

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.....IAPQLKNYRWKKGINSNGKK.TSGNVLAMTEIEVRRERLDAQHIKIKKKLKKGSISFITK.....ISHRVKGK	68
NTDB id 1113 AAA85695.1 219..1451()	MKAT.....QTLPLKNYRWKKGINSNGKK.VSQQLAISIEIEVRDKLKDQHIQIKKKLKKGSVSLAR.....LTHRVKSK	70
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSFAFTEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	70
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSFAFTEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	67
NTDB id 1016 ACIAD RS01680 WP 004920476.1	.MDK.....NSPPLILT FHYQGINKAGQK.MEGDIQARS LAIAKADLRKQGIVTNKVVKRKPFLFDR.....KNKKKITQA	69
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAK.....KTQVMPVFAFEGVDRKGKIK.LKGELPARNMALAKVTLRKQGITRTIREKRKNIFEG....LLKKKVKPL	69
NTDB id 403971 GNT44 RS27510 WP 003094649.1	MAVK.....KAQMMPTFAYEGVDRKGKIK.LKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKKKVTTL	66
NTDB id 1198 PSJM300 03950 AFN76868.1	.MAD.....KALKTSVFWEGTDKKGKTK.VKGELSSQNPTLVKAQLRKQGITPVKVRKKGISLLG.....AGKKIKPM	66
consensus	.MAQ.....KAIKNSVFTWEGLDRQGAK.TKGELSGVSPALVKAQLRKQGINPQKVRKKKSISLFS.....AGKKIKPM	66

logo

NTDB id 1029 TT RS02230 WP 011228203.1	DITIFTRQLATMAGYPLVQAFELVAGHEPMPRELLMEIKVEGSSSALRKHPQYFDLYCNLVAGEQSGI	144
NTDB id 1402 DSB67 RS12670 WP 010643257.1	DLAIFSRQLATMLGAGLTLLQALAILERQTEENRKFREILKQVRTDVEGGMAFSEALS KH.KIFSRLYVNLVRAGETSGGL	147
NTDB id 1169 A1552VC RS11075 WP 000648511.1	DITIFTRQIATMLMTGVPIVQALKLVSENHKKAEKMSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNL	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 403971 GNT44 RS27510 WP 003094649.1	DITIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLIESGEQSGAL	146
NTDB id 1198 PSJM300 03950 AFN76868.1	DIALFTRQMATMMKAGVPLVQAFDIISSEGFNDPNMNRKLVVEIKQEVAGGNSLANSLRKKPKQYFDSLYCNLVDAGEQSGAL	146
consensus	DIALFTRQMATMMKAGVPLVQAFDIISSEGFNDPNMNRKLVDDLKQEVAAAGNSFASSLRKKPKQYFDDLYCNLVDAGEQSGSL	146

logo

NTDB id 1029 TT RS02230 WP 011228203.1	EILLDRYAYKYEKTELRKIKKAMYPVIVVAVAGVYLLLVWPFFQSVAGFAGELPAETQVVMSSQYWL	224
NTDB id 1402 DSB67 RS12670 WP 010643257.1	DLILDRLASFLEKELELRGKIRSAMTYPIVVFVAVGVAYFLLTGIVPQFAQILTDLGSSELPLLTRFLIAVSDLLRAATL	227
NTDB id 1169 A1552VC RS11075 WP 000648511.1	SQVFERLATYREKSEQLRAKVIKALIYPMAMVVLVALGVSYLMLTRVPIPEFEKMFMTGFGADLPFTQMVNLNSAWTQNWGP	228
NTDB id 1113 AAA85695.1 219..1451()	PEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVPIPEFESMFKGFGAELPWFTQQVVKLSHWVQAYSL	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	EIMLDRVAIYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPFTQVVMNMSNMWQDYWF	229
NTDB id 403971 GNT44 RS27510 WP 003094649.1	ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFASFGADLPFTQVVMNMSNMWQDYWF	226
NTDB id 1198 PSJM300 03950 AFN76868.1	ETLLDRVATYKEKTEALKAKIKKAMTYPIAVIVVAIIVSAILLIKVVPQFQSVFEGFAGELPAFTMMVINISNVLQEWL	226
consensus	ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVVLVAVIVTAILLIKVVPQFQDVVFANFGAELPAFTLMVIGLSEALQAWWY	226

