

logo

NTDB id 1323 RAOC RS07335 WP 004916218.1	MSLAIVYSRASIGVAPLVTVVHLSNGPGETLVGLPETTVKESDRVRSALINSQEFPAKRITVNLAPADLPKEGGR	78
NTDB id 1271 LPP RS03220 WP 011213198.1	.MLVKKVYGSAIHGVSAQTTITIEVNVDDGV.GYHLVGLPDNAIKESSHRISAALKNVGYKLPKKITINMAPADLRKEGSA	80
NTDB id 1248 GC085 RS03150 WP 011213198.1	MSLAFTTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETAVKESKDRVRSALINSQFEFPCKRITVNLGPANLPKGTGSG	80
NTDB id 1028550 AB4090 RS24840 WP 002883134.1	MSLAFTTKTRSTIGIVAQPVSVEVHLSNGLPSFTMVGLAETAVKESKDRVRSALINSQFEFPCKRITVNLGPANLPKGTGSG	80
NTDB id 1397 DSB67 RS15690 WP 005535577.1	MSLAIVYTRAALGIEAPLITVEVHLSNGLPGLTMVGLPETTVKEARDRVRSALINSQYAFPAKKITINLAPADLPKEGGR	80
NTDB id 1153 A1552VC RS00115 WP 000521788.1	MGLAIIHSRASVGVQAPSVSVEVHISNGMPGFTLVGLPETTVKESKDRVRSALVNSNFQFPAKRITVNLAPADLPKEGGR	80
NTDB id 1349 HI 1117 AAC22771.1	MGLAIIHSRASIGVQAPPVTVVEVHISNGMPGFTLVGLPETTVKESRDRVRSALINSRFEFPKAKRITVNLAPADLPKEGGR	80
NTDB id 1387 A4U84 RS06900 WP 020457569.1	MSLAIVYSRASMGVQAPLVITIEVHLSNGKPGFTLVGLPEKTVKEAQDRVRSALMNAQFKYPAKRITVNLAPADLPKEGGR	80
consensus	MSLAIIYSRASIGVEAPLVITIEVHISGGSPGLTLVGLPEKSVKEAQDRVRSALMNAFDPARRITINLAPADLPKEGGR	80

logo

NTDB id 1323 RAOC RS07335 WP 004916218.1	FDLPIALGILAASQQLITLKNYEFYELALGGLRGVGYLPAALAAKDRLLIVPNAEASLVGLQGVYAA	158
NTDB id 1271 LPP RS03220 WP 011213198.1	YDLSTIALGILAASGQIIAPETIERYLIMGELSLDGGQLPIKGVLPPIARAREEGFGKTIILPKQNTREAAIVNDLEVYGVEN	159
NTDB id 1248 GC085 RS03150 WP 011213198.1	FDLPIALGILAASEQIPLTNLANHEFIGELALSGELRGVSAIIPAVLAAHKD.NQHLLIIANANAAEASLTGHQKVFTANN	159
NTDB id 1028550 AB4090 RS24840 WP 002883134.1	FDLPIALGILAASEQIPLTNLANHEFIGELALSGELRGVSAIIPAVLAAHKD.NQHLLIIANANAAEASLTGHQKVFTANN	159
NTDB id 1397 DSB67 RS15690 WP 005535577.1	YDLPIALALLVASEQLNTTRLNQYEFVGELALTGGLRGVPGAIPSSAMEAIKA.GRRIVVSSDNAAEVGLTGGSDCLVADH	159
NTDB id 1153 A1552VC RS00115 WP 000521788.1	FDLPIALGILAASEQIATDKLNQYEFVGELALSGGLRTVKGVLPAALAAANKK.QRHLVVPHANGDQAALVGKEQHKSAQS	159
NTDB id 1349 HI 1117 AAC22771.1	FDLPIALGILAASDQIARNKLESYEFIGELALSGEIRGVKGVLPAALAAANQV.ERCLVVPHSNGDQAALVGVERHKSQAQS	159
NTDB id 1387 A4U84 RS06900 WP 020457569.1	FDLPIALGILAASDQLDASHLKQFEFVAELALTGQLRGVHGVIPAILAAQKS.KRELIIAKQNANEASLVSDQNTYFAQT	159
consensus	FDLPIALGILAASGQIDSDKLKRIFELGELSLTGHLRGVHGAIPAVLAASKA.KRETIIVPQQNANEVSLVSNQTQYCAST	159

