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NTDB id 1323 RAOC RS07335 WP 004916218.1	MSLAIVYSRASIGVAPPVTVVHLSNGPGETLVGLPETTVKESDRVRSALINSQEEPAKRITVNLAPADLPKEGGR	78
NTDB id 1271 LPP RS03220 WP 011213198.1	.MLVKKVYGSAIHGVSAQTTITIEVNVDDGV.GYHLVGLPDNAIKESSHRISAALKNVGYKLPKKITINMAPADLRKEGSA	80
NTDB id 1248 GC085 RS03150 WP 011213198.1	MSLAFTTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETAVKESKDRVRSAINSQFEFPCRKITVNLGPANLPKGTGSG	80
NTDB id 1010768 ABR099 RS23305 WP 000058964.1	MSLAFTTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETAVKESKDRVRSAINSQFEFPCRKITVNLGPANLPKGTGSG	80
NTDB id 1153 A1552VC RS00115 WP 000521788.1	MSLSIVHTRALGLVNAPPITVEVHISKGLPGLTMVGLPETTVKEARDRVRSAINSGYEYPAKKITINLAPADLPKEGGR	80
NTDB id 1397 DSB67 RS15690 WP 005535577.1	MGLAIIHSRASIGVQAPPVTVEVHISNGMPGFTLVGLPETTVKESRDRVRSAINSRFEFPAKRITVNLAPADLPKEGGR	80
NTDB id 1349 HI 1117 AAC22771.1	MGLAIIHSRASVGVQAPSVSVEVHISNGMPGFTLVGLPETTVKESKDRVRSAINVSNFQFPAKRITVNLAPADLPKEGGR	80
NTDB id 1387 A4U84 RS06900 WP 020457569.1	MSLAIVYSRASMGVQAPLVTIEVHLSNGKPGFTLVGLPEKTVKEAQDRVRSALMNAQFKYPAKRITVNLAPADLPKEGGR	80
consensus	MSLAIIYSRASIGVEAPLVTIEVHISGGSPLTLVGLPEKSVKEAQDRVRSALMNANFDYPARRITINLAPADLPKEGGR	80



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NTDB id 1323 RAOC RS07335 WP 004916218.1	FDLPIALGILAASQQLTANKLKNYEFYGLALGSLRGVKGVLPAALAAKRLIYLPKQNADEASLVGQVYAN	158
NTDB id 1271 LPP RS03220 WP 011213198.1	YDLSTIALGILAASGQIIAPEIERYLIMGELSLDGGQLPIKGVLPPIARAREEGFGKTIILPKQNTREAAIVNDLEVYGVEN	159
NTDB id 1248 GC085 RS03150 WP 011213198.1	FDLPIALGILAASEQIPLTNLANHEFIGELALSGELRGVSAIIPAVLAAHKD.NQHLLIIANANAAEASLTGHQKVFTANN	159
NTDB id 1010768 ABR099 RS23305 WP 000058964.1	FDLPIALGILAASEQIPLTNLANHEFIGELALSGELRGVSAIIPAVLAAHKD.NQHLLIIANANAAEASLTGHQKVFTANN	159
NTDB id 1153 A1552VC RS00115 WP 000521788.1	YDLPIAIALLAASEQLTANKLDEYELVGLALTGALRGVPGAIISSATEAIKS.GRKLIVAKDNEDEVGLINGEGCLIADH	159
NTDB id 1397 DSB67 RS15690 WP 005535577.1	FDLPIALGILAASDQIARNKLESYEFIGELALSGEIRGVKGVLPAAALANQV.ERCLVVPHSNGDQAALVGVERHKSQAS	159
NTDB id 1349 HI 1117 AAC22771.1	FDLPIALGILAASEQIATDKLKNYEFVGLALSGGLRRTVKGVLPAAALAAKQK.QRHLVVPHANGDQAALVGKEQHKSAQS	159
NTDB id 1387 A4U84 RS06900 WP 020457569.1	FDLPIAIGILAASDQLDASHLKQFEFVAELALTGQLRGVHGVIPAILAAQKS.KRELIIAKQNANEASLVSDQNTYFAQT	159
consensus	FDLPIAIGILAASGQIDSDKLKRIFELGELSLTGHLRGVHGAIPAVLAASKA.KRETIIVPQQNANEVSLVSNQTQYCAST	159



