

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	MAKN	72
NTDB id 407319 GPY27 RS02135 WP 031830115.1	MAKNTQ.....TLPLKNYRWKGINNSGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLLKKGVSILAR.LTHRVRVKSKDITI	71
NTDB id 1402 DSB67 RS12670 WP 010643257.1	.MKTTT.....TPQLKNFRWKGVNSSGKK.TSGQTLAMSEVEVRERLDAQHIKIKKLLKKGSSISFLT.LSHRVKVKGDITV	71
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MKTI.....APQLKNYRWKGINNSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLLKKGSSISFITK.ISHRVVKGDITI	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.....SPPLTLFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGI VTNKVVKRKP L FDR.KNKKITQADITV	70
NTDB id 1016 ACIAD RS01680 WP 004920476.1	.MAQK.....AIKNSVFTWGLDRQGAQK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPMDIAL	73
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAKK.....TQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKVKPLDIAI	73
consensus	MAVKK.....AQMMPTFA YEGVDRKGIVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVVTTLDITI	73

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	FTRQLATM	152
NTDB id 407319 GPY27 RS02135 WP 031830115.1	FTRQISTMLVTGVPLVQALKLVSDNHKKAEMKSI LMSVTRAVEAGTPMSKAMRTASNHFDPPLYTDLIATGEQSGNLAEVF	151
NTDB id 1402 DSB67 RS12670 WP 010643257.1	FTRQIATMLMTGVPIVQALKLVSENHKKAEMKSI LMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQVF	151
NTDB id 1112 NGFG RS09215 WP 003689811.1	FTRQLSTMIKAGLPLMQAFEIVARGHGPNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL	154
NTDB id 1113 AAA85695.1 219..1451()	FTRQLSTMINAGLPLMQAFEIVARGHGPNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL	154
NTDB id 1252 GC085 RS07730 WP 011213805.1	FTRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHD IETGLTLAESLIKHPLYFNE LFCNLVDAGEKSGSLDIML	151
NTDB id 1198 PSJM300 03950 AFN76868.1	FTRQMATMMKAGVPLQSFDIIGEGFDNPNMRKLVDL LKQEVAAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETLL	150
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FTRQLATMMLKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIML	153
NTDB id 1059 ABD1 RS01610 WP 000279215.1	FTRQLATMMLKAGVPLVQGF EIVAEGLENPAMREVVLG IKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETML	153
consensus	FTRQLATMMLKAGVPLVQAFEIVAEGLENPAMREVVLG IKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETML	153

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	DRLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIP EFESMFKGFGAELPWFTQQVLKLSHWVQAVSLWAFI	232
NTDB id 407319 GPY27 RS02135 WP 031830115.1	ERLATYREKNEQLRAKVIKALIY PAMVILVALGVSFIMLT KVIPEFEKMFVGFAGELPWFTTRQVLDLSAWTQNWSPFTIAL	231
NTDB id 1402 DSB67 RS12670 WP 010643257.1	ERLATYREKSEQLRAKVIKALIY PAMVVLVALGVSYLMLTRV IPEFEKMF TGFAGDLPAFTQMVLNLSAWTQNWGPFGIL	231
NTDB id 1112 NGFG RS09215 WP 003689811.1	DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVLI	234
NTDB id 1113 AAA85695.1 219..1451()	DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVLI	234
NTDB id 1252 GC085 RS07730 WP 011213805.1	DKVATYKEKIEIKKKIKKALTYP IAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYIIFG	231
NTDB id 1198 PSJM300 03950 AFN76868.1	DRVATYKEKTEALKAKIKKAMNYP IAVVLVAVIVTATILLIKVVPQFQDV FANFGAELPAFTLMVIGLSEALQAWWYVVL A	230
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFTSFGADLP AFTQLVNMNSNMWQDYWFILIL	233
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFASFGADLP AFTQMVMNMSKWMQYWFIMII	233
consensus	ERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIP EFESMFKGFGAELPWFTQQVLKLSHWVQAVSLWAFI	233

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	AIAAAIFGLKALRKNSFQIRLKT SR LGLKFPITGNVLAKASTIAKFSRTLATSFAAGIPILASLKT TAKTSGNVHFETAIN	312
NTDB id 407319 GPY27 RS02135 WP 031830115.1	GSISVVCISARVLSKRSDSFR LMLNRSVLKFPVLGAVLSKAAIAKFSRTLATSFTAGIPILTS LKTTSKTS SGNMHYQLAIE	311
NTDB id 1402 DSB67 RS12670 WP 010643257.1	SFVSL LISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTS SGNMHYQLAIE	311
NTDB id 1112 NGFG RS09215 WP 003689811.1	ALGFAIYGF LK LARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAAGNLIYEATR	314
NTDB id 1113 AAA85695.1 219..1451()	ALGFAIYRFLK LARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAAGNLIYEATR	314
NTDB id 1252 GC085 RS07730 WP 011213805.1	ALGGVVSFFYAKNHSLEFAQTIDRVMLKL PVI GP ILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATD	311
NTDB id 1198 PSJM300 03950 AFN76868.1	GFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVG DILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFERSATN	310
NTDB id 1016 ACIAD RS01680 WP 004920476.1	VIGAATAGFLEARKRSKRFRDQLDRLVLR LPIVGDLVYKAI IARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAVL	313
NTDB id 1059 ABD1 RS01610 WP 000279215.1	AIGAVIAAFLEARKRSKRFRDGLDKLALKLPIFGDLVYKAI IARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAVM	313
consensus	AIAAAIFGLKALRKNSFQIRLKT SR LGLKFPITGNVLAKASTIAKFSRTLATSFAAGIPILASLKT TAKTSGNVHFETAIN	313

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NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

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[illegible][illegible]

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