

logo

NTDB id 1029 TT RS02230 WP 011228203.1	MAK	65
NTDB id 1402 DSB67 RS12670 WP 010643257.1	MPVYQYKARDRQGRLLVEATTEAEDLRTAARLLRDRGLFVAEIKKEPGKGLQAEVRIPALERGPGGLK	67
NTDB id 1169 A1552VC RS11075 WP 000648511.1	.MKT.....IAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRRERLDAQHIKIKKKLKKGSISFITK.....ISHRVKGK	68
NTDB id 1113 AAA85695.1 219..1451()	MKAT.....QTLPLKNYRWKGINSGKK.VSQMLAISEIEVRDKLKDQHIQIKKKLKKGSVSLAR.....LTHRVKSK	70
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSATETEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	70
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSATETEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	67
NTDB id 1016 ACIAD RS01680 WP 004920476.1	.MDK.....NSPPLILTFFHYQGINKAGQK.MEGDIQARSLAIKADLRKQGIIVTNKVVKRKPFLFDR.....KNKKKITQA	69
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAK.....KTQVMPVFAFEGVDRKGKIK.LKGELPARNMALAKVTLRKQGITRTIREKRKNIFEG....LLKKKVKPL	69
NTDB id 400790 GJV02 RS28480 WP 003161763.1	MAVK.....KAQMMPTFAYEGVDRKGKIK.LKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFFKKVTTTL	66
NTDB id 1198 PSJM300 03950 AFN76868.1	.MAD.....KALKTSVFFVWEGTDKKGKTK.VKGELSSQNPTLVKAQLRKQGITPVKVRKKGISLLG.....AGKKIKPM	66
consensus	.MAQ.....KAIKNSVFTWEGLDRQGAK.TKGELSGVSPALVKAQLRKQGINPQKVRKKKSISLFS.....AGKKIKPM	66

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NTDB id 1029 TT RS02230 WP 011228203.1	DITIFTRQLATMAGYPLVQAEIVAEHNPMBRELLMEIKVEGSSSALRKHPQYFDLYCNLVAGEQSGI	144
NTDB id 1402 DSB67 RS12670 WP 010643257.1	DLAIFSRQLATMLGAGLTLLQALATILERQTEENRKFREILKQVRTDVEGGMAFSEALSKEH.KIFSRLYVNLVRAGETSGGL	147
NTDB id 1169 A1552VC RS11075 WP 000648511.1	DITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNL	148
NTDB id 1113 AAA85695.1 219..1451()	DITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLIVETGEMSGNL	150
NTDB id 1112 NGFG RS09215 WP 003689811.1	DITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL	150
NTDB id 1252 GC085 RS07730 WP 011213805.1	DITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL	147
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELCNLDVAGEKSGSL	149
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSL	149
NTDB id 400790 GJV02 RS28480 WP 003161763.1	DITIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLIESGEQSGAL	146
NTDB id 1198 PSJM300 03950 AFN76868.1	DIALFTRQMATMMKAGVPLVQAFDIISSEGFNDPNMNRKLVVEIKQEVAGGNSLANSLRKKPKQYFDSLYCNLVDAGEQSGAL	146
consensus	DIALFTRQMATMMKAGVPLVQAFDIISSEGFNDPNMNRKLVDDLKQEVAAAGNSFASSLRKKPKQYFDDLYCNLVDSEGEQSGSL	146

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NTDB id 1029 TT RS02230 WP 011228203.1	EILLDRYAYKYEKTELRKIKKAMYPVVAIVVIGTYLLIWPDFEYFAGELPAETQVNMDSQYWL	224
NTDB id 1402 DSB67 RS12670 WP 010643257.1	DLILDRLASFLEKELELRGKIRSAMTYPIVVFVAVGVAYFLLTGIVPQFAQILTDLGSSELPLLTRFLIAVSDLLRAATL	227
NTDB id 1169 A1552VC RS11075 WP 000648511.1	SQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVPIPEFEKMFMTGFGADLPFTQMVNLNSAWTQNWGP	228
NTDB id 1113 AAA85695.1 219..1451()	PEVFERLATYREKSEQLRAKVIKALIYPMSVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVCLKSHVQAYSL	230
NTDB id 1112 NGFG RS09215 WP 003689811.1	ESLLDKLAIYKEKTQAIRKKVKKTALTYPVSVIAVAIGLVFVMMIFVLPAPFKEVYANMGAELPALTQTVMDMSDFFVSYGW	230
NTDB id 1252 GC085 RS07730 WP 011213805.1	ESLLDKLAIYKEKTQAIRKKVKKTALTYPVSVIAVAIGLVFVMMIFVLPAPFKEVYANMGAELPALTQTVMDMSDFFVSYGW	227
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DIMLDKVATYKEKIEIKKKIKKALTYPPIAVMVVALLVTAGLLIYVVPQFESLFKGFAGDLPAMTRAVITMSEFMQAYWY	229
NTDB id 1059 ABD1 RS01610 WP 000279215.1	EIMLDRVAIYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPFTQVLMVNMNSNMWQDYWF	229
NTDB id 400790 GJV02 RS28480 WP 003161763.1	ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFASFGADLPFTQMVNMNSNMWQDYWF	226
NTDB id 1198 PSJM300 03950 AFN76868.1	ETLLDRVATYKEKTEALKAKIKKAMTYPIAVIVVAIIVSAILLIKVVPVQFQSVFEGFGAELPAFTQMVINISNVLQEWL	226
consensus	ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVVLVAVIVTAILLIKVVPVQFQDVVFANFGAELPAFTLMVIGLSEALQAWWY	226