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NTDB id 1323 RAOC RS07335 WP 004916218.1	LLEVCDELGGQTSGLLQPKPKLNNYERDLSDIIGQQHAKRALEIAAGGHNLLFLGPPGTGKTMLASRLCDLL	238
NTDB id 1271 LPP RS03220 WP 011213198.1	LREVCDELQCGTSLQSLPPKPDLLNNYELDWSDIKQQHAKNAMVIAACGGHSILLSGAPGSGKTMMAKRFSTLL	235
NTDB id 1248 GC085 RS03150 WP 011213198.1	LREVCDELQCGTSLQSLPPKPDLLNNYELDWSDIKQQHAKNAMVIAACGGHSILLSGAPGSGKTMMAKRFSTLL	235
NTDB id 1010768 ABR099 RS23305 WP 000058964.1	LQAVCAFLQKHALERPCKPTDA...VSRALQHDLSDVIGQEQKRGLEITAAGGHNLLFLGPPGTGKTMLASRLINGLL	234
NTDB id 1153 A1552VC RS00115 WP 000521788.1	LLEVCADLCGQQTLSLFQSSPSV...QQVSQTRDLQDIIGQQQKRALEIAAAGNHNLLFLGPPGTGKTMLASRLCDLL	235
NTDB id 1397 DSB67 RS15690 WP 005535577.1	LLEVCDELQCGHQLNLYQTPKKK...ELKAHGRDLQDIIGQQQKRALEIAAAGNHNLLFLGPPGTGKTMLASRLCDLL	235
NTDB id 1349 HI 1117 AAC22771.1	LLDVVQFLNGQEKPLATEIVKESAVNFSGKNTLLDIIGQQHAKRALTIAAAGQHNLLFLGPPGTGKTMLASRLTGLL	239
NTDB id 1387 A4U84 RS06900 WP 020457569.1	LLQVVNFLNNRDQLPIAQQLSQNIAEN.RPLVSRDLTDIIGQQHAKRALTIAAAGQHNLLFLGPPGTGKTMLASRLADLL	238
consensus	LLEVCDELQCGTSLQSLPPKPDLLNNYELDLSDIIGQQHAKRALEIAAGGHNLLFLGPPGTGKTMLASRLCDLL	238



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NTDB id 1323 RAOC RS07335 WP 004916218.1	PEMSDEALEETASISLVQENFHNWKRPFRAPHHSASMAALVGGGSIKPKGEISLAHNGVFLDELPEFERKVLDA	318
NTDB id 1271 LPP RS03220 WP 011213198.1	PELSETQALECAAINSIRGKLPDF.REWRLLPFRAPHHTASPVVALVGGGNPPKPEISLAHHGVFLDELPEFNRQVLET	314
NTDB id 1248 GC085 RS03150 WP 011213198.1	PELSETQALECAAINSIRGKLPDF.REWRLLPFRAPHHTASPVVALVGGGNPPKPEISLAHHGVFLDELPEFNRQVLET	314
NTDB id 1010768 ABR099 RS23305 WP 000058964.1	PDLSENEALESAAISLVNAESVQ.KQWRQRPFRSPHHSASLTAMVGGGATPGPEISLAHNGVFLDELPEFERRTLDA	313
NTDB id 1153 A1552VC RS00115 WP 000521788.1	PEMSDEEAMETASIASLTQQEINQ.HNWKLRPFRAPHHSSMAALVGGGTIPRPGEISLAHNGLLFLDEMPEFERKVLDS	314
NTDB id 1397 DSB67 RS15690 WP 005535577.1	PEMSDEEAMETASVASLTQSEINE.HNWKTRPFRAPHHSSMAALVGGGSVPRPGEISLAHNGLLFLDEMPEFDRKVLDS	314
NTDB id 1349 HI 1117 AAC22771.1	PEMTDLEAIETASVTSLVQNELNF.HNWKQRPFRAPHHSASMPALVGGGTIPKPEISLATNGVFLDELPEFERKVLDA	318
NTDB id 1387 A4U84 RS06900 WP 020457569.1	PEMTDLEAIETASVTSLVQNELNF.HNWKKRPFRSPHHSASMPALVGGGSIPKPEISLAHNGVFLDELPEFERKVLDA	317
consensus	PEMSDEALEETASISLVQENFHNWKRPFRAPHHSASMAALVGGGSIKPKGEISLAHNGVFLDELPEFERKVLDA	318



