

NTDB	id	617	LCA	RS06480	WP	011375001.1	.MSTEEKLTTLLKHCAKQRVQDLYFTPTIGGWRLTERRQSGLVTNQELDKPTGTRYLNRLKYMAGMDISETRRAQTGRSELQLAD	84
NTDB	id	586	KW2	RS10855	WP	011836048.1	..MVQKKKAQELIQKAIEMEASDIYLIASGNLYKIYIRQQLGRTLTJEEVNQEIGLALLTHFKFLAGMNTGERRRVQLCACWVELEG	83
NTDB	id	584	DLJ51	RS00890	WP	019777327.1	MVEVQELGKLELRQAVEEQAQDDIYLLPAPVKYKIYLRFGEKRHLITCPPEQAAGLISHFKFLAGMNVGEKRRSQLGCADYAFAAD	85
NTDB	id	385	SMU	RS09035	WP	002263435.1	..MVQKLGRKIIAEAVQNKAQDIYIIPKKESEYELMRIGNERRFIDVDHFFMANLISHFKFVAGMNVGEKRRSQLGSCDYSDYE	83
NTDB	id	394	FSA28	RS09405	WP	002291652.1	..MVQKLGRKIIAEAVQNKAQDIYIIPKKESEYELMRIGNERRFIDVDHFFMANLISHFKFVAGMNVGEKRRSQLGSCDYSDYE	83
NTDB	id	34595	SSU	RS00780	WP	011921718.1	..MIQEKARKMIEEAADRVSADIYLVPRGECYQVYHRIMDDREFVQDLAAEEEVTAIISHFKFLAGLNVGEKRRSQQGSCDYDYGS	83
NTDB	id	429	SGO	RS09420	WP	012130942.1	..MVQKIAAQIVRQAKEECAQDIYFVPKLDCCYELMYRIGDERRFITQTYDFQLAAYISHFKFLAGMNVGEKRRSQLGSCDYRYDD	83
NTDB	id	500	SM12261	RS00945	WP	000249545.1	..MVQEIAQEIIIRSARKKGAQDIYFVPKLDAYELHMVRGDERCKIGSYDFEKFPAAVISHFKFVAGMNVGEKRRSQLGSCDYEDDQ	83
NTDB	id	270	KZH43	RS09265	WP	000249564.1	..MVQEIAQEIIIRSARKKGTQDIYFVPKLDAYELHMVRGDERCKIGSYDFEKFPAAVISHFKFVAGMNVGEKRRSQLGSCDYAYDH	83
NTDB	id	229	SPD	RS09895	WP	000249564.1	..MVQEIAQEIIIRSARKKGTQDIYFVPKLDAYELHMVRGDERCKIGSYDFEKFPAAVISHFKFVAGMNVGEKRRSQLGSCDYAYDH	83
NTDB	id	195	SPR	RS09430	WP	000249564.1	..MVQEIAQEIIIRSARKKGTQDIYFVPKLDAYELHMVRGDERCKIGSYDFEKFPAAVISHFKFVAGMNVGEKRRSQLGSCDYAYDH	83
NTDB	id	160	SP	RS10380	WP	000249564.1	..MVQEIAQEIIIRSARKKGTQDIYFVPKLDAYELHMVRGDERCKIGSYDFEKFPAAVISHFKFVAGMNVGEKRRSQLGSCDYAYDH	83
consensus							***** * * ! * ! * * * * ! * * * * ! * * * * ! * * * * ! * * * * ! * * * * ! * * * *	

Position	Sequence	Conservation Score
1	Q.TIY	168
2	SSAKR	165
3	GETA	169
4	GKVI	167
5	GKVI	167
6	G.EI	166
7	K.ET	166
8	K.MA	166
9	K.IA	166
10	K.IA	166
11	K.IA	166
12	K.IA	166

[illegible]

logo

NTDB id 617 LCA RS06480 WP 011375001.1	QLRACLTGIAVQSLVTKDDVVQAH...YELLTGSDYFSKKE.....GGCDV.....	296
NTDB id 586 KW2 RS10855 WP 011836048.1	ELKNGLEAVVYQRLIAGKGVLDIAKSKFDTWSPKKWNEKIENTLYANGHLTAIEEAEREKISINQASKIDTTDGESFE	326
NTDB id 584 DLJ51 RS00890 WP 019777327.1	ELDNCLAGIAYQRLIGGGGLIDFAQDHFQNHQAECWNEKIDQLLAAGHLTEEEAAAEEKIKD.....	315
NTDB id 385 SMU RS09035 WP 002263435.1	ELQNALRGIVYQRLIGGGGIIDFAKGDYQNHSACKWNNKQIYDLFTAGYITEGEAQAEIIE.....	313
NTDB id 394 FSA28 RS09405 WP 002291652.1	ELQNALCGIVYQRLIGGGGIIDFAKGDYQNHSACKWNNKQIYDLFTAGYITEGEAQAEIIE.....	313
NTDB id 34595 SSU RS00780 WP 011921718.1	ELNNALQGIAYQRLIGGGGVVDFAKGNYQNHSADQWNAQIDRLFAAGHISLRQAETEKITLGSPA.....	316
NTDB id 429 SGO RS09420 WP 012130942.1	ELKIVLQGICYQRLIGGGGVIDFASDNYQEHEPTVWNQQIDQLLAAGHIHPEQAEAEKIRNQQAKTSY.....	319
NTDB id 500 SM12261 RS00945 WP 000249545.1	ELAVVLQGVICYQRLIGGGGIVDFANKDYQEHQSTSWNAQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id 270 KZH43 RS09265 WP 000249564.1	ELAVVLQGVICYQRLIGGGGIVDFASRDYQEHQAACKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id 229 SPD RS09895 WP 000249564.1	ELAVVLQGVICYQRLIGGGGIVDFASRDYQEHQAACKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id 195 SPR RS09430 WP 000249564.1	ELAVVLQGVICYQRLIGGGGIVDFASRDYQEHQAACKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
NTDB id 160 SP RS10380 WP 000249564.1	ELAVVLQGVICYQRLIGGGGIVDFASRDYQEHQAACKWNEQIDQLLKDGHITSLQAETEKISYS.....	313
consensus	*! !*** !!*!***** ** * ** ** ** ** ** ** ** ** ** ** **	

- non conserved
- similar
- ≥ 50% conserved