

NTDB	id	617	LCA	RS06480	WP	011375001.1	.MSTEEKLTTLLKHCAKQRVQDLYFTPTIGGWRLTERRQSDLVTNQELDKPTGTRYLNRLKYMAGMDISETTRAQTGRSELQLAD	84
NTDB	id	586	KW2	RS10855	WP	011836048.1	..MVQKKKAQELIQKAIEMEASDIYLIASGNLYKIYIRQQLGRTLTIEVNNQIEIGLALLTHFKFLAGMNTGERRRVQLGACWVELEG	83
NTDB	id	584	DLJ51	RS00890	WP	019777327.1	MVEVQELGKLEIRQAVEEQAQDIYLLPCKPAVYKIYLRFGKEKRLITCPPEQAAGLISHFKFLAGMNVGEKRRSQLGACDYAFAD	85
NTDB	id	385	SMU	RS09035	WP	002263435.1	..MVQKLGKRIIAEAVQNKAAQDIYIIPKKESEYELMYRIGNERRFIDVDYHHFMANLISHFKFVAGMNVGEKRRSQLGSCDYSDE	83
NTDB	id	394	FSA28	RS09405	WP	002291652.1	..MVQKLGKRIIAEAVQNKAAQDIYIIPKKESEYELMYRIGNERRFIDVDYHHFMANLISHFKFVAGMNVGEKRRSQLGSCDYSDE	83
NTDB	id	500	SM12261	RS00945	WP	000249545.1	..MVQEIAQEIIIRSARKKGAQDIYFVPKLDAYELHMRVGDERCKIGCYDFEKFKAIVISHFKFVAGMNVGEKRRSQLGSCDYEYDQ	83
NTDB	id	270	KZH43	RS09265	WP	000249564.1	..MVQEIAQEIIIRSARKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFKAIVISHFKFVAGMNVGEKRRSQLGSCDYAYDH	83
NTDB	id	229	SPD	RS09895	WP	000249564.1	..MVQEIAQEIIIRSARKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFKAIVISHFKFVAGMNVGEKRRSQLGSCDYAYDH	83
NTDB	id	195	SPR	RS09430	WP	000249564.1	..MVQEIAQEIIIRSARKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFKAIVISHFKFVAGMNVGEKRRSQLGSCDYAYDH	83
NTDB	id	160	SP	RS10380	WP	000249564.1	..MVQEIAQEIIIRSARKKGTQDIYFVPKLDAYELHMRVGDERCKIGSYDFEKFKAIVISHFKFVAGMNVGEKRRSQLGSCDYAYDH	83
NTDB	id	61495	SCRE	RS08600	WP	006268058.1	..MVQNIQAIIICQAKAERAQDIYFVPKENVYELMYRIGDERRRFIRNYGFEELAAVISHFKFTAGMNVGEKRRSQLGSCDYQYSD	83
NTDB	id	429	SGO	RS09420	WP	012130942.1	..MVQKIAQAIIVRQAKKECAQDIYFVPKDDCYELMYRIGDERRRFIQTYDFDQLAAVISHFKFLAGMNVGEKRRSQLGSCDYRYD	83
consensus								83
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K	A	S	R	L	S	T	V	G	D	Y	R	G	E	S	L	V	I	R	L	H	D	E	E	Q	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	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	F	I	Y	P	I	G	A	I	Y	H	C	D	Q	Q	I	L	A	Q	L	T	Q	M	S	R	Q	S	G	L	I	L	F	A	G	P	T	G	S	G	K	T	T	S	L	Y	H	L	A	Q	Q	S	M	S	A	K	M	V	V	A	I	E	D
S	S	A	K	R	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	T	L	M	F	D	L	A	H	R	F	S	A	N	Q	V	I	T	I	E	D
G	E	T	A	L	R	L	S	T	V	G	D	Y	Q	G	R	E	S	L	V	I	R	L	F	D	R	K	R	E	L	K	F	W	F	D	.	G	I	N	A	L	L	P	K	I	E	I	R	G	L	Y	L	F	S	G	P	V	G	S	G	K	T	T	L	M	H	E	L	V	S	R	K	Y	P	D	S	Q	I	T	I	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	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	T	S	L	M	Y	Q	L	V	K	L	R	F	E	T	K	Q	V	I	T	I	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	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	T	S	L	M	Y	Q	L	V	K	L	R	F	E	T	K	Q	V	I	T	I	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																																			

PVEIKQDRLMLQLQLNEAIGLTYENLIKLSLRHRPDLLIIGEIRDLETARAVRASLTGATVFSTIHAKSIRGVYERLLELGVSEE																																																																																				
P	I	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	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	D	R	L	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	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	250
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	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	254
P	V	E	I	K	Q	D	N	M	L	Q	L	Q	L	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	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	252
P	V	E	I	K	Q	D	N	M	L	Q	L	Q	L	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	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	252
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	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	251
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	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	251
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	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	251
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	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	251
P	V	E	I	K	Q	D</																																																																														

logo

NTDB id 617 LCA RS06480 WP 011375001.1	QLRACLTGIAVQSLVTKDDVVQA...HYELLTGSDYFSKKEGGCDV.....	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	ELAVVLQGVICYQRLIGGGGIVDFANKDYQEHQSTSWNAQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id 270 KZH43 RS09265 WP 000249564.1	ELAVVLQGVICYQRLIGGGGIVDFASRDYQEHQAANKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id 229 SPD RS09895 WP 000249564.1	ELAVVLQGVICYQRLIGGGGIVDFASRDYQEHQAANKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id 195 SPR RS09430 WP 000249564.1	ELAVVLQGVICYQRLIGGGGIVDFASRDYQEHQAANKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id 160 SP RS10380 WP 000249564.1	ELAVVLQGVICYQRLIGGGGIVDFASRDYQEHQAANKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id 61495 SCRE RS08600 WP 006268058.1	ELKIVLQGICYQRLIAGKGVDFVVSERYQEHEPSDWNKQIDQLYAAGHITFEQAETEKIIHS.....	313
NTDB id 429 SGO RS09420 WP 012130942.1	ELKIVLQGICYQRLIGGGGVIDFASDNYQEHEPTVWNQQIDQLLAAGHIHPEQAEAEKIRNQQAKTSY.....	319
consensus	*! **!*****!!*!***** ** ** ** **	

- ⓧ non conserved
- ✖ similar
- ⓧ ≥ 50% conserved