

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	MAKN	72
NTDB id 397248 GH799 RS06155 WP 005493981.1	MAKNTQ.....TLPLKNYRWKGINNSGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLLKKGVSILAR.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 FEGRHSASDKLVNVEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQEDITV	74
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MAKNGGFSLF AKKEKRFI FEGRHSASDKLVNVEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQEDITV	71
NTDB id 1198 PSJM300 03950 AFN76868.1	.MDKN.....SPPLTLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGI VTNKVVKKKRPLFDR.KNKKITQADITV	70
NTDB id 1016 ACIAD RS01680 WP 004920476.1	.MAQK.....AIKNSVFTWGLDRQGAQK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSSISLFS..AGKKIKPMDIAL	73
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAKK.....TQVMPVFAFEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPLDIAI	73
consensus	MAVKK.....AQMMPTFAFEGVDRKGIVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVKTTLDITI	73

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	FTRQLATM	152
NTDB id 397248 GH799 RS06155 WP 005493981.1	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	FTRQLATMIESGPIPLVQAFDIVAKGQSNKRLKDLIETIKHD IETGLTLAESLIKHPLYFNEFCNLVDAGEKSGSLDIML	151
NTDB id 1198 PSJM300 03950 AFN76868.1	FTRQMATMMKAGVPLQSFDIIGEGFDNPNMRKLVDLQKQEVAAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETLL	150
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FTRQLATMMAKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIML	153
NTDB id 1059 ABD1 RS01610 WP 000279215.1	FTRQLATMMAKAGVPLVQGFIEIVAEGLENPAMREVVLG IKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETML	153
consensus	FTRQLATMMAKAGVPLVQGFIEIVAEGLENPAMREVVLG IKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETML	153

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	ERLATYREKSEQLRRAKVIKALYPSMVVLVALGVSYLMLTMVIPFESFMFKGFGAELPWFTQQVLKLSHWVQAYSLWAFI	232
NTDB id 397248 GH799 RS06155 WP 005493981.1	ERLATYREKNEQLRAKVIKALYIPAMVILVALGVSFIMLTKVIPFEEKMFVGFGAELPWFTQVLDLSAWTQNWSPFTIAL	231
NTDB id 1402 DSB67 RS12670 WP 010643257.1	ERLATYREKSEQLRRAKVIKALYIPAMVVLVALGVSYLMLTRVIPFEEKMFTGFGADLPFTQMVNLMSAWTQNWGPFGIL	231
NTDB id 1112 NGFG RS09215 WP 003689811.1	DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPFAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVLI	234
NTDB id 1113 AAA85695.1 219..1451()	DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPFAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVLI	234
NTDB id 1252 GC085 RS07730 WP 011213805.1	DKVATYKEKIEIKKKIKKALTYPPIAMVVALLVTAGLLIYVVPQFESLFKGFAGADLPAMTRAVITMSEFMQAYWYIIFG	231
NTDB id 1198 PSJM300 03950 AFN76868.1	DRVATYKEKTEALKAKIKKAMNYPPIAVVLVAVIVTATILLIKVVPQFQDVAFNFGAELPAFTLMVIGLSEALQAWWYVVL	230
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFTSFGADLPFTQLVNVNMSNWMQDYWFILIL	233
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFASFGADLPFTQMNVNMSKWMQYWFIMII	233
consensus	ERLATYREKSEQLRRAKVIKALYPSMVVLVALGVSYLMLTMVIPFESFMFKGFGAELPWFTQQVLKLSHWVQAYSLWAFI	233

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	AIAAAIFGLKALRKNSFQIRLKTSLGLKFPITGNVLAKASTIAKFSRTLATSFAAGIPILASLKTAKTSGNVHFETAIN	312
NTDB id 397248 GH799 RS06155 WP 005493981.1	GSISVFISARVLSKRSDSFRLLMNRSLVKFPVLGAVLSKAAIAKFSRTLATSFTAGIPILTSKLTTSKTSGNMHHYQLAIE	311
NTDB id 1402 DSB67 RS12670 WP 010643257.1	SFVSLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHHYQLAIE	311
NTDB id 1112 NGFG RS09215 WP 003689811.1	ALGFAIYGLFLKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	314
NTDB id 1113 AAA85695.1 219..1451()	ALGFAIYRFLKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	314
NTDB id 1252 GC085 RS07730 WP 011213805.1	ALGGVVSFFYAKNHSLEFAQTIIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGPLPLVEALKSVAGATGNIIYAKATD	311
NTDB id 1198 PSJM300 03950 AFN76868.1	FGVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDIYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFERSATN	310
NTDB id 1016 ACIAD RS01680 WP 004920476.1	VIGAATAGFLEARKRSKRFRDQLDLRLVLRPIVGDLVYKAI IARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAVL	313
NTDB id 1059 ABD1 RS01610 WP 000279215.1	AIGAVIAAFLEARKRSKKFRDGLDKLALKLPVIGDLVYKAI IARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAVM	313
consensus	AIAAAIFGLKALRKNSFQIRLKTSLGLKFPITGNVLAKASTIAKFSRTLATSFAAGIPILASLKTAKTSGNVHFETAIN	313

```

NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 397248 GH799 RS06155 WP 005493981.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1112 NCFG 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

```

392
391
391
394
394
391
390
393
393

logo

```

NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 397248 GH799 RS06155 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

```

[illegible]

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