

logo

NTDB id 587 KW2 RS10850 WP 042211510.1	MQT	DILRLILRPKGGKKLALIKQAKLIQLMGNLLNNGFNLG	EVINFLALSKLVEKEFVFKM	59	
NTDB id 222897 A6J31 RS08680 WP 142390728.1	MPVKISKAIRQSAGTNSWKAWLNK	DISLKGISKGKKLQINQFKVIQLFKQLLKA	GFTEIVAFLE	RSRSHLLKESSLSLM	80
NTDB id 395 FSA28 RS09400 WP 257638827.1	MTFLQQ	DISLKEKHKQKKLKIKKQKQKVIQLFNNLFTSGFN	LTEIIDFLERSHLLAEIYTKKM	62	
NTDB id 386 SMU RS09030 WP 255262721.1	MTFLQQ	DISLKEKHKQKKLKIKKQKQKVIQLFNNLFTSGFN	LTEIIDFLERSHLLAEIYTKKM	62	
NTDB id 430 SGO RS09415 WP 012130941.1	MISFLQQ	DISILSKQKQKKLGT	SKQKQVIELFNNLFSSGFHLAETVDFLGRSALL	EKNYVQQM	63
NTDB id 271 KZH43 RS09260 WP 074196785.1		MDISQVFRLLRRKKLATAKQKNIITLFNNLFSSGFHL	VETISFLDRSALLDKQCVTQM	57	
NTDB id 230 SPD RS09890 WP 074196785.1		MDISQVFRLLRRKKLATAKQKNIITLFNNLFSSGFHL	VETISFLDRSALLDKQCVTQM	57	
NTDB id 196 SPR RS09425 WP 074196785.1		MDISQVFRLLRRKKLATAKQKNIITLFNNLFSSGFHL	VETISFLDRSALLDKQCVTQM	57	
NTDB id 161 SP RS10375 WP 074196785.1		MDISQVFRLLRRKKLATAKQKNIITLFNNLFSSGFHL	VETISFLDRSALLDKQCVTQM	57	
NTDB id 529 SMSK321 RS09235 WP 080550783.1		MDISQVFRLLRRKKLATAKQKNIITLFNNLFSSGFHL	VETISFLDRSALLDKQCVTQM	57	
NTDB id 501 SM12261 RS00950 WP 004238896.1		MDISQVFRLLRRKKLATAKQKNIITLFNNLFSSGFHL	VETISFLDRSALLDKQCVTQM	57	
consensus		*****	*****	*****	*****

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NTDB id 587 KW2 RS10850 WP 042211510.1	HQGLSSGKSLSEILESLSFSKN	VVTQLALVEVHGNLVG	TMQLVELHLKKQLKVKKKLIEVATYP	VVLLVFLIGIMWGLKN	139
NTDB id 222897 A6J31 RS08680 WP 142390728.1	KASLMRGDRLDQMFASVGFSDN	IVTQIALADKHGNLLGSLTKIETY	MLRMTKVRKKLMEVATYP	ILLGFLILIMLGLKN	160
NTDB id 395 FSA28 RS09400 WP 257638827.1	RQGLLNGLHLAEIMSSSLGFSD	VVTQLALSEVHGNTQKSL	LKIESYLNLLILVKKKLVEVITY	PIILLIFLVVIMLGLKN	142
NTDB id 386 SMU RS09030 WP 255262721.1	RQGLLNGLHLAEIMSSSLGFSD	VVTQLALSEVHGNTQKSL	LKIESYLNLLILVKKKLVEVITY	PIILLIFLVVIMLGLKN	142
NTDB id 430 SGO RS09415 WP 012130941.1	RQGLANGQAFSEIMASLGFSD	AVVTQLSLAE	LHGNLSLALLKIEEYLDNLAKVKKKLIEVATYP	MMLLGFLVLIMIGLRN	143
NTDB id 271 KZH43 RS09260 WP 074196785.1	RVGLSQGKSFSEMMESLGC	SSAIVTQLSLAEVHGNLHLS	LGKIEEYLDNLAKVKKKLIEVATY	PLILLGFLLLIMLGLRN	137
NTDB id 230 SPD RS09890 WP 074196785.1	RVGLSQGKSFSEMMESLGC	SSAIVTQLSLAEVHGNLHLS	LGKIEEYLDNLAKVKKKLIEVATY	PLILLGFLLLIMLGLRN	137
NTDB id 196 SPR RS09425 WP 074196785.1	RVGLSQGKSFSEMMESLGC	SSAIVTQLSLAEVHGNLHLS	LGKIEEYLDNLAKVKKKLIEVATY	PLILLGFLLLIMLGLRN	137
NTDB id 161 SP RS10375 WP 074196785.1	RVGLSQGKSFSEMMESLGC	SSAIVTQLSLAEVHGNLHLS	LGKIEEYLDNLAKVKKKLIEVATY	PLILLGFLLLIMLGLRN	137
NTDB id 529 SMSK321 RS09235 WP 080550783.1	RTDLSQGKSFSEMMESLGFSSA	IVTQLSLAEVHGNLHLS	LGKIEEYLDNLAKVKKKLIEVATY	PLILLGFLLSIMLGLRN	137
NTDB id 501 SM12261 RS00950 WP 004238896.1	RAGLSQGKSFSEMMESLGFSSA	IVTQLSLAEVHGNLHLS	LGKIEEYLDNLAKVKKKLIEVATY	PLILLGFLLLIMLGLRN	137
consensus	* * ! *				

