

logo

NTDB	id	617	LCA	RS06480	WP	011375001.1	.MSTEEKLTTLLKHCAKQRVQDLYFTPTIGGWRLTERRQSDLVTNQELDKPTGTRYINHLKYMAGMDISETRRRAQTGRSELQLAD	84
NTDB	id	586	KW2	RS10855	WP	011836048.1	..MVQKKKAQELIQQKAIEMEAASDIYLLTASGNLYKTIYIRQQLGRTLTJEEVNVQIEIGLALLTHFKFLAGMNTGERRRVQLGACWYELEG	83
NTDB	id	584	DLJ51	RS00890	WP	019777327.1	MVEVQELGKGLIRQAVEEQAQDIYLLPKPAVYKIIYLRFGKEKRHLIQTCPPPEQAAGLISHFKFLAGMNVGEKRRRAQLGACDYAFAD	85
NTDB	id	385	SMU	RS09035	WP	002263435.1	..MVQKGLGRKIIAEAVQNKAQDIYIIPKKESYELYMRIICNERRFIDVYDHHFMANLISHFKFVAGMNVGEKRRSQLGSCDYSYDE	83
NTDB	id	394	FSA28	RS09405	WP	002291652.1	..MVQKGLGRKIIAEAVQNKAQDIYIIPKKESYELYMRIICNERRFIDVYDHHFMANLISHFKFVAGMNVGEKRRSQLGSCDYSYDE	83
NTDB	id	500	SM12261	RS00945	WP	000249545.1	..MVQEIAQEIIRSARKKGAQDIYFVPKLDAYELHMRVGDERCKIGCYDFEKFAAVISHFKFVAGMNVGEKRRSQLGSCDYEYDQ	83
NTDB	id	270	KZH43	RS09265	WP	000249564.1	..MVQEIAQEIIRSARKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFAAVISHFKFVAGMNVGEKRRSQLGSCDYYDH	83
NTDB	id	229	SPD	RS09895	WP	000249564.1	..MVQEIAQEIIRSARKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFAAVISHFKFVAGMNVGEKRRSQLGSCDYYDH	83
NTDB	id	195	SPR	RS09430	WP	000249564.1	..MVQEIAQEIIRSARKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFAAVISHFKFVAGMNVGEKRRSQLGSCDYYDH	83
NTDB	id	160	SP	RS10380	WP	000249564.1	..MVQEIAQEIIRSARKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFAAVISHFKFVAGMNVGEKRRSQLGSCDYYDH	83
NTDB	id	58487	I872	RS09745	WP	015605921.1	..MVQKIAKEMIQLARQEAAQDIYLLPKSSCYELMVRGDERRRFQTYDFDILLSSVISHFKFVSGMNVGEKRRSQLGSCDYDCGD	83
NTDB	id	429	SGO	RS09420	WP	012130942.1	..MVQKIAQAIIVRQAKEECQDIYFVPKDCYELMVRIGDERRRFQTYDFDQLAAVISHFKFLAGMNVGEKRRSQLGSCDYYD	83
consensus								83
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NTDB	id	617	LCA	RS06480	WP	011375001.1	.QTTIYLRRLATVGDFLNRNRESLVIRFITYPIGAIYHCDQQGLLAQLTQMSRQSGLILFAGPTGSGKTTSLYHLAQQSMSAKMVVAIED	168
NTDB	id	586	KW2	RS10855	WP	011836048.1	SSAKRLRLSTVGDFECNESLVIRLLHDQKQLEFWF.DDK.LLQDFRCKRGLYLFAGPVGSKGTSLMFDLAHRHFSNAQVITIEE	165
NTDB	id	584	DLJ51	RS00890	WP	019777327.1	GETAALRLSTVGDDYQGRESLVIRLLFDRKRELKFWF.DGILNALLPKIIGRGLYLFSPGVSGKTTLMYELVSRRYPDSQTITIED	169
NTDB	id	385	SMU	RS09035	WP	002263435.1	GKVISLRLSVGDYRGYESLVIRLLFSGRHLDFKFWF.NSMDLLINEIKGRGLYLFSPGVSGKTSLMYQQLVKRLFETKQVITIED	167
NTDB	id	394	FSA28	RS09405	WP	002291652.1	GKVISLRLSVGDYRGYESLVIRLLFSGRHLDFKFWF.NSMDLLINEIKGRGLYLFSPGVSGKTSLMYQQLVKRLFETKQVITIED	167
NTDB	id	500	SM12261	RS00945	WP	000249545.1	.KMASLRRLSTVGDDYRGHESLVIRLLHDEEQDLHFWE.QDIEELGKQYRQRGLYLFAGPVGSKGTTLMHELSKSLEFKGQQVMSSIED	166
NTDB	id	270	KZH43	RS09265	WP	000249564.1	.KITASLRRLSTVGDDYRGHESLVIRLLHDEEQDLHFWE.QDIEELGKQYRQRGLYLFAGPVGSKGTTLMHELSKSLEFKGQQVMSSIED	166
NTDB	id	229	SPD	RS09895	WP	000249564.1	.KITASLRRLSTVGDDYRGHESLVIRLLHDEEQDLHFWE.QDIEELGKQYRQRGLYLFAGPVGSKGTTLMHELSKSLEFKGQQVMSSIED	166
NTDB	id	195	SPR	RS09430	WP	000249564.1	.KITASLRRLSTVGDDYRGHESLVIRLLHDEEQDLHFWE.QDIEELGKQYRQRGLYLFAGPVGSKGTTLMHELSKSLEFKGQQVMSSIED	166
NTDB	id	160	SP	RS10380	WP	000249564.1	.KITASLRRLSTVGDDYRGHESLVIRLLHDEEQDLHFWE.QDIEELGKQYRQRGLYLFAGPVGSKGTTLMHELSKSLEFKGQQVMSSIED	166
NTDB	id	58487	I872	RS09745	WP	015605921.1	.VTVISLRRLSTVGDDYRGYESLVIRLLHDEERELRFWF.DNLDPDLRKKVNSRGLYLFSPGVSGKTTLMHQLAQMRFEGQQQVMSSIED	166
NTDB	id	429	SGO	RS09420	WP	012130942.1	.KETISLRRLSTVGDDYRGYESLVIRLLHDEETELKFWE.THFPELREKFKNDRLGYLFSPGVSGKTTLMHQAQLKLEFKGQQVMSSIED	166
consensus							* * * * * ! ! ! ! ! * * * * * ! ! ! ! ! * * * * * ! ! ! ! ! * * * * * ! ! ! ! ! * * * * * ! ! ! ! ! * * * * * ! ! ! ! ! * * * * *	