NTDB	id	1029	TT	RS02230	WP	011228203.1	PL	L	L	L	L	A	V	A	L	F	F	A	Y	R	.	W	Y	Y	G	T	P	Q	G	R	R	V	I	D	R	L	K	L	R	L	P	V	F	G	N	L	N	R	K	T	A	V	A	R	F	S	R	T	L	A	L	L	S	S	G	V	N	I	V	E	A	L	D	I	T	K	G	T	A	G	N	S	V	V	E		303
NTDB	id	1402	DSB67	RS12670	WP	010643257.1	F	I	G	L	S	F	V	S	L	I	S	G	K	I	M	S	Q	R	S	D	S	F	R	L	L	A	A	R	S	S	L	R	V	P	I	L	G	P	V	L	S	K	A	A	I	A	K	F	S	R	T	L	A	T	S	F	S	A	G	I	P	I	L	T	A	L	K	T	T	S	K	T	S	G	N	M	H	Y	Q		307
NTDB	id	1169	A1552VC	RS11075	WP	000648511.1	W	A	F	I	A	T	A	A	A	I	F	G	L	K	A	L	R	K	N	S	F	Q	I	R	L	K	T	S	R	L	G	L	K	F	P	I	I	G	N	V	L	A	K	A	I	A	K	F	S	R	T	L	A	T	S	F	A	A	G	I	P	I	L	A	S	L	K	T	T	A	K	T	S	G	N	V	H	F	E		308
NTDB	id	1113	AAA85695.1			219..1451()	M	V	L	I	A	L	G	F	A	I	Y	R	F	L	K	L	K	A	R	S	I	K	I	Q	R	R	M	D	A	I	L	R	M	P	I	F	G	D	I	V	R	K	T	A	I	A	R	W	G	R	T	T	A	T	L	F	A	A	G	V	P	L	V	D	S	T	A	G	A	A	G	N	L	I	Y	E		310			
NTDB	id	1112	NGFG	RS09215	WP	003689811.1	M	V	L	I	A	L	G	F	A	I	Y	R	F	L	K	L	K	A	R	S	I	K	I	Q	R	R	M	D	A	I	L	R	M	P	I	F	G	D	I	V	R	K	T	A	I	A	R	W	G	R	T	T	A	T	L	F	A	A	G	V	P	L	V	D	S	T	A	G	A	A	G	N	L	I	Y	E		310			
NTDB	id	1252	GC085	RS07730	WP	011213805.1	I	I	F	G	A	L	G	G	V	V	S	F	F	Y	A	K	N	H	S	L	E	F	A	Q	T	I	D	R	V	M	L	K	L	P	V	I	G	P	I	L	E	K	A	A	I	A	R	F	A	R	T	L	S	I	T	F	A	A	G	L	P	L	V	E	A	L	K	S	V	A	G	A	T	G	N	I	I	Y	A		307
NTDB	id	1016	ACIAD	RS01680	WP	004920476.1	I	L	I	L	V	I	G	A	A	I	A	G	F	L	E	A	R	K	R	S	K	R	F	R	D	Q	L	D	R	L	V	L	R	L	P	I	V	G	D	L	V	Y	K	A	I	A	R	Y	S	R	T	L	A	T	T	F	A	A	G	V	P	L	I	D	A	L	A	S	T	A	G	A	T	N	N	T	V	Y	E		309
NTDB	id	1059	ABD1	RS01610	WP	000279215.1	I	M	I	I	A	I	G	A	V	I	A	A	F	L	E	A	K	K	R	S	K	K	F	R	D	G	L	D	K	L	A	L	K	L	P	I	F	G	D	L	V	Y	K	A	I	A	R	Y	S	R	T	L	A	T	T	F	A	A	G	V	P	L	I	D	A	L	E	S	T	A	G	A	T	N	N	V	I	Y	E		309
NTDB	id	400790	GJV02	RS28480	WP	003161763.1	L	V	L	L	M	M	G	G	A	G	F	L	L	N	H	A	Y	K	R	S	E	K	F	R	D	A	T	D	R	T	V	L	K	L	P	I	V	G	A	I	L	Y	K																																						

