

[illegible][illegible]

NTDB id 361	SMU RS01310 WP 002262737.1	SGGMRQRAVIAIALATNFEILVADEPTTALDVTIQAQIHLHMKELIQKNTDSIIIFITHDLGVVGADRVAVVMYAGKTIVE	236
NTDB id 977842	MGAS37834 RS08210 WP 010921893.1	SGGMRQRIVIAIALACRPDIILICDEPTTALDVTIQAQIVELLKSLQREYHFITIIIFITHDLGVVASIADKVAVMYAGEIIVE	240
NTDB id 478	HSISS4 RS06985 WP 021143811.1	SGGMRQRIVIAIALACRPDVLICDEPTTALDVTIQAQIIDLLKSLKEEYGFSVIFITHDLGVVASIADKVAVMYAGEIIE	240
NTDB id 327	STU RS16115 WP 011226304.1	SGGMRQRIVIAIALACRPDVLICDEPTTALDVTIQAQIIDLLKSLKEEYGFSVIFITHDLGVVASIADKVAVMYAGEIIE	240
NTDB id 295	STER RS06915 WP 011226304.1	SGGMRQRIVIAIALACRPDVLICDEPTTALDVTIQAQIIDLLKSLKEEYGFSVIFITHDLGVVASIADKVAVMYAGEIIE	240
consensus		* * * * *	

NTDB id 361	SMU RS01310	WP 002262737.1	YGTVDDEVFYNPQHPPYTWGLLNSMPTTNTAS	GSLSHSIPGTPPDLLQPPQGDAFAPRNEFALDIDLKEEPPFFKVSDDSHYAA	316
NTDB id 977842	MGAS37834	RS08210 WP 010921893.1	FGTVEEIFYDPRHPYTWSLLSSLPQLADES	GELIYAIPGTPPSLYSPIIGDAFALRSEYAMVLDFEKAPPAINVSETHWAK	320
NTDB id 478	HSISS4	RS06985 WP 021143811.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDK	GELFSIPGTPPSLYTTPVVGDAFALRSDYAMQIDFEEKAPQFQVSDTHWAK	320
NTDB id 327	STU RS16115	WP 011226304.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDN	GKLFSSIPGTPPSLYTTPVVGDAFALRSDYALQIDFEEKAPQFQVSDTHWAK	320
NTDB id 295	STER RS06915	WP 011226304.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDN	GKLFSSIPGTPPSLYTTPVVGDAFALRSDYALQIDFEEKAPQFQVSDTHWAK	320
consensus			*****	*****	

NTDB id 361	SMU RS01310 WP 002262737.1	TWLLDTRAPKTPPERILRLWEKWKSLOGEKHND.....	350
NTDB id 977842	MGAS37834 RS08210 WP 010921893.1	TWLLHPEAPKVQKPEVIQDLHQIKLRKMSQQEEGV.....	356
NTDB id 478	HSISS4 RS06985 WP 021143811.1	TWLLHEDAPKVVKPAVIQNLEHKIRANMGMFAHLGDEEEGNA	361
NTDB id 327	STU RS16115 WP 011226304.1	TWLLHEDAPKVVKPAVIQNLEHKILANMGMFAHLGDEEEGNA	361
NTDB id 295	STER RS06915 WP 011226304.1	TWLLHEDAPKVVDKPAVIQNLEHKILANMGMFAHLGDEEEGNA	361
consensus		!! ! ! * * * * ! ! ! * * * * ! ! ! * * * * ! ! ! * * * * ! ! ! * * * * ! ! ! * * * *	

 non conserved
 similar
 $\geq 50\%$ conserved