

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	MAKN	72
NTDB id 419094 GSR97 RS12520 WP 005462561.1	MAKNTQ.....TLPLKNYRWKGINNSGKK..VSGQMLAISIEIEVRDKLKDQHIQIKKKLKKGSVSLAR.LTHRVRVKSKDITI	71
NTDB id 1402 DSB67 RS12670 WP 010643257.1	.MKTTT.....TPQLKNFRWKGVNSSGKK.TSGQTLAMSEIEVRERLDAQHIKIKKKLKKSSISFLT.LSHRVKVKGDITV	71
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MKTI.....APQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKKLKKGSISFITK.ISHRVVKGDITI	74
NTDB id 1113 AAA85695.1 219..1451()	.MAKNGGFSLF AKKEKRFI FEGRHSASDKLVNVEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQEDITV	74
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MAKNGGFSLF AKKEKRFI FEGRHSASDKLVNVEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQEDITV	71
NTDB id 1198 PSJM300 03950 AFN76868.1	.MDKN.....SPPLTLFHYQGINKAGQK.MEGDIQARSLAIADLRKQGI VTNKVVKRKP 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.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKVKPLDIAI	73
consensus	MAVKK.....AQMMPTFA YEGVDRKGIVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVKTTLDITI	73

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	FTRQLATM	152
NTDB id 419094 GSR97 RS12520 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	FTRQLATMIESGPIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNEFCNLVDAGEKSGSLDIML	151
NTDB id 1198 PSJM300 03950 AFN76868.1	FTRQMATMMKAGVPLQSFDIIGEGFDNPNMRKLVDDLKQEVAAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETLL	150
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPPQYFDNLFCSLIESGEQSGSLEIML	153
NTDB id 1059 ABD1 RS01610 WP 000279215.1	FTRQLATMMKAGVPLVQGFIEIVAEGLENPAMREVVLGKGEVEGGSTFASALRKYPPQHFDNLFCSLVESGEQSGALETML	153
consensus	FTRQLATM KAGVPLVQAFEIVAEGHNPMSLMSIKVEAGTSSALRKHPYFDLYCNLVAGFESGSL EIM	153

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	DRLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPFESFMFKGFGAELPWFTQQVLKLSHWVQAVSLWAFI	232
NTDB id 419094 GSR97 RS12520 WP 005462561.1	ERLATYREKNEQLRAKVIKALIY PAMVILVALGVSFIMLT KVIPFEEKMFVGFGAELPWFTTRQVLDLSAWTQNWSPFTIAL	231
NTDB id 1402 DSB67 RS12670 WP 010643257.1	ERLATYREKSEQLRAKVIKALIY PAMVVLVALGVSYLMLTRVIPFEEKMFTGFGADLPFTQMVNLNSAWTQNWGPFGIL	231
NTDB id 1112 NGFG RS09215 WP 003689811.1	DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMIFVLPFAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVLI	234
NTDB id 1113 AAA85695.1 219..1451()	DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMIFVLPFAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVLI	234
NTDB id 1252 GC085 RS07730 WP 011213805.1	DKVATYKEKIEIKKKIKKALTYPPIAMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYIIFG	231
NTDB id 1198 PSJM300 03950 AFN76868.1	DRVATYKEKTEALKAKIKKAMNYPPIAVVLVAVIVTATILLIKVVPQFQDV FANFGAELPAFTLMVIGLSEALQAWWYVVL	230
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFTSFGADLPFTQLVNVNMSNWMQDYWFILIL	233
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFASFGADLPFTQMNVNMSKWMQYWFIMII	233
consensus	ERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPFESFMFKGFGAELPWFTQQVLKLSHWVQAVSLWAFI	233

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	AIAAAIFGLKALRKNSFQIRLKTSSRLGLKFPITGNVLAKASTIAKFSRTLATSFAAGIPILASLKTAKTSGNVHFETAIN	312
NTDB id 419094 GSR97 RS12520 WP 005462561.1	GSISLFI SARVLSKRSDSFRLLMNRSLVKFPVLGAVLSKAAIAKFSRTLATSFTAGIPILTSKLTTSKTS 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()	ALGFAIYRFLKLRARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	314
NTDB id 1252 GC085 RS07730 WP 011213805.1	ALGGVVSFFYAKNHSLEFAQTI DRVMLKL PVI GP ILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATD	311
NTDB id 1198 PSJM300 03950 AFN76868.1	FGVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDI LYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFERSATN	310
NTDB id 1016 ACIAD RS01680 WP 004920476.1	VIGAATAGFLEARKRSKRFRDQLDRLVLRLPVIGDLVYKAI IARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAVL	313
NTDB id 1059 ABD1 RS01610 WP 000279215.1	AIGAVIAAFLEARKRSKKFRDGLDKLALKLPIFGDLVYKAI IARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAVM	313
consensus	AIAAAIFGLKALRKNSFQIRLKTSSRLGLKFPITGNVLAKASTIAKFSRTLATSFAAGIPILASLKTAKTSGNVHFETAIN	313

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NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1252 GCO85 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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NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 419094 GSR97 RS12520 WP 005462561.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1252 GCO85 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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V V A M Y L P I F N L S V L G . 408
V T A M Y L P I F N L M S V L G . 407
V T A M Y L P I F N L M S V L G . 407
L V A M Y L P I F N L G N V V A . 410
L V A M Y L P I F N L G N V V A * 410
V V A M Y L P I F K L G S A V . 406
T I A M Y L P I F Q M G S V V . 405
V I A M Y L P I F Q M G S V V . 408
V I A M Y L P I F Q M G S V V . 408

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