

NTDB id 587 KW2 RS10850 WP 042211510.1	MQT	DILRL	LLRPK	GKKL	ALIK	QAKLI	QLMGN	LNNGF	NLGEV	INFLA	LSKL	VEKE	EFVFK	MHQ	GLSS	GKSL	SEILE	SLSFS	SKN	81			
NTDB id 395 FSA28 RS09400 WP 257638827.1	.MTFL	QQDIS	LKEK	HKKQ	KKLKI	KKQK	RVII	QLFNN	LFTSG	FNLT	TEIID	FLERS	HLLAE	IYTK	KMRQ	GLLN	GLHL	ABIM	SSLGF	SDD	84		
NTDB id 386 SMU RS09030 WP 255262721.1	.MTFL	QQDIS	LKEK	HKKQ	KKLKI	KKQK	RVII	QLFNN	LFTSG	FNLT	TEIID	FLERS	HLLAE	IYTK	KMRQ	GLLN	GLHL	ABIM	SSLGF	SDD	84		
NTDB id 271 KZH43 RS09260 WP 074196785.1		MDISQ	VFRL	RRKK	LATA	KQKNI	ITL	FNNL	FSSG	FHLV	ETIS	FLDR	SALL	DKQ	CVTQ	MRV	GLS	QKSF	SEMME	SLGC	SSA	79	
NTDB id 230 SPD RS09890 WP 074196785.1		MDISQ	VFRL	RRKK	LATA	KQKNI	ITL	FNNL	FSSG	FHLV	ETIS	FLDR	SALL	DKQ	CVTQ	MRV	GLS	QKSF	SEMME	SLGC	SSA	79	
NTDB id 196 SPR RS09425 WP 074196785.1		MDISQ	VFRL	RRKK	LATA	KQKNI	ITL	FNNL	FSSG	FHLV	ETIS	FLDR	SALL	DKQ	CVTQ	MRV	GLS	QKSF	SEMME	SLGC	SSA	79	
NTDB id 161 SP RS10375 WP 074196785.1		MDISQ	VFRL	RRKK	LATA	KQKNI	ITL	FNNL	FSSG	FHLV	ETIS	FLDR	SALL	DKQ	CVTQ	MRV	GLS	QKSF	SEMME	SLGC	SSA	79	
NTDB id 529 SMSK321 RS09235 WP 080550783.1		MDISQ	VFRL	RRKK	LATA	KQKNI	ITL	FNNL	FSSG	FHLV	ETIS	FLDR	SALL	DKQ	CVTQ	MRD	TL	SQKSF	SEMME	SLGF	SSA	79	
NTDB id 501 SM12261 RS00950 WP 004238896.1		MDISQ	VFRL	RRKK	LATA	KQKNI	ITL	FNNL	FSSG	FHLV	ETIS	FLDR	SALL	DKQ	CVTQ	MR	A	GLS	QKSF	SEMME	SLGF	SSA	79
NTDB id 61916 SIR RS18230 WP 021003258.1	MQQ	DISIL	NRQK	RKKL	STV	KQK	QVVE	LNN	FFSSG	FHLAE	ITID	FLKRS	ALLE	EKAY	VEKM	KEGL	ATG	KPFS	D	IMAS	SLGFS	DN	81
NTDB id 430 SGO RS09415 WP 012130941.1	MISFL	QQDIS	ILSK	QKQK	KKLGT	SKQK	QVIE	LNNL	FSSG	FHLAE	ITVDF	FLGR	SALL	EKNY	VQ	QMRQ	GLANG	QA	FSEIM	ASLGF	S	85	
consensus			*	!	!	*	*	*	*	*	!	!	*	*	*	*	!	!	*	*	*	*	

VVTQLALVEVHGNLHLSLGLKIEEYLDNLAKVKKKLEI VATYPVVLIVFLIGIMWGLKNYLLPQLDKGN	NFATLLINHLPLVFFSV	166
VVTQLALSEVHGNTQKSLLKIESYLNLLIVKKKLEVIETYPITILLIFLVIMLGLKNYLLPQLBK	GFATRLISNFPILFLG	168
VVTQLALSEVHGNTQKSLLKIESYLNLLIVKKKLEVIETYPITILLIFLVIMLGLKNYLLPQLBK	GFATRLISNFPILFLG	168
IVTQLSLAEVHGNLHLSLGLKIEEYLDNLAKVKKKLEI VATYPLILLGFLLLIMLGLRNYLLPQLDSS	NIATQIIGNLPQIFLGM	163
IVTQLSLAEVHGNLHLSLGLKIEEYLDNLAKVKKKLEI VATYPLILLGFLLLIMLGLRNYLLPQLDSS	NIATQIIGNLPQIFLGM	163
IVTQLSLAEVHGNLHLSLGLKIEEYLDNLAKVKKKLEI VATYPLILLGFLLLIMLGLRNYLLPQLDSS	NIATQIIGNLPQIFLGM	163
IVTQLSLAEVHGNLHLSLGLKIEEYLDNLAKVKKKLEI VATYPLILLGFLLLIMLGLRNYLLPQLDSS	NIATQIIGNLPQIFLGM	163
IVTQLSLAEVHGNLHLSLGLKIEEYLDNLAKVKKKLEI VATYPLILLGFLLLIMLGLRNYLLPQLDSS	NIATQIIGNLPQIFLGM	163
IVTQLSLAEVHGNLHLSLGLKIEEYLDNLAKVKKKLEI VATYPLILLGFLLLIMLGLRNYLLPQLDSS	NIATQIIGNLPQIFLGM	163
VVTQLSLAEIHGNLSLSLSKIEEYLDNLAKVKKKLEI VATYPLIFLIFLVFIMLGLRNYLLPQLBSQ	NIATQLISRLPQIFLGS	165
VVTQLSLAEIHGNLSLSLSKIEEYLDNLAKVKKKLEI VATYPLIMLLGFLVIMLGLRNYLLPQLSSQ	NFATQLIGHLPTIFLGT	169

