV ALVGGGNPPKPGGEISLAHNGVFLDELPEFNRQVLET	313
NTDB id 1397 DSB67 RS15690 WP 005535577.1	PPLSNQEALESAAILSLVDSRHAM.KNWRRLPFRAPHHSSSLAAMVGGGSTIPAPGEISLAHNGVFLDELPEFERVLD	314
NTDB id 1153 A1552VC RS00115 WP 000521788.1	PEMSDEEAMETASVASLTQSEINE.HNWKTRPFRAPHHSSSMAALVGGGSVPRPGEISLAHNGLLFLDEMPEFDRKVLDS	314
NTDB id 1349 HI 1117 AAC22771.1	PEMSDEEAMETASIASLTQQEINQ.HNWKLRPFRAPHHSSSMAALVGGGTIPRPGGEISLAHNGLLFLDEMPEFERKVLDS	314
NTDB id 1387 A4U84 RS06900 WP 020457569.1	PEMTDLEAIETASVTSLVQNELNF.HNWKRPFRAPHHSSASMPALVGGGTIPKPGGEISLATNGVFLDELPEFERKVLDA	318
consensus	PEMTDLEAIETASVTSLVQNELNF.QNWKRPFRSPHHSASMAALVGGGSIPKPGGEISLAHNGVFLDELPEFERKVLDA	317



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NTDB id 1323 RAOC RS07335 WP 004916218.1	LREPLESGEIIISRAAKIIFPAFQLYAAMNPSPTCGYGSONRISPPQRIIRYLRLSGPFLDRFDMSIEIPALPQG	397
NTDB id 1271 LPP RS03220 WP 011213198.1	MRQPLEDRVITISRAKFTVNYPASFMLVASMNPSPSGFFPDDPNNT.SSSFEMQRYLNLKLSGPLLDRIDITHIEVQKVEFD	394
NTDB id 1248 GC085 RS03150 WP 011213198.1	LREPLESGHICISRAAAQIEFPAKFQLIAAMNPPCGQWGNISQANCMCTPDRIISRYLAKLSAPLLDRIDMQVTIHALSQE	394
NTDB id 1009342 ABNK32 RS30255 WP 032693771.1	LREPLESGHICISRAAAQIEFPAKFQLIAAMNPPCGQWGNISQANCMCTPDRIISRYLAKLSAPLLDRIDMQVTIHALSQE	391
NTDB id 1397 DSB67 RS15690 WP 005535577.1	LREPLESGEIIISRAQKTRFPAFQIVGALNPSPGTGYEGNQAR..TNPQATILRYLGRLSGPFLDRFDLSIEIPLPPPG	392
NTDB id 1153 A1552VC RS00115 WP 000521788.1	LREPLESGEIVISRAQKTRFPAFQIVGALNPSPGTGYEGSQAR..ANPQSILRYLSRLSGPFLDRFDMSIEIPALPKG	392
NTDB id 1349 HI 1117 AAC22771.1	LRQPLESGEIIISRAQKTRFPAFQIVGALNPSPGTGYEGNQAR..ANPQSILRYLSRLSGPFLDRFDMSIEIPALPKG	396
NTDB id 1387 A4U84 RS06900 WP 020457569.1	LRQPLESGEIIISRAQKTRFPAFQIVGALNPSPGTGYEGNQAR..ANPQSILRYLSRLSGPFLDRFDMSIEIPALPKG	395
consensus	*!*****!!!!* *** *!!!!*****!!!!* * ** * ** *!!!! *!!!!*!!!!*!!!!***** ** *	

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NTDB id 1323 RAOC RS07335 WP 004916218.1	QLSDK..RKGESSEIRQRVLKAREIQERYQDLAISYNAQMGPKEIEHFCELDVSLLLIKNAMEKLNLSARAYDRILK	475
NTDB id 1271 LPP RS03220 WP 011213198.1	ELIKPNTHLEKQSLAIREKVTMKHEIQMARQDS...LNANLNSKTCCEMVCELGSEEQLFLREVMSKLLKSARGYHRLIK	470
NTDB id 1248 GC085 RS03150 WP 011213198.1	ELIKPNTHLEKQSLAIREKVTMKHEIQMARQDS...LNANLNSKTCCEMVCELGSEEQLFLREVMSKLLKSARGYHRLIK	470
NTDB id 1009342 ABNK32 RS30255 WP 032693771.1	VLSQGT.NEESSACVRQRVLAARERQLSRQKK...LNAHLGNDEMCKICRRLHKDPAVWLEQTLIQLGLSTRAWQRLIK	466
NTDB id 1397 DSB67 RS15690 WP 005535577.1	TLSEG.GDRGEPTAIVKERVNQARDCLARSGK...VNALLGSREIEAFQPLQKSDAEFLENALHRLGLSIRAYHRIIK	467
NTDB id 1153 A1552VC RS00115 WP 000521788.1	TLANG.GDRGESTAAVRQRVWVARERMLARSGK...VNALLGSREIEQYCPLLKADAEFLESALHRLGLSIRAYHRIIK	467
NTDB id 1349 HI 1117 AAC22771.1	SLQNT.GDRGETSAQVREKVLKVREIQMERAGK...INAYLNSKEIERDCCKLNDKDAFFLEKALNKLGLSVRAYHRILK	471
NTDB id 1387 A4U84 RS06900 WP 020457569.1	ALQNNTDQRGETTEQARKRVLEARHLQFNRRGK...INAQLTTKEIEQDCCKLTDRDAFLFLENALTKLGLSVRAYHRILK	471
consensus	! **** * *! ***** ! * *!! * ***** !! ***** * *!*****!!*****!!	

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NTDB id 1323 RAOC RS07335 WP 004916218.1	VSRTIADLERETNIQSHHIAEAIQYRSLDRDFWKV.....	510
NTDB id 1271 LPP RS03220 WP 011213198.1	VSRTIADMNSSKKVLLNHLQQALSQKQNLHLPK.....	503
NTDB id 1248 GC085 RS03150 WP 011213198.1	VSRTIADMNSSKKVLLNHLQQALSQKQNLHLPK.....	503
NTDB id 1009342 ABNK32 RS30255 WP 032693771.1	VSRTIADIEAVERIERHHLQEALGYRAIDRMLSHLQKMMA	506
NTDB id 1397 DSB67 RS15690 WP 005535577.1	VARTIADLEGSPQIERTHLAEALGYRAMDRLLKQLTAQAV	507
NTDB id 1153 A1552VC RS00115 WP 000521788.1	VARTIADLQCEAQIARPHLAEALGYRAMDRLLKQLSAQNV	507
NTDB id 1349 HI 1117 AAC22771.1	VSRTIADLQCEQIQIFQPHLAEALGYRAMVRLLQKLSNM..	509
NTDB id 1387 A4U84 RS06900 WP 020457569.1	VSRTIADLACEAQIQPHLAEALGYRAMDRLLQRLQGES.	510
consensus	!*****! * ** !***** * *	

- X non conserved
- X similar
- X ≥50% conserved