

NTDB id	1323	RAOC RS07335 WP	004916218.1	.MLVVKYVGSAIHGVSAQTITIEVNVDQGV.GYHLVLGLPDNATIKESSHRISAAIKNVGYKLPCKKITINMAPADLRKEGSA	78
NTDB id	1271	LPP RS03220 WP	011213198.1	MSLAFTKRSTIGTIVAQPVSVVEVHLSNGLPSFTMVGLAETAVKESKDVRVSAINSQFEFPCRKITVNLGPANLPKTGS	80
NTDB id	1248	GCO85 RS03150 WP	011213198.1	MSLAFTKTRSTIGTIVAQPVSVVEVHLSNGLPSFTMVGLAETAVKESKDVRVSAINSQFEFPCRKITVNLGPANLPKTGS	80
NTDB id	101193	ABS743 RS24740 WP	000058957.1	MSLSITVHTRAALGVNAAPPITVEVHISKPLPGLTMVGLPETTVKEARDRVRSAINSGYEYPAKKITINLAPADLPKEGGR	80
NTDB id	1153	A1552VC RS00115 WP	000521788.1	MGLAIITHSRASIGVQAAPPVTVEVHLSNGMPGFLLVGLPETTVKESRDVRVSAINSNRFEFPACKRITVNLAPADLPKEGGR	80
NTDB id	1397	DSB67 RS15690 WP	005535577.1	MGLAIITHSRASVGVQAAPSVSVEVHLSNGMPGFLLVGLPETTVKESKDVRVSAINSNRFQEPACKRITVNLAPADLPKEGGR	80
NTDB id	1349	HI 1117 AAC22771.1		MSLAIVYSRASMGVQAPLVLTIEVHLSNGKPGFLLVGLPEKVTKEAQRDVRVSALMNAQFKYPAKRITVNLAPADLPKEGGR	80
NTDB id	1387	A4U84 RS06900 WP	020457569.1	MSLAIIYSRASIGVEAPLVLTIEVHISGGSPGLTLVGLPEKSVEKAQRDVRVSALMNANFDYPARRITINLAPADLPKEGGR	80
consensus				* * * * *	80

NTDB id	1323	RAOC RS07335 WP	O04916218.1		YDLSIALGILAASGGTIIAPEIERVYLIMGELSLDGGLQPIKGVLPATIRAREEGFGKITLTKQNRTREAAALVNMLEVYGVEN	158
NTDB id	1271	LPP RS03220 WP	O11213198.1		FDLPIALGILAASEQTPLTNLANHEFIGELALSCELRGVSATIPAVLAAHKD.NQHLLIANANAAEASTLGHKVFETANN	159
NTDB id	1248	GCO85 RS03150 WP	O11213198.1		FDLPIALGILAASEQTPLTNLANHEFIGELALSCELRGVSATIPAVLAAHKD.NQHLLIANANAAEASTLGHKVFETANN	159
NTDB id	1011193	ABS743 RS24740 WP	O00058957.1		YDLPIAIAALAASEQTANKLDEVELVGELALTGALRGVPGAITSSATEAIKS.GRKTIIVAKDNEDEVGLINGECGLIADH	159
NTDB id	1153	A1552VC RS00115 WP	O00521788.1		FDLPIALGILAASDIARNKLSESYEFIGELALSGETIRGVKGVLPAALAAHQV.ERCLLVPHSNGDQAALVGVERHKSACS	159
NTDB id	1397	DSB67 RS15690 WP	O05535577.1		FDLPIALGILAASEQIATDKLKNYEFVGEALSGGLRLTVKGVLPAAALAAKK.QRHLLVPHANGDQAALVGKEQHKSACS	159
NTDB id	1349	HI 1117 AAC22771.1			FDLPIAITGILAAAGLDASHLKFEEFVAELATIQHLRGVHGVIAPAILAAQS.KRELIIIAKQNAANEASLVSDQNTTYFACT	159
NTDB id	1387	A4U84 RS06900 WP	O20457569.1		FDLPIAIGILAASQLIDSKLRRIELLGELSITHGRGVHGAIPAVLAASKA.KREITIIVPQQNANEASLVSNLTQTTTCYST	159
consensus					*!!*!*!***!!!!!!!*!* * !!**!**!!*!!*****!!**!!*****	

