

[illegible][illegible]

NTDB id 361	SMU RS01310 WP 002262737.1	SGGMRQRAVIAIALATNFEILVADEPTTALDVTIQAQLHLMKELIQKNTDSIIFFITHDLGVVGAMDRVAVVMYAGKTVE	236
NTDB id 977898	MGAS37833 RS08215 WP 010921893.1	SGGMRQRIVIAIALACRPDIILICDEPTTALDVTIQAQIVELLKSLLRQRYHFTIIFITHDLGVVASIADKVAVMYAGEIVE	240
NTDB id 478	HSISS4 RS06985 WP 021143811.1	SGGMRQRIVIAIALACRPDVLCDEPTTALDVTIQAQIIDLLKSLKEEYGFSVFIFITHDLGVVASIADKVAVMYAGEIIE	240
NTDB id 327	STU RS16115 WP 011226304.1	SGGMRQRIVIAIALACRPDVLCDEPTTALDVTIQAQIIDLLKSLKEEYGFSVFIFITHDLGVVASIADKVAVMYAGEIIE	240
NTDB id 295	STER RS06915 WP 011226304.1	SGGMRQRIVIAIALACRPDVLCDEPTTALDVTIQAQIIDLLKSLKEEYGFSVFIFITHDLGVVASIADKVAVMYAGEIIE	240
consensus		* * * * *	*

NTDB id 361	SMU RS01310 WP 002262737.1	YGTVDDEVFYNPQHPPYTWGLLNSMPTTNTAS	GSLSHSIPGTPPDLLQPPQGDAFAPRNEFALDIDLKEPPFFKVS	SHYAA	316
NTDB id 977898	MGAS37833 RS08215 WP 010921893.1	FGTVEEIFYDPRHPYTWSLLSSLPQLADESGE	LAYAIPTGTPPSLYSPIIGDAFALRSEYAMVLDFEKAPPA	INVSETHWAK	320
NTDB id 478	HSIS4 RS06985 WP 021143811.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDK	GELFSIPGTPPSLYTTPVVGDAFALRSDYAMQIDFEEKAPQ	FQVSDTHWAK	320
NTDB id 327	STU RS16115 WP 011226304.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDN	GKLFSSIPGTPPSLYTTPVVGDAFALRSDYALQIDFEEKAPQ	FQVSDTHWAK	320
NTDB id 295	STER RS06915 WP 011226304.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDN	GKLFSSIPGTPPSLYTTPVVGDAFALRSDYALQIDFEEKAPQ	FQVSDTHWAK	320
consensus		*** ** ** ** **	*** ** ** ** **	*** ** ** ** *	

[illegible]

 non conserved
 similar
 $\geq 50\%$ conserved