

NTDB id	611 V4T04 RS07970 WP 003129593.1	MGYL	VPTVIEQSSRGERAYDIYSRLRKDRIIMLTGPVEDG	MANSIIAQLLFDAQDN TKDIYLYVNTPGGSVSAG	75
NTDB id	183018 LLJM3 RS03435 WP 011675637.1	MGYL	VPTVIEQSSRGERAYDIYSRLRKDRIIMLTGPVEDG	MANSIIAQLLFDAQDN TKDIYLYVNTPGGSVSAG	75
NTDB id	602 KW2 RS03060 WP 011834647.1	MGYL	VPTVIEQSSRGERAYDIYSRLRKDRIIMLTGPVEDG	MANSIIAQLLFDAQDN TKDIYLYVNTPGGSVSAG	75
NTDB id	330 STU RS11365 WP 002949732.1	MIPV	VIEQTSRGERSYDIYSRLRKDRIIMLTGP	IEDNMANSIIAQLLFDAQDN TKDIYLYVNTPGGSVSAG	72
NTDB id	298 STER RS01925 WP 002949732.1	MIPV	VIEQTSRGERSYDIYSRLRKDRIIMLTGP	IEDNMANSIIAQLLFDAQDN TKDIYLYVNTPGGSVSAG	72
NTDB id	282 KZH43 RS03215 WP 000613477.1	MIPV	VIEQTSRGERSYDIYSRLRKDRIIMLTGP	VEDNMANSVIAQLLFDAQDS TKDIYLYVNTPGGSVSAG	72
NTDB id	246 SPD RS03495 WP 000613477.1	MIPV	VIEQTSRGERSYDIYSRLRKDRIIMLTGP	VEDNMANSVIAQLLFDAQDS TKDIYLYVNTPGGSVSAG	72
NTDB id	244 SPR RS03300 WP 000613477.1	MIPV	VIEQTSRGERSYDIYSRLRKDRIIMLTGP	VEDNMANSVIAQLLFDAQDS TKDIYLYVNTPGGSVSAG	72
NTDB id	242 SP RS03655 WP 000613477.1	MIPV	VIEQTSRGERSYDIYSRLRKDRIIMLTGP	VEDNMANSVIAQLLFDAQDS TKDIYLYVNTPGGSVSAG	72
NTDB id	376 SMU RS07595 WP 255262720.1	MELKEKYS	MIPVVIEQTSRGERSYDIYSRLRKDRIIMLTGP	VEDNMANSIIAQLLFDAQDN TKDIYLYINSPGGSVSAG	80
NTDB id	446 SpyM6JRS4 RS01695 WP 002985850.1	MIPV	VIEQTSRGERSYDIYSRLRKDRIIMLTGP	VEDNMANSVIAQLLFDAQDN TKDIYLYVNTPGGSVSAG	72
NTDB id	445 SPYM3 RS01720 WP 002985850.1	MIPV	VIEQTSRGERSYDIYSRLRKDRIIMLTGP	VEDNMANSVIAQLLFDAQDN TKDIYLYVNTPGGSVSAG	72
NTDB id	1223 Cj0192c YP 002343650.1	MFIP	YVIEKSSRGRSYDIYSRLRKDRIIML	SGETHDELAASIVAQLLFLEAEDPTKDIYLYINSPGGVITS	73
NTDB id	86 BSU 34540 NP 391334.1	MNL	IPTVIEQTNRGERAYDIYSRLRKDRIIML	GSAIDNVANSIVSQLLFLAAEDPEKEISLYINSPGGSI	74
consensus		***	* * * * *	*****	