NTDB id 1323	RAOC RS07335 WP 004916218.1	I	K	E	V	I	D	F	F	N	E	N	C	P	L	E	P	T	K	V	N	T	R	E	E	F	H	K	R	V	N	L	F	P	F	D	F	S	E	V	K	G	Q	E	T	A	K	R	A	M	E	V	A	A	A	G	G	H	N	I	L	I	L	G	P	P	G	S	G	K	T	M	L	A	K	R	I	P	S	I	L		238
NTDB id 1271	LPP RS03220 WP 011213198.1	L	R	E	V	C	D	I	L	C	Q	G	T	S	L	Q	S	L	P	P	K	P	D	L	...	L	L	N	N	Y	E	L	D	W	S	D	I	K	G	Q	Q	H	A	K	N	A	M	V	I	A	A	C	G	G	H	S	I	L	L	S	C	A	P	G	S	G	K	T	M	A	K	R	F	S	T	L		235					
NTDB id 1248	GC085 RS03150 WP 011213198.1	L	R	E	V	C	D	I	L	C	Q	G	T	S	L	Q	S	L	P	P	K	P	D	L	...	L	L	N	N	Y	E	L	D	W	S	D	I	K	G	Q	Q	H	A	K	N	A	M	V	I	A	A	C	G	G	H	S	I	L	L	S	C	A	P	G	S	G	K	T	M	A	K	R	F	S	T	L		235					
NTDB id 101193	ABS743 RS24740 WP 000058957.1	L	Q	A	V	C	A	E	L	G	K	H	A	L	E	H	P	K	P	T	N	A	...	V	S	R	A	L	Q	H	D	L	S	D	V	G	Q	E	K	R	G	L	E	I	T	A	A	G	G	H	N	L	I	L	G	P	P	G	T	G	K	T	M	L	A	S	R	I	N	G	L		234										
NTDB id 1153	A1552VC RS00115 WP 000521788.1	L	L	E	V	C	A	D	I	L	C	G	Q	Q	T	S	L	F	Q	S	S	P	S	V	...	Q	Q	V	S	Q	T	R	D	L	Q	D	I	I	G	Q	Q	Q	K	R	A	L	E	I	A	A	A	G	N	H	N	L	L	F	L	G	P	P	G	T	G	K	T	M	L	A	S	R	L	C	D	L		235					
NTDB id 1397	DSB67 RS15690 WP 005535577.1	L	L	E	V	C	A	E	L	C	G	Q	H	L	N	L	Y	Q	T	P	K	K	...	E	L	K	A	H	G	R	D	L	Q	D	I	I	G	Q	Q	Q	K	R	A	L	E	I	A	A	A	G	N	H	N	L	L	F	L	G	P	P	G	T	G	K	T	M	L	A	S	R	L	C	D	L		235							
NTDB id 1349	HI 1117 AAC22771.1	L	L	D	V	V	Q	F	L	N	G	Q	E	K	L	P	L	A	T	E	I	V	K	E	S	A	V	N	F	S	G	K	N	T	L	D	L	T	D	I	I	G	Q	Q	H	A	K	R	A	L	T	I	A	A	A	G	Q	H	N	L	L	F	L	G	P	P	G	T	G	K	T	M	L	A	S	R	L	T	G	L		239	
NTDB id 1387	A4U84 RS06900 WP 020457569.1	L	L	Q	V	N	F	L	N	N	R	D	L	P	I	A	Q	Q	L	S	Q	N	I	A	E	N	.	R	P	L	V	S	R	D	L	T	D	I	I	G	Q	Q	H	A	K	R	A	L	I	I	A	A	S	G	Q	H	N	L	L	F	L	G	P	P	G	T	G	K															

[illegible]

