

[illegible][illegible]

NTDB id 361	SMU RS01310 WP 002262737.1	SGGMRQRAVIAIALATNFEILVADEPTTALDVTIQAQIHLHMKIEIQKNTDSSIIFITHDLGVVAGMADRVAVMYAGKIVE	236
NTDB id 978177	MGAS37826 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	YGTVDDEVFYNPQHPPYTWGLLNSMPTTNTAS	GSLSHSIPGTTPD LL QPPQGDAFAPRNEFALDIDLKEEPPFFKVS DS HYAA	316
NTDB id 978177	MGAS37826	RS08210 WP 010921893.1	FGTVEEIFYDPRHPYTWSLLSSLPQLADES	GELYAIPGTTPPSLYSPIIGDAFALRSEYAMVLDFEKAPPAINVSETHWAK	320
NTDB id 478	HSISS4	RS06985 WP 021143811.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDK	GELFSIPGTTPPSLYTPVVGDAFALRSDYAMQIDFEEKAPQFQVSDTHWAK	320
NTDB id 327	STU RS16115	WP 011226304.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDN	GKLFSSIPGTTPPSLYTPVVGDAFALRSDYALQIDFEEKAPQFQVSDTHWAK	320
NTDB id 295	STER RS06915	WP 011226304.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDN	GKLFSSIPGTTPPSLYTPVVGDAFALRSDYALQIDFEEKAPQFQVSDTHWAK	320
consensus			*****	*****	

NTDB id 361	SMU RS01310 WP 002262737.1	TWLLDTRAPKTPPERILRLRWEKWKSLOGEKHND.....	350
NTDB id 978177	MGAS37826 RS08210 WP 010921893.1	TWLLHPEAPKVQKPEVIQDLHQILRKMSQQEEGV.....	356
NTDB id 478	HSISS4 RS06985 WP 021143811.1	TWLLHEDAPKVDEKPAVIQNLEHKIRANMGFAHLGDEEEGNA	361
NTDB id 327	STU RS16115 WP 011226304.1	TWLLHEDAPKVDEKPAVIQNLEHKILANMGFAHLGDEEEGNA	361
NTDB id 295	STER RS06915 WP 011226304.1	TWLLHEDAPKVDEKPAVIQNLEHKILANMGFAHLGDEEEGNA	361
consensus		!! ! ! * * * * ! ! ! * * * * ! ! ! * * * * ! ! ! * * * * ! ! ! * * * * ! ! ! * * * *	

 non conserved
 similar
 $\geq 50\%$ conserved