logo

NTDB id 1323 RAOC RS07335 WP 004916218.1	LLEVCDELCCQTSLSLQCKPKLNNYERDLSDIIGQQAHRALIAAAGHNLLFGPPGTGKTMLASRLSDLL	238
NTDB id 1271 LPP RS03220 WP 011213198.1	LKEVIDFFNENCPLEPTKVNTREEFHKRVNLPFPDFSEVKGQETAKRAMEVAAAGGHNIIILGPPGSGKTMMAKRIPSTIL	235
NTDB id 1248 GC085 RS03150 WP 011213198.1	LREVC DYLCQGTSLQSLPPKPDLL...LLNNYELDWS DIKGQQHAKNAMVIAACGGHSILLSGAPGSGKTMMAKRFTSTLL	235
NTDB id 1028550 AB4090 RS24840 WP 002883134.1	LREVC DYLCQGTSLQSLPPKPDLL...LLNNYELDWS DIKGQQHAKNAMVIAACGGHSILLSGAPGSGKTMMAKRFTSTLL	234
NTDB id 1397 DSB67 RS15690 WP 005535577.1	LQEVCAFLAGQTSLSPLAE...PARDERYEDLLDVIGQQQ GKRALEIIVAAGGHNLLILGPPGTGKTMLASRLPGLL	235
NTDB id 1153 A1552VC RS00115 WP 000521788.1	LLEVCAELCGQHQLNLYQTPKKK...ELKAHGRDLQDIIGQQQ GKRALEIAAAGHNLLFLGPPGTGKTMLASRLCDLL	235
NTDB id 1349 HI 1117 AAC22771.1	LLEVCADLCGQQTLSLFQSSPSV...QQVQSTRDLQDIIGQQQ GKRALEIAAAGHNLLFLGPPGTGKTMLASRLCDLL	239
NTDB id 1387 A4U84 RS06900 WP 020457569.1	LLQVVNFLNNRDQLPIAQQLSQNIAEN.RPLVSRDLTDIIGQQHAKRALIAAAGQHNLLFLGPPGTGKTMLASRLADLL	238
consensus	LLEVCDELCCQTSLSLQCKPKLNNYERDLSDIIGQQAHRALIAAAGHNLLFGPPGTGKTMLASRLSDLL	

logo

NTDB id 1323 RAOC RS07335 WP 004916218.1	PEMSDEALEETASISLVQKEPNEHNWKRPFRAPHHSASMAALVGGGSIIPGGEISLAHNGVFLDELPEFERVLD	318
NTDB id 1271 LPP RS03220 WP 011213198.1	PPLTLKEALETTKIHSVAGKMGAEATSLMTIRPFRSPHHTISDVVALVGGGSIYPQGEISLAHNGVFLDEMPFEKRTVLEV	314
NTDB id 1248 GC085 RS03150 WP 011213198.1	PELSETQALECAAINSIRGKLPDF.REWRLLPFRAPHHTASPVVALVGGGNPPKPGEISLAHNGVFLDELPEFNRQVLET	314
NTDB id 1028550 AB4090 RS24840 WP 002883134.1	PELSETQALECAAINSIRGKLPDF.REWRLLPFRAPHHTASPVVALVGGGNPPKPGEISLAHNGVFLDELPEFNRQVLET	313
NTDB id 1397 DSB67 RS15690 WP 005535577.1	PPLSNQEALESAAIQSLVNLHTAK.TRWRRQRPFRAPHHSASLAAMVGGGSIIPVPGEISLAHNGVFLDELPEFERVLD	314
NTDB id 1153 A1552VC RS00115 WP 000521788.1	PEMSDEEAMETASVASLTQSEINE.HNWKTRPFRAPHHSSMAALVGGGSIIPVPGEISLAHNGVFLDELPEFERVLD	314
NTDB id 1349 HI 1117 AAC22771.1	PEMSDEEAMETASIASLTQSEINQ.HNWKLRPFRAPHHSSMAALVGGGSIIPVPGEISLAHNGVFLDELPEFERVLD	314
NTDB id 1387 A4U84 RS06900 WP 020457569.1	PEMTDLEAIETASVTSLVQNELNF.HNWKRPFRAPHHSASMPALVGGGTIPKPGEISLATNGVFLDELPEFERKVLDA	318
consensus	PEMTDLEAIETASVTSLVQNELNF.HNWKRPFRAPHHSASMPALVGGGSIIPKPGEISLAHNGVFLDELPEFERKVLDA	317