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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	LREPLESGHICISRAAAQIEFPAKFQLIAAMNPPCGQWGNSSQANCMCTPDRIISRYLAKLSAPLLDRIDMQVTIHALSQE	394
NTDB id 1011193 ABS743 RS24740 WP 000058957.1	LREPLESGHICISRAAAQIEFPAKFQLIAAMNPPCGQWGNSSQANCMCTPDRIISRYLAKLSAPLLDRIDMQVTIHALSQE	391
NTDB id 1153 A1552VC RS00115 WP 000521788.1	LREPIESGQIHLSRTRAKITYPARFQLVAAMNPSPTGHHYQGNHN..RCTPEQTLRYLNRLSGPFLDRFDLSLEIPLPPPG	392
NTDB id 1397 DSB67 RS15690 WP 005535577.1	LREPLESGEIVISRAQKTRFPAFQLVGALNPSPTGYYEGSSQA..RANPQSILRYLSRLSGPLLDRFDMSTIEIPALPKG	392
NTDB id 1349 HI 1117 AAC22771.1	LREPLESGEIIISRAQKTRFPAFQIVGALNPSPTGYYEGNQA..RTNPQAAILRYLGRLSGPLLDRFDMSTIEIPALPKG	396
NTDB id 1387 A4U84 RS06900 WP 020457569.1	LRQPLESGEIIISRANAKIQFPAFQLVAAAMNPSPTGHYTGTHN..RTSPQQIMRYLNRLSGPFLDRFDLSIEVPLLPQG	395
consensus	*!***** *!!* *** *!!*!*****!!*!!* * ** * ** *!!!! *!!!!*!!!!*!***** ** *	

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NTDB id 1323 RAOC RS07335 WP 004916218.1	QNSKNDLGESESAAYRERVKAREQMAKQKNAQNSKEIECKLSEDALEFENALKGLSARAYHRLK	475
NTDB id 1271 LPP RS03220 WP 011213198.1	QLSD..KRKGESSEIRQRVLKAREIQQERYQDLAISYNAQMGPKEIEHFCELDVSLLLIKNAMEKLNLSARAYDRILK	470
NTDB id 1248 GC085 RS03150 WP 011213198.1	ELIKPNTHLEKQSLAIREKVTMKHEIQMARQDS...LNANLNSKTCCEMVCELGSEEQFLREVMSKIKLSARGYHRLK	470
NTDB id 1011193 ABS743 RS24740 WP 000058957.1	ELIKPNTHLEKQSLAIREKVTMKHEIQMARQDS...LNANLNSKTCCEMVCELGSEEQFLREVMSKIKLSARGYHRLK	466
NTDB id 1153 A1552VC RS00115 WP 000521788.1	ILSKT.VVPGENSTTVKQRVMAARERQFKRQNK...LNAWLDNPEIRQFCKLESEDAQWLEETLIHLGLSTRAWQRLK	467
NTDB id 1397 DSB67 RS15690 WP 005535577.1	TLANG.GDRGESTAAVRQRVWVARERMLARSGK...VNALLQSREIEQYCPLLKADAEFLESALHRLGLSIRAYHRIK	467
NTDB id 1349 HI 1117 AAC22771.1	TLSEG.GDRGEPTAIVKERVNQARDCMLARSGK...VNALLQSREIEAFCPQLKSDAEFLENALHRLGLSIRAYHRIK	471
NTDB id 1387 A4U84 RS06900 WP 020457569.1	SLQNT.GDRGETSAQVREKVLKVREIQMERAGK...INAYLNSKEIERDCKLNDKDAFFLEKALNKLGLSVRAYHRILK	471
consensus	ALQNNTDQRGETTEQARKRVLEARHLQFNRRGK...INAQLITKEIEQDCKLITDRDALFLENALTKLGLSVRAYHRILK	
	! *** * * * *! ***** ! * *!!* * ***** ! ! ** *** ** *!!!!*!*****!!*	

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NTDB id 1323 RAOC RS07335 WP 004916218.1	VSRTIADLERETNIQSHHIAEAIQYRSIDRDFWKV.....	510
NTDB id 1271 LPP RS03220 WP 011213198.1	VSRTIADLNSSKKVLLNHLQQALSYPKQNLHLPK.....	503
NTDB id 1248 GC085 RS03150 WP 011213198.1	VSRTIADLNSSKKVLLNHLQQALSYPKQNLHLPK.....	503
NTDB id 1011193 ABS743 RS24740 WP 000058957.1	VARTIADIDQSDIITRQHLQEAVSYRAIDRLLIHLLQKLLT	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	VSRTIADLQGEQIFQPHLAEALGYRAMVRLKQLSNM..	509
NTDB id 1387 A4U84 RS06900 WP 020457569.1	VSRTIADLAGEAQIQPHLAEALGYRAMDRLLQRLQGES.	510
consensus	!*****! ** !****! * !***** *	

- ☒ non conserved
- ☒ similar
- ☒ ≥ 50% conserved