

NTDB id 1029	TT RS02230 WP 011228203.1	MPVYQYKARDRQGRLLVEATTEAEDLRATAARL	LRDRGLFVAETIKPEPGKG	LQAEVRIPALER	RGPGLK	65				
NTDB id 1402	DSB67 RS12670 WP 010643257.1	.MKT.....IAPQKNYRWKGINSSGKK	.TSGNVLAMTEIEVRER	LDAQHIKIKKLK	KGSI	67				
NTDB id 1169	A1552VC RS11075 WP 000648511.1	MKAT.....QTLPLKNYRWKGINSGKK	.VSGQMLAISEIEVRDK	LKDQHIQIKKLK	KGSVSL	68				
NTDB id 1113	AAA85695.1 219..1451()	.MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVS	AFTEEEARKKLAKRGIRPLQITRVK	TS.....SKR	KITQE	70				
NTDB id 1112	NGFG RS09215 WP 003689811.1	.MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVS	AFTEEEARKKLAKRGIRPLQITRVK	TS.....SKR	KITQE	70				
NTDB id 1252	GC085 RS07730 WP 011213805.1	.MDK.....NSPPLTFHYQGINKAGQK	.MEGDIQARSLATAKAD	LRKQGVITNKVV	KKRKP	67				
NTDB id 1016	ACIAD RS01680 WP 004920476.1	MAAK.....KTQVMPVFAYEGVDRKGKIK	.LKGEIPARNMALAKVT	LRKQGITIRTI	REKRKN	69				
NTDB id 1059	ABD1 RS01610 WP 000279215.1	MAVK.....KAQMMPTFAYEGVDRKGKIK	.LKGEIPAKNMALAKVT	LRKQGVITVRNI	REKRKN	69				
NTDB id 1036485	ACA097 RS17670 WP 371364859.1	.MAE.....KALKTSVFIFEGTDRKGGK	.IKGELSGTNAALVKAQ	LRKQGINPTKVR	KKGIS	66				
NTDB id 1198	PSJM300 03950 AFN76868.1	.MAE.....KAIKNSVFTWEGLDQGA	.IKGELSGVSPALVKAQ	LRKQGINPTKVR	KKGIS	66				
consensus		***	* *	* ** ** *	* *	* * * * *	! * * * * *	* * * * *	*	***

NTDB id	1029	TT RS02230 WP	011228203.1	DLAIFSRQLATMIGAGITLLQALATLERQTENRKFREILKQVVRTDVEGGMAFSEALSKH.KIFSRLYVNLVRAGETSGGI	144
NTDB id	1402	DSB67 RS12670 WP	010643257.1	DITIFTRQIATMTGTGVPDIVQALKLVSENHKKAEKMSILMSVTRAWEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNL	147
NTDB id	1169	A1552VC RS11075 WP	000648511.1	DITIILTRQLATMLTTGVPDIVQALKLVGDNHRKAEMKSILAQITKTSVEAGTPLSKAMRTASAHFDTLYVDLTVETGEMSGNL	148
NTDB id	1113	AAA85695.1	219..1451()	DITVFTRQLSTMINAGLPLMQAFEIVARGHGPNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAAGETGGVL	150
NTDB id	1112	NGFG RS09215 WP	003689811.1	DITVFTRQLSMTIKAGLPLMQAFEIVARGHGPNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAAGETGGVL	150
NTDB id	1252	GC085 RS07730 WP	011213805.1	DITVFSRQLATMIESGIPLVQAFFDIVAKGQSNKRCLKDLTIETIKHDIIETGLTLAESLIKHPPLYFNELFCNLVDAGEKSGSL	147
NTDB id	1016	ACIAD RS01680 WP	004920476.1	DIAIFTRQLATMYKAGVPLVQAFFEIVAEGLENPAMRDVVIGLKNEVEGGNTFAGALRKYPQYFDNFLFCSLIESGEQSGSL	149
NTDB id	1059	ABD1 RS01610 WP	000279215.1	DITIFTRQLATMYKAGVPLVQGFIVEAEGLENPAMREVVIGIKGEVEGGSTFASALRKYPQHFDNFLFCSLVESGEQSGAL	149
NTDB id	1036485	ACA097 RS17670 WP	371364859.1	DIALFTRQMATTMYKAGVPLLQAFDIADGFDPNNMRKLVDIDIKQEVAAGNSLANSLRKKPKQYFDDLYCNLVDAGEQSGAL	146
NTDB id	1198	PSJM300 03950 AFN76868.1		DIALFTRQMATTMYKAGVPLLQSFDIIGEGFDNPNNMRKLVDIDIKQEVAAGNSLFASLRKKPKQYFDDLYCNLVDSEGEQSGSL	146
consensus				!*****!!**!* *!*****!***** ** * **** * !**** * !*** * !*****!*****!!**!	

NTDB id 1029	TT RS02230 WP 011228203.1	DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSSELPLLTRFLIAVSDLLRAATL	224
NTDB id 1402	DSB67 RS12670 WP 010643257.1	SQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFITGFGADLPFTQMVLNLSAMTQNWGP	227
NTDB id 1169	A1552VC RS11075 WP 000648511.1	PEVFERLATYREKSEQLRAKVIKALIYPMSVVLVALGVSYLMLTMVPEFESMFKFGGAELPWFTQVVLKLSHWVQAYSL	228
NTDB id 1113	AAA85695.1 219..1451()	ESLCLKLATIYKEKTAIRKKVKLTALTYPSVIAVAIGLVFVMMIFVLPAFKEVYANMGALPALTQVTMDMSDFVSYGW	230
NTDB id 1112	NGFG RS09215 WP 003689811.1	ESLCLKLATIYKEKTAIRKKVKLTALTYPSVIAVAIGLVFVMMIFVLPAFKEVYANMGALPALTQVTMDMSDFVSYGW	230
NTDB id 1252	GC085 RS07730 WP 011213805.1	DIMLDKVATYKEKTEIIRKKIKKKALTYPIAVMVVALLVITAGLLIYVVPQFESLFKGFADLPAMTRAVITMSEFMQAYWY	227
NTDB id 1016	ACIAD RS01680 WP 004920476.1	EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVVPVFKDLFTSFGADLPFTQLVNNMNSNMQDYWF	229
NTDB id 1059	ABD1 RS01610 WP 000279215.1	ETMLDRVATYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVVPVFKDLFASFGADLPFTQMNVNMSKWMQEYWF	229
NTDB id 1036485	ACA097 RS17670 WP 371364859.1	ETLDRVATYKEKTESLKAKIKKAMTYPVIAVVAVIVSAILLIKVVPQFQEVFANFGAELPFTLMVIHLSLILQKWWL	226
NTDB id 1198	PSJM300 03950 AFN76868.1	ETLDRVATYKEKTEALKAKIKKAMNYPVIAVVLVAVIVTALLIKVVPQFQDVFANFGAELPFTLMVIGLSEALQAWWY	226
consensus		*****!***!*?* *?*****!***!*?* *?*****!***!*?* *?*****!***!*?* *?*****!***!*?* *?	

