

NTDB id	602	KW2	RS03060	WP	011834647.1	MGYL	VPTVIEQSSRGERAYDIYSRLKDRIIIMLTGPVEDGMANS	IIAQLFLDQAQN	TKDIYLYVNTPGGSVSAG	75
NTDB id	611	V4T04	RS07970	WP	003129593.1	MGYL	VPTVIEQSSRGERAYDIYSRLKDRIIIMLTGPVEDGMANS	IIAQLFLDQAQN	TKDIYLYVNTPGGSVSAG	75
NTDB id	330	STU	RS11365	WP	002949732.1	MIP	VVIEQTSGERSYDIYSRLKDRIIIMLTGPIEDNMANS	IIAQLFLDQAQN	TKDIYLYVNTPGGSVSAG	72
NTDB id	298	STER	RS01925	WP	002949732.1	MIP	VVIEQTSGERSYDIYSRLKDRIIIMLTGPIEDNMANS	IIAQLFLDQAQN	TKDIYLYVNTPGGSVSAG	72
NTDB id	282	KZH43	RS03215	WP	000613477.1	MIP	VVIEQTSGERSYDIYSRLKDRIIIMLTGPVEDNMANS	VIAQLFLDAQDS	TKDIYLYVNTPGGSVSAG	72
NTDB id	246	SPD	RS03495	WP	000613477.1	MIP	VVIEQTSGERSYDIYSRLKDRIIIMLTGPVEDNMANS	VIAQLFLDAQDS	TKDIYLYVNTPGGSVSAG	72
NTDB id	244	SPR	RS03300	WP	000613477.1	MIP	VVIEQTSGERSYDIYSRLKDRIIIMLTGPVEDNMANS	VIAQLFLDAQDS	TKDIYLYVNTPGGSVSAG	72
NTDB id	242	SP	RS03655	WP	000613477.1	MIP	VVIEQTSGERSYDIYSRLKDRIIIMLTGPVEDNMANS	VIAQLFLDAQDS	TKDIYLYVNTPGGSVSAG	72
NTDB id	446	SpyM6JRS4	RS01695	WP	002985850.1	MIP	VVIEQTSGERSYDIYSRLKDRIIIMLTGPVEDNMANS	VIAQLFLDQAQN	TKDIYLYVNTPGGSVSAG	72
NTDB id	445	SPYM3	RS01720	WP	002985850.1	MIP	VVIEQTSGERSYDIYSRLKDRIIIMLTGPVEDNMANS	VIAQLFLDQAQN	TKDIYLYVNTPGGSVSAG	72
NTDB id	376	SMU	RS07595	WP	255262720.1	MELKEKYS	MIPVVIEQTSGERSYDIYSRLKDRIIIMLTGPVEDNMANS	IIAQLFLDQAQN	TKDIYLYINSPGGSVSAG	80
NTDB id	1223	Cj0192c	YP	002343650.1	MF	IPIPVIEKSSRGERSYDIYSRLKDRIIIMLTGSEIHDELAAS	IVAQLLFLAEADP	TKDIYLYINSPGGVITSG	73	
NTDB id	403911	GD442	RS13060	WP	001092372.1	MNT	IPYVVEEQTKLGRERSYDIYSRLKDRIIITIGSEINDQVASS	VVAQLLFLAEADA	EKKDIYLYINSPGGSTITAG	74
NTDB id	86	BSU	34540	NP	391334.1	MNL	IPTVIEQTNRGERAYDIYSRLKDRIIIMLTGSAIDNVANS	IVSQLLFLAAEDPE	KEISLYINSPGGSIATG	74
consensus							***!?!?*****!!*!!!!!!!!!!!!!!*!*!*****!***!****!***!****!			

