

NTDB id	602	KW2 RS03060 WP 011834647.1	MGYLVPTVIEQSSRGERAYDIYSRLKDRIIMLTGPVEDGMANSIIAQLFLDQAQDN	TCKDIYLYVNTPGGSVSAG	75
NTDB id	611	V4T04 RS07970 WP 003129593.1	MGYLVPTVIEQSSRGERAYDIYSRLKDRIIMLTGPVEDGMANSIIAQLFLDQAQDN	TCKDIYLYVNTPGGSVSAG	75
NTDB id	330	STU RS11365 WP 002949732.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIMLTGPIEDNMANSIIAQLFLDQAQDN	TCKDIYLYVNTPGGSVSAG	72
NTDB id	298	STER RS01925 WP 002949732.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIMLTGPIEDNMANSIIAQLFLDQAQDN	TCKDIYLYVNTPGGSVSAG	72
NTDB id	282	KZH43 RS03215 WP 000613477.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIMLTGPVEDNMANSVIAQLFLDQAQS	TCKDIYLYVNTPGGSVSAG	72
NTDB id	246	SPD RS03495 WP 000613477.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIMLTGPVEDNMANSVIAQLFLDQAQS	TCKDIYLYVNTPGGSVSAG	72
NTDB id	244	SPR RS03300 WP 000613477.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIMLTGPVEDNMANSVIAQLFLDQAQS	TCKDIYLYVNTPGGSVSAG	72
NTDB id	242	SP RS03655 WP 000613477.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIMLTGPVEDNMANSVIAQLFLDQAQS	TCKDIYLYVNTPGGSVSAG	72
NTDB id	446	SpyM6JRS4 RS01695 WP 002985850.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIMLTGPVEDNMANSVIAQLFLDQAQDN	TCKDIYLYVNTPGGSVSAG	72
NTDB id	445	SPYM3 RS01720 WP 002985850.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIMLTGPVEDNMANSVIAQLFLDQAQDN	TCKDIYLYVNTPGGSVSAG	72
NTDB id	376	SMU RS07595 WP 255262720.1	MELKEKYS MIPVVIEQTSGRSERSYDIYSRLKDRIIMLTGPVEDNMANSIIAQLFLDQAQDN	TCKDIYLYINSPPGGSVSAG	80
NTDB id	1223	Cj0192c YP 002343650.1	MFIPYVIEKSSRGERSYDIYSRLKDRIIMLSGETIHDELAASIVAQLLFLAEADP	TCKDIYLYINSPGGVITSG	73
NTDB id	61011	RBAU RS16890 WP 003151513.1	MNLIPTVIEQTNRGERAYDIYSRLKDRIIMLGSAIDNVANSIVSQQLLFLEADEDPEKDISTIYNISPPGGSITAG	74	
NTDB id	86	BSU 34540 NP 391334.1	MNLIPTVIEQTNRGERAYDIYSRLKDRIIMLGSAIDNVANSIVSQQLLFLAAEDEDPEKEISLIYNISPPGGSITAG	74	
consensus					
!**!!**!!!!!!!*****!*****!****!*~*~*~*~*~*~*~*~*~*~*~*~*~*~*~*~*~*~*					

