

NTDB id 1029	TT RS02230 WP 011228203.1	MPVYQYKARDRQGR.LVEATIEAEDLRTAARLRDRGLFVAEIKPEPGKGLQAEVRIPALER	60
NTDB id 1169	A1552VC RS11075 WP 000648511.1	MKATQTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDCLKDQHIQIKKLLKKGVSLLAR.....LTH	63
NTDB id 1402	DSB67 RS12670 WP 010643257.1	MKTIIAPQLKNYRWKGINSNGKK.TSGNVLAMATEIEVRERLDAQHIKIKKLLKKGVSISFITK.....ISH	62
NTDB id 1112	NGFG RS09215 WP 003689811.1	MAKNGGFSFLAKKEKRFYFEGRHSASDKLVNGEVSATFEEEARKKLAKRGIRPLQITRV.....KTS...SSKR	65
NTDB id 1113	AAA85695.1 219..1451()	MAKNGGFSFLAKKEKRFYFEGRHSASDKLVNGEVSATFEEEARKKLAKRGIRPLQITRV.....KTS...SSKR	65
NTDB id 159094	APY29 RS05905 WP 033836749.1	MSVARNVIKKQPADRSNSQMMPFVWEGTDKRGIK.MKGEQAARNVNMRLAELRRQGITPTVVKPKPKPLFGA.....AGK	74
NTDB id 1252	GC085 RS07730 WP 011213805.1	MDKNSPPLLTFFHYQGINKAGQK.MEGDIQARSLAIKADLRKQGIVTNKVVKKRKPLFDR.....KNK	62
NTDB id 1198	PSJM300 03950 AFN76868.1	MAQKAIKNSVFTWEGLDKRGQAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKKSISLFS.....AGK	61
NTDB id 1016	ACIAD RS01680 WP 004920476.1	MAAKKTQVMPVYFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG....LLKK	64
NTDB id 1059	ABD1 RS01610 WP 000279215.1	MAVKKAMMPFTFAYEGVDRKGIVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKK	64
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NTDB id 1029	TT RS02230 WP 011228203.1	GPGLKDLAIFSRQLATMLGAGLTLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFSRLVYNLVRAGE	139
NTDB id 1169	A1552VC RS11075 WP 000648511.1	RVKSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDLTLYVDLLETGE	143
NTDB id 1402	DSB67 RS12670 WP 010643257.1	RVGKGKDITIFTFRQIATMLMTGVPIVQALKLVSENHKKAEEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPPLYTDLTATGE	142
NTDB id 1112	NGFG RS09215 WP 003689811.1	KITQEDITVFTRQLSTMINKAGLPMLQAFAEIVARGHGNSPMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGE	145
NTDB id 1113	AAA85695.1 219..1451()	KITQEDITVFTRQLSTMINAGLPLMQAFEIVARHGHNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGE	145
NTDB id 159094	APY29 RS05905 WP 033836749.1	KVGPKDIAFFSRQMATTMMKSGVPVIGSLEITIGEGHKNPRMRKMVGQIRTDIIEGSSSLHEATISKHPVQFDELYRNLVRAGE	154
NTDB id 1252	GC085 RS07730 WP 011213805.1	KITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNNKRLKDLIETIKHDIIETGLTLAESLIKHPLYFNELFCNLVDAGE	142
NTDB id 1198	PSJM300 03950 AFN76868.1	KIKPMDIALFTRQMATMMKAGVPLQSFIDIIGEGFDNPNNMRKLVDLKKQEVAAGNSFASSLRKKPPQYFDDLYCNLVDSDGE	141
NTDB id 1016	ACIAD RS01680 WP 004920476.1	KVKPLDIAIFTRQLATMMKAGVPLVQAFAEIVAEGLENPAMRDVVVLGLKNEVEGGNTFAGALRKYPQYFDNFLFCSLTESGE	144
NTDB id 1059	ABD1 RS01610 WP 000279215.1	KVTTLDTITIFTRQLATMMKAGVPLVQGEFIVAEGLENNPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNFLFCSLVESGE	144
consensus		** !*****!****!*!!!!!!*****!*****!*****!*****!*****!*****!*****!*****!	

NTDB	id	1029	TT	RS02230	WP	011228203.1	TSGGLDLILDRLASFLKELELRGKIRSAMTYPVIVFVFAVGVAIFYLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLL	219
NTDB	id	1169	A1552VC	RS11075	WP	000648511.1	MSGNLPPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMTVIPEFESMFKGFGAELPWFTQQVLKLSHWV	223.
NTDB	id	1402	DSB67	RS12670	WP	010643257.1	QSGNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLLTRVIPEFEKMTFTGFAGDLPFTAQMVLNLNSAWT	222
NTDB	id	1112	NGFG	RS09215	WP	003689811.1	TGGVLESLLDKLAITYKEKTQAIRKKVKTKALTYPVSVIAVAIGLVFVMIFVLPAFKFEVYANMGAELPALQTQTMMDMSDF	225
NTDB	id	1113	AAA85695.1	219..1451()			TGGVLESLLDKLAITYKEKTQAIRKKVKTKALTYPVSVIAVAIGLVFVMIFVLPAFKFEVYANMGAELPALQTQTMMDMSDF	225
NTDB	id	159094	APY29	RS05905	WP	033836749.1	GAGVLETVLDTVANYKENIEALKGKIKKALFYPMVVAVALIVSAILLIFVVPQFEVFKGFGAELPAFTQMIVAASRFM	234
NTDB	id	1252	GC085	RS07730	WP	011213805.1	KSGSLDIMLDKVATYKEKIEIIRKKIKKALTYPPIAVMMVALLVTAGLLIYVVPQFESLFKGFAGDLPAMTRAVITMSEFM	222
NTDB	id	1198	PSJM300	03950	AFN	76868.1	QSGSLETILDRVATYKEKTEALKAKIKKAMNPYIAVVLVAVIVTATILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEAL	221
NTDB	id	1016	ACIAD	RS01680	WP	004920476.1	QSGSLEIMLDRAVAYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVVPVFKDLFTSFAGDLPFTAQLVVNMNSWM	224
NTDB	id	1059	ABD1	RS01610	WP	000279215.1	QSGALEITMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVVPVFKDLFASFAGDLPFTAQMNVNMNSKM	224
consensus							* ! ***** * ** *** * * * * ***** * * * ***** * * * ***** * *	

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