

NTDB id	602 KW2 RS03060 WP 011834647.1	MGYLVPTVIEQSSRGERAYDIYSRLKDRIIIMLTGPVEDGMANSIIAQLFLDQAQDNTKDIYLYVNTPGGSVSAG	75
NTDB id	611 V4T04 RS07970 WP 003129593.1	MGYLVPTVIEQSSRGERAYDIYSRLKDRIIIMLTGPVEDGMANSIIAQLFLDQAQDNTKDIYLYVNTPGGSVSAG	75
NTDB id	330 STU RS11365 WP 002949732.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIIMLTGPIEDNMANSIIAQLFLDQAQDNTKDIYLYVNTPGGSVSAG	72
NTDB id	298 STER RS01925 WP 002949732.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIIMLTGPIEDNMANSIIAQLFLDQAQDNTKDIYLYVNTPGGSVSAG	72
NTDB id	282 KZH43 RS03215 WP 000613477.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIIMLTGPVEDNMANSVIAQLFLDQAQDS TKDIYLYVNTPGGSVSAG	72
NTDB id	246 SPD RS03495 WP 000613477.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIIMLTGPVEDNMANSVIAQLFLDQAQDS TKDIYLYVNTPGGSVSAG	72
NTDB id	244 SPR RS03300 WP 000613477.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIIMLTGPVEDNMANSVIAQLFLDQAQDS TKDIYLYVNTPGGSVSAG	72
NTDB id	242 SP RS03655 WP 000613477.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIIMLTGPVEDNMANSVIAQLFLDQAQDS TKDIYLYVNTPGGSVSAG	72
NTDB id	446 SpyM6JRS4 RS01695 WP 002985850.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIIMLTGPVEDNMANSVIAQLFLDQAQDN TKDIYLYVNTPGGSVSAG	72
NTDB id	445 SPYM3 RS01720 WP 002985850.1	MIPVVIEQTSGRSERSYDIYSRLKDRIIIMLTGPVEDNMANSVIAQLFLDQAQDN TKDIYLYVNTPGGSVSAG	72
NTDB id	376 SMU RS07595 WP 255262720.1	MELKEKYSMIPVVIEQTSGRSERSYDIYSRLKDRIIIMLTGPVEDNMANSIIAQLFLDQAQDN TKDIYLYINSPGGSVSAG	80
NTDB id	1223 Cj0192c YP 002343650.1	MFIPYVVEIKSSRGERSYDIYSRLKDRIIIMLSGEIHDELAASIVAQLLFLAEADPTKDIYLYINSPGGVITSG	73
NTDB id	32408 BCG9842 RS13445 WP 000991608.1	MNAPIPVVEEQTKIIGERSYDIYSRLKDRIIITIGSEINDQVASSVVAQLLFLAEADA EKDIYLYINSPGGSTITAG	74
NTDB id	86 BSU 34540 NP 391334.1	MNLIPTVIEQTNRGERAYDIYSRLKDRIIIMLGSAIDNVANSIVSQLLFLAAEDAPEKEISLIYNISPGGSI TAG	74
consensus		* * * ! * ! * ! * * * * ! * ! * ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! ! * * * * ! * * * ! * * * ! * * ! * ! * ! * ! * ! * ! * ! *	

