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NTDB id 1169 A1552VC RS11075 WP 000648511.1	MAKN	72
NTDB id 22752 VP RS12245 WP 005479682.1	MAKNTQ.....TLPLKNYRWKGINNSGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLLKKGVSILAR.LTHRVRKSKDITI	71
NTDB id 1402 DSB67 RS12670 WP 010643257.1	.MKTT.....TPQLKNFRWKGVNSSGKK.TSGQTLAMSEIEVRERLDAQHIKIKKLLKKGSSISFLT.LSHRVKKGKDITV	71
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MKTI.....APQLKNYRWKGINNSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLLKKGSSISFITK.ISHRVKKGKDI	74
NTDB id 1113 AAA85695.1 219..1451()	.MAKNGGFSLF AKKEKR FIFEGRHSASDKLVNGEVSAFTEEEARKKLA KRGI RPLQITRV.....KTSSKRKITQEDITV	74
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MAKNGGFSLF AKKEKR FIFEGRHSASDKLVNGEVSAFTEEEARKKLA 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.....AIKNSVFTWEG LDRQGA K.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPMDIAL	73
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAKK.....TQVMPVFAYEGVDRKG I.KGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPLDIAI	73
consensus	MAVKK.....AQMMPTFA YEGVDRKG V.KGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVKTTLDITI	73

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	FTRQLATM LKAGVPLVQAF EIVAE GHNP E KSLMS IK VEGTTSALRKHP YFDLYCNLVAG EESG L EIM	152
NTDB id 22752 VP RS12245 WP 005479682.1	LTRQLATMITTGVPIVQALKLVGDNHRKAEMKSI LAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLP E V F	151
NTDB id 1402 DSB67 RS12670 WP 010643257.1	FTRQISTMLVTGVPLVQALKLVSDNHKKAEMKSI LMSVTRAVEAGTPMSKAMRTASNHFDPPLYTDLIATGEQSGNLA E V F	151
NTDB id 1112 NGFG RS09215 WP 003689811.1	FTRQIATMLMTGVPIVQALKLVSENHKKAEMKSI LMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQV F	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	FTRQLATMIESG IPLVQAFDIVAKGQSNKRLKDLIETIKHD IETGLTLAESLIKHPLYFNE LFCNLVDAGEKSGSLDIML	150
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FTRQMATMMKAGVPL LQSFDIIGEGFDNPNMRKLVD LKQEVAAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETLL	153
NTDB id 1059 ABD1 RS01610 WP 000279215.1	FTRQLATMMLKAGVPLVQAFEIVAEGL ENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIML	153
consensus	FTRQLATMMLKAGVPLVQGF EIVAEGL ENPAMREVVLG IKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETML	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 Q V M S W Q Y W Y I Y L I	232
NTDB id 22752 VP RS12245 WP 005479682.1	ERLATYREKSEQLR AKVIKALIYPSMVVLVALGVSYLMLTMVIP EFESMFKGFGAELPWFTQQVLKLSHWVQAVSLWAFI	231
NTDB id 1402 DSB67 RS12670 WP 010643257.1	ERLATYREKNEQLRAKVIKALIY PAMVILVALGVSFIMLT KVIP EF EKMFVGFGAELPWFTTRQVLDLSAWTQNWSPFTIAL	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()	DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMIFVLP AFKEVYANMGAELPALTQTVM DMSDFVSYGWMVLI	234
NTDB id 1252 GC085 RS07730 WP 011213805.1	DKVATYKEKIEI IKKKIKKALTYP IAVMVVALLV TAGLLIYVVPQFESL FKGFGADLPAMTRAVITMSEFMQAYWYIIFG	230
NTDB id 1198 PSJM300 03950 AFN76868.1	DRVATYKEKTEAL KAKIKKAMNYP IAVVLVAVIVTATILLIKVVPQFQDV FANFGAELPAFTLMVIGLSEALQAWWYVVL A	233
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFTSFGADLP AFTQLVNMNSNMWQDYWFILIL	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 22752 VP RS12245 WP 005479682.1	ATIAAIFGLKALRKN SFQIRLKT SR LGLKFPITGNVLAKASTAKFSRTLATSFAAGIPILASLKT TAKTSGNVHFETAIN	311
NTDB id 1402 DSB67 RS12670 WP 010643257.1	GSISVFISARVLSKRSDSFR LMLNRSVLKFPVLGAVLSKAAIAKFSRTLATSFTAGIPILTS LKTTSKTS SGNMHYQLAIE	311
NTDB id 1112 NGFG RS09215 WP 003689811.1	SFVSLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTS SGNMHYQLAIE	314
NTDB id 1113 AAA85695.1 219..1451()	ALGFAIYGLFLKARSIKIQR RMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	314
NTDB id 1252 GC085 RS07730 WP 011213805.1	ALGFAIYRFLKLARSIKIQR RMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	311
NTDB id 1198 PSJM300 03950 AFN76868.1	ALGGVVSFFYAKNHSLEFAQTIDRVMLKL PVI GP ILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATD	310
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FGVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDI LYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFERSATN	313
NTDB id 1059 ABD1 RS01610 WP 000279215.1	VIGAATAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAI IARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAVL	313
consensus	AIGAVIAAFLEAKRSKRFRDGLDKLALKLPIFGDLVYKAI IARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAVM	313

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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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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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[illegible]

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