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NTDB id 1169 A1552VC RS11075 WP 000648511.1	MAKN	72
NTDB id 407279 GPY31 RS10835 WP 005479682.1	MAKNTQ.....TLPLKNYRWKGINSSGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLLKKGVSILAR.LTHRVRKSKDITI	71
NTDB id 1402 DSB67 RS12670 WP 010643257.1	.MKTT.....TPQLKNFRWKGVNSSGKK.TSGQTLAMSEIEVRERLDAQHIKIKKLLKKGSSISFLT.LSHRVKVKGDITV	71
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MKTI.....APQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLLKKGSSISFITK.ISHRVKVKGDITI	74
NTDB id 1113 AAA85695.1 219..1451()	.MAKNGGFSLF AKKEKRFI FEGRHSASDKLVNGEVS AFTEEEARKKLA KRGI RPLQITRV.....KTSSKRKITQEDITV	74
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MAKNGGFSLF AKKEKRFI FEGRHSASDKLVNGEVS AFTEEEARKKLA KRGI RPLQITRV.....KTSSKRKITQEDITV	71
NTDB id 1198 PSJM300 03950 AFN76868.1	.MDKN.....SPPLLT FHYQGINKAGQK.MEGDIQARS LAIAKADLRKQGI VTNKV VVKRKP L FDR.KNKKITQADITV	70
NTDB id 1016 ACIAD RS01680 WP 004920476.1	.MAQK.....AIKNSVFTWEG LDRQGA K.IKGELSGVSPALVKAQLR KQG INPQKV RKKSISLFS..AGKKIKPMDIAL	73
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAKK.....TQVMPVFAYEGVDRKG I.KGELPARNMALAKVT LRKQG ITIRTIREKRKN IFEGL LKKKVKPLDIAI	73
consensus	MAVKK.....AQMMPTFA YEGVDRKG V.KGELPAKNMALAKVT LRKQG VTVRNIREKRKN ILEGLFKKKVKTTLDITI	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 407279 GPY31 RS10835 WP 005479682.1	LTRQLATMITTGVPIVQALKLVGDNHRKAEMKSI LAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLP EVF	151
NTDB id 1402 DSB67 RS12670 WP 010643257.1	FTRQISTMLVTGVPLVQALKLVSDNHKKAEMKSI LMSVTRAVEAGTPMSKAMRTASNHFDPPLYTDLIATGEQSGNLA EVF	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	FTRQLATMIESG IPLVQAFDIVAKGQSNKRLKDLIETIKHD IETGLTLAESLIKHP LYFNELFCNLVDAGEKSGSLDIML	150
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FTRQMATMMKAGVPL LQSFDI IEGEFDNPNMRKLVDL LKQEVAAAGNSF ASSLRKKPQYFDDLYCNLVDSGEQSGSLETLL	153
NTDB id 1059 ABD1 RS01610 WP 000279215.1	FTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIML	153
consensus	FTRQLATMMKAGVPLVQGF EIVAEGLENPAMREVVLG IKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETML	153

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	DRLATYK EKE LRAKYKKAL YP VILVALV VVLP FEF EAG FGAEL PAETQ VVMS WQY YLYL	232
NTDB id 407279 GPY31 RS10835 WP 005479682.1	ERLATYREKSEQ LRAKVIKALIYPSMVVLVALGVSYLMLTMVIP EFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWAFI	231
NTDB id 1402 DSB67 RS12670 WP 010643257.1	ERLATYREKNEQLRAKVIKALIY PAMVILVALGVSFIMLT KVIPEFEKMFVGFGAELPWFTTRQVLDLSAWTQNWSPFTIAL	231
NTDB id 1112 NGFG RS09215 WP 003689811.1	ERLATYREKSEQ LRAKVIKALIY PAMVVLVALGVSYLMLTRV IPEFEKMF 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 FANFGAELPAFTLMVIGLSEALQAWVYVLA	233
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFTSFGADLP AFTQLV VNMNSNMWQDYWFILIL	233
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFASFGADLP AFTQM VNMNSKWMQYWFIMII	233
consensus	ERLATYREKSE LRAKVIKALIYPSMVVLVALGVSYLMLTMVIP EFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWAFI	233

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	ALGAAIYSELKKRSKFR DR LKPIGDIYKAAIARE SRTLATFAAGYPLYDAL KSTAGAGNLYEAT	312
NTDB id 407279 GPY31 RS10835 WP 005479682.1	ATIAAIFGLKALRKNSFQIRLKTSSRLGLKFPITGNVLAKASTAKFSRTLATSFAAGIPILASLKT TAKTSGNVHFETAIN	311
NTDB id 1402 DSB67 RS12670 WP 010643257.1	GSISVFISARVLSKRSDSFRLLMNRSVLKFPVLGAVLSKAAIAKFSRTLATSFTAGIPILTS LKTTSKTS SGNMHYQLAIE	311
NTDB id 1112 NGFG RS09215 WP 003689811.1	SFVSLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTS SGNMHYQLAIE	314
NTDB id 1113 AAA85695.1 219..1451()	ALGFAIYGLFLKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAGNLIYEATR	314
NTDB id 1252 GC085 RS07730 WP 011213805.1	ALGFAIYRFLKLARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAGNLIYEATR	311
NTDB id 1198 PSJM300 03950 AFN76868.1	ALGGVVSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATD	310
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FGVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDI LYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFERSATN	313
NTDB id 1059 ABD1 RS01610 WP 000279215.1	VIGAATAGFLEARKRSKRFRDQLDRLVLRLPVIGDLVYKAI IARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAVL	313
consensus	AIGAVIAAFLEAKRSKRFRDGLDKLALKLPVIGDLVYKAI IARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAVM	313

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NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1252 GCO85 RS07730 WP 011213805.1
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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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Sequence	392
EVYRDTAAGMPMYIAMRNTFAFPMVLQVMVIGEESQLDDMLNKKVATIEFEVDNTVDNLGKILEPLIIYFLGTIVVGG	392
EVYRDTAAGMPMYIAMRNCNVFPELVLMQVMIGEESGRDDMLNKKVATIEFEVDNTVDNLGKILEPLIIYFLGTIVVGG	391
EVYRDTAAGMPMYIAMRHCHVFPELVLMQVMIGEESGRDDMLNKKAAIEFEVDNTVDNLGKILEPLIIYFLGTIVVGG	391
EIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGRDDMLNKKAAIEFEVDNNAVGRLSAMMEPIIIVILGLVIGTL	394
EIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGRDDMLNKKAAIEFEVDNNAVGRLSAMMEPIIILGLVIGTL	394
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KIKSDVSSGMQLNFSMRRTGTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEEVDNMMVDGLTALMEPMIMAVLGLVGG	390
KIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHVDGLTSMMEPLIMAILGLVGG	393
KIREDVATGQQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNNAVDGLTSMMEPLIMAILGLVGG	393

V V A M Y L P I F N L M S V L G . 408
T 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
I 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
-  > 50% conserved