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NTDB id 1323 RAOC RS07335 WP 004916218.1	MSLAIVYSRASIGVAPLVTVVHLSNGPGETLVGLPETTVKESDRVRSALINSQEFPAKRITVNLAPADLPKEGGR	78
NTDB id 1271 LPP RS03220 WP 011213198.1	.MLVKKVYGSAIHGVSAQTTITIEVNVDQGV.GYHLVGLPDNAIKESSHRISAAIKNVGYKLPKGGKITINMAPADLRKEGSA	80
NTDB id 1248 GC085 RS03150 WP 011213198.1	MSLAFTTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETAVKESKDRVRSAINSQFEFPCKRITVNLGPANLPKGTGSG	80
NTDB id 1106468 ACN4IK RS22740 WP 022649778.1	MSLAFTTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETAVKESKDRVRSAINSQFEFPCKRITVNLGPANLPKGTGSG	80
NTDB id 1397 DSB67 RS15690 WP 005535577.1	MSLSVVYTRAIGVKAPLISVEVHLSNGLPGLTLVGLPETTVKEARDRVRSAINSGYAFPAKKITINLAPADLPKEGGR	80
NTDB id 1153 A1552VC RS00115 WP 000521788.1	MGLAIIHSRASVGVQAPSVSVEVHISNGMPGFTLVGLPETTVKESKDRVRSAINVSNFQFPAKRITVNLAPADLPKEGGR	80
NTDB id 1349 HI 1117 AAC22771.1	MGLAIIHSRASIGVQAPPVTVVEVHISNGMPGFTLVGLPETTVKESRDRVRSAINSRFEFPKAKRITVNLAPADLPKEGGR	80
NTDB id 1387 A4U84 RS06900 WP 020457569.1	MSLAIVYSRASMGVQAPLVTTIEVHLSNGKPGFTLVGLPEKTVKEAQDRVRSALMNAQFKYPAKRITVNLAPADLPKEGGR	80
consensus	MSLAIIYSRASIGVEAPLVTTIEVHISGGSPGLTLVGLPEKSVKEAQDRVRSALMNAFDPARRITINLAPADLPKEGGR	80



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NTDB id 1323 RAOC RS07335 WP 004916218.1	FDLPIALGILAASQQLRTIKKKNYEFYGEALALSGELRGVGVLPAAALAKNRLLVYPNQNAEASLVGLGVYVAA	158
NTDB id 1271 LPP RS03220 WP 011213198.1	YDLSTIALGILAASGQIIAPEIERYLIMGELSLDGGQLPIKGVLPPIARAREEGFGKTIILPKQNTREAAIVNDLEVYGVEN	159
NTDB id 1248 GC085 RS03150 WP 011213198.1	FDLPIALGILAASEQIPLTNLANHEFIGELALSGELRGVSAIIPAVLAAHKD.NQHLIIANANAAEASLTGHQKVFTANN	159
NTDB id 1106468 ACN4IK RS22740 WP 022649778.1	FDLPIALGILAASEQIPLTNLANHEFIGELALSGELRGVSAIIPAVLAAHKD.NQHLIIANANAAEASLTGHQKVFTANN	159
NTDB id 1397 DSB67 RS15690 WP 005535577.1	YDLPIAIALLAASEQLNTPGLSSCEFVGELALTGALRGVPGAISGALEAIRA.GRQTIIVANENASEVSLTAEKGCLVAGH	159
NTDB id 1153 A1552VC RS00115 WP 000521788.1	FDLPIALGILAASEQIATDKLKNYEFVGELALSGGLRTVKGVLPAALAANKK.QRHLVVPHANGDQAALVGKEQHKSAQS	159
NTDB id 1349 HI 1117 AAC22771.1	FDLPIALGILAASDQIARNKLESYEFIGELALSGEIRGVKGVLPAALAANKV.ERCLVVPHSNGDQAALVGVERHKSQAQS	159
NTDB id 1387 A4U84 RS06900 WP 020457569.1	FDLPIAIGILAASDQLDASHLKQFEFVAELALTGQLRGVHGVIPAILAAQKS.KRELIIAKQNANEASLVSDQNTYFAQT	159
consensus	FDLPIAIGILAASGQIDSDKLKRIELLGELSLTGHLRGVHGAIPAVLAASKA.KRETIIVPQQNANEVSLVSNTQTFCAST	159



