

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	MAKN	72
NTDB id 132557 FORC4 RS12355 WP 005462561.1	MAKNTQ.....TLPLKNYRWKGINNSGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLLKKGVSILAR.LTHRVRVKSKDITI	71
NTDB id 1402 DSB67 RS12670 WP 010643257.1	.MKTT.....TPQLKNFRWKGVNSSGKK.TSGQTLAMSEIEVRERLDAQHIKIKKLLKKGSSISFLT.LSHRVKVKGDITV	71
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MKTI.....APQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLLKKGSSISFITK.ISHRVVKGDITI	74
NTDB id 1113 AAA85695.1 219..1451()	.MAKNGGFSLF AKKEKR FIFEGRHSASDKLVNVEVS AFTEEEARKKLA KRGI RPLQITRV.....KTSSKRKITQEDITV	74
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MAKNGGFSLF AKKEKR FIFEGRHSASDKLVNVEVS AFTEEEARKKLA KRGI RPLQITRV.....KTSSKRKITQEDITV	71
NTDB id 1198 PSJM300 03950 AFN76868.1	.MDKN.....SPPLLT FHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGI VTNKV VVKRKP L FDR.KNKKITQADITV	70
NTDB id 1016 ACIAD RS01680 WP 004920476.1	.MAQK.....AIKNSVFTWGLDRQGAQK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSSISLFS..AGKKIKPMDIAL	73
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAKK.....TQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPLDIAI	73
consensus	MAVKK.....AQMMPTFA YEGVDRKGIVK.IKGELPAKNMALAKVTLRKQGITVRNIREKRKNILEGLFKKKVKTTLDITI	73

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	FTRQLATM	152
NTDB id 132557 FORC4 RS12355 WP 005462561.1	FTRQISTMLVTGVPLVQALKLVSDNHKKAEMKSI LMSVTRAVEAGTPMSKAMRTASNHFDPPLYTDLIATGEQSGNLAIEVF	151
NTDB id 1402 DSB67 RS12670 WP 010643257.1	FTRQIATMLMTGVPIVQALKLVSENHKKAEMKSI LMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQVF	151
NTDB id 1112 NGFG RS09215 WP 003689811.1	FTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL	154
NTDB id 1113 AAA85695.1 219..1451()	FTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL	154
NTDB id 1252 GC085 RS07730 WP 011213805.1	FTRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHD IETGLTLAESLIKHPLYFNE LFCNLVDAGEKSGSLDIML	151
NTDB id 1198 PSJM300 03950 AFN76868.1	FTRQMATMMKAGVPLQSFDIIGEGFDNPNMRKLVDDLKQEVAAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETLL	150
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIML	153
NTDB id 1059 ABD1 RS01610 WP 000279215.1	FTRQLATMMKAGVPLVQGFIEIVAEGLENPAMREVVLG IKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETML	153
consensus	FTRQLATM KAGVPLVQAFEIVAEGHNPMSLMSIKVEAGTTSALRKHPYFDLYCNLVAGFESGSL EIM	153

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	DRLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIP EFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWAFI	232
NTDB id 132557 FORC4 RS12355 WP 005462561.1	ERLATYREKNEQLRAKVIKALIY PAMVILVALGVSFIMLT KVIPEFEKMFVGFGAELPWFTTRQVLDLSAWTQNWSPFTIAL	231
NTDB id 1402 DSB67 RS12670 WP 010643257.1	ERLATYREKSEQLRAKVIKALIY PAMVVLVALGVSYLMLTRV IPEFEKMF TGF GADLPAFTQMVNL SAWTQNWGPFGIL	231
NTDB id 1112 NGFG RS09215 WP 003689811.1	DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVLI	234
NTDB id 1113 AAA85695.1 219..1451()	DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVLI	234
NTDB id 1252 GC085 RS07730 WP 011213805.1	DKVATYKEKIEIKKKIKKALTYP IAVMVVALLV TAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYIIFG	231
NTDB id 1198 PSJM300 03950 AFN76868.1	DRVATYKEKTEALKAKIKKAMNYP IAVVLVAVIVTATILLIKVVPQFQDV FANFGAELPAFTLMVIGLSEALQAWWYVVL A	230
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFTSFGADLPAFTQLVNVNMSNWMQDYWFILIL	233
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFASF GADLPAFTQM VNVNMSKWMQEYWFIMII	233
consensus	ERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIP EFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWAFI	233