NTDB id	602	KW2	RS03060	WP	011834647.1	LAIVDTMNFIKS	DVQTI	VMGMAASMG	TIASSGT	TGKGRFMLPNAEYL	LHQP	MGGAGQG	TGQTQD	MAIVA	EAEQLL	KTRKR	LEQ	155
NTDB id	611	V4T04	RS07970	WP	003129593.1	LAIVDTMNFIKS	DVQTI	VMGMAASMG	TIASSGT	TGKGRFMLPNAEYL	LHQP	MGGTGQG	TGQTQD	MAIVA	EAEQLL	KTRKR	LEQ	155
NTDB id	330	STU	RS11365	WP	002949732.1	LAIVDTMNFIKS	DVQTI	VMGMAASMG	TIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGT	TGQTQD	MAIAA	EAHL	LLKTRNN	LEQ		152	
NTDB id	298	STER	RS01925	WP	002949732.1	LAIVDTMNFIKS	DVQTI	VMGMAASMG	TIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGT	TGQTQD	MAIAA	EAHL	LLKTRNN	LEQ		152	
NTDB id	282	KZH43	RS03215	WP	000613477.1	LAIVDTMNFIKS	DVQTI	VMGMAASMG	TIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGT	TGQTQD	MAIAA	EAHL	LLKTRNT	LEK		152	
NTDB id	246	SPD	RS03495	WP	000613477.1	LAIVDTMNFIKS	DVQTI	VMGMAASMG	TIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGT	TGQTQD	MAIAA	EAHL	LLKTRNT	LEK		152	
NTDB id	244	SPR	RS03300	WP	000613477.1	LAIVDTMNFIKS	DVQTI	VMGMAASMG	TIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGT	TGQTQD	MAIAA	EAHL	LLKTRNT	LEK		152	
NTDB id	242	SP	RS03655	WP	000613477.1	LAIVDTMNFIKS	DVQTI	VMGMAASMG	TIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGT	TGQTQD	MAIAA	EAHL	LLKTRNT	LEK		152	
NTDB id	446	SpyM6JRS4	RS01695	WP	002985850.1	LAIVDTMNFIKS	DVQTI	VMGMAASMG	TIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGT	TGQTQD	MAIAA	EAHL	LLKTRHR	LEK		152	
NTDB id	445	SPYM3	RS01720	WP	002985850.1	LAIVDTMNFIKS	DVQTI	VMGMAASMG	TIASSGT	TGKGRFMLPNAEYMIHQPMGGTGGGT	TGQTQD	MAIAA	EAHL	LLKTRHR	LEK		152	
NTDB id	376	SMU	RS07595	WP	255262720.1	LAIVDTMNFIKS	DVQTI	VMGMAASMG	TIASSGT	TGKGRFMLPNAEYL	LHQP	MGGTGGGTQQ	SDMAIAA	EAEQLL	KTRKK	LEK	160	
NTDB id	1223	Cj0192c	YP	002343650.1		FSLIYDTMNLIK	PVQTCICIGQAASMGAFILLSCGAEGKRFALPN	SRI	MIHQPLGGARG..	QATDIEIQAKEILRLK	ITILND						151	
NTDB id	403911	GD442	RS13060	WP	001092372.1		FAILIDTMNLIIKP	DVQTCICMGFAASFALLLSGAKGKRFALPN	SE	MIHQPLGGAQG..	QATEIEITAKRILKLKH	DKIN					152	
NTDB id	86	BSU	34540	NP	391334.1		MAIYDTMQFIKPKVSTI	CIGMAASMGAFLLAAAGEKGKRYALPN	SE	MIHQPLGGAQG..	QATEIEIAAKRILL	RDLKLNK					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	ILADNSGQPPIEKVHVDAERDNWMSAQETLEYGFIDEIMTNQLK.	196
NTDB id	298	STER	RS01925	WP	002949732.1	ILADNSGQPPIEKVHVDAERDNWMSAQETLEYGFIDEIMTNQLK.	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	ILAKNTTKKKVAKIADTDTERDFFMASQAQEAKEYGLIDKIVLEKSFK..	194	
NTDB id	403911	GD442	RS13060	WP	001092372.1	MIAEKTGGPPIERVAHDTDERDYFMTAEEAKAYGIVDVVTKK....	193
NTDB id	86	BSU	34540	NP	391334.1	VLAERTGGPLEVIERDDTRDNEFKSAEEALEYGLIDKILTHTEDKK	197
consensus						*****!***!* **!* ****!	

 non conserved
 similar
 $\geq 50\%$ conserved