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NTDB id 1029	TT RS02230 WP 011228203.1	MAK	65
NTDB id 1402	DSB67 RS12670 WP 010643257.1	MPVYQYKARDRQGRLLVEATTEAEDLRTAARLLRDRGLFVAEIKKEPGKGLQAEVRIPALERGPGGLK	67
NTDB id 1169	A1552VC RS11075 WP 000648511.1	.MKT.....IAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRRERLDAQHIKIKKKLKKGSISFITK.....ISHRVKKGK	68
NTDB id 1113	AAA85695.1 219..1451()	MKAT.....QTLPLKNYRWKGINSSGKK.VSQMLAISEIEVRDKLKDQHIQIKKKLKKGSVSLAR.....LTHRVKSK	70
NTDB id 1112	NGFG RS09215 WP 003689811.1	.MAKNGGFSFLFAKKEKRFIFEGRHSASDKLVNGEVSFAFTEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	70
NTDB id 1252	GCO85 RS07730 WP 011213805.1	.MAKNGGFSFLFAKKEKRFIFEGRHSASDKLVNGEVSFAFTEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	67
NTDB id 1016	ACIAD RS01680 WP 004920476.1	.MDK.....NSPPLILTFFHYQGINKAGQK.MEGDIQARSLAIKADLRKQGIIVTNKVVKRKPFLFDR.....KNKKKITQA	69
NTDB id 1059	ABD1 RS01610 WP 000279215.1	MAAK.....KTQVMPVFAFEGVDRKGKIK.LKGELPARNMALAKVTLRKQGITRTIREKRKNIFEG....LLKKKVKPL	69
NTDB id 161118	ATC05 RS16350 WP 003161763.1	MAVK.....KAQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGITVRNIREKRKNILEG....LFFKKKVTTL	66
NTDB id 1198	PSJM300 03950 AFN76868.1	.MAD.....KALKTSVFFVWEGTDKKGKTK.VKGELSSQNPTLVKAQLRKQGITPVKVRKKGISLLG.....AGKKIKPM	66
consensus		.MAQ.....KAIKNSVFTWGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKKSISLFS.....AGKKIKPM	66

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NTDB id 1029	TT RS02230 WP 011228203.1	DITIFTRQLATMAGYPLVQAEIVAEHNPMBRELLMEIKVEGSSSALRKHPQYFDLYCNLVAGEQSGI	144
NTDB id 1402	DSB67 RS12670 WP 010643257.1	DLAIFSRQLATMLGAGLTLLQALATILERQTEENRKFREILKQVRTDVEGGMAFSEALSKEH.KIFSRLYVNLVRAGETSGGL	147
NTDB id 1169	A1552VC RS11075 WP 000648511.1	DITIFTRQLATMLTGGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNL	148
NTDB id 1113	AAA85695.1 219..1451()	DITIFTRQLATMLTGGVPIVQALKLVSENHKKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLIVETGEMSGNL	150
NTDB id 1112	NGFG RS09215 WP 003689811.1	DITVFTRQLSTMINGAGLPLMQAFEIVARGHGNSPMTLEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAGAGETGGVL	150
NTDB id 1252	GCO85 RS07730 WP 011213805.1	DITVFTRQLSTMINGAGLPLMQAFEIVARGHGNSPMTLEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAGAGETGGVL	147
NTDB id 1016	ACIAD RS01680 WP 004920476.1	DITVFTRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNFELFCNLVDAGEKSGSL	149
NTDB id 1059	ABD1 RS01610 WP 000279215.1	DIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSL	149
NTDB id 161118	ATC05 RS16350 WP 003161763.1	DITIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLIESGEQSGAL	146
NTDB id 1198	PSJM300 03950 AFN76868.1	DIALFTRQMATMMKAGVPLVQAFDIIEGFDNPNMRKLVDEEIKQEVAGGNSLANSLRKKPKQYFDSLYCNLVDSGEQSGAL	146
consensus		DIALFTRQMATMMKAGVPLVQAFDIIEGFDNPNMRKLVDDLKQEVAAAGNSFASSLRKKPKQYFDDLYCNLVDSGEQSGSL	

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NTDB id 1029	TT RS02230 WP 011228203.1	EILDRYAYKEKTELRKIKKAMYPVVAIVVIGTYLLIWPDFEAEFGAELPAETQVNMDSQYWL	224
NTDB id 1402	DSB67 RS12670 WP 010643257.1	DLILDRLASFLEKELELRGKIRSAMTYPIVVFVAVGVAYFLLTGIVPQFAQILTDLGSSELPLLTRFLIAVSDLLRAATL	227
NTDB id 1169	A1552VC RS11075 WP 000648511.1	SQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVPIPEFEKMFMTGFGADLPFTQMVNLNSAWTQNWGP	228
NTDB id 1113	AAA85695.1 219..1451()	PEVFERLATYREKSEQLRAKVIKALIYPMSVVLVALGVSYLMLTMVPIPEFESMFKGFGAELPWFTQQVCLKSHVQAYSL	230
NTDB id 1112	NGFG RS09215 WP 003689811.1	ESLLDKLAIYKEKTQAIRKKVKKTALTYPVSVIAVAIGLVFVMMIFVLPAPFKEVYANMGAELPALTQTVMDMSDFFVSYGW	230
NTDB id 1252	GCO85 RS07730 WP 011213805.1	ESLLDKLAIYKEKTQAIRKKVKKTALTYPVSVIAVAIGLVFVMMIFVLPAPFKEVYANMGAELPALTQTVMDMSDFFVSYGW	227
NTDB id 1016	ACIAD RS01680 WP 004920476.1	DIMLDKVATYKEKIEIKKKIKKALTYPPIAVMVVALLVTAGLLIYVVPQFESLFKGFAGDLPAMTRAVITMSEFMQAYWY	229
NTDB id 1059	ABD1 RS01610 WP 000279215.1	EIMLDRVAIYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPFTQVNVNMSNMWQDYWF	229
NTDB id 161118	ATC05 RS16350 WP 003161763.1	ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFPQDLFASFGADLPFTQMVVNMSKMWQDYWF	226
NTDB id 1198	PSJM300 03950 AFN76868.1	ETLLDRVATYKEKTEALKAKIKKAMTYPIAVIVVAIVVSAILLIKVVPQFQSVFEGFGAELPAFTQMVINISNVLQEWL	226
consensus		ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVVLVAVIVTAILLIKVVPQFQDVVFANFGAELPAFTLMVIGLSEALQAWWY	

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