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	AIAAAIFGLKALRKNSFQIRLKTSTR LGLKFPITGNVLAKASTIAKFSRTLATSFAAGIPILASLKT TAKTSGNVHFETA IN	312
NTDB id 132557 FORC4 RS12355 WP 005462561.1	GSISLFI SARVLSKRSDSFR LMLNRSVLKFPVLGAVLSKAAIAKFSRTLATSFTAGIPILTS LKTTSKTS SGNMHYQLAIE	311
NTDB id 1402 DSB67 RS12670 WP 010643257.1	SFVSL LISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTS SGNMHYQLAIE	311
NTDB id 1112 NGFG RS09215 WP 003689811.1	ALGFAIYGLFLKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	314
NTDB id 1113 AAA85695.1 219..1451()	ALGFAIYRFLKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	314
NTDB id 1252 GC085 RS07730 WP 011213805.1	ALGGVVSFFYAKNHSLEFAQTIDRVMLKLVPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATD	311
NTDB id 1198 PSJM300 03950 AFN76868.1	FGVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDI LYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFERSATN	310
NTDB id 1016 ACIAD RS01680 WP 004920476.1	VIGAATAGFLEARKRSKRFRDQLDRLVLR LPIVGDLVYKAI IARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAVL	313
NTDB id 1059 ABD1 RS01610 WP 000279215.1	AIGAVIAAFLEARKRSKKFRDGLDKLALKLPIFGDLVYKAI IARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAVM	313
consensus	AIAAAIFGLKALRKNSFQIRLKTSTR LGLKFPITGNVLAKASTIAKFSRTLATSFAAGIPILASLKT TAKTSGNVHFETA IN	313

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NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 132557 FORC4 RS12355 WP 005462561.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1112 N6GF RS09215 WP 003689811.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

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Sequence	Position
EIRDVATGQMLNMRNINLFPNMLQMAIGEESGALDDMLNKVATIYEFVDNVTVDNLGKILEPLIIVFLGTVVGG	392
EYVRDTAAGMPMYIAMRNTAEAFPEMVLQMVMIIGEESGRLDDMLNKVATIYEFVDNVTVDNLSKILEPLIIVFLGTVVGG	391
EYVRDTAAGMPMYIAMRHCHVFPFELVLQMVMIIGEESGRLDDMLNKTAIYEFVDNVTVDNLSKILEPLIIVFLGTVVGG	391
EIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYDEVDNAVGRLSAMMEPTIIIVILGLVIGTL	394
EIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYDEVDNAVGWLSAMMEPTIIILILGLVIGTL	394
KIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALDKMLSKVADFYEEVNNAVDALSSILEPIIMSILGILVGG	391
KIKSDVSSGQMLNFSMRTVNGRFPSPMAVQMTAIGEESGALDEMLSKVATFYDEVDNMVDGLTALMEPMIMAVLGVLVGG	390
KIREDDVSTGQQLNFAMRVTSNTRFSPMAIQMTAIGEESGALDEMLDKVANFYEYSEVDHVDGLTSMMEPLIMAILGILVGG	393
KIREDDVATGQQLQFAMRISNRFPSPMAIQMTAIGEESGALDSMLDKVATYYENVEVDNAVGLTSMMEPLIMAILGVLVGG	393

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NTDB	id	1169	A1552VC	RS11075	WP	000648511.1	VV	AM	YLP	IF	NLM	SV	LG	.	408	
NTDB	id	132557	FORC4	RS12355	WP	005462561.1	VT	AM	YLP	IF	NLM	SV	LG	.	407	
NTDB	id	1402	DSB67	RS12670	WP	010643257.1	VT	AM	YLP	IF	NLM	SV	LG	.	407	
NTDB	id	1112	NGFG	RS09215	WP	003689811.1	LV	AM	YLP	LF	NL	GN	VV	A	.	410
NTDB	id	1113	AAA85695.1	219..1451()			LV	AM	YLP	LF	NL	GN	VV	A	*	410
NTDB	id	1252	GC085	RS07730	WP	011213805.1	VV	AM	YLP	IF	K	LG	SA	V	..	406
NTDB	id	1198	PSJM300	03950	AFN76868.1		II	AM	YLP	IF	Q	MG	SV	V	..	405
NTDB	id	1016	ACIAD	RS01680	WP	004920476.1	VI	AM	YLP	IF	Q	MG	SV	V	..	408
NTDB	id	1059	ABD1	RS01610	WP	000279215.1	VI	AM	YLP	IF	Q	MG	SV	V	..	408
consensus							***!!!!!!*!*****									

WYAMLPFNLGSW
LTAMLPFNLGSW

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