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NTDB	id	617	LCA	RS06480	WP	011375001.1	P	T	E	I	V	A	P	E	F	L	Q	L	Q	V	N	D	N	A	G	L	S	Y	A	E	L	L	K	I	S	L	R	L	R	P	D	T	L	I	G	E	I	R	D	L	E	T	A	Q	Y	V	V	S	A	A	L	S	C	H	L	V	L	S	T	I	H	A	R	S	T	Q	G	V	V	A	R	L	L	D	L	G	I	S	E	L	253
NTDB	id	586	KW2	RS10855	WP	011836048.1	P	V	E	L	I	D	S	D	F	I	Q	L	Q	V	N	D	V	I	G	N	S	Y	D	E	L	I	K	L	S	L	R	H	R	P	D	L	L	I	V	G	E	I	R	D	Q	T	A	R	A	V	I	R	A	S	L	T	G	Y	T	V	F	S	T	I	H	A	S	V	K	G	V	V	A	R	L	L	E	L	G	I	S	D	W	250	
NTDB	id	584	DLJ51	RS00890	WP	019777327.1	P	V	E	I	K	Q	D	N	M	L	Q	L	Q	L	N	P	S	I	G	M	T	Y	D	H	L	I	K	L	S	L	R	H	R	P	D	V	L	I	G	E	I	R	D	E	T	A	Q	A	V	I	R	A	S	L	T	G	I	R	V	F	S	T	I	H	A	K	S	I	P	G	V	Y	A	R	L	E	L	G	V	S	E	Q	254		
NTDB	id	385	SMU	RS09035	WP	002263435.1	P	V	E	I	K	Q	D	N	M	L	Q	L	Q	L	N	E	S	I	G	M	T	Y	D	N	L	I	K	L	S	L	R	H	R	P	D	L	L	I	G	E	I	R	D	K	E	T	A	R	A	V	I	R	A	S	L	T	G	A	M	V	F	S	T	I	H	A	K	S	I	P	G	V	Y	A	R	L	E	L	G	T	S	E	252		
NTDB	id	394	FSA28	RS09405	WP	002291652.1	P	V	E	I	K	Q	D	N	M	L	Q	L	Q	L	N	E	S	I	G	M	T	Y	D	N	L	I	K	L	S	L	R	H	R	P	D	L	L	I	G	E	I	R	D	K	E	T	A	R	A	V	I	R	A	S	L	T	G	A	M	V	F	S	T	I	H	A	K	S	I	P	G	V	Y	A	R	L	E	L	G	T	S	E	252		
NTDB	id	500	SM12261	RS00945	WP	000249545.1	P	V	E	I	K	Q	D	N	M	L	Q	L	Q	L	N	E	A	I	G	L	T	Y	E	N	L	I	K	L	S	L	R	H	R	P	D	L	L	I	G	E	I	R	D	S	E	T	A	R	A	V	I	R	A	S	L	T	G	A	T	V	F	S	T	I	H	A	K	S	I	P	G	V	Y	E	R	L	L	E	L	G	V	S	E	E	251
NTDB	id	270	KZH43	RS09265	WP	000249564.1	P	V	E	I	K	Q	D	N	M	L	Q	L	Q	L	N	E	A	I	G	L	T	Y	E	N	L	I	K	L	S	L	R	H	R	P	D	L	L	I	G	E	I	R	D	S	E	T	A	R	A	V	I	R	A	S	L	T	G	A	T	V	F	S	T	I	H	A	K	S	I	P	G	V	Y	E	R	L	L	E	L	G	V	S	E	E	251
NTDB	id	229	SPD	RS09895	WP	000249564.1	P	V	E	I	K	Q	D	N	M	L	Q	L	Q	L	N	E	A	I	G	L	T	Y	E	N	L	I	K	L	S	L	R	H	R	P	D	L	L	I	G	E	I	R	D	S	E	T	A	R	A	V	I	R	A	S	L	T	G	A	T	V	F	S	T	I	H	A	K	S	I	P	G	V	Y	E	R	L	L	E	L	G	V	S	E	E	251
NTDB	id	195	SPR	RS09430	WP	000249564.1	P	V	E	I	K	Q	D	N	M																																																																												