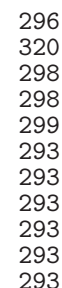
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NTDB id 587 KW2 RS10850 WP 042211510.1	YLLPQLDKG...NNFATLL	LINHLPLVFFSVG	ALIVLLTSLS	IIIFKHIS	SALTNFT	FLVKVPLVSS	FIRLYLTAY	FSREW	216
NTDB id 222897 A6J31 RS08680 WP 142390728.1	YLLPQLLEGDGKENW	AVQLVQIFPKLFFVT	LCGLLVLSL	ILYLWVKRQP	ALVFYRRMAKIP	FIQGTVRLY	MTAYYAREW	G	240
NTDB id 395 FSA28 RS09400 WP 257638827.1	YLLPQLEK....GNFATRL	LISNFPILFLLGCCFFIL	LVGIFTFFSRKIS	RLHLIGFCS	SHLPFVGKYL	QLYLTA	YAREW	G	218
NTDB id 386 SMU RS09030 WP 255262721.1	YLLPQLER....GNFATRL	LISNFPILFLLGCCFFIL	LVGIFTFFSRKIS	RLHLIGFCS	SHLPFAGKYL	QLYLTA	YAREW	G	218
NTDB id 430 SGO RS09415 WP 012130941.1	YLLPQLSS....QNFATQL	LIGHLPITIFLLTVL	MLLGLTGAIYLV	FKGQKRIPVYS	SFLARLPFVGS	FVRIYLT	YAREW	G	219
NTDB id 271 KZH43 RS09260 WP 074196785.1	YLLPQLDS....SNIATQI	IGNLPQIFLGMVGLVSVL	ALLALTFYKR	SKMSVFS	SILARLPF	IGIFVQTYLT	YAREW	G	213
NTDB id 230 SPD RS09890 WP 074196785.1	YLLPQLDS....SNIATQI	IGNLPQIFLGMVGLVSVL	ALLALTFYKR	SKMSVFS	SILARLPF	IGIFVQTYLT	YAREW	G	213
NTDB id 196 SPR RS09425 WP 074196785.1	YLLPQLDS....SNIATQI	IGNLPQIFLGMVGLVSVL	ALLALTFYKR	SKMSVFS	SILARLPF	IGIFVQTYLT	YAREW	G	213
NTDB id 161 SP RS10375 WP 074196785.1	YLLPQLDS....SNIATQI	IGNLPQIFLGMVGLVSVL	ALLALTFYKR	SKMSVFS	SILARLPF	IGIFVQTYLT	YAREW	G	213
NTDB id 529 SMSK321 RS09235 WP 080550783.1	YLLPQLDS....SNIATQI	IGNLPQIFLGMVGLVSL	TLTLLALTFYKR	SKMRVFS	SILARIPFL	GIFVQTYLT	YAREW	G	213
NTDB id 501 SM12261 RS00950 WP 004238896.1	YLLPQLDS....SNIATQI	IGNLPQIFLGMVGF	VSVGVLLALTFYKR	G	SKMRVFS	SILARIPFL	GIFVQTYLT	YAREW	213
consensus	!!!!!!**	*!*!*****	*!*!*****	*****	***	*****	!*****	!!!!!!	

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consensus



- ☐ non conserved
- ☒ similar
- ☒ $\geq 50\%$ conserved