

NTDB id 1029	TT RS02230 WP 011228203.1	MPVYQYKARDRQGR.L	VEATIEAEDLRTAARLRDRGLFVAETKEPGKGLQAEVRIPALER	60
NTDB id 1169	A1552VC RS11075 WP 000648511.1	MKATQTLPLKKNYRWKGINSGKK	VSGQMLAISEIEVRDKLKDQHIQIKKLKKGVSLSLLA....RLTH	63
NTDB id 1402	DSB67 RS12670 WP 010643257.1	MKTIAAPQLKKNYRWKGINSSGKK	TSGNVLAMTEIEVRERLDAQHIKIKKLKKGKSISFIT....KISH	62
NTDB id 1112	NGFG RS09215 WP 003689811.1	MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVS	AFTEEEAARKKLAKRGIRPLQITRVK....T....SSKR	65
NTDB id 1113	AA85695.1 219..1451()	MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVS	AFTEEEAARKKLAKRGIRPLQITRVK....T....SSKR	65
NTDB id 1198	PSJM300 03950 AFN76868.1	MAQKAIAKNSVFTWEGLDLRQGAK	IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS....AGK	61
NTDB id 1016	ACIAD RS01680 WP 004920476.1	MAAKKTQVMPVFAYEGVDRKGIK	LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG...LLKK	64
NTDB id 1059	ABD1 RS01610 WP 000279215.1	MAVKKAQMMPTFAYEGVDRKGIVK	IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG...LFKK	64
NTDB id 348346	EYR03 RS17250 WP 024743356.1	MSVARSAIKKQPVDRNTMSLQTFVWEGADKRGVVK	MKGEGQARNANMLRAELRRQGIVPSMVKKQKPKPLLG....AAGK	74
NTDB id 1252	GC085 RS07730 WP 011213805.1	MDKNSPPLLTTHYQGGINKAGQK	MEGDIQARSLAIAKADLRKQGIVTNKKVKKRKPLFD....RKNK	62
consensus		* * * * *	! * * * * *	

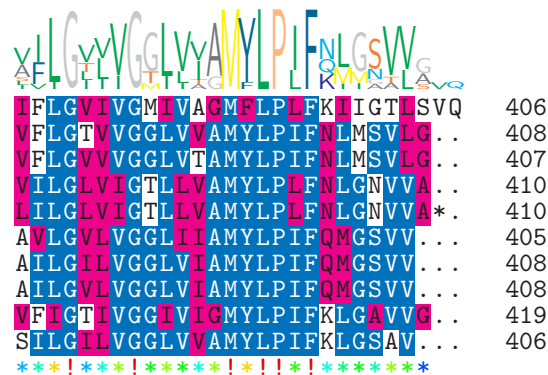
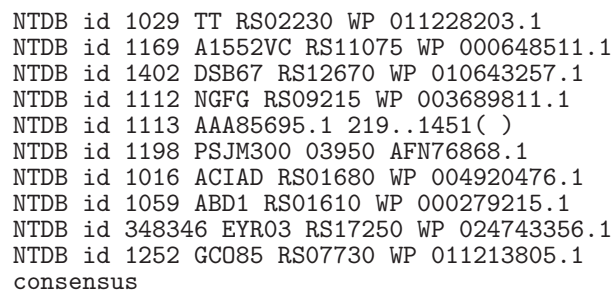
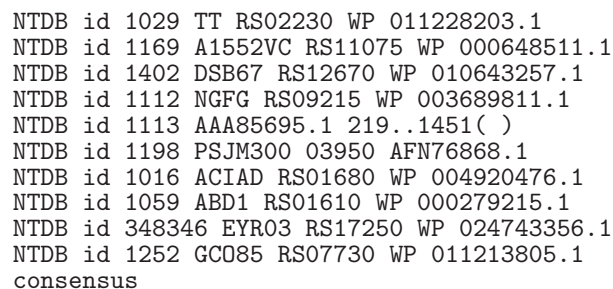
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NTDB id 1169	A1552VC RS11075 WP 000648511.1	RVKSKDITILTTRQLATMLTTGVPIVQALKLVGDNRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLVVDLVEETGE	143
NTDB id 1402	DSB67 RS12670 WP 010643257.1	RVGKGDIITFTRQIATMLMTGVPIVQALKLVSENHHKAEMKSILMSVTRAWEAGTPMSKAMRTASTHFDPPLYTDLIATAGE	142
NTDB id 1112	NGFG RS09215 WP 003689811.1	KITQEDITVFTRQLSTMIAKAGLPMLQAFAIVARGHGPNPSMTEMLMEIRGQVEEQSSLSRAFSNHPKYFDRFYCNLVAAGE	145
NTDB id 1113	AAA85695 0.219..1451()	KITQEDITVFTRQLSTMIAAGLPMLQAFAIVARGHGPNPSMTEMLMEIRGQVEEQSSLSRAFSNHPKYFDRFYCNLVAAGE	145
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NTDB id 1016	ACIAD RS01680 WP 004920476.1	KVKPLDIAIFTRQLATMMKAGVPLVQAFAIVAEGLENPAMRDVVVLGLKNEVEGGNTFAGALRKKYPQYFDNFLFCSLIESGE	144
NTDB id 1059	ABD1 RS01610 WP 000279215.1	KVTITLDITFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKEGEVEGGSTFASALRKKYPQHFDNFLFCSLVESGE	144
NTDB id 348346	EYR03 RS17250 WP 024743356.1	KITPKDIAFFSRQMATTMMKSGVPITVSSLLEITIGEGHKNNPRMKKMVGIRTDTIEGSSSLEYESTISKHPVQFDELYRNLRAGE	154
NTDB id 1252	GC085 RS07730 WP 011213805.1	KITQADITVFTRQLATMLESGIPLVQAFDIVAKGQSNKRLLKDLETIKHDIIETGLTLAESLLIKHPLYNFELFCNLVDAGE	142
consensus		***** !*****!*****!*****!*****!*****!*****!*****!*****!*****!*****!	

