

NTDB	id	617	LCA	RS06480	WP	011375001.1	.MSTEEKLTTLLKHCAKQRVQDLYFTPTIGGWR	LERRQSDLVTNQELDKPTGTRYINHLKYMAGMDISERRAQTGRSELQLAD	84
NTDB	id	586	KW2	RS10855	WP	011836048.1	..MVQKKKAQELIQKAIEMEASDIYLLTASGNLYKTIYIRQQLGRITLIEEVNQEIGLALLTHFKFLAGMNTGERRRVQLGACWYELEG	83	
NTDB	id	584	DLJ51	RS00890	WP	019777327.1	MVEVQELGKLEKQAVEEQAQDIYLLIPKPAVYKTYLRFGEKRRHLIQTCPPBQAAGLISHFKFLAGMNVGEKRRQLGACDYAFAD	85	
NTDB	id	385	SMU	RS09035	WP	002263435.1	..MVQKLGKRLIIAEAVQNKAQDIYLLIPKKESEYELMRIENRRFIDVYDHHFMANLISHFKFVAGMNVGEKRRSQLGSCDYSYDE	83	
NTDB	id	394	FSA28	RS09405	WP	002291652.1	..MVQKLGKRLIIAEAVQNKAQDIYLLIPKKESEYELMRIENRRFIDVYDHHFMANLISHFKFVAGMNVGEKRRSQLGSCDYSYDE	83	
NTDB	id	500	SM12261	RS00945	WP	000249545.1	..MVQEIAQEIIRSARKKGAQDIYFVPKLDAYELHMRVGDERCKIGCYDFEKFAAVISHFKFVAGMNVGEKRRSQLGSCDYEYDQ	83	
NTDB	id	270	KZH43	RS09265	WP	000249564.1	..MVQEIAQEIIRSARKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFAAVISHFKFVAGMNVGEKRRSQLGSCDYYDHY	83	
NTDB	id	229	SPD	RS09895	WP	000249564.1	..MVQEIAQEIIRSARKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFAAVISHFKFVAGMNVGEKRRSQLGSCDYYDHY	83	
NTDB	id	195	SPR	RS09430	WP	000249564.1	..MVQEIAQEIIRSARKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFAAVISHFKFVAGMNVGEKRRSQLGSCDYYDHY	83	
NTDB	id	160	SP	RS10380	WP	000249564.1	..MVQEIAQEIIRSARKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFAAVISHFKFVAGMNVGEKRRSQLGSCDYYDHY	83	
NTDB	id	61639	SANR	RS01165	WP	003033431.1	..MVQNIQAQAIICQAKEERAQDIYFVPKENVYELMRIENRRFIRNYDFEELAAVISHFKFLTAGMNVGEKRRSQLGSCDYYQYGD	83	
NTDB	id	429	SGO	RS09420	WP	012130942.1	..MVQKIIQAIVRQAKEECQAQDIYFVPKDCYELMRIENRRFIQTYDFEQLAAVISHFKFLTAGMNVGEKRRSQLGSCDYYD	83	
consensus							*****	*****	*****

