

NTDB id	602	KW2	RS03060	WP	011834647.1	MGYLVPTVIEQSSRGERAYDIYSRLKDRIIMLTGPVEDGMANSIIAQLFLDAQDNTKDIYLYVNTPGGSVSAG	75
NTDB id	611	V4T04	RS07970	WP	003129593.1	MGYLVPTVIEQSSRGERAYDIYSRLKDRIIMLTGPVEDGMANSIIAQLFLDAQDNTKDIYLYVNTPGGSVSAG	75
NTDB id	282	KZH43	RS03215	WP	000613477.1	MIPVVIEQTSGERSYDIYSRLKDRIIMLTGPVEDNMANSVIAQLFLDAQDS TKDIYLYVNTPGGSVSAG	72
NTDB id	246	SPD	RS03495	WP	000613477.1	MIPVVIEQTSGERSYDIYSRLKDRIIMLTGPVEDNMANSVIAQLFLDAQDS TKDIYLYVNTPGGSVSAG	72
NTDB id	244	SPR	RS03300	WP	000613477.1	MIPVVIEQTSGERSYDIYSRLKDRIIMLTGPVEDNMANSVIAQLFLDAQDS TKDIYLYVNTPGGSVSAG	72
NTDB id	242	SP	RS03655	WP	000613477.1	MIPVVIEQTSGERSYDIYSRLKDRIIMLTGPVEDNMANSVIAQLFLDAQDS TKDIYLYVNTPGGSVSAG	72
NTDB id	330	STU	RS11365	WP	002949732.1	MIPVVIEQTSGERSYDIYSRLKDRIIMLTGPIEDNMANSIIAQLFLDAQDNTKDIYLYVNTPGGSVSAG	72
NTDB id	298	STER	RS01925	WP	002949732.1	MIPVVIEQTSGERSYDIYSRLKDRIIMLTGPIEDNMANSIIAQLFLDAQDNTKDIYLYVNTPGGSVSAG	72
NTDB id	376	SMU	RS07595	WP	255262720.1	MELKEKYS MIPVVIEQTSGERSYDIYSRLKDRIIMLTGPVEDNMANSIIAQLFLDAQDNTKDIYLYINSPGGSVSAG	80
NTDB id	49696	SSU12	RS07480	WP	002937303.1	MIPVVIEQTSGERSYDIYSRLKDRIIMLTGPVEDNMANSIIAQLFLDAQDP TKDIYLYVNTPGGSVSAG	72
NTDB id	446	SpyM6JRS4	RS01695	WP	002985850.1	MIPVVIEQTSGERSYDIYSRLKDRIIMLTGPVEDNMANSVIAQLFLDAQDNTKDIYLYVNTPGGSVSAG	72
NTDB id	445	SPYM3	RS01720	WP	002985850.1	MIPVVIEQTSGERSYDIYSRLKDRIIMLTGPVEDNMANSVIAQLFLDAQDNTKDIYLYVNTPGGSVSAG	72
NTDB id	1223	Cj0192c	YP	002343650.1	MFIPYVIEKSSRGRSYDIYSRLKDRIIMLSGEIHDELAAASIVAQLLFLAEADPTKDIYLYINSPGGVITSG	73	
NTDB id	86	BSU	34540	NP	391334.1	MNLIPTVIEQTNRGERAYDIYSRLKDRIIMLGSAIDDNVANSIVSQLLFLAAEDPEKEISLYINSPGGISITAG	74
consensus						**!*!*****!!*!!!!!!!!!!!!!!**!*!*****!!*!!!!!!!!!!!!!!**!*!*****!!*!!!!!!!!!!!!!!**!*!*****!!*!!!!!!!!!!!!!!	