NTDB id 1029	TT RS02230 WP 011228203.1	EIVEAAKLKIQQGDPLNLTLAQHPFVFPMPVSSMVAIGEETGALDTMLS	SKVADFYER	EVDEAVAS	LTAAIIEPLMIIFLGV	383		
NTDB id 1402	DSB67 RS12670 WP 010643257.1	LAIEEVYRDTAAGMPMYIAMR.HCHVFPELVLMQVMIGEESGRLLDMLNK	IAAIYEF	EV DNTVDNL	SKITILEPLIIVFLGV	386		
NTDB id 1169	A1552VC RS11075 WP 000648511.1	TAINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLN	KVATIYEF	EV DNTVDNL	LGKITILEPLIIVFLGT	387		
NTDB id 1113	AAA85695.1 219..1451()	EATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMS	SIGEESGLDDMLN	KAAEFYED	EV DNAVGL	LSAMMEPIIILILGI	389	
NTDB id 1112	NGFG RS09215 WP 003689811.1	EATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMS	SIGEESGLDDMLN	KAAEFYED	EV DNAVGL	LSAMMEPIIIVILGI	389	
NTDB id 1252	GC085 RS07730 WP 011213805.1	KATDKIREEVAATGQQMFIAE.NTHLFPNMVIQMVAIGEESGAL	EKMLS	SKVADFYEEEV	NNAVDAL	LSSLEPIIMSILGI	386	
NTDB id 1016	ACIAD RS01680 WP 004920476.1	QAVLKIREDDVSTGQQQLNFAMR.VSNRFPTMAIQMVAIGEESGAL	DEMLDKVAN	YYE	SEVDHAVDGL	TSMMEPLIMAILGI	388	
NTDB id 1059	ABD1 RS01610 WP 000279215.1	KAVMKIREDVATGQQQLQFAMR.ISNRFPSMAIQMVAIGEESGAL	DSMLDKVAT	YYENE	EV DNAVGL	TSMMEPLIMAILGV	388	
NTDB id 400790	GJV02 RS28480 WP 003161763.1	DAVGKIKQDVSTGMQLNFSMR.TTNTIFPSMAIQMTAIGEESGAL	DDMLK	AVG	FYE	QEV DNAV	DLTALMEPMIMAVLGV	385
NTDB id 1198	PSJM300 03950 AFN76868.1	SATNKIKSDVSTSGMQLNFSMR.TTGTFPMAVQMTAIGEESGAL	DEMLSKVAT	FYED	EV DNMVDG	LTLALMEPMIMAVLGV	385	
consensus		*****	*****	*****	*****	*****		

NTDB id 1029	TT RS02230 WP 011228203.1	IVGMIVAGMFLPLFKIIGT	LSVQ	406
NTDB id 1402	DSB67 RS12670 WP 010643257.1	VVGGLVITAMYLPIFNLMSV	LG..	407
NTDB id 1169	A1552VC RS11075 WP 000648511.1	VVGGLVVAMYLPIFNLMSV	LG..	408
NTDB id 1113	AAA85695.1 219..1451()	VIGTLLVAMYLPLFNLGNV	VVA*	410
NTDB id 1112	NGFG RS09215 WP 003689811.1	VIGTLLVAMYLPLFNLGNV	VVA..	410
NTDB id 1252	GCO85 RS07730 WP 011213805.1	LVGGLVVAMYLPIFKLGS	AV...	406
NTDB id 1016	ACIAD RS01680 WP 004920476.1	LVGGLVIAMYLPIFQMG	SVV...	408
NTDB id 1059	ABD1 RS01610 WP 000279215.1	LVGGLVIAMYLPIFQMG	SVV...	408
NTDB id 400790	GJV02 RS28480 WP 003161763.1	LVGGIIAMYLPIFQLGN	VV...	405
NTDB id 1198	PSJM300 03950 AFN76868.1	LVGGLIIAMYLPIFQMG	SVV...	405
consensus		***!*****!*	*****	

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