NTDB id	602	KW2	RS03060	WP	011834647.1	LAIVDTMNFIKS	DVQTI	VMGMAASMG	TIASSGT	TGKGRFMLPNAEYL	LHQPMGGAGQG	TQTQTDMAIVA	EAEQLLKRKRLE	Q	155
NTDB id	611	V4T04	RS07970	WP	003129593.1	LAIVDTMNFIKS	DVQTI	VMGMAASMG	TIASSGT	TGKGRFMLPNAEYL	LHQPMGGTGQG	TQTQTDMAIVA	EAEQLLKRKRLE	Q	155
NTDB id	330	STU	RS11365	WP	002949732.1	LAIVDTMNFIKS	DVQTI	VMGMAASMG	TIASSGT	TGKGRFMLPNAEYMIHQP	MGGTGGGTQQT	TDMAIAAAEHLLKTRNN	LE	Q	152
NTDB id	298	STER	RS01925	WP	002949732.1	LAIVDTMNFIKS	DVQTI	VMGMAASMG	TIASSGT	TGKGRFMLPNAEYMIHQP	MGGTGGGTQQT	TDMAIAAAEHLLKTRNN	LE	Q	152
NTDB id	282	KZH43	RS03215	WP	000613477.1	LAIVDTMNFIKA	DVQTI	VMGMAASMG	TVIASSG	AKGGRFMLPNAEYMIHQP	MGGTGGGTQQT	TDMAIAAAEHLLKTRNT	LE	K	152
NTDB id	246	SPD	RS03495	WP	000613477.1	LAIVDTMNFIKA	DVQTI	VMGMAASMG	TVIASSG	AKGGRFMLPNAEYMIHQP	MGGTGGGTQQT	TDMAIAAAEHLLKTRNT	LE	K	152
NTDB id	244	SPR	RS03300	WP	000613477.1	LAIVDTMNFIKA	DVQTI	VMGMAASMG	TVIASSG	AKGGRFMLPNAEYMIHQP	MGGTGGGTQQT	TDMAIAAAEHLLKTRNT	LE	K	152
NTDB id	242	SP	RS03655	WP	000613477.1	LAIVDTMNFIKA	DVQTI	VMGMAASMG	TVIASSG	AKGGRFMLPNAEYMIHQP	MGGTGGGTQQT	TDMAIAAAEHLLKTRNT	LE	K	152
NTDB id	446	SpyM6JRS4	RS01695	WP	002985850.1	LAIVDTMNFIKA	DVQTI	VMGMAASMG	TVIASSG	TGKGRFMLPNAEYMIHQP	MGGTGGGTQQT	TDMAIAAAEHLLKTRHR	LE	K	152
NTDB id	445	SPYM3	RS01720	WP	002985850.1	LAIVDTMNFIKA	DVQTI	VMGMAASMG	TVIASSG	TGKGRFMLPNAEYMIHQP	MGGTGGGTQQT	TDMAIAAAEHLLKTRHR	LE	K	152
NTDB id	376	SMU	RS07595	WP	255262720.1	LAIVDTMNFIKS	DVQTI	VMGTAASMG	TIASSGT	AKGGRFMLPNAEYLI	HQPMGGTGGGTQQ	SDMAIAAEQLLKRKK	LE	K	160
NTDB id	1223	Cj0192c	YP	002343650.1	FSIYDTMNVIKP	DVCTICIGQAASMG	AFLILSCGAEGKRFALPN	SRI	MIHQPLGGARG..	QATDIEIQAKEILRLK	ITILND				
NTDB id	61011	RBAU	RS16890	WP	003151513.1	MAIYDTMQFIKPKVS	TCICGMAASMG	AFLLAAGEKGKRYALPN	SEVMIHQPLGGAQG..	QATEIEIAAKRILLRLDKLN	K				
NTDB id	86	BSU	34540	NP	391334.1	MAIYDTMQFIKPKVS	TCICGMAASMG	AFLLAAGEKGKRYALPN	SEVMIHQPLGGAQG..	QATEIEIAAKRILLRLDKLN	K				
consensus						**!!**!!!!*	*!*	*!*!!*	*!*****!	*!!****!!*	*!*****!	*!*****!	*!*****!	*!*****!	*!*

NTDB id 602 KW2 RS03060 WP 011834647.1	ILADNSNRSLQIHKDAERDHWMDAKETLEYGFIDEIMENNSLK..	199
NTDB id 611 V4T04 RS07970 WP 003129593.1	ILADNSNRSLQIHKDAERDHWMDAKETLEYGFIDEIMENNSLK..	199
NTDB id 330 STU RS11365 WP 002949732.1	ILADNSGQPIEKVHVDAERDNWMSAQETLEYGFIDEIMTNNQLK..	196
NTDB id 298 STER RS01925 WP 002949732.1	ILADNSGQPIEKVHVDAERDNWMSAQETLEYGFIDEIMTNNQLK..	196
NTDB id 282 KZH43 RS03215 WP 000613477.1	ILAE NSGQSMEKVVHADAERDNWMSAQETLEYGFIDEIMANNSLN..	196
NTDB id 246 SPD RS03495 WP 000613477.1	ILAE NSGQSMEKVVHADAERDNWMSAQETLEYGFIDEIMANNSLN..	196
NTDB id 244 SPR RS03300 WP 000613477.1	ILAE NSGQSMEKVVHADAERDNWMSAQETLEYGFIDEIMANNSLN..	196
NTDB id 242 SP RS03655 WP 000613477.1	ILAE NSGQSMEKVVHADAERDNWMSAQETLEYGFIDEIMANNSLN..	196
NTDB id 446 SpyM6JRS4 RS01695 WP 002985850.1	ILAQNAGKTIKQIHKDAERDYWMSAEETLAYGFIDEIMENNELK..	196
NTDB id 445 SPYM3 RS01720 WP 002985850.1	ILAQNAGKTIKQIHKDAERDYWMSAEETLAYGFIDEIMENNELK..	196
NTDB id 376 SMU RS07595 WP 255262720.1	ILSDNSGKTIKQIHKDAERDYWMDAKETLKYGFIDEIMENNELK..	204
NTDB id 1223 Cj0192c YP 002343650.1	ILAKNTIKQKVAKIAKDTTERDFFMSAQEAKLEYGLIDKVLKSFK...	194
NTDB id 61011 RBAU RS16890 WP 003151513.1	VLAERTGQPLEVIERDTRDNNFKSADAEALEYGLIDKVLTRNTEDQK	198
NTDB id 86 BSU 34540 NP 391334.1	VLAERTGQPLEVIERDTRDNNFKSADAEALEYGLIDKILTHTEDKK.	197
consensus	!*!***** **!*!*****! !*****! !***** ** **	

 non conserved
 similar
 $\geq 50\%$ conserved