Q	T	I	Y	L	R	L	A	T	V	G	D	F	L	N	R	E	S	L	V	I	R	L	H	D	E	E	Q	D	L	H	F	W	F	Q	D	I	E	E	L	G	K	Q	Y	R	Q	R	G	L	Y	L	F	A	G	P	V	G	S	G	K	T	T	L	M	H	E	L	A	K	S	L	F	K	Q	Q	V	M	S	I	E	D			
Q	.	T	I	Y	L	R	L	A	T	V	G	D	F	L	N	R	E	S	L	V	I	R	L	H	D	E	E	Q	D	I	E	E	L	G	K	Q	Y	R	Q	R	G	L	Y	L	F	A	G	P	T	G	S	G	K	T	T	S	L	Y	H	T	A	Q	Q	S	M	S	A	K	M	V	V	A	I	E	D								
SS	A	K	T	L	R	L	S	T	V	G	D	F	E	G	N	E	S	L	V	I	R	L	L	H	D	E	E	Q	K	Q	E	L	F	W	F	D	.	D	K	.	L	Q	D	F	R	C	K	R	G	L	Y	L	F	A	G	P	V	G	S	G	K	T	S	L	M	F	D	L	A	H	R	H	F	S	N	A	Q	V	I	T	E	E	
G	E	T	A	L	R	L	S	T	V	G	D	Y	Q	G	R	E	S	L	V	I	R	L	L	F	D	R	K	E	L	K	F	W	F	D	.	G	L	N	A	L	L	P	K	I	G	R	G	L	Y	L	F	S	G	P	V	G	S	G	K	T	T	L	M	H	E	L	S	R	K	Y	P	D	S	I	T	E	D						
G	K	V	I	S	L	R	L	S	V	G	D	Y	R	G	Y	E	S	L	V	I	R	L	L	F	S	G	R	H	D	L	K	F	W	F	N	.	S	M	D	L	I	L	N	E	I	K	R	G	L	Y	L	F	S	G	P	V	G	S	G	K	T	S	L	M	Y	Q	L	V	K	L	R	F	E	T	K	Q	V	I	T	E	D		
G	K	V	I	S	L	R	L	S	V	G	D	Y	R	G	Y	E	S	L	V	I	R	L	L	F	S	G	R	H	D	L	K	F	W	F	N	.	S	M	D	L	I	L	N	E	I	K	R	G	L	Y	L	F	S	G	P	V	G	S	G	K	T	S	L	M	Y	Q	L	V	K	L	R	F	E	T	K	Q	V	I	T	E	D		
K	.	M	A	S	L	R	L	S	T	V	G	D	Y	R	G	H	E	S	L	V	I	R	L	L	H	D	E	E	Q	D	L	H	F	W	F	Q	.	D	I	E	E	L	G	K	Q	Y	R	Q	R	G	L	Y	L	F	A	G	P	V	G	S	G	K	T	T	L	M	H	E	L	A	K	S	L	F	K	Q	Q	V	M	S	I	E	D
K	.	I	A	S	L	R	L	S	T	V	G	D	Y	R	G	H	E	S	L	V	I	R	L	L	H	D	E	E	Q	D	L	H	F	W	F	Q	.	D	I	E	E	L	G	K	Q	Y	R	Q	R	G	L	Y	L	F	A	G	P	V	G	S	G	K	T	T	L	M	H	E	L	S	K	S	L	F	K	Q	Q	V	M	S	I	E	D
K	.	I	A	S	L	R	L	S	T	V	G	D	Y	R	G	H	E	S	L	V	I	R	L	L	H	D	E	E	Q	D	L	H	F	W	F	Q	.	D	I	E	E	L	G	K	Q	Y	R	Q	R	G	L	Y	L	F	A	G	P	V	G	S	G	K	T	T	L	M	H	E	L	S	K	S	L	F	K	Q	Q	V	M	S	I	E	D
K	.	I	A	S	L	R	L	S	T	V	G	D	Y	R	G	H	E	S	L	V	I	R	L	L	H	D	E	E	Q	D	L	H	F	W	F	Q	.	D	I	E	E	L	G	K	Q	Y	R	Q	R	G	L	Y																															

