

NTDB	id	602	KW2	RS03060	WP	011834647.1		MGYL	VPTVIEQSSRGERAYDIYSRLRKDRIIMLTGPVEDGMANSIIAQLLFDAQDNTKDIYLYVNTPGGSVSAG	75
NTDB	id	611	V4T04	RS07970	WP	003129593.1		MGYL	VPTVIEQSSRGERAYDIYSRLRKDRIIMLTGPVEDGMANSIIAQLLFDAQDNTKDIYLYVNTPGGSVSAG	75
NTDB	id	48980	STH8232	RS02005	WP	002949732.1			MIPVVIEQTSRGERSYDIYSRLRKDRIIMLTGPIEDNMANSIIAQLLFDAQDNTKDIYLYVNTPGGSVSAG	72
NTDB	id	330	STU	RS11365	WP	002949732.1			MIPVVIEQTSRGERSYDIYSRLRKDRIIMLTGPIEDNMANSIIAQLLFDAQDNTKDIYLYVNTPGGSVSAG	72
NTDB	id	298	STER	RS01925	WP	002949732.1			MIPVVIEQTSRGERSYDIYSRLRKDRIIMLTGPIEDNMANSIIAQLLFDAQDNTKDIYLYVNTPGGSVSAG	72
NTDB	id	282	KZH43	RS03215	WP	000613477.1			MIPVVIEQTSRGERSYDIYSRLRKDRIIMLTGPVEDNMANSVIAQLLFDAQDS TKDIYLYVNTPGGSVSAG	72
NTDB	id	246	SPD	RS03495	WP	000613477.1			MIPVVIEQTSRGERSYDIYSRLRKDRIIMLTGPVEDNMANSVIAQLLFDAQDS TKDIYLYVNTPGGSVSAG	72
NTDB	id	244	SPR	RS03300	WP	000613477.1			MIPVVIEQTSRGERSYDIYSRLRKDRIIMLTGPVEDNMANSVIAQLLFDAQDS TKDIYLYVNTPGGSVSAG	72
NTDB	id	242	SP	RS03655	WP	000613477.1			MIPVVIEQTSRGERSYDIYSRLRKDRIIMLTGPVEDNMANSVIAQLLFDAQDS TKDIYLYVNTPGGSVSAG	72
NTDB	id	446	SpyM6JRS4	RS01695	WP	002985850.1			MIPVVIEQTSRGERSYDIYSRLRKDRIIMLTGPVEDNMANSVIAQLLFDAQDNTKDIYLYVNTPGGSVSAG	72
NTDB	id	445	SPYM3	RS01720	WP	002985850.1			MIPVVIEQTSRGERSYDIYSRLRKDRIIMLTGPVEDNMANSVIAQLLFDAQDNTKDIYLYVNTPGGSVSAG	72
NTDB	id	376	SMU	RS07595	WP	255262720.1	MELKEKYS	MIPVVIEQTSRGERSYDIYSRLRKDRIIMLTGPVEDNMANSIIAQLLFDAQDNTKDIYLYINS PGGSVSAG	80	
NTDB	id	86	BSU	34540	NP	391334.1		MNL	IPTVIEQTNRGERAYDIYSRLRKDRIIMLGSAIDDNVANISVSQLFLAEDEPEKETISLYINSPGGSTITAG	74
NTDB	id	1223	Cj0192c	YP	002343650.1			MF	IPYVIEKSSRGERSYDIYSRLRKDRIIMLSGEIHDELAAASIV AQLLFLEAEDPTTKDIYLYINSPGGVITSG	73
									* * * * *	

NTDB id	602 KW2 RS03060 WP 011834647.1	LAIVDTMNFIKSDVQTI VMGMAASMGTTIASSGT KGKRFMLPNAEYL I HQPMGGAGQG GTQTQDMAI VAEQL LKTRKRLEQ	155
NTDB id	611 V4T04 RS07970 WP 003129593.1	LAIVDTMNFIKSDVQTI VMGMAASMGTTIASSGT KGKRFMLPNAEYL I HQPMGGTGCG GTQTQDMAI VAEQL LKTRKRLEQ	155
NTDB id	48980 STH8232 RS02005 WP 002949732.1	LAIVDTMNFIKSDVQTI VMGMAASMGTTIASSGT KGKRFMLPNAEYMIHQ PMGGTGGGT QQT DMAIA AEHL LKTRNNLEQ	152
NTDB id	330 STU RS11365 WP 002949732.1	LAIVDTMNFIKSDVQTI VMGMAASMGTTIASSGT KGKRFMLPNAEYMIHQ PMGGTGGGT QQT DMAIA AEHL LKTRNNLEQ	152
NTDB id	298 STER RS01925 WP 002949732.1	LAIVDTMNFIKSDVQTI VMGMAASMGTTIASSGT KGKRFMLPNAEYMIHQ PMGGTGGGT QQT DMAIA AEHL LKTRNNLEQ	152
NTDB id	282 KZH43 RS03215 WP 000613477.1	LAIVDTMNFIKADVQTI VMGMAASMGTVI ASSGA KGKRFMLPNAEYMIHQ PMGGTGGGT QQT DMAIA AEHL LKTRN TLEK	152
NTDB id	246 SPD RS03495 WP 000613477.1	LAIVDTMNFIKADVQTI VMGMAASMGTVI ASSGA KGKRFMLPNAEYMIHQ PMGGTGGGT QQT DMAIA AEHL LKTRN TLEK	152
NTDB id	244 SPR RS03300 WP 000613477.1	LAIVDTMNFIKADVQTI VMGMAASMGTVI ASSGA KGKRFMLPNAEYMIHQ PMGGTGGGT QQT DMAIA AEHL LKTRN TLEK	152
NTDB id	242 SP RS03655 WP 000613477.1	LAIVDTMNFIKADVQTI VMGMAASMGTVI ASSGA KGKRFMLPNAEYMIHQ PMGGTGGGT QQT DMAIA AEHL LKTRN TLEK	152
NTDB id	446 SpyM6JRS4 RS01695 WP 002985850.1	LAIVDTMNFIKADVQTI VMGMAASMGTVI ASSGT KGKRFMLPNAEYMIHQ PMGGTGGGT QQT DMAIA AEHL LKTRH RLEK	152
NTDB id	445 SPYM3 RS01720 WP 002985850.1	LAIVDTMNFIKADVQTI VMGMAASMGTVI ASSGT KGKRFMLPNAEYMIHQ PMGGTGGGT QQT DMAIA AEHL LKTRH RLEK	152
NTDB id	376 SMU RS07595 WP 255262720.1	LAIVDTMNFIKSDVQTI VMGI AASMGTII ASSGA KGKRFMLPNAEYL I HQPMGGTGGGT QQ SDMAIA AEQL LKTRKKLEK	160
NTDB id	86 BSU 34540 NP 391334.1	MAI YD TM QFIKP KVSTICIGMAA SMC AFLL AAGEKGKRYALPNSEVM IHQP LGCAQG...QA TEIEIAAKRI LLRDKLNK	152
NTDB id	1223 Cj0192c YP 002343650.1	F SI Y DTM N F IK P DVCTICIGQA ASMC GAFLL SC GAEGK RF AL PN SRIMIH QPL GGARG...QA TD IE IQAKE IL RL KTILND	151
consensus		** * * * * * *	

[illegible]

 non conserved
 similar
 $\geq 50\%$ conserved