logo

NTDB id 1323 RAOC RS07335 WP 004916218.1	LREPLESGEIIISRAAKIIFPAFQLYAAMNPSPTCGYGQNRISPGQILRYLRLSGPFLDRFDMSIEIPALPQG	397
NTDB id 1271 LPP RS03220 WP 011213198.1	MRQPLEDRVITISRAKFTVNYPASFMLVASMNPSPSGFFPDDPNNT.SSSFEMQRYLNLKLSGPLLDRIDITHIEVQKVVEFD	394
NTDB id 1248 GC085 RS03150 WP 011213198.1	LREPLESGHICISRAAAQIEFPAKFQLIAAMNPPCGQWGNISQANCMCTPDRIISRYLAKLSAPLLDRIDMQVTIHALSQE	394
NTDB id 1028550 AB4090 RS24840 WP 002883134.1	LREPLESGHICISRAAAQIEFPAKFQLIAAMNPPCGQWGNISQANCMCTPDRIISRYLAKLSAPLLDRIDMQVTIHALSQE	391
NTDB id 1397 DSB67 RS15690 WP 005535577.1	LREPLESGEIIISRAQKTRFPAFQIVGALNPSPGTGYEGNQAR..TNPQATILRYLGRLSGPFLDRFDLSLEIPLPPPG	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	Q L S D . . K R K G E S S E I T 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...LNANLNSKTCCEMVCELGSEEQLFLREVMSKLLKLSARGYHRLK	470
NTDB id 1248 GC085 RS03150 WP 011213198.1	ELIKPNTHLEKQSLAIREKVTMKHEIQMARQDS...LNANLNSKTCCEMVCELGSEEQLFLREVMSKLLKLSARGYHRLK	470
NTDB id 1028550 AB4090 RS24840 WP 002883134.1	ILSQG.SQGEESATVRQRVLAARERQMLRQNK...LNAHLENREMKNCRLRREDAVWLEQTLTQLGLSTRAWQRLK	466
NTDB id 1397 DSB67 RS15690 WP 005535577.1	TLSEG.GDRGEPTAIVKERVNQARDCLARSGK...VNALLGSREIEAFQPLQKSDAEFLENALHRLGLSIRAYHRIK	467
NTDB id 1153 A1552VC RS00115 WP 000521788.1	TLANG.GDRGESTAAVRQRVVVARERMLARSGK...VNALLGSREIEQYCPLLKADAEFLESALHRLGLSIRAYHRIK	467
NTDB id 1349 HI 1117 AAC22771.1	SLQNT.GDRGETSAQVREKVLKVREIQMERAGK...INAYLNSKEIERDCKLNDKDAFFLEKALNKLGLSVRAYHRILK	471
NTDB id 1387 A4U84 RS06900 WP 020457569.1	ALQNNTDQRGETTEQARKRVLEARHLQFNRRGK...INAQLTTKEIEQDCKLTDRDAFLFLENALTKLGLSVRAYHRILK	471
consensus	! **** * * ! * **** * ! * * ! ! * **** * ! ! **** * * * ! ! ! ! ! ! ! ! ! ! ! !	

logo

NTDB id 1323 RAOC RS07335 WP 004916218.1	VSRTIADLERETNIQSHHIAEAIQYRSLDRDFWKV.....	510
NTDB id 1271 LPP RS03220 WP 011213198.1	VSRTIADLNSSKKVLLNHLQQALSYPKQNLHLPK.....	503
NTDB id 1248 GC085 RS03150 WP 011213198.1	VSRTIADLNSSKKVLLNHLQQALSYPKQNLHLPK.....	503
NTDB id 1028550 AB4090 RS24840 WP 002883134.1	VARTIADLAEEVEETIERCHLQEALSYRAIDRMLNHLQKMMA	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