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NTDB id 1323 RAOC RS07335 WP 004916218.1	MSLAIVYSRASIGVAPLVTVVHLSNGPGETLVGLPETTVKESDRVRSALINSQEFPAKRITVNLAPADLPKEGGR	78
NTDB id 1271 LPP RS03220 WP 011213198.1	.MLVKKVYGSAIHGVSAQTTITIEVNVDDGV.GYHLVGLPDNAIKESSHRISAALKNVGYKLPKGGKITINMAPADLRKEGSA	80
NTDB id 1248 GC085 RS03150 WP 011213198.1	MSLAFTTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETAVKESKDRVRSAINSQFEFPCRKITVNLGPANLPKGTGSG	80
NTDB id 1036009 AB7D97 RS22645 WP 022649778.1	MSLAFTTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETAVKESKDRVRSAINSQFEFPCRKITVNLGPANLPKGTGSG	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	MGLAIIHSRASIGVQAPPVTVVEVHISNGMPGFTLVGLPETTVKESRDRVRSAINSRFEFPAKRITVNLAPADLPKEGGR	80
NTDB id 1387 A4U84 RS06900 WP 020457569.1	MSLAIVYSRASMGVQAPLVTTIEVHLSNGKPGFTLVGLPEKTVKEAQDRVRSALMNAQFKYPAKRITVNLAPADLPKEGGR	80
consensus	MSLAIIYSRASIGVEAPLVTTIEVHISGGSPGLTLVGLPEKSVKEAQDRVRSALMNAFDPARRITINLAPADLPKEGGR	80



logo

NTDB id 1323 RAOC RS07335 WP 004916218.1	FDLPIALGILAASQQLITIAPEIERYLIMGELSLDGGQLPIKGVLPPIAIRAREEGFGKTIILPKQNTREAAIVNDLEVYGVEN	158
NTDB id 1271 LPP RS03220 WP 011213198.1	FDLPIALGILAASEQIPLTNLANHEFIGELALSGELRGVSAIIPAVLAAHKD.NQHLLIIANANAAEASLTGHQKVFTANN	159
NTDB id 1248 GC085 RS03150 WP 011213198.1	FDLPIALGILAASEQIPLTNLANHEFIGELALSGELRGVSAIIPAVLAAHKD.NQHLLIIANANAAEASLTGHQKVFTANN	159
NTDB id 1036009 AB7D97 RS22645 WP 022649778.1	YDLPIAIALLAASEQLNTPGLSSCEFVGELALTGALRGVPGAISGALEAIRA.GRQTIIVANENASEVSLTAEKGCLVAGH	159
NTDB id 1397 DSB67 RS15690 WP 005535577.1	FDLPIALGILAASEQIATDKLKNYEFVGELALSGGLRTVKGVLPAALAAANKK.QRHLVVPHANGDQAALVGKEQHKSAQS	159
NTDB id 1153 A1552VC RS00115 WP 000521788.1	FDLPIALGILAASDQIARNKLESYEFIGELALSGEIRGVKGVLPAALAAANQV.ERCLVVPHSNGDQAALVGVERHKSQAQS	159
NTDB id 1349 HI 1117 AAC22771.1	FDLPIAIGILAASDQLDASHLKQFEFVAELALTGQLRGVHGVIPAILAAQKS.KRELIIAKQNANEASLVSDQNTYFAQT	159
NTDB id 1387 A4U84 RS06900 WP 020457569.1	FDLPIAIGILAASGQIDSDKLKRIELLGELSLTGHLRGVHGAIPAVLAASKA.KRETIIVPQQNANEVSLVSNTQT YCAST	159
consensus	FDLPIAIGILAASGQIDSDKLKRIELLGELSLTGHLRGVHGAIPAVLAASKA.KRETIIVPQQNANEVSLVSNTQT YCAST	159



