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NTDB id 1029 TT RS02230 WP 011228203.1	MAK	65
NTDB id 1402 DSB67 RS12670 WP 010643257.1	MPVYQYKARDRQGRLLVEATTEAEDLRTAARLLRDRGLFVAEIKPEPGKGLQAEVRIPALERGPGGLK	67
NTDB id 1169 A1552VC RS11075 WP 000648511.1	.MKT.....IAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRRERLDAQHIKIKKLLKKGSIKFITK.....ISHRVKKGK	68
NTDB id 1113 AAA85695.1 219..1451()	MKAT.....QTLPLKNYRWKGINSGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLLKKGSIKLAR.....LTHRVKSK	70
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MAKNGGFSLFAKKEKRFFIEGRHSASDKLVNGEVSATFEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	70
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MAKNGGFSLFAKKEKRFFIEGRHSASDKLVNGEVSATFEEEARKKLAKRGIRPLQITRVK.....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 174855 AXW93 RS24845 WP 003107299.1	MAVK.....KAQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGITVRNIREKRKNILEG....LFFKKKVTTL	66
NTDB id 1198 PSJM300 03950 AFN76868.1	.MAD.....KALKTSVFFVWEGTDKKGKTK.VKGELSSQNPTLVKAQLRKQGITPVKVRKKGISLLG.....AGKKIKPM	66
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NTDB id 1169 A1552VC RS11075 WP 000648511.1	DITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNL	148
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NTDB id 1252 GC085 RS07730 WP 011213805.1	DITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL	147
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NTDB id 174855 AXW93 RS24845 WP 003107299.1	DITIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLIESGEQSGAL	146
NTDB id 1198 PSJM300 03950 AFN76868.1	DIALFTRQMSMTMMAAGVPLLQSFDIISEGFDNPNMRKLVVEIKQEVAGGNSLANSLRKKPKQYFDSLYCNLVDAGEQSGAL	146
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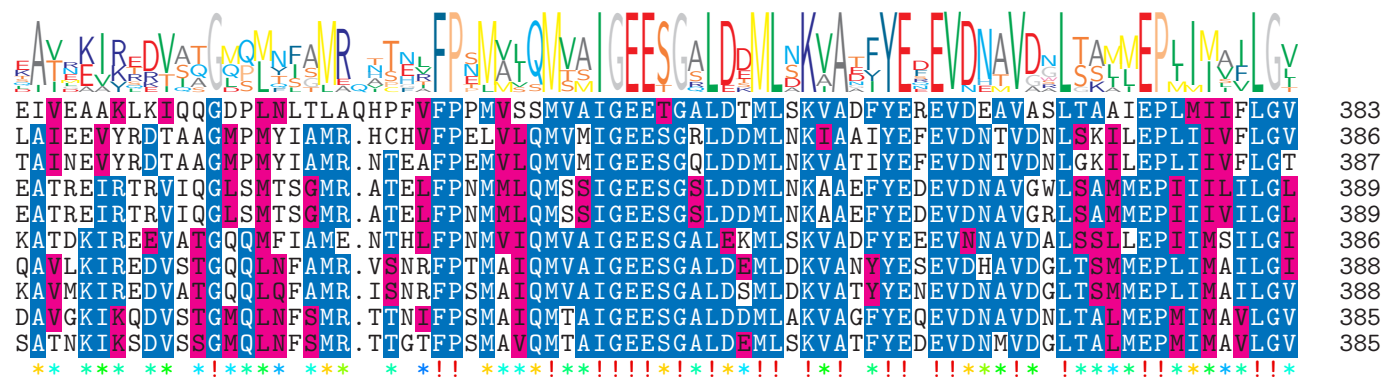
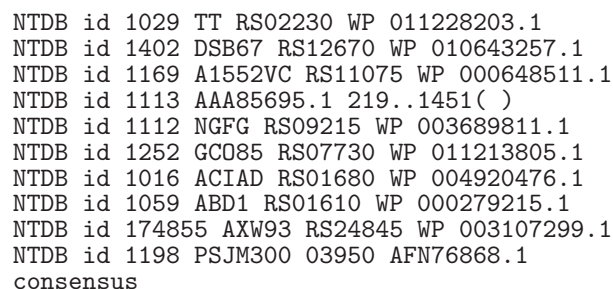
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NTDB id 1059 ABD1 RS01610 WP 000279215.1	EIMLDRVAIYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPFTQVLMVNMNSNMWQDYWF	229
NTDB id 174855 AXW93 RS24845 WP 003107299.1	ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFPQDLFASFGADLPFTQVLMVNMNSNMWQDYWF	226
NTDB id 1198 PSJM300 03950 AFN76868.1	ETLLDRVATYKEKTEALKAKIKKAMTYPIAVIVVAIIVSAILLIKVVPQFQSVFEGFGAELPAFTMMVINISNVLQEWL	226
consensus	ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVVLVAVIVTAILLIKVVPQFQDVVFANFGAELPAFTLMVIGLSEALQAWWY	226

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consensus

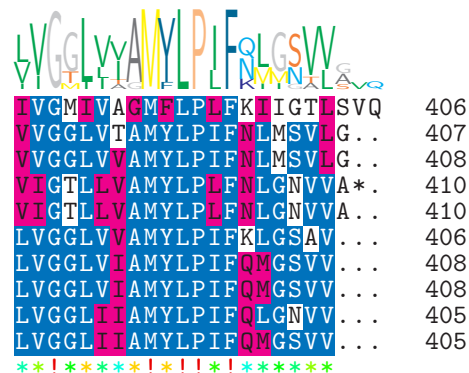
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consensus

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