

NTDB id 602 KW2 RS03060 WP 011834647.1	MGYL	VPTVIEQSSRGERAYDIYSRLKDRIMLTGPVEDGMANS	IIAQLFLDAQDN	TKDIIYLYVNTPGGSVSAG	75
NTDB id 611 V4T04 RS07970 WP 003129593.1	MGYL	VPTVIEQSSRGERAYDIYSRLKDRIMLTGPVEDGMANS	IIAQLFLDAQDN	TKDIIYLYVNTPGGSVSAG	75
NTDB id 330 STU RS11365 WP 002949732.1		MIPVVIEQTSRGRERSYDIYSRLKDRIMLTGPTEDNMANS	IIAQLFLDAQDN	TKDIIYLYVNTPGGSVSAG	72
NTDB id 298 STER RS01925 WP 002949732.1		MIPVVIEQTSRGRERSYDIYSRLKDRIMLTGPTEDNMANS	IIAQLFLDAQDN	TKDIIYLYVNTPGGSVSAG	72
NTDB id 282 KZH43 RS03215 WP 000613477.1		MIPVVIEQTSRGRERSYDIYSRLKDRIMLTGPVEDNMANS	VIAQLFLDAQDS	STKDIYLYVNTPGGSVSAG	72
NTDB id 246 SPD RS03495 WP 000613477.1		MIPVVIEQTSRGRERSYDIYSRLKDRIMLTGPVEDNMANS	VIAQLFLDAQDS	STKDIYLYVNTPGGSVSAG	72
NTDB id 244 SPR RS03300 WP 000613477.1		MIPVVIEQTSRGRERSYDIYSRLKDRIMLTGPVEDNMANS	VIAQLFLDAQDS	STKDIYLYVNTPGGSVSAG	72
NTDB id 242 SP RS03655 WP 000613477.1		MIPVVIEQTSRGRERSYDIYSRLKDRIMLTGPVEDNMANS	VIAQLFLDAQDS	STKDIYLYVNTPGGSVSAG	72
NTDB id 446 SpyM6JRS4 RS01695 WP 002985850.1		MIPVVIEQTSRGRERSYDIYSRLKDRIMLTGPVEDNMANS	VIAQLFLDAQDN	TKDIIYLYVNTPGGSVSAG	72
NTDB id 445 SPYM3 RS01720 WP 002985850.1		MIPVVIEQTSRGRERSYDIYSRLKDRIMLTGPVEDNMANS	VIAQLFLDAQDN	TKDIIYLYVNTPGGSVSAG	72
NTDB id 376 SMU RS07595 WP 255262720.1	MELKEKYS	MIPVVIEQTSRGRERSYDIYSRLKDRIMLTGPVEDNMANS	IIAQLFLDAQDN	TKDIIYLYINSPGGSVSAG	80
NTDB id 1223 Cj0192c YP 002343650.1	MFIP	YVIEKSSRGRERSYDIYSRLKDRIMLTGSETHDELAAS	IVAQLFLFEAEDP	TKDIIYLYINSPGGVITSG	73
NTDB id 24993 GBAA RS13750 WP 000991625.1	MNA	IPYVVEQTKLGRERSYDIYSRLKDRIMLTGSEINDQVASS	VVAQLFLFEAEDA	EKDIFLYINSPGGSTITAG	74
NTDB id 86 BSU 34540 NP 391334.1	MNL	IPTVIEQTNRGERAYDIYSRLKDRIMLTGSAIDDNVANS	IVSQQLLFLAAED	PEKEISLYINSPGGSTITAG	74
consensus		*** ** * * * * * *	*** ** * * * * *	*** ** * * * * *	

[illegible][illegible]

 non conserved
 similar
 $\geq 50\%$ conserved