VGLVSVL	LALLAL	TFYKR	SKMS	VFSIL	ARLP	PF	GIFV	QTYL	TAYY	AREW	GNM	ISQ	GL	QIFQM	QEQS	QLF	KE	V	QD	L	AA	L	251																																																											
GALIV	LITS	LSII	IFKH	SALTN	FT	FLVK	VP	VSSFI	R	LYLT	AYFS	REWGN	LIA	QGV	ELR	QI	EL	MKK	QKS	RL	FA	EV	G	IK	LD	L	L	252																																																						
CCFFIL	LVG	IFTF	FSRK	IS	RLH	LIGFC	SHLP	FG	KYL	QL	LYLT	AYYAREW	GN	LIG	QGV	MA	QIV	RL	MQD	QKS	QLF	RE	IGY	D	ME	K	A	253																																																						
CCFFIL	LVG	IFTF	FSRK	IS	RLH	LIGFC	SHLP	FG	KYL	QL	LYLT	AYYAREW	GN	LIG	QGV	MA	QIV	RL	MQD	QKS	QLF	RE	IGY	D	ME	K	A	253																																																						
VGLVSVL	LALLAL	TFYKR	SSKMS	VFSIL	ARLP	PF	GIFV	QTYL	TAYY	AREW	GNM	ISQ	G	MELT	QIFQ	M	MQE	QGS	QLF	KE	V	QD	L	AQ	T	L	248																																																							
VGLVSVL	LALLAL	TFYKR	SSKMS	VFSIL	ARLP	PF	GIFV	QTYL	TAYY	AREW	GNM	ISQ	G	MELT	QIFQ	M	MQE	QGS	QLF	KE	V	QD	L	AQ	T	L	248																																																							
VGLVSVL	LALLAL	TFYKR	SSKMS	VFSIL	ARLP	PF	GIFV	QTYL	TAYY	AREW	GNM	ISQ	G	MELT	QIFQ	M	MQE	QGS	QLF	KE	V	QD	L	AQ	T	L	248																																																							
VGLVSVL	LALLAL	TFYKR	SSKMS	VFSIL	ARLP	PF	GIFV	QTYL	TAYY	AREW	GNM	ISQ	G	MELT	QIFQ	M	MQE	QGS	QLF	KE	V	QD	L	AQ	T	L	248																																																							
VGLVSVL	LALLAL	TFYKR	SSKMR	VFSIL	AR	IP	FL	GIFV	QTYL	TAYY	AREW	GNM	ISQ	G	MELT	QIFQ	I	M	Q	E	Q	G	S	Q	L	F	K	E	I	G	D	L	A	Q	S	L	248																																													
VG	FVS	GV	LL	AL	TFYKR	G	SKMR	VFSIL	AR	IP	FL	GIFV	QTYL	TAYY	AREW	GNM	ISQ	G	MELT	QIFQ	I	M	Q	E	Q	G	S	Q	L	F	K	E	I	G	D	M	A	H	A	L	248																																									
VG	V	F	A	L	F	A	I	G	F	Y	W	F	R	K	S	S	Q	I	R	V	F	S	L	S	R	L	P	F	W	G	T	F	V	Q	T	Y	L	T	A	Y	Y	A	R	E	W	G	N	M	I	G	Q	G	L	E	L	S	Q	I	F	Q	M	M	Q	G	Q	R	S	A	M	F	Q	E	I	G	K	D	L	E	V	A	L	250
VL	M	L	L	G	L	T	G	A	I	Y	L	V	F	K	G	K	R	I	P	V	S	F	L	A	R	L	P	F	V	G	S	F	V	R	I	Y	L	T	A	Y	Y	A	R	E	W	G	N	M	I	G	Q	G	L	E	L	S	Q	I	F	Q	I	M	Q	E	Q	R	S	V	L	F	Q	E	I	G	D	L	G	A	L	254		

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consensus

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- X non conserved
- X similar
- X $\geq 50\%$ conserved