NTDB id 611 V4T04 RS07970 WP 003129593.1	LAIVDTMNF	IKSDVQ	TIVMGMAAS	MGTTI	ASSG	TGKGRF	MPLPNAEY	L	I	HQPMGGT	Q	G	TQQTDM	AI	V	A	E	Q	L	L	K	R	K	R	L	E	Q	155																																															
NTDB id 183018 LLJM3 RS03435 WP 011675637.1	LAIVDTMNF	IKSDV	L	TIVMGMAAS	MGTTI	ASSG	TGKGRF	MPLPNAEY	L	I	HQPMGG	A	Q	G	TQQTDM	AI	V	A	E	Q	L	L	K	R	K	R	L	E	Q	155																																													
NTDB id 602 KW2 RS03060 WP 011834647.1	LAIVDTMNF	IKSDVQ	TIVMGMAAS	MGTTI	ASSG	TGKGRF	MPLPNAEY	L	I	HQPMGG	A	Q	G	TQQTDM	AI	V	A	E	Q	L	L	K	R	K	R	L	E	Q	155																																														
NTDB id 330 STU RS11365 WP 002949732.1	LAIVDTMNF	IKSDVQ	TIVMGMAAS	MGTTI	ASSG	TGKGRF	MPLPNAEY	M	I	HQPMGGT	GGG	T	Q	Q	TDM	AI	A	A	E	H	L	L	K	R	T	R	N	L	E	Q	152																																												
NTDB id 298 STER RS01925 WP 002949732.1	LAIVDTMNF	IKSDVQ	TIVMGMAAS	MGTTI	ASSG	TGKGRF	MPLPNAEY	M	I	HQPMGGT	GGG	T	Q	Q	TDM	AI	A	A	E	H	L	L	K	R	T	R	N	L	E	Q	152																																												
NTDB id 282 KZH43 RS03215 WP 000613477.1	LAIVDTMNF	IKADVQ	TIVMGMAAS	MGTTI	ASSG	A	K	G	K	R	F	M	L	P	N	A	E	Y	M	I	H	Q	P	M	G	G	T	G	G	T	Q	Q	TDM	AI	A	A	E	H	L	L	K	R	T	R	N	L	E	Q	152																										
NTDB id 246 SPD RS03495 WP 000613477.1	LAIVDTMNF	IKADVQ	TIVMGMAAS	MGTTI	ASSG	A	K	G	K	R	F	M	L	P	N	A	E	Y	M	I	H	Q	P	M	G	G	T	G	G	T	Q	Q	TDM	AI	A	A	E	H	L	L	K	R	T	R	N	L	E	Q	152																										
NTDB id 244 SPR RS03300 WP 000613477.1	LAIVDTMNF	IKADVQ	TIVMGMAAS	MGTTI	ASSG	A	K	G	K	R	F	M	L	P	N	A	E	Y	M	I	H	Q	P	M	G	G	T	G	G	T	Q	Q	TDM	AI	A	A	E	H	L	L	K	R	T	R	N	L	E	Q	152																										
NTDB id 242 SP RS03655 WP 000613477.1	LAIVDTMNF	IKADVQ	TIVMGMAAS	MGTTI	ASSG	A	K	G	K	R	F	M	L	P	N	A	E	Y	M	I	H	Q	P	M	G	G	T	G	G	T	Q	Q	TDM	AI	A	A	E	H	L	L	K	R	T	R	N	L	E	Q	152																										
NTDB id 376 SMU RS07595 WP 255262720.1	LAIVDTMNF	IKSDVQ	TIVMG	TI	A	A	S	M	G	T	I	A	S	S	G	A	K	G	K	R	F	M	L	P	N	A	E	Y	L	I	H	Q	P	M	G	G	T	G	G	T	Q	Q	TDM	AI	A	A	E	H	L	L	K	R	K	L	E	Q	160																		
NTDB id 446 SpyM6JRS4 RS01695 WP 002985850.1	LAIVDTMNF	IKADVQ	TIVMGMAAS	MGTTI	ASSG	TGKGRF	MPLPNAEY	M	I	HQPMGGT	GGG	T	Q	Q	TDM	AI	A	A	E	H	L	L	K	R	T	R	H	R	L	E	Q	152																																											
NTDB id 445 SPYM3 RS01720 WP 002985850.1	LAIVDTMNF	IKADVQ	TIVMGMAAS	MGTTI	ASSG	TGKGRF	MPLPNAEY	M	I	HQPMGGT	GGG	T	Q	Q	TDM	AI	A	A	E	H	L	L	K	R	T	R	H	R	L	E	Q	152																																											
NTDB id 1223 Cj0192c YP 002343650.1	FS	I	Y	D	T	M	N	I	K	P	D	V	C	T	I	C	I	G	A	A	S	M	G	A	F	L	S	C	G	A	E	G	K	R	F	A	L	P	N	S	R	I	M	I	H	Q	P	L	G	G	A	R	G	..	Q	A	T	D	I	E	I	Q	A	K	E	L	L	R	L	K	T	I	N	D	151
NTDB id 86 BSU 34540 NP 391334.1	MA	I	Y	D	T	M	N	I	K	P	K	V	S	T	I	C	I	G	A	A	S	M	G	A	F	L	A	A	G	E	K	G	K	R	F	A	L	P	N	S	E	V	M	I	H	Q	P	L	G	G	A	Q	..	Q	A	T	E	I	E	I	A	A	K	R	I	L	L	R	D	K	L	N	K	152	
consensus	**	*	*	*	*																																																																						

[illegible]

 non conserved
 similar
 $\geq 50\%$ conserved