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NTDB id 1323 RAOC RS07335 WP 004916218.1	LLEVCDFCCGRTSLLQENCKYLNNTIRDLSDIIGQQHAKRALEIAAGGHNLLFGPPGTGKTMLASRLSDLL	238
NTDB id 1271 LPP RS03220 WP 011213198.1	IKVEIDFFNENCPLEPTKVNTREEFHKRVNLPFPDFSEVKGQETAKRAMEVAAAGGHNIIILGPPGSGKTMLAKRIPSTIL	235
NTDB id 1248 GC085 RS03150 WP 011213198.1	LREVCDFLCQGTSLQSLPPKPDLL...LLNNYELDWSDIKGQQHAKNAMVIAACGGHSILLSGAPGSGKTMMAKRFSTLL	235
NTDB id 1106468 ACN4IK RS22740 WP 022649778.1	LREVCDFLCQGTSLQSLPPKPDLL...LLNNYELDWSDIKGQQHAKNAMVIAACGGHSILLSGAPGSGKTMMAKRFSTLL	234
NTDB id 1397 DSB67 RS15690 WP 005535577.1	LQEVCAWLEGRHELAEPQENEEV...VADSPDDLSDIMGQEQGKRALEITAAGGHNLLILGPPGTGKTMLASRLSGLL	235
NTDB id 1153 A1552VC RS00115 WP 000521788.1	LLEVCAELCGQHQLNLYQTPKKK...ELKAHGRDLQDIIGQQQKRALEIAAAGNHNLLFLGPPGTGKTMLASRLCDLL	235
NTDB id 1349 HI 1117 AAC22771.1	LLEVCADLCGQQTLSLFQSSPSV...QQVSQTRDLQDIIGQQQKRALEIAAAGNHNLLFLGPPGTGKTMLASRLCDLL	239
NTDB id 1387 A4U84 RS06900 WP 020457569.1	LLQVVNFLNNRDQLPIAQQLSQNIAEN.RPLVSRDLTDIIGQQHAKRALIIAASGQHNNLLFLGPPGTGKTMLASRLADLL	238
consensus	LLEVCDFCCGRTSLLQENCKYLNNTIRDLSDIIGQQHAKRALEIAAGGHNLLFGPPGTGKTMLASRLSDLL	



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NTDB id 1323 RAOC RS07335 WP 004916218.1	PEMSDIEALEETASISLVQKEPNEHNWKRPFRAPHHSASMVVGVGGSIIPGGEISLAHNGVFLDELPEFERKVLDA	318
NTDB id 1271 LPP RS03220 WP 011213198.1	PPLTLKEALETTKIHSVAGKMGAEATSLMTIRPFRSPHHTISDVVALVGGGSYPQPGGEISLAHNGVFLDEMPEFKRTVLEV	314
NTDB id 1248 GC085 RS03150 WP 011213198.1	PELSETQALECAAINSIRGKLPDF.REWRLLPFRAPHHTASPVVALVGGGNPPKPGGEISLAHNGVFLDELPEFNRQVLET	314
NTDB id 1106468 ACN4IK RS22740 WP 022649778.1	PELSETQALECAAINSIRGKLPDF.REWRLLPFRAPHHTASPVVALVGGGNPPKPGGEISLAHNGVFLDELPEFNRQVLET	313
NTDB id 1397 DSB67 RS15690 WP 005535577.1	PPLNNHEALESAAIFSLVSSISLH.KQWRRRPFRSPHHSASLTAMVGGGSIPGPGGEISLAHNGVFLDELPEFERVLD	314
NTDB id 1153 A1552VC RS00115 WP 000521788.1	PEMSDEEAMETASVASLTQSEINE.HNWKTRPFRAPHHSSMAALVGGGSVPRPGEISLAHNGVFLDEMPEFDRKVLDS	314
NTDB id 1349 HI 1117 AAC22771.1	PEMSDEEAMETASIASLTQEQINQ.HNWKLRPFRAPHHSSMAALVGGGTIPRPGGEISLAHNGVFLDEMPEFERKVLDS	314
NTDB id 1387 A4U84 RS06900 WP 020457569.1	PEMTDLEAIIETASVTSLVQNELNF.HNWKRPFRAPHHSASMPALVGGGTIPKPGGEISLAHNGVFLDELPEFERKVLDA	318
consensus	PEMTDLEAIIETASVTSLVQNELNF.HNWKRRPFRSPHHSASMPALVGGGSIPKPGGEISLAHNGVFLDELPEFERKVLDA	317



