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NTDB id 1169 A1552VC RS11075 WP 000648511.1	MKATQTLP	VSCQMLAIS	LAR.LT	67
NTDB id 1402 DSB67 RS12670 WP 010643257.1	MKTIA	TSGNVLAMTE	ISHRVKG	66
NTDB id 1112 NGFG RS09215 WP 003689811.1	MAKNGGFS	LNGEVS	TSSKRKITQ	69
NTDB id 1113 AAA85695.1 219..1451()	MAKNGGFS	LNGEVS	TSSKRKITQ	69
NTDB id 1198 PSJM300 03950 AFN76868.1	MAQKA	IKGELS	AGKKIKP	65
NTDB id 1016 ACIAD RS01680 WP 004920476.1	MAAKKTQ	LKGELP	IFEGLLK	68
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAVKKA	IKGELP	LEGLFK	68
NTDB id 1102209 Q9285 RS06745 WP 011408067.1	MSVARSAIKKQ	MKCEQT	AGKKITP	78
NTDB id 1252 GC085 RS07730 WP 011213805.1	MDKN	MKCEQT	FDR.KN	66
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logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	KDITILTRQLATMTTGVPLVQALKLVGDNHRKAEMKSSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDL	147
NTDB id 1402 DSB67 RS12670 WP 010643257.1	KDITIFTRQIATMTTGVPLVQALKLVSENHKKAEMKSSILMSVTRAVEAGTPMSKAMRTASTHFDP	146
NTDB id 1112 NGFG RS09215 WP 003689811.1	EDITVFRQLSTMIAKACPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCN	149
NTDB id 1113 AAA85695.1 219..1451()	EDITVFRQLSTMIAAGPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCN	149
NTDB id 1198 PSJM300 03950 AFN76868.1	MDIALFTRQMATMNAKAGVPLLSQSFDTIGEGFDNPNMRKLVDDLKQEVAAAGNSFASLSLRKKPQYFDD	145
NTDB id 1016 ACIAD RS01680 WP 004920476.1	LDIALFTRQLATMNAKAGVPLVQAFEIVAEGLNPAMRDVVVLGLKNEVEGNTFAGALRKYPQYFDNLF	148
NTDB id 1059 ABD1 RS01610 WP 000279215.1	LDITIFTRQLATMNAKAGVPLVQCFEIVAEGLNPAMREVVILGIKGEVEGSSFTFASALRKYPQHFDN	148
NTDB id 1102209 Q9285 RS06745 WP 011408067.1	KEIAFFSRQMATMNAKGVPTVSSLEITEGEHNPRMKMKMGQIRTDIEGSSLYESISKHPVQFDELYRNL	158
NTDB id 1252 GC085 RS07730 WP 011213805.1	ADITVFSRQLATMTESGIPLVQAQFDIVAKQGSNKRLKDLIETIKHDIETGLTLAEASLIKHPLYFNL	146
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NTDB id 1169 A1552VC RS11075 WP 000648511.1	LPEVFERLATYREKSEQLRAKVIKALITYPSMVVLVALGVSYLMLTMVPIEFESMFKGFGAELPWFTTQQVLKLSHWVQAYS	227
NTDB id 1402 DSB67 RS12670 WP 010643257.1	LSQVFERLATYREKSEQLRAKVIKALITYPAMVVLVALGVSYLMLTRVPIEFEKMFTFGFGADLPFAFTQMVNLNSAWTQNWG	226
NTDB id 1112 NGFG RS09215 WP 003689811.1	LESLLDKLATYKEKTAIRKKVKLTALTYPSVSVIAVAIGLVFVMMIFVLPAFKKEVYANMGAELPLTQTVMDSDFVSYG	229
NTDB id 1113 AAA85695.1 219..1451()	LESLLDKLATYKEKTAIRKKVKLTALTYPSVSVIAVAIGLVFVMMIFVLPAFKKEVYANMGAELPLTQTVMDSDFVSYG	229
NTDB id 1198 PSJM300 03950 AFN76868.1	LETILDRVATYKEKTEALKAKIKKAMNYPIAVVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWW	225
NTDB id 1016 ACIAD RS01680 WP 004920476.1	LETIMLDRVATYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPFAFTQLVVNMNSNMQDYW	228
NTDB id 1059 ABD1 RS01610 WP 000279215.1	LETIMLDRVATYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPFAFTQMVVNMSKMQEYW	228
NTDB id 1102209 Q9285 RS06745 WP 011408067.1	LETVLETVATYKENIEALKGKIKKALFYPMVVAIVVTSATLLIFVVPQFEVLFKSFGAELPAFTQLLVNNSKRFMVSYW	238
NTDB id 1252 GC085 RS07730 WP 011213805.1	LDIMLDKVATYKEKTEITKKKIKKALTYPiAVMVVALLVITAGLLIYVVPQFESLFKGFAGADLPAMTRAVITMSEFMQAYW	226
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NTDB id 1169 A1552VC RS11075 WP 000648511.1	LWAFIAIAAAIFGLKAL	PKNSFQIRLKTSRLGLKFP	IIIGNVLAKASIAK	FSRTLATSFAAGIPILASLKT	TTAKTSGNVHF	307
NTDB id 1402 DSB67 RS12670 WP 010643257.1	PFITGLSFSVSLISGKIMSQR	SDSFRLLAARSSLRV	PILGPVLSKAAIAK	FSRTLATSFSAGIPILTALK	TTSKTSGNMHY	306
NTDB id 1112 NGFG RS09215 WP 003689811.1	WMVLIAGLGAFAIYCF	LKLARSIIQRRMDAIL	LRMPIFGDIVRKG	TIARWGRTTATLFAAGVPLVDVLD	STAGAAGNLIY	309
NTDB id 1113 AAA85695.1 219..1451()	WMVLIAGLGAFAIYCF	LKLARSIIQRRMDAIL	LRMPIFGDIVRKG	TIARWGRTTATLFAAGVPLVDVLD	STAGAAGNLIY	309
NTDB id 1198 PSJM300 03950 AFN76868.1	YVVIAGFVGAAYAFKQA	HTRSEKFRNWFDR	MLKVPVVDILYKSS	VARFARTLSTTFAAGVPLVDALD	SVAGATGNVVF	305
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FILILVIGAAIAGFL	EAFKRSKRFRDQL	DRLVLRLPIVGD	LVYKAIIRARYS	RTLATTTFAAGVPLIDALASTAGATNN	TVY
NTDB id 1059 ABD1 RS01610 WP 000279215.1	FIMIIAIGAVIAAF	LEAKRSKSKFRDGL	DKLALKLPIFG	DLVYKAIIRARYS	RTLATTTFAAGVPLIDALEASTAGATNN	VIY
NTDB id 1102209 Q9285 RS06745 WP 011408067.1	WLMLIVTVGSSVVG	CFIAYKRSPRMQHG	LDRLLTKVPVIG	QIMHNSIARFARTTAV	TFKAGVPLVEALGIVAGATGN	KLY
NTDB id 1252 GC085 RS07730 WP 011213805.1	YIIFGALGGVYVS	EFYAKNLSLE	FAQTTDRVM	LKLPIVIGPILEKAA	IARFARTLSITFAAGVPLVEALKSVAGATGN	IY
consensus	*****	*****	*****	*****	*****	*****

