

logo

NTDB id 478 HSISS4 RS06985 WP 021143811.1	MTENKNVILSARDIVVEFDVDRDVLTAIRGVSLDLVEGEVLALVGESGSGKSVLT	80
NTDB id 327 STU RS16115 WP 011226304.1	MTENKNVILSARDIVVEFDVDRDVLTAIRGVSLDLVEGEVLALVGESGSGKSVLT	80
NTDB id 295 STER RS06915 WP 011226304.1	MTENKNVILSARDIVVEFDVDRDVLTAIRGVSLDLVEGEVLALVGESGSGKSVLT	80
NTDB id 1119742 EL077 RS01555 WP 012678544.1	..MTNETILSVKNLHVDFKTYAGDVKAIRNLSFELKKGETLAVGESGSGKSVT	77
NTDB id 361 SMU RS01310 WP 002262737.1	..MSKEKILQVNLHVNFHTYAGEVKAIRDVSFYLEKGETLAVGESGSGKSVT	77
consensus	*****!!*****!!*****!!!!*!*!*!*!*!*!!!!!!*!*!*!*!*!*!*!*!*!*!*!	

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NTDB id 478 HSISS4 RS06985 WP 021143811.1	TKLKSHQDWAHIRGAKIATIFQDPMTSLDPIKTIGSQI	160
NTDB id 327 STU RS16115 WP 011226304.1	TKLKSHQDWAHIRGAKIATIFQDPMTSLDPIKTIGSQI	160
NTDB id 295 STER RS06915 WP 011226304.1	TKLKSHQDWAHIRGAKIATIFQDPMTSLDPIKTIGSQI	160
NTDB id 1119742 EL077 RS01555 WP 012678544.1	NELK.EEEWVKVVRGNEIAMIFQDPMTSLDPTMTIGMQIAEATMTHQSIHKTEAL	156
NTDB id 361 SMU RS01310 WP 002262737.1	NDLK.EEDWVHIRGNDISMIQDPMTSLDPTMRIGLQIAEPTIKHEKVTKKEAL	156
consensus	***!*****!* *!!*!*!*!*!!!!!!*!*!*!*!*!*!!!!!!*!*!*!*!*!*!!!!!!*!*!	

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NTDB id 478 HSISS4 RS06985 WP 021143811.1	SGGMRQRIVIAIALACRPDYLICDEPTTALDVTIQAQI	240
NTDB id 327 STU RS16115 WP 011226304.1	SGGMRQRIVIAIALACRPDVLICDEPTTALDVTIQAQI	240
NTDB id 295 STER RS06915 WP 011226304.1	SGGMRQRIVIAIALACRPDVLICDEPTTALDVTIQAQI	240
NTDB id 1119742 EL077 RS01555 WP 012678544.1	SGGMRQRAVIAIALAANPDILIADEPTTALDVTIQAQIKLMDIQSQTASSIF	236
NTDB id 361 SMU RS01310 WP 002262737.1	SGGMRQRAVIAIALATNPETLVADEPTTALDVTIQAQIHLMKELQKNTDSSIF	236
consensus	!!!!!!!!*!!!!!!!!!!*!*!*!*!!!!!!!!!!!!!!!!!!!!!!!!!!*!*!*!!!!!!!!!!*!*!*!!!!!!!!!!*!*!	

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NTDB id 478 HSISS4 RS06985 WP 021143811.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDNGKLF	320
NTDB id 327 STU RS16115 WP 011226304.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDNGKLF	320
NTDB id 295 STER RS06915 WP 011226304.1	YATVEEIFYEPCHPYTWSLLSSLPQLADDNGKLF	320
NTDB id 1119742 EL077 RS01555 WP 012678544.1	YGTVDDEVFYHPQHPYTWGLLSMPTTATAAGSLRSIPGTPPDLLNPPKGDAFA	316
NTDB id 361 SMU RS01310 WP 002262737.1	YGTVDDEVFYNPQHPYTWGLLSMPTTNTASGSLHSIPGTPPDLLQPPQGDAFA	316
consensus	!*!*!*!*!*!*!!!!!!!!!!*!*!*!*!*!*!!!!!!!!!!*!*!*!*!*!*!!!!!!!!!!*!*!*!*!*!*!!!!!!!!!!*!*!	

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NTDB id 478 HSISS4 RS06985 WP 021143811.1	TWLLHEDAPKVEKPAVIQNLHEKILANMGFAHLGDEEEGNA	361
NTDB id 327 STU RS16115 WP 011226304.1	TWLLHEDAPKVDKPAVIQNLHEKILANMGFAHLGDEEEGNA	361
NTDB id 295 STER RS06915 WP 011226304.1	TWLLHEDAPKVDKPAVIQNLHEKILANMGFAHLGDEEEGNA	361
NTDB id 1119742 EL077 RS01555 WP 012678544.1	TWLLDERAPKLTTPPLPIRKRWAKWQEMEERKA.....	348
NTDB id 361 SMU RS01310 WP 002262737.1	TWLLDDRAPKLTTPPERILRWKWKSLQGEKHND.....	350
consensus	!!!!*!*!*!*!*!*!!!!!!!!!!*!*!*!*!*!*!!!!!!!!!!*!*!*!*!*!*!!!!!!!!!!*!*!*!*!*!*!!!!!!!!!!*!*!	

 non conserved
 similar
 $\geq 50\%$ conserved