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NTDB id 617 LCA RS06480 WP 011375001.1	QLRACLTGIAVYQSLVTKDDVVQA...HYELLTGSDYFSKKEG.....GCDV.....	296
NTDB id 586 KW2 RS10855 WP 011836048.1	ELKNGLEAVVYQRLIAGKGVLDIAKSKFDTWSPKKWNEKTENLYANGHLTAIEEAEREKISINQASKIDTTDGESFE	326
NTDB id 584 DLJ51 RS00890 WP 019777327.1	ELDNCLAGIAYQRLIGGGGLIDFAQDHFQNHQAECWNEKIDQLLAAGHLTEEEAAAEEKIKD.....	315
NTDB id 385 SMU RS09035 WP 002263435.1	ELQNALRGIVYQRLIGGGGIIDFAKGDYQNHSAKKWNKQIYDLFTAGYITEGEAQAEIIE.....	313
NTDB id 394 FSA28 RS09405 WP 002291652.1	ELQNALCGIVYQRLIGGGGIIDFAKGDYQNHSAKKWNKQIYDLFTAGYITEGEAQAEIIE.....	313
NTDB id 500 SM12261 RS00945 WP 000249545.1	ELAVVLQGVCYQRLIGGGGIVDFANKDYQEHQSTSWNAQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id 270 KZH43 RS09265 WP 000249564.1	ELAVVLQGVCYQRLIGGGGIVDFASRDYQEHQAANKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id 229 SPD RS09895 WP 000249564.1	ELAVVLQGVCYQRLIGGGGIVDFASRDYQEHQAANKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id 195 SPR RS09430 WP 000249564.1	ELAVVLQGVCYQRLIGGGGIVDFASRDYQEHQAANKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id 160 SP RS10380 WP 000249564.1	ELAVVLQGVCYQRLIGGGGIVDFASRDYQEHQAANKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id 58487 I872 RS09745 WP 015605921.1	ELRMVLQGVCYQRLIGGGGVIDFVNQDYQKHEASLWNQQIDQLFADGHITADQRQAEEKIYA.....	313
NTDB id 429 SGO RS09420 WP 012130942.1	ELKIVLQGTICVQRLIGGGGVIDFASDNYQEHEPTVWNQQIDQLLAAGHIHPEQAEAEKIRNQQAKTSY.....	319
consensus	*! **!*****!***** ***** **	

- non conserved
- similar
- ≥ 50% conserved