NTDB id	602	KW2 RS03060 WP 011834647.1	LAIVDTMNFIKS	DVQTI VMGMAASMGTVIASSGT	TGKGRFMLPNAEYL	LHQPMGGAGQGTTQQTDMAIVAEQLLKT	RKRLEQ	155
NTDB id	611	V4T04 RS07970 WP 003129593.1	LAIVDTMNFIKS	DVQTI VMGMAASMGTVIASSGT	TGKGRFMLPNAEYL	LHQPMGGTGQGTQQTDMAIVAEQLLKT	RKRLEQ	155
NTDB id	282	KZH43 RS03215 WP 000613477.1	LAIVDTMNFKA	DVQTI VMGMAASMGTVIASSG	AKGKRFMLPNAEYMIHQPMGGTGGGTQQTDMAIAA	EHLLKTRNTLEK		152
NTDB id	246	SPR RS03495 WP 000613477.1	LAIVDTMNFIKS	DVQTI VMGMAASMGTVIASSG	AKGKRFMLPNAEYMIHQPMGGTGGGTQQTDMAIAA	EHLLKTRNTLEK		152
NTDB id	244	SPR RS03300 WP 000613477.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSG	AKGKRFMLPNAEYMIHQPMGGTGGGTQQTDMAIAA	EHLLKTRNTLEK		152
NTDB id	242	SP RS03655 WP 000613477.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSG	AKGKRFMLPNAEYMIHQPMGGTGGGTQQTDMAIAA	EHLLKTRNTLEK		152
NTDB id	330	STU RS11365 WP 002949732.1	LAIVDTMNFIKS	DVQTI VMGMAASMGTVIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGTQQTDMAIAA	EHLLKTRNNLEQ		152
NTDB id	298	STER RS01925 WP 002949732.1	LAIVDTMNFIKS	DVQTI VMGMAASMGTVIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGTQQTDMAIAA	EHLLKTRNNLEQ		152
NTDB id	376	SMU RS07595 WP 255262720.1	LAIVDTMNFIKS	DVQTI VMGTAASMGTVIASSG	AKGKRFMLPNAEYL	LHQPMGGTGGGTQQSDMAIAAEQLLKTR	KKLEK	160
NTDB id	49696	SSU12 RS07480 WP 002937303.1	LAIVDTMNFIKA	DVQTI VMGTAASMGTVIASSG	AKGKRFMLPNAEYMIHQPMGGTGGGTQQTDMAIAA	EHLLKTRNKLEK		152
NTDB id	446	SpyM6JRS4 RS01695 WP 002985850.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGTQQTDMAIAA	EHLLKTRHRLEK		152
NTDB id	445	SPYM3 RS01720 WP 002985850.1	LAIVDTMNFIKA	DVQTI VMGMAASMGTVIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGTQQTDMAIAA	EHLLKTRHRLEK		152
NTDB id	1223	Cj0192c YP 002343650.1	FSIYDTMNFIKP	DVCTICIGQAASMGAFLLSCGAEGKRFALPN	SRIMIHQPLGGARG..QATDIEIQAKE	TLRLKITLND		151
NTDB id	86	BSU 34540 NP 391334.1	MAYIDTMQFIKPKVS	TCICGMAASMGAFLLAAAGEKGRKYALPNSEVM	IHQPLGGARG..QATEIEIAAKRILL	LRDLKNK		152
consensus			*****	* ** ! * ! * ! * ! *	* ** ! * ! * ! * ! * ! * ! * ! * ! * ! *	* ** ! * ! * ! * ! * ! * ! * ! * ! * ! *	* ** ! * ! * ! * ! * ! * ! * ! * ! * ! *	

NTDB id 602 KW2 RS03060 WP 011834647.1	ILADNSNRSL	EQIHKDAERDHWMDAK	ETLEYGFIDEIMENNSLK.	199
NTDB id 611 V4T04 RS07970 WP 003129593.1	ILADNSNRSL	EQIHKDAERDHWMDAK	ETLEYGFIDEIMENNSLK.	199
NTDB id 282 KZH43 RS03215 WP 000613477.1	ILAE	NSGQSMEKVVHADAERDNWMSAQ	ETLEYGFIDEIMANNSLN.	196
NTDB id 246 SPD RS03495 WP 000613477.1	ILAE	NSGQSMEKVVHADAERDNWMSAQ	ETLEYGFIDEIMANNSLN.	196
NTDB id 244 SPR RS03300 WP 000613477.1	ILAE	NSGQSMEKVVHADAERDNWMSAQ	ETLEYGFIDEIMANNSLN.	196
NTDB id 242 SP RS03655 WP 000613477.1	ILAE	NSGQSMEKVVHADAERDNWMSAQ	ETLEYGFIDEIMANNSLN.	196
NTDB id 330 STU RS11365 WP 002949732.1	ILADNSGQPI	EKVHVDAERDNWMSAQ	ETLEYGFIDEIMTNNQLK.	196
NTDB id 298 STER RS01925 WP 002949732.1	ILADNSGQPI	EKVHVDAERDNWMSAQ	ETLEYGFIDEIMTNNQLK.	196
NTDB id 376 SMU RS07595 WP 255262720.1	ILSDNSGKTI	QIKHKDAERDYWMDAK	ETLKYGFIDEIMENNELK.	204
NTDB id 49696 SSU12 RS07480 WP 002937303.1	ILADNSGKTV	KVKIHKDAERDYWMSAE	ETLAYGFIDQIMDNTKVK.	196
NTDB id 446 SpyM6JRS4 RS01695 WP 002985850.1	ILAQ	NAGKTIKQIHKDAERDYWMSAE	ETLAYGFIDEIMENNELK.	196
NTDB id 445 SPY3 RS01720 WP 002985850.1	ILAQ	NAGKTIKQIHKDAERDYWMSAE	ETLAYGFIDEIMENNELK.	196
NTDB id 1223 Cj0192c YP 002343650.1	ILAK	NTKQKVAKIAKDTERDFFMSAQ	EAKLEYGLIDKVLKFSFK.	194
NTDB id 86 BSU 34540 NP 391334.1	VLAERTGQPLE	VIERDTRDNEFKSAEE	ALEYGLIDKILTHTDKK	197
consensus	*!*****	*****!*****!	*****!*****!*****!*****!*****	

 non conserved
 similar
 $\geq 50\%$ conserved