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NTDB id 1029	TT RS02230 WP 011228203.1	MPVYQYKARDRQGRLLVEATTEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALER	60
NTDB id 1169	A1552VC RS11075 WP 000648511.1	MKATQTLPLKNYRWKGINSGKKVSGQMLAISEIEVRDKLKDDHIQIKKKLKGVSLLAR....LTH	63
NTDB id 1402	DSB67 RS12670 WP 010643257.1	MKTIIAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKKLKGSSIFITK....ISH	62
NTDB id 1112	NGFG RS09215 WP 003689811.1	MAKNGGFSLFAKKEKRFIIEGRHSASDKLVNGEVSATFEEEEARKKLAIRGIRPLQITRVK.....T....SSKR	65
NTDB id 1113	AAA85695.1 219..1451()	MAKNGGFSLFAKKEKRFIIEGRHSASDKLVNGEVSATFEEEEARKKLAIRGIRPLQITRVK.....T....SSKR	65
NTDB id 1043080	ABQU55 RS06275 WP 039525808.1	MSVARNAVNKNQPVSRNTSLQQPFFVWEGTDKRGVK.MKGEQTARNANMLRAELRRQGITPTVVAKPKPLFGS....AGK	74
NTDB id 1252	GC085 RS07730 WP 011213805.1	MDKNSPPLLTFFHYQGINKAGQK.MEGDIQARSLAIKADLRKQGIVTNKVVKKRKPLFDR....KNK	62
NTDB id 1198	PSJM300 03950 AFN76868.1	MAQKAIKNSVFTWEGLDKQGAIKGELSGVSPALVKAQLRKQGINPQKVRKKSSISLFS....AGK	61
NTDB id 1016	ACIAD RS01680 WP 004920476.1	MAAKKTQVMPVFAIEGVDRKGKIKGELPARNMALAKVTLRKQGITTIRTIKREKRKNIFEG....LLKK	64
NTDB id 1059	ABD1 RS01610 WP 000279215.1	MAVKKAQMMPTFAYIEGVDRKGKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFFK	64
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NTDB id 1029	TT RS02230 WP 011228203.1	GPGCLKDLAIFSRQLATMLGAGLTLLQALATLERQTENNRKFFREILKQVRTDVEGGMAFSEALSCHKK.IFSRLYVNLVRAGE	139
NTDB id 1169	A1552VC RS11075 WP 000648511.1	RVKSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVEATGE	143
NTDB id 1402	DSB67 RS12670 WP 010643257.1	RVKGGDITIFTRQIATMLTTGVPIVQALKLVSENHKKAEKMSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLTIATGE	142
NTDB id 1112	NGFG RS09215 WP 003689811.1	KITIQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGPNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGE	145
NTDB id 1113	AAA85695.1 219..1451()	KITIQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGPNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGE	145
NTDB id 1043080	ABQU55 RS06275 WP 039525808.1	RISSKDIAFFSRQMATMMKSGIPIVSSLEIIGEGHKNPRMKQMVGQIRSDIEGGSSSLQEAISKHPVQFDELYRNLVRAGE	154
NTDB id 1252	GC085 RS07730 WP 011213805.1	KITIQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGE	142
NTDB id 1198	PSJM300 03950 AFN76868.1	KIKPMDIALFTRQMATMMKAGVPLQLSFDIIGEGFDNPNMRKLVDLDDLKQEVAAAGNSFASSLRKPKPYFDDLYCNLVDSEGE	141
NTDB id 1016	ACIAD RS01680 WP 004920476.1	KVKPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGE	144
NTDB id 1059	ABD1 RS01610 WP 000279215.1	KVITLDTITIFTRQLATMMKAGVPLVQGEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGE	144
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NTDB id 1029	TT RS02230 WP 011228203.1	TSGGLDLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAIFYLLTGIVPQFAQILTDLGSSELPPLLTRFLIAVSDLL	219
NTDB id 1169	A1552VC RS11075 WP 000648511.1	MSGNLPVFERLATYREKSEQLRKAVIKALIYPSMVLVALGVSYLMLTMVPIPEFESMFKGFGAELPWFTQQLKLSHWV	223
NTDB id 1402	DSB67 RS12670 WP 010643257.1	QSGNLSQVFERLATYREKSEQLRKAVIKALIYPSMVLVALGVSYLMLTRVIPEFEKMFTEGFGADLPAFTQMVNLNSAWT	222
NTDB id 1112	NGFG RS09215 WP 003689811.1	TGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAPFKEVYANMGAELPPLTQTVMDSDF	225
NTDB id 1113	AAA85695.1 219..1451()	TGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAPFKEVYANMGAELPALTQTVMDSDF	225
NTDB id 1043080	ABQU55 RS06275 WP 039525808.1	GAGVLETIVLDTVATYKENIEALKGKIKKALFYPSMVLVAIVSAIILLIFVVPQFEVFKSFGAELPAFTQIIVNASRFM	234
NTDB id 1252	GC085 RS07730 WP 011213805.1	KSGSLDIMLDKVATYKEKIEIKKKIKKALTYPIAVMVALLVITAGLLIYVVPQFESLFKGFAGADLPAMTRAVITMSEFM	222
NTDB id 1198	PSJM300 03950 AFN76868.1	QSGSLETLLDRVATYKEKTEALKAKIKKAMNYPVAVLVAVIVTALLIKVVPQFQDVVFANFGAELPAFTLMVIGLSEAL	221
NTDB id 1016	ACIAD RS01680 WP 004920476.1	QSGSLEIMLDRVAIVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVNNMSNWM	224
NTDB id 1059	ABD1 RS01610 WP 000279215.1	QSGALETMLDRVAIVYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFASFGADLPAFTQMVVNNMSKWM	224
consensus		*****	

