

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	MAKN	72
NTDB id 1402 DSB67 RS12670 WP 010643257.1	APPLTKFYEINSAGKVGKESAEAKLRKQGLPSKKKKRKSLEFRSSKKKITQDITY	71
NTDB id 1113 AAA85695.1 219..1451()	MAKNGGFSFLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIPLQITRV....KTSSKRKITQEDITV	74
NTDB id 1112 NGFG RS09215 WP 003689811.1	MAKNGGFSFLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIPLQITRV....KTSSKRKITQEDITV	74
NTDB id 193190 BE845 RS00890 WP 011215549.1	MDKN.....SPPLLTFHYQGINKAGQK.MEGDIQARSLATAKADLRKQGIIVTNKVVKRRKPLFDR.KNKKITQADITV	71
NTDB id 1252 GC085 RS07730 WP 011213805.1	MDKN.....SPPLLTFHYQGINKAGQK.MEGDIQARSLATAKADLRKQGIIVTNKVVKRRKPLFDR.KNKKITQADITV	71
NTDB id 1198 PSJM300 03950 AFN76868.1	MAQK.....AIKNSVFTWGLDRQGAQK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSSISLFS..AGKKIKPMDIAL	70
NTDB id 1016 ACIAD RS01680 WP 004920476.1	MAAKK.....TQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKVKPLDIAI	73
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAVKK.....AQMMPTFAVEGVDRKGVK.IKGELPAKNMALAKVTLRKQGITVRNIREKRKNILEGLFKKKVTTLDITI	73
consensus	*** * * * * ! * * ! * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * *	

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	FTRQLATMKAQVPLVQAFIVAGHNPMEKMTIKVEGGLAALRKHPYFDLYCNVAGFESGGLIEM	152
NTDB id 1402 DSB67 RS12670 WP 010643257.1	LTRQLATMITTGVPIVQALKLVGDNRHKAEMKSIILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLIVETGEMSGNLPVEVF	151
NTDB id 1113 AAA85695.1 219..1451()	FTRQIATMLMTGVPIVQALKLVSENHKKAEKMSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQVF	154
NTDB id 1112 NGFG RS09215 WP 003689811.1	FTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL	154
NTDB id 193190 BE845 RS00890 WP 011215549.1	FTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL	151
NTDB id 1252 GC085 RS07730 WP 011213805.1	FSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDIML	151
NTDB id 1198 PSJM300 03950 AFN76868.1	FSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDIML	150
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FTRQMATMMKAGVPLQSFDIIGEGFDNPNMRKLVDDLKQVEVAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETLL	153
NTDB id 1059 ABD1 RS01610 WP 000279215.1	FTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIML	153
consensus	***** ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * *	

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	DRVATYKEKSELKKKKIKKALYPVIVVAVVGTALLIKVVPFESLFAEGADLPAFETQVMSWQYWIYIFL	232
NTDB id 1402 DSB67 RS12670 WP 010643257.1	ERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWAFI	231
NTDB id 1113 AAA85695.1 219..1451()	ERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTRVIPFEEKMFTGFGADLPFTQMVNLNSAWTQNWGPFTIGL	234
NTDB id 1112 NGFG RS09215 WP 003689811.1	DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFMMIFVLPAFKEVYANMGAELPALTQTVMMDMSDFVSYGWMVLI	234
NTDB id 193190 BE845 RS00890 WP 011215549.1	DKVATYKEKIEIKKKIKKALTYPPIAVMVVALLVTAGLLIYVVPQFESLFKGFAGADLPAMTRAVITMSEFMQAYWYIIFG	231
NTDB id 1252 GC085 RS07730 WP 011213805.1	DKVATYKEKIEIKKKIKKALTYPPIAVMVVALLVTAGLLIYVVPQFESLFKGFAGADLPAMTRAVITMSEFMQAYWYIIFG	230
NTDB id 1198 PSJM300 03950 AFN76868.1	DRVATYKEKTEALKAKIKKAMNYPPIAVVLVAVIVTALLIKVVPQFQDVAFNFGAELPAFTLMVIGLSEALQAWWYVVLIA	233
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPFTQLVNVNMSNWMQDYWFILIL	233
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DRVAIYKEKSELKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFASFGADLPFTQMVNVNMSKWMQYWFIMII	
consensus	***** ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * *	

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	ALGAIYSEAKRSFRDRILKPIGLIKAAIARERTLATFAAGVPLVDALKSTAGAGNVIYEAT	312
NTDB id 1402 DSB67 RS12670 WP 010643257.1	ATIAAIFGLKALRKNSFQIRLKTSSRLGLKFPITGNVLAKASTAKFSRTLATSFAAGIPILASLKTAKTSGNVHVFETAIN	311
NTDB id 1113 AAA85695.1 219..1451()	SFVSLIISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSTSGNMHYQLAIE	314
NTDB id 1112 NGFG RS09215 WP 003689811.1	ALGFAYIRFLKLKARSIKIQRMDAAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEATR	314
NTDB id 193190 BE845 RS00890 WP 011215549.1	ALGFAYIRFLKLKARSIKIQRMDAAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEATR	311
NTDB id 1252 GC085 RS07730 WP 011213805.1	ALGGVYYSFFYAKNHSLEFAQTIIDRVMLKFPVIGPILEKAAIARFARTLSITFAAGPLVEALKSVAGATGNIYAKATD	311
NTDB id 1198 PSJM300 03950 AFN76868.1	ALGGVYYSFFYAKNHSLEFAQTIIDRVMLKFPVIGPILEKAAIARFARTLSITFAAGPLVEALKSVAGATGNIYAKATD	310
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FGVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDIYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFERSATN	313
NTDB id 1059 ABD1 RS01610 WP 000279215.1	VIGAATAGFLEARKRSKRFRDQLDLRLVLRPIVGDVYKAIARIYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAVL	313
consensus	***** ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * *	