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NTDB id 1323 RAOC RS07335 WP 004916218.1	LREPLESGEIIISRAAKIIFPAFQLYAAMNPSPTCGYGSONRITPQRIIRYLNRLSGPIIDREFDMSIEIPALPQG	397
NTDB id 1271 LPP RS03220 WP 011213198.1	MRQPLEDRVETISRAKFTVNYPASFMLVASMNPSPSGFFPDDPNNT.SSSFEMQRYLNKLSGPLLDRIDITHIEVQKVVEFD	394
NTDB id 1248 GC085 RS03150 WP 011213198.1	LREPLESGHICISRAAAQIEFPAKFQLI AAMNPPCGQWGN SQANCMCTPDRIISRYLAKLSAPLLDRIDMQVTIHALSQE	394
NTDB id 1010768 ABR099 RS23305 WP 000058964.1	LREPLESGHICISRAAAQIEFPAKFQLI AAMNPPCGQWGN SQANCMCTPDRIISRYLAKLSAPLLDRIDMQVTIHALSQE	391
NTDB id 1153 A1552VC RS00115 WP 000521788.1	LREPLESGEIVISRAQKTRFPAFQLVGALNPSPGTGYEGSSQA..RANPQSILRYLSRLSGPLLDRFDMSTIEIPALPKG	392
NTDB id 1397 DSB67 RS15690 WP 005535577.1	LREPLESGEIIISRAQKTRFPAFQIVGALNPSPGTGYEGNQA..RTNPQAAILRYLGRLSGPLLDRFDMSTIEIPALPKG	392
NTDB id 1349 HI 1117 AAC22771.1	LRQPLESGEIIISRAANAKIQFPAFQLV AAMNPSPGTGHYTGT HN..RTSPQQIMRYLNRLSGPF LDRFDLSIEVPLLPQG	396
NTDB id 1387 A4U84 RS06900 WP 020457569.1	LRQPLESGEIIISRAANAKVFFPAFQLI AAMNPSPGTGHYQGT HN..RTSPQQLMRYLNRLSGPF LDRFDLSIEVPLLPQG	395
consensus	*!***** *!!* *** *!!*!*****!!*!!* * ** * ** *!!!! *!!!!*!!!!*!***** ** *	

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NTDB id 1323 RAOC RS07335 WP 004916218.1	Q L S D . . K R K G E S S E I I R Q R V L K A R E I Q Q E R Y Q D L A I S Y N A Q M G P K E I E H F C E L D E V S L L I T K N A M E K L N L S A R A Y D R I L K	475
NTDB id 1271 LPP RS03220 WP 011213198.1	ELIKPNTHLEKQSLAIREKVTMKHEIQMARQDS...LNANLNSKTCCEMVCELGSEEQLFLREVMSKLLKSARGYHRLK	470
NTDB id 1248 GC085 RS03150 WP 011213198.1	ELIKPNTHLEKQSLAIREKVTMKHEIQMARQDS...LNANLNSKTCCEMVCELGSEEQLFLREVMSKLLKSARGYHRLK	470
NTDB id 1010768 ABR099 RS23305 WP 000058964.1	ILSKT.VVPGESSATVQKRVMAARERQFKRQNK...LNAWLDSPETIRQFCKLESEDAMWLEGTLIHLGLSTRAWQRLK	466
NTDB id 1153 A1552VC RS00115 WP 000521788.1	TLANG.GDRGESTAAVRQRVVVARERMLARSGK...VNALLQSREIEQYCPLLKADAEFLESALHRLGLSIRAYHRIK	467
NTDB id 1397 DSB67 RS15690 WP 005535577.1	TLSEG.GDRGEPTAIVKERVNQARDCMLARSGK...VNALLQSREIEAFCP LQKSDAEFLENALHRLGLSIRAYHRIK	467
NTDB id 1349 HI 1117 AAC22771.1	SLQNT.GDRGETSAQVREKVLKVREIQMERAGK...INAYLNSKEIERDCKLNDKDAFFLEKALNKLGLSVRAYHRILK	471
NTDB id 1387 A4U84 RS06900 WP 020457569.1	ALQNNTDQRGETTEQARKRVLEARHLQFNRRGK...INAQLTKEIEQDCKLTDRDAFLFLENALT KLGLSVRAYHRILK	471
consensus	! **** * * * ! * * * * * ! * * * ! ! * * * * * ! ! * * * * * * * * ! * ! * ! * ! * ! * ! * ! * !	

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NTDB id 1323 RAOC RS07335 WP 004916218.1	VSRTIADLERETNIQSHHIAEAIQYRSIDRDFWKV.....	510
NTDB id 1271 LPP RS03220 WP 011213198.1	VSRTIADMNSSKKVLLNHLQQALS YKQNLHLPK.....	503
NTDB id 1248 GC085 RS03150 WP 011213198.1	VSRTIADMNSSKKVLLNHLQQALS YKQNLHLPK.....	503
NTDB id 1010768 ABR099 RS23305 WP 000058964.1	VARTIADIDQSDIITRQHLQEAVSYRAIDRLLIH LQKLLT	506
NTDB id 1153 A1552VC RS00115 WP 000521788.1	VARTIADLQGEAQIARPHLAEALGYRAMDRLLKQLSAQNV	507
NTDB id 1397 DSB67 RS15690 WP 005535577.1	VARTIADLEGSPQIERTHLAEALGYRAMDRLLKQLTAQAV	507
NTDB id 1349 HI 1117 AAC22771.1	VSRTIADLQGEQ QIFQPHLAEALGYRAMVRL LKQLSNM..	509
NTDB id 1387 A4U84 RS06900 WP 020457569.1	VSRTIADLAGEAQIQPHLAEALGYRAMDRLLQRLQGES.	510
consensus	! * ! ! ! ! ! * * * ! * * ! * * * * * *	

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