NTDB id	1029	TT RS02230 WP	O11228203.1	TSGGLDLILDRLASHLEKEELERLGRKIRSAMTYPIVIVFAVGVAIFLLTGIVPQFAQLITDGLSELPLLRFLIAVSDDL	219
NTDB id	1169	A1552VC RS11075 WP	000648511.1	MGNLPPEVFERRLATYREKSEQLRAKVIKALIYPMSVVVLVALGVSYLMMLTMIPEFESMFKGFGAELPWFTQQVKLSHWV	223
NTDB id	1402	DSB67 RS12670 WP	O10643257.1	QSCNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAPTQMVLNLASAT	222
NTDB id	1112	NGFG RS09215 WP	003689811.1	TGGVLESLLDKLATYKEKTQAIRKKVKLTALTPYSVIAIVAIGLVFMVMIFVLPAFKEVYANMGAELPPLTQTVMDSDF	225
NTDB id	1113	AAA85695 L	219..1451()	TGGVLESLLDKLATYKEKTQAIRKKVKLTALTPYSVIAIVAIGLVFMVMIFVLPAFKEVYANMGAELPALTTQTVMDMSDF	225
NTDB id	1198	PSJM300 O3950 AFN76868.1		QSCLSLETLDLRVATYKEKTEALKAKIKKANMPYIADVLLAVIVTAAILLIKVPVPFQDVFNAGAELPAFTLMVIGLSEAL	221
NTDB id	1016	ACIAD RS01680 WP	O04920476.1	QSCSLETIMDRVAIVYEKSEVLLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAPTQLVVNMNSNW	224
NTDB id	1059	ABD1 RS01610 WP	O00279215.1	QSGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFASFAGADLPAPTQM VVNMSKW	224
NTDB id	348346	EYR03 RS17250 WP	O24743356.1	GAGVLETVLETVATYKENIEALKGKIKKAMFPATVVAIVAIIVSAILLIFVVPQFEQVFKSFGAELPAFTQLLVNASRF	234
NTDB id	1252	GC085 RS07730 WP	O11213805.1	KGSCLDETMLDKVATYKEKIEIIKKIKKALTPTIAMMVALLTAGLLIIVVPQFESLFKGFAGADLPAMTRAIVITMSEFM	222
consensus				* ! * * * * * * ! * * ! * * * * * * * * ! * * * * * * * * ! * * * * * * * * ! * * * * * * * *	

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NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
NTDB id 348346 EYR03 RS17250 WP 024743356.1
NTDB id 1252 GC085 RS07730 WP 011213805.1
consensus

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- X non conserved
- X similar
- X > 50% conserved