NTDB	id	1029	TT	RS02230	WP	011228203.1	P	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	T	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	S	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	C	F	A	I	Y	R	F	L	K	L	K	A	S	I	K	I	Q	R	R	M	D	A	I	L	L	R	M	P	I	F	G	D	I	V	R	K	G	T	I	A	R	W	G	R	T	T	A	T	L	F	A	A	G	V	P	L	V	D	L	S	T	A	G	A	G	N	L	I	Y	E		310				
NTDB	id	1112	NGCF	RS09215	WP	003689811.1	M	V	L	I	A	L	C	F	A	I	Y	R	F	L	K	L	K	A	S	I	K	I	Q	R	R	M	D	A	I	L	L	R	M	P	I	F	G	D	I	V	R	K	G	T	I	A	R	W	G	R	T	T	A	T	L	F	A	A	G	V	P	L	V	D	L	S	T	A	G	A	G	N	L	I	Y	E		310				
NTDB	id	1252	GCO85	RS07730	WP	011213805.1	I	I	F	G	A	L	C	G	V	V	S	F	F	Y	A	K	N	S	L	E	F	A	Q	T	I	D	R	V	M	L	K	P	V	I	G	P	I	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	C	A	A	T	A	C	F	L	E	A	R	K	R	S	K	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	T	C	A	V	I	A	A	F	L	E	A	K	K	R	S	K	K	F	R	D	G	L	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	403971	GNT44	RS27510	WP	003094649.1	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	S	A	V	A	R																																		

NTDB id 1029	TT RS02230 WP 011228203.1	EIVAAKILKIQQCDPLNLTLAQHPPVFPMPVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAGIEPLMIIFLVG	383
NTDB id 1402	DSB67 RS12670 WP 010643257.1	LATEEVRDRTAACGPMPIAMR.HCHVPFPELVLMVMIGEESGRLDMLNKIAAIYEFVDNITVDNLISKIILEPLIIIVFLGV	386
NTDB id 1169	A1552VC RS11075 WP 000648511.1	TAINEVYRDRTAACGPMPIAMR.NTEAFPEPMVLQMVMIGEESGLDDMLNKKVATIIYEFVDNITVDNLGKIILEPLIIIVFLGT	387
NTDB id 1113	AAA85695.1 219..1451()	EATREIRTRVIQLSMTSGMR.ATELFPNMMLQMSSSIGEESSLDDMLNKAAEFYEDVDNAVGGWLSAMMEPIIILILGL	389
NTDB id 1112	NGCF RS09215 WP 003689811.1	EATREIRTRVIQLSMTSGMR.ATELFPNMMLQMSSSIGEESSLDDMLNKAAEFYEDVDNAVGGWLSAMMEPIIIVILGL	389
NTDB id 1252	GCO85 RS07730 WP 011213805.1	KATDKIREEVAITGQQMFIAEM.NTHLPNMVIMQMAIGEESGALDEKMLSKVADFYEVEVNNAVDALLSSIILEPIIMSILGI	386
NTDB id 1016	ACIAD RS01680 WP 004920476.1	QAVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGI	388
NTDB id 1059	ABD1 RS01610 WP 000279215.1	KAVMKIREDVATGQQLGFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVGGTSMMEPLIMAILGV	388
NTDB id 403971	GNT44 RS27510 WP 003094649.1	DVGKIKIQDVSTGMQLNFSMR.TTNIFPMSMAIQMTAIGEESSGALDDMLAKVAGFYEQVDNAVNDLTALMEPMIMAVLVG	385
NTDB id 1198	PSJM300 03950 AFN76868.1	SATNKIKIDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESSGALDEMLSKVATFIYEDVDNMVDDGLTALMEPMIMAVLVG	385
consensus		* * * * *	

NTDB id 1029	TT RS02230 WP 011228203.1	IVGMIVAGMFLPLFKIIGTISVQ	406
NTDB id 1402	DSB67 RS12670 WP 010643257.1	VVGGLVTIAMYLPIFNLMSVLG..	407
NTDB id 1169	A1552VC RS11075 WP 000648511.1	VVGGLVVIAMYLPIFNLMSVLG..	408
NTDB id 1113	AAA85695.1 219..1451()	VIGTLLVIAMYLPLFNLGNVVA*	410
NTDB id 1112	NGFC RS09215 WP 003689811.1	VIGTLLVIAMYLPLFNLGNVVA..	410
NTDB id 1252	CQ085 RS07730 WP 011213805.1	VVGGLVVIAMYLPIFKLGSAV...	406
NTDB id 1016	ACIAD RS01680 WP 004920476.1	LVGGLVIAMYLPIFQMGSVV...	408
NTDB id 1059	ABD1 RS01610 WP 000279215.1	LVGGLVIAMYLPIFQMGSVV...	408
NTDB id 403971	GNT44 RS27510 WP 003094649.1	VVGGLIIAMYLPIFQLGNVVG..	406
NTDB id 1198	PSJM300 03950 AFN76868.1	LVGGLIIAMYLPIFQMGSVV...	405
consensus		***!*****!*****!	

- X non conserved
- X similar
- X > 50% conserved