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NTDB id 1169 A1552VC RS11075 WP 000648511.1	MAKN	72
NTDB id 407186 GPY21 RS11160 WP 005493981.1	MAKNTQ.....TLPLKNYRWKGINNSGKK.VSGQMLAISIEIEVRDKLKDQHIQIKKLLKKGVSILAR.LTHRVRKSKDITI	71
NTDB id 1402 DSB67 RS12670 WP 010643257.1	.MKTT.....TPQLKNFRWKGVNSSGKK.TSGQTLAMSETEVRERLDAQHIKIKKLLKKGSSISFLT.LSHRVKVKGDITV	71
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MKTI.....APQLKNYRWKGINNSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLLKKGSSISFITK.ISHRVKVKGDITI	74
NTDB id 1113 AAA85695.1 219..1451()	.MAKNGGFSLF AKKEKRFI FEGRHSASDKLVNVEVS AFTEEEARKKLA KRGI RPLQITRV.....KTSSKRKITQEDITV	74
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MAKNGGFSLF AKKEKRFI FEGRHSASDKLVNVEVS AFTEEEARKKLA KRGI RPLQITRV.....KTSSKRKITQEDITV	71
NTDB id 1198 PSJM300 03950 AFN76868.1	.MDKN.....SPPLLT FHYQGINKAGQK.MEGDIQARSLAI AKADLRKQGI VTNKV VVKRKPLFDR.KNKKITQADITV	70
NTDB id 1016 ACIAD RS01680 WP 004920476.1	.MAQK.....AIKNSVFTWEG LDRQGA K.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPMDIAL	73
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAKK.....TQVMPVFAYEGVDRKG I.KGELPARNMALAKVT LRKQGITIRTIREKRKNIFEGLLKKVKVPLDIAI	73
consensus	MAVKK.....AQMMPTFA YEGVDRKG V.KGELPAKNMALAKVT LRKQGVTVRNIREKRKNILEGLFKKKVKTTLDITI	73

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	FTRQLATM LKA GVP LVA F E I V A E G H N P M K S L M S I K V E A T T S A L R K P Y F D L Y C N L V A G E Q S G L E I M	152
NTDB id 407186 GPY21 RS11160 WP 005493981.1	LTRQLATMITTGVPIVQALKLVGDNHRKAEMKSI LAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLPVEVF	151
NTDB id 1402 DSB67 RS12670 WP 010643257.1	FTRQISTMLVTGVPLVQALKLVSDNHKKAEMKSI LMSVTRAVEAGTPMSKAMRTASNHFDPPLYTDLIATGEQSGNLAEVF	151
NTDB id 1112 NGFG RS09215 WP 003689811.1	FTRQIATMLMTGVPIVQALKLVSENHKKAEMKSI LMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQVF	154
NTDB id 1113 AAA85695.1 219..1451()	FTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL	154
NTDB id 1252 GC085 RS07730 WP 011213805.1	FTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL	151
NTDB id 1198 PSJM300 03950 AFN76868.1	FTRQIATMIESG IPLVQAFDIVAKGQSNKRLKDLIETIKHD IETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDIML	150
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FTRQMATMMKAGVPL LQSFDI IGE GFDNPNMRKLVD LKQEVAA GNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETLL	153
NTDB id 1059 ABD1 RS01610 WP 000279215.1	FTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIML	153
consensus	FTRQLATMMKAGVPLVQGF EIVAEGLENPAMREVLG IKGVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETML	153

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	DRLATYK E K E L R A K Y K K A L Y P A M V I L V A L G T E I M L L I K V Y P F E D V A G F G A E L P A E T O V M S W Q Y W Y I Y L I	232
NTDB id 407186 GPY21 RS11160 WP 005493981.1	ERLATYREKSEQLR AKVIKALIYPSMVVLVALGVSYLMLTMVIP EFESMFKGFGAELPWFTQQVLKLSHWVQAVSLWAFI	231
NTDB id 1402 DSB67 RS12670 WP 010643257.1	ERLATYREKNEQLRAKVIKALIY PAMVILVALGVSFIMLT KVIPEFEKMFVGFGAELPWFTTRQVLDLSAWTQNWSPFTIAL	231
NTDB id 1112 NGFG RS09215 WP 003689811.1	ERLATYREKSEQLR AKVIKALIY PAMVVLVALGVSYLMLTRVIP EF EKMF TGF GADLP AFTQMVNL SAWTQNWGPFGIL	234
NTDB id 1113 AAA85695.1 219..1451()	DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVLI	234
NTDB id 1252 GC085 RS07730 WP 011213805.1	DKVATYKEKIEI IKKKIKKALTYP IAVMVVALLV TAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYIIFG	231
NTDB id 1198 PSJM300 03950 AFN76868.1	DRVATYKEKTEAL KAKIKKAMNYP IAVVLVAVIVTATILLIKVVPQFQDV FANFGAELPAFTLMVIGLSEALQAWWYVVL A	230
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFTSFGADLP AFTQLVVMNSNMWQDYWFILIL	233
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFASFGADLP AFTQMVMNSKWMQYWFIMII	233
consensus	ERLATYREKSEQLR AKVIKALIYPSMVVLVALGVSYLMLTMVIP EFESMFKGFGAELPWFTQQVLKLSHWVQAVSLWAFI	233

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	AIAGAIYSELKKRSKFRDR LKPIGDIYKAAIARESR TLATFAAGYPLVDALKSTAGAGNLYEAT	312
NTDB id 407186 GPY21 RS11160 WP 005493981.1	AIAGAIYSELKKRSKFRDR LKPIGDIYKAAIARESR TLATFAAGYPLVDALKSTAGAGNLYEAT	311
NTDB id 1402 DSB67 RS12670 WP 010643257.1	GSISVFISARVLSKRSDSFRLLMNRSVLKFPVLGAVLSKAAIAKFSRTLATSFTAGIPILTSKLTTSKTS SGNMHYQLAIE	311
NTDB id 1112 NGFG RS09215 WP 003689811.1	SFVSLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFTAGIPILTSKLTTSKTS SGNMHYQLAIE	314
NTDB id 1113 AAA85695.1 219..1451()	ALGFAIYGLFLKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	314
NTDB id 1252 GC085 RS07730 WP 011213805.1	ALGFAIYRFLKLRARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	311
NTDB id 1198 PSJM300 03950 AFN76868.1	ALGGVVSFFYAKNHSLEFAQTIDRVMLKLVPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATD	310
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FGVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDIYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFERSATN	313
NTDB id 1059 ABD1 RS01610 WP 000279215.1	VIGAATAGFLEAKRKRFRDQDLRLVLRPIVGDVYKAI IARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAVL	313
consensus	AIAGAVIAAFLEAKRKRFRDQDLRLVLRPIVGDVYKAI IARYSRTLATTFAAGVPLIDALESTAGATNNTVYEQAVL	313

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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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NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 407186 GPY21 RS11160 WP 005493981.1
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 M S V L G . 408
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

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