

[illegible]

NTDB id 361 SMU RS01310 WP 002262737.1	NDLK.EEDWVHIRGNDISMFQDPMTSLDPTMRIGLQIAEPIIKHEKVTKKEALKRALDMMKEKVGIPNAQEHINDYPHQW	156
NTDB id 977730 MGAS37837 RS08210 WP 010921893.1	TDLKTNKEWAKIRGSKIATIFQDPMTSLSPIKTIGSQITEVIKHKQVSHAKAKEMALDYMKNKVGIPNAKRRFEDYPFY	160
NTDB id 478 HSIS4 RS06985 WP 021143811.1	TKLKSHQDWAHIRGAKIATIFQDPMTSLDPIKTIGSQIVEVIVKHGQKSAKEAKKMAIDYMDKVGIPDAEKRFNEYPFQY	160
NTDB id 327 STU RS16115 WP 011226304.1	TKFKSHQDWAAIRGAKIATIFQDPMTSLNPIKTIGSQIEVIVKHGQKTAKEAKKMAIDYMDKVGIPDAEKRFNEYPFQY	160
NTDB id 295 STER RS06915 WP 011226304.1	TKFKSHQDWAAIRGAKIATIFQDPMTSLNPIKTIGSQIEVIVKHGQKTAKEAKKMAIDYMDKVGIPDAEKRFNEYPFQY	160
consensus	*****	

[illegible]

NTDB id 361	SMU RS01310 WP 002262737.1	YGTVDDEVFYNPQHPPYTWGLLNSMPTTINTAS	GSLHSIPGTPPDLLQPPQGDAFAPRNEFALDIDLKEEPFFKVSDDSHYAA	316
NTDB id 977730	MGAS37837 RS08210 WP 010921893.1	FGTVEEIFYDPRHPYTWSLLSSLPQLADES	GELYAIPGTPPSLYSPIIGDAFALRSEYAMVLDFEKAPPAINVSETHWAK	320
NTDB id 478	HSISS4 RS06985 WP 021143811.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDK	GELFSIPGTPPSLYTPVVGDFAFALRSDYAMQIDFEEDKAPQFQVSDTHWAK	320
NTDB id 327	STU RS16115 WP 011226304.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDN	GKLFSIPGTPPSLYTPVVGDFAFALRSDYALQIDFEEDKAPQFQVSDTHWAK	320
NTDB id 295	STER RS06915 WP 011226304.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDN	GKLFSIPGTPPSLYTPVVGDFAFALRSDYALQIDFEEDKAPQFQVSDTHWAK	320
consensus		*****	*****	

NTDB id 361	SMU RS01310 WP 002262737.1	TWLLDTRAPKTPPERILRLRWEKWKSLOGEKHND.....	350
NTDB id 977730	MGAS37837 RS08210 WP 010921893.1	TWLLHPEAPKVQKPEVIQDLHQIKLRKMSQQEEGV.....	356
NTDB id 478	HSISS4 RS06985 WP 021143811.1	TWLLHEDAPKVDEKPAVIQNLEHKIRANMGFAHLGDDEEEGNA	361
NTDB id 327	STU RS16115 WP 011226304.1	TWLLHEDAPKVDEKPAVIQNLEHKILANMGFAHLGDDEEEGNA	361
NTDB id 295	STER RS06915 WP 011226304.1	TWLLHEDAPKVDEKPAVIQNLEHKILANMGFAHLGDDEEEGNA	361
consensus		!!!!!!**!*! ! ! * ! * ! * ! * ! * ! * ! * ! * ! * ! *	

 non conserved
 similar
 $\geq 50\%$ conserved