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NTDB id 1029 TT RS02230 WP 011228203.1	MAKN	65
NTDB id 1402 DSB67 RS12670 WP 010643257.1	MPVYQYKARDRQGRLLVEATTEAEDLRTAARLLRDRGLFVAEIKPEPGKGLQAEVRIPALERGPGLK	67
NTDB id 1169 A1552VC RS11075 WP 000648511.1	MKTTI.....APQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKKLKKGSISFITK.....ISHRVKKGK	68
NTDB id 1112 NGFG RS09215 WP 003689811.1	MKATQ.....TLPLKNYRWKGINSSGKK.VSQMLAISEIEVRDKLKDQHIQIKKKLKKGSVSLAR.....LTHRVKSK	70
NTDB id 1113 AAA85695.1 219..1451()	MAKNGGFSLF AKKEKR FIFEGRHSASDKLVNGEVS AFTEEEARKKLAKRGIRPLQITRVKT.....S....SKRKITQE	70
NTDB id 1252 GC085 RS07730 WP 011213805.1	MAKNGGFSLF AKKEKR FIFEGRHSASDKLVNGEVS AFTEEEARKKLAKRGIRPLQITRVKT.....S....SKRKITQE	67
NTDB id 1016 ACIAD RS01680 WP 004920476.1	MDKN.....SPPLILT FHYQGINKAGQK.MEGDIQARSLAI AKADLRKQGI VTNKVVKRK KPLFDR.....KNKKITQA	69
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAKK.....TQVMPV FAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITRTIREKRKNIFEGGL...LKKKV KPL	69
NTDB id 77149 H7K70 RS05510 WP 182851840.1	MAVKK.....AQMMPT FAYEGVDRKGIV.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL...FKKKVTTL	66
NTDB id 1198 PSJM300 03950 AFN76868.1	MADQ.....AVKVS VFKWEGTDKRGAK.ITGEITGANPALVKAQLRKQGINPLKVKKKGTSLFS.....KGKKIKPM	66
consensus	MAKNGGFSLF AKKEKR FIFEGRHSASDKLVNGEVS AFTEEEARKKLAKRGIRPLQITRVKT.....S....SKRKITQE	

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NTDB id 1029 TT RS02230 WP 011228203.1	DITIFTRQLATMMAKAGVPLVQAFELVAEGHEPMMRELLMGLKVEGGEFSAALRKHPYFDLYCNLVESGEQSGI	144
NTDB id 1402 DSB67 RS12670 WP 010643257.1	DITIFTRQLATMMAKAGVPLVQAFELVAEGHEPMMRELLMGLKVEGGEFSAALRKHPYFDLYCNLVESGEQSGI	147
NTDB id 1169 A1552VC RS11075 WP 000648511.1	DITIFTRQLATMMAKAGVPLVQAFELVAEGHEPMMRELLMGLKVEGGEFSAALRKHPYFDLYCNLVESGEQSGI	148
NTDB id 1112 NGFG RS09215 WP 003689811.1	DITIFTRQLATMMAKAGVPLVQAFELVAEGHEPMMRELLMGLKVEGGEFSAALRKHPYFDLYCNLVESGEQSGI	150
NTDB id 1113 AAA85695.1 219..1451()	DITIFTRQLATMMAKAGVPLVQAFELVAEGHEPMMRELLMGLKVEGGEFSAALRKHPYFDLYCNLVESGEQSGI	150
NTDB id 1252 GC085 RS07730 WP 011213805.1	DITIFTRQLATMMAKAGVPLVQAFELVAEGHEPMMRELLMGLKVEGGEFSAALRKHPYFDLYCNLVESGEQSGI	147
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DITIFTRQLATMMAKAGVPLVQAFELVAEGHEPMMRELLMGLKVEGGEFSAALRKHPYFDLYCNLVESGEQSGI	149
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DITIFTRQLATMMAKAGVPLVQAFELVAEGHEPMMRELLMGLKVEGGEFSAALRKHPYFDLYCNLVESGEQSGI	149
NTDB id 77149 H7K70 RS05510 WP 182851840.1	DITIFTRQLATMMAKAGVPLVQAFELVAEGHEPMMRELLMGLKVEGGEFSAALRKHPYFDLYCNLVESGEQSGI	146
NTDB id 1198 PSJM300 03950 AFN76868.1	DITIFTRQLATMMAKAGVPLVQAFELVAEGHEPMMRELLMGLKVEGGEFSAALRKHPYFDLYCNLVESGEQSGI	146
consensus	DITIFTRQLATMMAKAGVPLVQAFELVAEGHEPMMRELLMGLKVEGGEFSAALRKHPYFDLYCNLVESGEQSGI	

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NTDB id 1029 TT RS02230 WP 011228203.1	ELLDRLASFLKELELRGKIRSAMTYPVIVFVFAVGVAFFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	224
NTDB id 1402 DSB67 RS12670 WP 010643257.1	SQVFERLATYREKSEQLRRAKVIKALIYPMAMVVLVALGVSYLMLTRVPIPEFEKMFMTGFGADLPFTQMVNLNSAWTQNWGP	227
NTDB id 1169 A1552VC RS11075 WP 000648511.1	PEVFERLATYREKSEQLRRAKVIKALIYPMAMVVLVALGVSYLMLTRVPIPEFEKMFMTGFGADLPFTQMVNLNSAWTQNWGP	228
NTDB id 1112 NGFG RS09215 WP 003689811.1	ESLLDKLAIYKEKTQAIRKKVKKTALTYPVSVIAVAIGLVFVMMIFVLPAPFKEVYANMGAELPPLTQTVMMDSDFFVSYGW	230
NTDB id 1113 AAA85695.1 219..1451()	ESLLDKLAIYKEKTQAIRKKVKKTALTYPVSVIAVAIGLVFVMMIFVLPAPFKEVYANMGAELPALTQTVMMDSDFFVSYGW	230
NTDB id 1252 GC085 RS07730 WP 011213805.1	DIMLDKVATYKEKIEIKKKIKKALTYPVAVMVVALLVTAGLLIYVVPQFESLFKGFAGDLPAMTRAVITMSEFMQAYWY	227
NTDB id 1016 ACIAD RS01680 WP 004920476.1	EIMLDRVAIYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPFTQVNVNMSNMWQDYWF	229
NTDB id 1059 ABD1 RS01610 WP 000279215.1	ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPFTQVNVNMSNMWQDYWF	229
NTDB id 77149 H7K70 RS05510 WP 182851840.1	ETLLDRVATYKEKTEALKAKIKKAMNYPVAVVLAIVVSMILLIKVVPQFEEVFKNFGAELPAFTRMVIGISEVLQEWYW	226
NTDB id 1198 PSJM300 03950 AFN76868.1	ETLLDRVATYKEKTEALKAKIKKAMNYPVAVVLAIVVSMILLIKVVPQFQDVVFANFGAELPAFTLMVIGLSEALQAWWY	226
consensus	ELLDRLASFLKELELRGKIRSAMTYPVIVFVFAVGVAFFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	

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