PVEIKQDRLMLQLQLNEAIGLTYENLIKLSLRHRPDLLIIGEIRDETARAVRASLTGATVFSTIHAKSIRGVYERLLELGVSEE																																																																																					
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	I	K	L	S	L	R	H	R	P	D	L	L	I	I	G	E	I	R	D	L	E	T	A	R	A	V	R	A	S	L	T	G	A	T	V	F	S	T	I	H	A	K	S	I	R	G	V	Y	E	R	L	L	E	L	G	V	S	E	E	253
P	V	E	I	K	Q	D	N	L	M	L	Q	L	Q	N	E	S	I	D	M	T	Y	D	N	L	I	K	L	S	L	R	H	R	P	D	L	L	I	I	G	E	I	R	D	K	E	T	A	R	A	V	R	A	S	L	T	G	A	T	V	F	S	T	I	H	A	K	S	I	R	G	V	Y	E	R	L	L	E	L	G	V	S	E	E	250	
P	V	E	I	K	Q	D	N	L	M	L	Q	L	Q	N	E	S	I	D	M	T	Y	D	N	L	I	K	L	S	L	R	H	R	P	D	L	L	I	I	G	E	I	R	D	K	E	T	A	R	A	V	R	A	S	L	T	G	A	T	V	F	S	T	I	H	A	K	S	I	R	G	V	Y	E	R	L	L	E	L	G	V	S	E	E	254	
P	V	E	I	K	Q	D	N	L	M	L	Q	L	Q	N	E	S	I	D	M	T	Y	D	N	L	I	K	L	S	L	R	H	R	P	D	L	L	I	I	G	E	I	R	D	K	E	T	A	R	A	V	R	A	S	L	T	G	A	T	V	F	S	T	I	H	A	K	S	I	R	G	V	Y	E	R	L	L	E	L	G	V	S	E	E	252	
P	V	E	I	K	Q	D	N	L	M	L	Q	L	Q	N	E	S	I	D	M	T	Y	D	N	L	I	K	L	S	L	R	H	R	P	D	L	L	I	I	G	E	I	R	D	K	E	T	A	R	A	V	R	A	S	L	T	G	A	T	V	F	S	T	I	H	A	K	S	I	R	G	V	Y	E	R	L	L	E	L	G	V	S	E	E	252	
P	V	E	I	K	Q	D	N	L	M	L	Q	L	Q	N	E	S	I	D	M	T	Y	D	N	L	I	K	L	S	L	R	H	R	P	D	L	L	I	I	G	E	I	R	D	K	E	T	A	R	A	V	R	A	S	L	T	G	A	T	V	F	S	T	I	H	A	K	S	I	R	G	V	Y	E	R	L	L	E	L	G	V	S	E	E	251	
P	V	E	I	K	Q	D	N	L	M	L	Q	L	Q	N	E	S	I	D	M	T	Y	D	N	L	I	K	L	S	L	R	H	R	P	D	L	L	I	I	G	E	I	R	D	K	E	T	A	R	A	V	R	A	S	L	T	G	A	T	V	F	S	T	I	H	A	K	S	I	R	G	V	Y	E	R	L	L	E	L	G	V	S	E	E	251	
P	V	E	I	K	Q	D	N	L	M	L	Q	L	Q	N	E	S	I	D	M	T	Y	D	N	L	I	K	L	S	L	R	H	R	P	D	L	L	I	I	G	E	I	R	D	K	E	T	A	R	A	V	R	A	S	L	T	G	A	T	V	F	S	T	I	H	A	K	S	I	R	G	V	Y	E	R	L	L	E	L	G	V	S	E	E	251	
P	V	E	I	K	Q	D	N	L	M	L	Q	L	Q	N	E	S	I	D	M	T	Y	D	N	L	I	K	L	S	L	R	H	R	P	D	L	L	I	I	G	E	I	R	D	K	E	T	A	R	A	V	R	A	S	L	T	G	A	T	V	F	S	T	I	H	A	K	S	I	R	G	V	Y	E	R	L	L	E	L	G	V	S	E	E	251	
P	V	E	I	K	Q																																																																																

NTDB id	617	LCA RS06480 WP 011375001.1	QLRACLTGIAVQSLVTKDDVVQAHA...YELLTGSDYFSKKEG.....GCDV.....	296
NTDB id	586	KW2 RS10855 WP 011836048.1	ELKNGLAENVYQRRLIAGKGVIDIAKSKFDTWSPKKWNEKIENLYANGHLTAIEAREKTSINQASKIDTTDGESFE	326
NTDB id	584	DLJ51 RS00890 WP 019777327.1	ELDNCLAGIAVQRLIGGGGLIDFAKDHFQNHQAECKWEKIDQLLAAGHLTEEAAAAEKIKD.....	315
NTDB id	385	SMU RS09035 WP 002263435.1	ELQNALRGIVYQRLIGGGGIIDFAKGDYQNHSAKKWNKQIYDLFTAGYITEGEAAQEIED.....	313
NTDB id	394	FSA28 RS09405 WP 002291652.1	ELQNALCGIVYQRLIGGGGIIDFAKGDYQNHSAKKWNKQIYDLFTAGYITEGEAAQEIED.....	313
NTDB id	500	SM12261 RS00945 WP 000249545.1	ELAVVLQGVVCYQRLIGGGGIVDFANKDYQEHQSTSWNAQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id	270	KZH43 RS09265 WP 000249564.1	ELAVVLQGVVCYQRLIGGGGIVDFASRDYQEHQAACKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id	229	SPD RS09895 WP 000249564.1	ELAVVLQGVVCYQRLIGGGGIVDFASRDYQEHQAACKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id	195	SPR RS09430 WP 000249564.1	ELAVVLQGVVCYQRLIGGGGIVDFASRDYQEHQAACKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id	160	SP RS10380 WP 000249564.1	ELAVVLQGVVCYQRLIGGGGIVDFASRDYQEHQAACKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id	61639	SANR RS01165 WP 003033431.1	ELKIVVLQGICYQRLIAGGGIVDFVSERYQEHEPIDWNRQIDQLHAAAGHINLEQAASEKIIHG.....	313
NTDB id	429	SGO RS09420 WP 012130942.1	ELKIVVLQGCICRYRLIGGGGIVDFASDNYYQEHEPTVWNQQIDQLLAAGHIHPAQEAEEKIRNQAKTSY.....	319
consensus			*! **!*!!!!!!** * * * * * * * * * * * * * *	

-  non conserved
-  similar
-  $\geq 50\%$ conserved