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NTDB id 1323 RAOC RS07335 WP 004916218.1	LREPLESGEIIISRAAKIIFPAFQLYAAMNPSPTCGYGSONRTTPQQLRYLRLSGPFLDRFDMSIEIPALPQG	397
NTDB id 1271 LPP RS03220 WP 011213198.1	MRQPLEDRVITISRAKFTVNYPASFMLVASMNPSPSGFFPDDPNNT.SSSFEMQRYLNKLSGPLLDRIDITHIEVQKVVEFD	394
NTDB id 1248 GC085 RS03150 WP 011213198.1	LREPLESGHICISRAAAQIEFPAKFQLIAAMNPPCGQWGNSSQANCMCTPDRIISRYLAKLSAPLLDRIDMQVTIHALSQE	394
NTDB id 1106468 ACN4IK RS22740 WP 022649778.1	LREPLESGHICISRAAAQIEFPAKFQLIAAMNPPCGQWGNSSQANCMCTPDRIISRYLAKLSAPLLDRIDMQVTIHALSQE	391
NTDB id 1397 DSB67 RS15690 WP 005535577.1	LREPESGEIHLSTRAKISYPAQFQLVAAMNPSPTGHHYQGNHN..RCTPEQTLRYLSKLSGPFLLDRFDLSLEIPLPPPG	392
NTDB id 1153 A1552VC RS00115 WP 000521788.1	LREPLESGEIIISRAQKTRFPAQFQIVGALNPSPTGYYEGNQA..RTNPQATILRYLGRLSGPPLDRFDMSLEIPALPKG	392
NTDB id 1349 HI 1117 AAC22771.1	LREPLESGEIVISRAQKTRFPAQFQIVGALNPSPTGYYEGSSQA..RANPQSILRYLSRLSGPPLDRFDMSIEIPALPKG	396
NTDB id 1387 A4U84 RS06900 WP 020457569.1	LRQPLESGEIIISRANAKIQFPAQFQIVGALNPSPTGHHYTGTHN..RTSPQQIMRYLNRLSGPFLDRFDLSIEVPLLPQG	395
consensus	*!***** *!* ** *!*!*!!!!!!!!!!!!!! * ** * ** *!!!! *!!!!*!!!!!!*!!!!***** ** *	

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NTDB id 1323 RAOC RS07335 WP 004916218.1	QNSD..KRKGESSEIRQVRLKAREIQQERYQDLAISYNAQMGPKEIEHFCELDVSLLLTKNAMEKLNLSARAYDRILK	475
NTDB id 1271 LPP RS03220 WP 011213198.1	ELIKPNTHLEKQSLAIQREKVTMKHEIQMARQDS...LNANLNSKTCCEMVCELGSEEQLFLREVMSKLLKSARGYHRLK	470
NTDB id 1248 GC085 RS03150 WP 011213198.1	ELIKPNTHLEKQSLAIQREKVTMKHEIQMARQDS...LNANLNSKTCCEMVCELGSEEQLFLREVMSKLLKSARGYHRLK	470
NTDB id 1106468 ACN4IK RS22740 WP 022649778.1	LLRQT.GIKGESSAVVRERVIAAQAQYARQNR...LNARLDNSGTRQFCSLNAEDAGWLEETLTRFGLSTRAWQRLK	466
NTDB id 1397 DSB67 RS15690 WP 005535577.1	TLSEG.GDRGEPTAIVKERVNQARDCLARSGK...VNALLGSREIEAFQPLQKSDAEFLENALHRLGLSIRAYHRIK	467
NTDB id 1153 A1552VC RS00115 WP 000521788.1	TLANG.GDRGESTAAVRQVWVARERMLARSGK...VNALLGSREIEQYCPLLKADAEFLESALHRLGLSIRAYHRIK	467
NTDB id 1349 HI 1117 AAC22771.1	SLQNT.GDRGETSAQVREKVLKVREIQMERAGK...INAYLNSKEIERDCKLNDKDAFFLEKALNKLGLSVRAYHRILK	471
NTDB id 1387 A4U84 RS06900 WP 020457569.1	ALQNNTDQRGETTEQARKRVLEARHLQFNRRGK...INAQLTKEIEQDCKLTDRDALFLENALTKLGLSVRAYHRILK	471
consensus	! ***** *!!!! *!!!!*!!!!!! * *!!!! * *!!!! *!!!!*!!!!!!*!!!!***** *!!!!*!!!!!!*!!!!***** *!!!!*!!!!!!*!!!!***** *!!!!*!!!!!!*!!!!*****	

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NTDB id 1323 RAOC RS07335 WP 004916218.1	VSRTIADLERETNIQSHHIAEAIQYRSILDRDFWKV.....	510
NTDB id 1271 LPP RS03220 WP 011213198.1	VSRTIADMNSSKKVLLNHLQQAISYKQNLHLPK.....	503
NTDB id 1248 GC085 RS03150 WP 011213198.1	VSRTIADMNSSKKVLLNHLQQAISYKQNLHLPK.....	503
NTDB id 1106468 ACN4IK RS22740 WP 022649778.1	VARTVADVEGCPGIERRHLQEALSYRAIDRLLHLQKMLA	506
NTDB id 1397 DSB67 RS15690 WP 005535577.1	VARTIADLEGSPQIERTHLAEALGYRAMDRLLKQLTAQAV	507
NTDB id 1153 A1552VC RS00115 WP 000521788.1	VARTIADLQGEAQIARPHLAEALGYRAMDRLLKQLSAQNV	507
NTDB id 1349 HI 1117 AAC22771.1	VSRTIADLQGEQIFQPHLAEALGYRAMVRLKQLSNM..	509
NTDB id 1387 A4U84 RS06900 WP 020457569.1	VSRTIADLAGEAQIQPHLAEALGYRAMDRLLQRLQGES.	510
consensus	!*****! * * *!!!! *!!!!*!!!!!! *!!!!*!!!!!!*!!!!***** *!!!!*!!!!!!*!!!!*****	

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