

[illegible][illegible]

NTDB id 361	SMU RS01310 WP 002262737.1	SGGMRQRAVIAIALATNFEILVADEPTTALDVTIQAQIHLHMKIEIQKNTDSSIIFITHDLGVVAGMADRVAVMYAGKIVE	236
NTDB id 977058	MGAS37859 RS08210 WP 010921893.1	SGGMRQRIVIAIALACRPDILICDEPTTALDVTIQAQIVELLKSLQREYHFTIIFITHDLGVVASIADKVAVMYAGEIVE	240
NTDB id 478	HSISS4 RS06985 WP 021143811.1	SGGMRQRIVIAIALACRPDVLICDEPTTALDVTIQAQIIDLLKSLKEEYGFVIFITHDLGVVASIADKVAVMYAGEIIE	240
NTDB id 327	STU RS16115 WP 011226304.1	SGGMRQRIVIAIALACRPDVLICDEPTTALDVTIQAQIIDLLKSLKEEYGFVIFITHDLGVVASIADKVAVMYAGEIIE	240
NTDB id 295	STER RS06915 WP 011226304.1	SGGMRQRIVIAIALACRPDVLICDEPTTALDVTIQAQIIDLLKSLKEEYGFVIFITHDLGVVASIADKVAVMYAGEIIE	240
consensus		*****	

NTDB id 361	SMU RS01310 WP 002262737.1	YGTVDDEVFYNPQHYPYTWGLLNSMPTTNTAS	GSLHSIPGTPPDLLQPPQGDAFAPRNEFALDIDLKEPPFKVSDSHYAA	316
NTDB id 977058	MGAS37859 RS08210 WP 010921893.1	FGTVEEIFYDPRHPYTWSLLSSLPQLADESGEL	YAIAGTPPSPLYSPIIGDAFALRSEYAMVLDFEKAPPAINVSETHWAK	320
NTDB id 478	HSIS4 RS06985 WP 021143811.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDKG	ELFSIPGTPPSLYTTPVVGDAFALRSDYAMQIDFEEKAPQFQVSDTHWAK	320
NTDB id 327	STU RS16115 WP 011226304.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDNG	KLFSIPGTPPSLYTTPVVGDAFALRSDYALQIDFEEKAPQFQVSDTHWAK	320
NTDB id 295	STER RS06915 WP 011226304.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDNG	KLFSIPGTPPSLYTTPVVGDAFALRSDYALQIDFEEKAPQFQVSDTHWAK	320
consensus		*** ** ** ** **	*** ** ** ** **	

NTDB id 361	SMU RS01310 WP 002262737.1	TWLLD D RAPK I TPPERIL L RWEKWKSLSQGEKHND.....	350
NTDB id 977058	MGAS37859 RS08210 WP 010921893.1	TWLLHPEAPKVQKPEVIQDLHQIKLRKMSQQEEGV....	356
NTDB id 478	HSISS4 RS06985 WP 021143811.1	TWLLHEDAPKVEKPAVIGNLHEKILANMGMFAHLGDEEEGNA	361
NTDB id 327	STU RS16115 WP 011226304.1	TWLLHEDAPKVDKPAVIGNLHEKILANMGMFAHLGDEEEGNA	361
NTDB id 295	STER RS06915 WP 011226304.1	TWLLHEDAPKVDKPAVIGNLHEKILANMGMFAHLGDEEEGNA	361
consensus		***** *** ** ***** ***** *****	

 non conserved
 similar
 $\geq 50\%$ conserved