logo

NTDB id 1323 RAOC RS07335 WP 004916218.1	LLEVCDFCCGRTSLLQENCKYLNNTIRDLSDIIGQQHAKRALEIAAGGHNLLFLGPPGTGKTMLASRLSDLL	238
NTDB id 1271 LPP RS03220 WP 011213198.1	LREVCDFLCQGTSLQSLPPKPDLLNNYELDWSDIKQQQHAKNAMVIAACGGHSILLSGAPGSGKTMMAKRFSTLL	235
NTDB id 1248 GC085 RS03150 WP 011213198.1	LREVCDFLCQGTSLQSLPPKPDLLNNYELDWSDIKQQQHAKNAMVIAACGGHSILLSGAPGSGKTMMAKRFSTLL	235
NTDB id 1036009 AB7D97 RS22645 WP 022649778.1	LQEVCAWLEGRHELAEPQENEEV...VADSPDDLSDIMGQEQGKRALEITAAGGHNLLFLGPPGTGKTMLASRLSGLL	234
NTDB id 1397 DSB67 RS15690 WP 005535577.1	LLEVCAELCGQHQLNLYQTPKKK...ELKAHGRDLQDIIGQQQKRALEIAAAGNHNLLFLGPPGTGKTMLASRLCDLL	235
NTDB id 1153 A1552VC RS00115 WP 000521788.1	LLEVCADLCGQQTLSLFQSSPSV...QQVSQTRDLQDIIGQQQKRALEIAAAGNHNLLFLGPPGTGKTMLASRLCDLL	235
NTDB id 1349 HI 1117 AAC22771.1	LLDVVQFLNGQEKPLATEIVKESAVNFGSKNTLDLTDIIGQQHAKRALTIAAAGQHNLLFLGPPGTGKTMLASRLTGLL	239
NTDB id 1387 A4U84 RS06900 WP 020457569.1	LLQVVNFLNNRDQLPIAQQLSQNIAEN.RPLVSRDLTDIIGQQHAKRALTIAAAGQHNLLFLGPPGTGKTMLASRLADLL	238
consensus	LLEVCDFCCGRTSLLQENCKYLNNTIRDLSDIIGQQHAKRALEIAAGGHNLLFLGPPGTGKTMLASRLSDLL	238



logo

NTDB id 1323 RAOC RS07335 WP 004916218.1	PEMSDIEALEETASISLVQKEPNEHNWKRPFRAPHHSASMAALVGGGSIIPGGEISLAHNGVFLDELPEFERKVLDA	318
NTDB id 1271 LPP RS03220 WP 011213198.1	PELSETQALECAAINSIRGKLPDF.REWRLLPFRAPHHTASPVALVGGGNPPKPGEISLAHHGVFLDELPEFNRQVLET	314
NTDB id 1248 GC085 RS03150 WP 011213198.1	PELSETQALECAAINSIRGKLPDF.REWRLLPFRAPHHTASPVALVGGGNPPKPGEISLAHHGVFLDELPEFNRQVLET	314
NTDB id 1036009 AB7D97 RS22645 WP 022649778.1	PPLNNHEALESAAIFSLVSSISLH.KQWRRRPFRSPHHSASLTAMVGGGSTIPGGEISLAHNGTFLDELPEFERVLD	313
NTDB id 1397 DSB67 RS15690 WP 005535577.1	PEMSDEEAMETASVASLTQSEINE.HNWKTRPFRAPHHSSMAALVGGGSVPRPGEISLAHNGLLFLDEMPEFDRKVLDS	314
NTDB id 1153 A1552VC RS00115 WP 000521788.1	PEMSDEEAMETASIASLTQEQINQ.HNWKLRPFRAPHHSSMAALVGGGTIPRPGGEISLAHNGLLFLDEMPEFERKVLDS	314
NTDB id 1349 HI 1117 AAC22771.1	PEMTDLEAIETASVTSLVQNELNF.HNWKRPFRAPHHSASMPALVGGGTIPKPGEISLATNGVFLDELPEFERKVLDA	318
NTDB id 1387 A4U84 RS06900 WP 020457569.1	PEMTDLEAIETASVTSLVQNELNF.HNWKRRPFRSPHHSASMPALVGGGSTIPKPGEISLAHNGVFLDELPEFERKVLDA	317
consensus	PEMSDIEALEETASISLVQKEPNEHNWKRPFRAPHHSASMAALVGGGSIIPGGEISLAHNGVFLDELPEFERKVLDA	318