NTDB id	602	KW2 RS03060 WP 011834647.1	LAIVDTMNFIKS	DVQTI VMGMAASMGTTIASSGT	TGKGRFMLPNAEYLIHQPMGGAGQG	TQTQTDMAIVAEEQLLKTRKRLEQ	155
NTDB id	611	V4T04 RS07970 WP 003129593.1	LAIVDTMNFIKS	DVQTI VMGMAASMGTTIASSGT	TGKGRFMLPNAEYLIHQPMGGTGQG	TQTQTDMAIVAEEQLLKTRKRLEQ	155
NTDB id	330	STU RS11365 WP 002949732.1	LAIVDTMNFIKS	DVQTI VMGMAASMGTTIASSGT	TGKGRFMLPNAEYMIHQPMGGTGCGT	TQTQTDMAIAAEHLLKTRNNLEQ	152
NTDB id	298	STER RS01925 WP 002949732.1	LAIVDTMNFIKS	DVQTI VMGMAASMGTTIASSGT	TGKGRFMLPNAEYMIHQPMGGTGCGT	TQTQTDMAIAAEHLLKTRNNLEQ	152
NTDB id	282	KZH43 RS03215 WP 000613477.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSGA	TGKGRFMLPNAEYMIHQPMGGTGCGT	TQTQTDMAIAAEHLLKTRNMLEK	152
NTDB id	246	SPD RS03495 WP 000613477.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSGA	TGKGRFMLPNAEYMIHQPMGGTGCGT	TQTQTDMAIAAEHLLKTRNMLEK	152
NTDB id	244	SPR RS03300 WP 000613477.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSGA	TGKGRFMLPNAEYMIHQPMGGTGCGT	TQTQTDMAIAAEHLLKTRNMLEK	152
NTDB id	242	SP RS03655 WP 000613477.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSGA	TGKGRFMLPNAEYMIHQPMGGTGCGT	TQTQTDMAIAAEHLLKTRNMLEK	152
NTDB id	446	SpyM6JRS4 RS01695 WP 002985850.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSGT	TGKGRFMLPNAEYMIHQPMGGTGCGT	TQTQTDMAIAAEHLLKTRHRLEK	152
NTDB id	445	SPYM3 RS01720 WP 002985850.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSGT	TGKGRFMLPNAEYMIHQPMGGTGCGT	TQTQTDMAIAAEHLLKTRHRLEK	152
NTDB id	376	SMU RS07595 WP 255262720.1	LAIVDTMNFIKS	DVQTI VMGTAASMGTTIASSGA	TGKGRFMLPNAEYLIHQPMGGTGCGTQQ	SDMAIAAEEQLLKTRKKLEK	160
NTDB id	1223	Cj0192c YP 002343650.1	FSLVDTMNYIKP	DVGTCICIGQAASMGAFILLSCG	AEGKRFALPNSSRI MIHQPLGGARG..	QATDIEIQAKEILRLKTILND	151
NTDB id	32408	BCG9842 RS13445 WP 000991608.1	FAILD TMNL IKP	DVQSTLCMGFAASF GALLLSG	AKGKRFALPNSEVI MIHQPLGGAQG..	QATEIEITAKRILKLKHDKIN	152
NTDB id	86	BSU 34540 NP 391334.1	MAYIDTMQFIKP	PKVSTJCIGMAASMGAFLLAAGE	GKGCRYALPNSEVM I HQPLGGAQG..	QATEIEIAAKRILLDLKLNK	152
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	ILADNSGQPIEKVHVDAERDNWMSAQETLEYGFIDEIMTNQLK.	196
NTDB id	298	STER	RS01925	WP	002949732.1	ILADNSGQPIEKVHVDAERDNWMSAQETLEYGFIDEIMTNQLK.	196
NTDB id	282	KZH43	RS03215	WP	000613477.1	ILAENSQGSMSEKVHADAERDNWMSAQETLEYGFIDEIMANNSLN.	196
NTDB id	246	SPD	RS03495	WP	000613477.1	ILAENSQGSMSEKVHADAERDNWMSAQETLEYGFIDEIMANNSLN.	196
NTDB id	244	SPR	RS03300	WP	000613477.1	ILAENSQGSMSEKVHADAERDNWMSAQETLEYGFIDEIMANNSLN.	196
NTDB id	242	SP	RS03655	WP	000613477.1	ILAENSQGSMSEKVHADAERDNWMSAQETLEYGFIDEIMANNSLN.	196
NTDB id	446	SpyM6JRS4	RS01695	WP	002985850.1	ILAAQNAGKTIKQIHKDAERDYWMSAEETLAYGFIDEIMENNELK.	196
NTDB id	445	SPYM3	RS01720	WP	002985850.1	ILAAQNAGKTIKQIHKDAERDYWMSAEETLAYGFIDEIMENNELK.	196
NTDB id	376	SMU	RS07595	WP	255262720.1	ILSDNSGKTIKQIHKDAERDYWMDAKETLKYGFIDEIMENNELK.	204
NTDB id	1223	Cj0192c	YP	002343650.1	ILAKNTIKQKVAKIAKDTTERDFFMSAQEAKKEYGLIDKIVLEKSFK..	194	
NTDB id	32408	BCG9842	RS13445	WP	000991608.1	MTAEKTIQGPIERVAHDTTERDYFMTAEEAKEYGIVDDVVTKK...	193
NTDB id	86	BSU	34540	NP	391334.1	VLAERTGGPLELVIERDTRDNLNFKSAEEALEYGLIDKIILTHTEDKK	197
consensus						*****!****!* ** *	

 non conserved
 similar
 $\geq 50\%$ conserved