

[illegible]

NTDB id	602	KW2 RS03060 WP 011834647.1	LAIVDTMNFIKS	DVQTI VMGMAASMGTTIASSGT	TGKGRFMLPNAEYL	LHQPMMGGAGQG	GTTQQTDMAIVA EQLLKTRKRLEQ	155
NTDB id	611	V4T04 RS07970 WP 003129593.1	LAIVDTMNFIKS	DVQTI VMGMAASMGTTIASSGT	TGKGRFMLPNAEYL	LHQPMMGGTGQG	GTTQQTDMAIVA EQLLKTRKRLEQ	155
NTDB id	330	STU RS11365 WP 002949732.1	LAIVDTMNFIKS	DVQTI VMGMAASMGTTIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGT	GTTQQTDMAIAAEHLKTRNNLEQ	152	
NTDB id	298	STER RS01925 WP 002949732.1	LAIVDTMNFIKS	DVQTI VMGMAASMGTTIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGT	GTTQQTDMAIAAEHLKTRNNLEQ	152	
NTDB id	282	KZH43 RS03215 WP 000613477.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSGA	TGKGRFMLPNAEYMIHQPMGGTGGGT	GTTQQTDMAIAAEHLKTRNMLEK	152	
NTDB id	246	SPD RS03495 WP 000613477.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSGA	TGKGRFMLPNAEYMIHQPMGGTGGGT	GTTQQTDMAIAAEHLKTRNMLEK	152	
NTDB id	244	SPR RS03300 WP 000613477.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSGA	TGKGRFMLPNAEYMIHQPMGGTGGGT	GTTQQTDMAIAAEHLKTRNMLEK	152	
NTDB id	242	SP RS03655 WP 000613477.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSGA	TGKGRFMLPNAEYMIHQPMGGTGGGT	GTTQQTDMAIAAEHLKTRNMLEK	152	
NTDB id	446	SpyM6JRS4 RS01695 WP 002985850.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGT	GTTQQTDMAIAAEHLKTRHRLEK	152	
NTDB id	445	SPYM3 RS01720 WP 002985850.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGT	GTTQQTDMAIAAEHLKTRHRLEK	152	
NTDB id	376	SMU RS07595 WP 255262720.1	LAIVDTMNFIKS	DVQTI VMTAASMGTTIASSGA	TGKGRFMLPNAEYL	LHQPMMGGTGGGTQQSDMAIAAEQLLKTRKKLEK	160	
NTDB id	983882	NST15 R516030 WP 007500118.1	MAIYDTMQFIKPKVSTICIGMAASMGAFLLAAEGEKGRYAALPNSEVMIHQPLGGAQG..QATIEIEIAAKRIILSLRDKLNQ	152				
NTDB id	86	BSU 34540 NP 391334.1	MAIYDTMQFIKPKVSTICIGMAASMGAFLLAAEGEKGRYAALPNSEVMIHQPLGGAQG..QATIEIEIAAKRIILLRDLKNL	152				
NTDB id	1223	Cj0192c YP 002343650.1	FSAIYDTMNVIKPKDVCTICIQAASMGAFLLSCGAEGKRFAFPNSRIMIHQPLGGARG..QATDIEIQAKEIIIRKLITIND	151				
consensus			**! ! * ! ! * ! ! *	* ! * ! ! * ! ! * ! ! * ! ! ! ! * ! ! ! ! * ! ! ! ! * ! ! ! ! * ! ! ! ! * ! ! ! ! * ! ! ! ! * ! ! ! ! *				

NTDB id 602 KW2 RS03060 WP 011834647.1	ILADNSNRSL	EQIHKDAERDHWMDAK	ETLEYGFIDEIMENNSL	..	199
NTDB id 611 V4T04 RS07970 WP 003129593.1	ILADNSNRSL	EQIHKDAERDHWMDAK	ETLEYGFIDEIMENNSL	..	199
NTDB id 330 STU RS11365 WP 002949732.1	ILADNSGQPI	EKVHVDAERDNWMSAQ	ETLEYGFIDEIMTNNQL	..	196
NTDB id 298 STER RS01925 WP 002949732.1	ILADNSGQPI	EKVHVDAERDNWMSAQ	ETLEYGFIDEIMTNNQL	..	196
NTDB id 282 KZH43 RS03215 WP 000613477.1	ILAE NSGQSM	EKVHADAERDNWMSAQ	ETLEYGFIDEIMANNSL	..	196
NTDB id 246 SPD RS03495 WP 000613477.1	ILAE NSGQSM	EKVHADAERDNWMSAQ	ETLEYGFIDEIMANNSL	..	196
NTDB id 244 SPR RS03300 WP 000613477.1	ILAE NSGQSM	EKVHADAERDNWMSAQ	ETLEYGFIDEIMANNSL	..	196
NTDB id 242 SP RS03655 WP 000613477.1	ILAE NSGQSM	EKVHADAERDNWMSAQ	ETLEYGFIDEIMANNSL	..	196
NTDB id 446 SpyM6JRS4 RS01695 WP 002985850.1	ILAAQNA	GKTIKQIHKDAERDYWMSAE	ETLAYGFIDEIMENNEL	..	196
NTDB id 445 SPYM3 RS01720 WP 002985850.1	ILAAQNA	GKTIKQIHKDAERDYWMSAE	ETLAYGFIDEIMENNEL	..	196
NTDB id 376 SMU RS07595 WP 255262720.1	ILSDNSGKTI	KQIHKDAERDYWMDAK	ETLKYGFIDEIMENNEL	..	204
NTDB id 983882 NST15 RS16030 WP 007500118.1	VLAERTGQPI	EVIERDTRDRNFKTAE	EALQYGLIDKVLTRN	TEEQK	198
NTDB id 86 BSU 34540 NP 391334.1	VLAERTGQPI	EVIERDTRDRNFKSAE	EALQYGLIDKIL	THTEDKK	197
NTDB id 1223 Cj0192c YP 002343650.1	ILAKNTIKQ	KVAKIAKDTERDFFMSAQ	EAKYGLIDKVL	LEKSF	194
consensus	!!*!*****	*****!*****!*****!	!*****!*****!*****	*****	

 non conserved
 similar
 $\geq 50\%$ conserved