logo

NTDB id 1323 RA0C RS07335 WP 004916218.1	LREPLESGEIIISRAAKIIFPAFQLYAAMNPSPTCGYGQONRITPQRIIRYLRLSGPFLDRFDMSIEIPALPQG	397
NTDB id 1271 LPP RS03220 WP 011213198.1	MRQPLEDRVITISRAKFTVNYPASFMLVASMNPSPSGFFPDDPNNT.SSSFEMQRYLNLKLSGPLLDRIDITHIEVQKVVEFD	394
NTDB id 1248 GC085 RS03150 WP 011213198.1	LREPLESGHICISRAAAQIEFPAKFQLIAAMNPPCGQWGNSSQANCMCTPDRIISRYLAKLSAPLLDRIDMQVTIHALSQE	394
NTDB id 1036009 AB7D97 RS22645 WP 022649778.1	LREPLESGHICISRAAAQIEFPAKFQLIAAMNPPCGQWGNSSQANCMCTPDRIISRYLAKLSAPLLDRIDMQVTIHALSQE	391
NTDB id 1397 DSB67 RS15690 WP 005535577.1	LREPESGEIHLSTRTRAKISYPAQFQLVAAMNPSPTGHHYQGNHN..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	LRQPLESGEIIISRAANAKIQFPAQFQIVGALNPSPTGHHYTGTHN..RTSPQQIMRYLNLRLSGPFLDRFDLSIEVPLLPQG	395
consensus	*!*!*!*!*!* *!*! * * * * *!*!*!*!*!*!*!*!* * * * * * * * * * * * * * * * * *	

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NTDB id 1323 RA0C RS07335 WP 004916218.1	LQNTGDRGESSAAYRERVKAREIQARQCKVALLSKEIECQLDALEFENALKGLSARAYHRLIK	475
NTDB id 1271 LPP RS03220 WP 011213198.1	QLSD..KRKGESSEIRQVRLKAREIQERYQDLAISYNAQMGPKEIEHFCELDEVSLLLIKNAMEKLNLSARAYDRILK	470
NTDB id 1248 GC085 RS03150 WP 011213198.1	ELIKPNTHLEKQSLAIREKVTMKHEIQMARQDS...LNANLNSKTCCEMVCELGSEEQLFLREVMSKIKLSARGYHRLIK	470
NTDB id 1036009 AB7D97 RS22645 WP 022649778.1	ELIKPNTHLEKQSLAIREKVTMKHEIQMARQDS...LNANLNSKTCCEMVCELGSEEQLFLREVMSKIKLSARGYHRLIK	466
NTDB id 1397 DSB67 RS15690 WP 005535577.1	LLRQT.GIKGESSAVVRERVIAAQAQYARQNR...LNARLDNSGTRQFCSLNAEDAGWLEETLTRFGLSTRAWQRLIK	467
NTDB id 1153 A1552VC RS00115 WP 000521788.1	TLSEG.GDRGEPTAIVKERVNQARDCLARSGK...VNALLGSREIEAFQPLQKSDAEFLENALHRLGLSIRAYHRIK	467
NTDB id 1349 HI 1117 AAC22771.1	TLANG.GDRGESTAAVRQRVVVARERMLARSGK...VNALLGSREIEQYCPLLKADAEFLESALHRLGLSIRAYHRIK	471
NTDB id 1387 A4U84 RS06900 WP 020457569.1	SLQNT.GDRGETSAQVREKVLKVREIQMERAGK...INAYLNSKEIERDCKLNDKDAFFLEKALNKLGLSVRAYHRILK	471
consensus	ALQNNTDQRGETTEQARKRVLEARHLQFNRRGK...INAQLITKEIEQDCKLITDRDALFLENALTKLGLSVRAYHRILK	
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NTDB id 1323 RA0C RS07335 WP 004916218.1	VSRTIADLERETNIQSHHIAEAIQYRSLDRDFWKV.....	510
NTDB id 1271 LPP RS03220 WP 011213198.1	VSRTIADLNSSKKVLLNHLQQAISYKQNLHLPK.....	503
NTDB id 1248 GC085 RS03150 WP 011213198.1	VSRTIADLNSSKKVLLNHLQQAISYKQNLHLPK.....	503
NTDB id 1036009 AB7D97 RS22645 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	VSRTIADLQGEQIFQPHLAEALGYRAMVRLLQKLSNM..	509
NTDB id 1387 A4U84 RS06900 WP 020457569.1	VSRTIADLAGEAQIQPHLAEALGYRAMDRLLQRLQGES.	510
consensus	! *	

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