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NTDB id 1029 TT RS02230 WP 011228203.1	MAK	65
NTDB id 1402 DSB67 RS12670 WP 010643257.1	MPVYQYKARDRQGRLLVEATTEAEDLRTAARLLRDRGLFVAEIKKEPGKGLQAEVRIPALERGPGGLK	67
NTDB id 1169 A1552VC RS11075 WP 000648511.1	.MKT.....IAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRRERLDAQHIKIKKKLKKGSISFITK.....ISHRVKKGK	68
NTDB id 1113 AAA85695.1 219..1451()	MKAT.....QTLPLKNYRWKGINSSGKK.VSQQLAISIEIEVRDKLKDQHIQIKKKLKKGSVSLAR.....LTHRVKSK	70
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MAKNGGFSFLFAKKEKRFIFEGRHSASDKLVNGEVSATFEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	70
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MAKNGGFSFLFAKKEKRFIFEGRHSASDKLVNGEVSATFEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	67
NTDB id 1016 ACIAD RS01680 WP 004920476.1	.MDK.....NSPPLILTFFHYQGINKAGQK.MEGDIQARS LAIAKADLRKQGIVTNKVVKRKPFLFDR.....KNKKKITQA	69
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAK.....KTQVMPVFAYEGVDRKGKIK.LKGELPARNMALAKVTLRKQGITRTIREKRKNIFEG....LLKKKVVKPL	69
NTDB id 176809 A4W92 RS10460 WP 003107299.1	MAVK.....KAQMMPTFAYEGVDRKGKIK.LKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFFKKKVTTL	66
NTDB id 1198 PSJM300 03950 AFN76868.1	.MAD.....KALKTSVFFVWEGTDKKGKTK.VKGELSSQNPTLVKAQLRKQGITPVKVRKKGISLLG.....AGKKIKPM	66
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logo

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	DITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNL	148
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NTDB id 1112 NGFG RS09215 WP 003689811.1	DITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL	150
NTDB id 1252 GC085 RS07730 WP 011213805.1	DITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL	147
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NTDB id 176809 A4W92 RS10460 WP 003107299.1	DITIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLIESGEQSGAL	146
NTDB id 1198 PSJM300 03950 AFN76868.1	DIALFTRQMSMTMMAAGVPLVQSFDIISEGFDNPNMRKLVVEIKQEVAGGNSLANSLRKKPKQYFDSLYCNLVDAGEQSGAL	146
consensus	DIALFTRQMATMMKAGVPLVQSFDIIGEGFDNPNMRKLVDDLKQEVAAAGNSFASSLRKKPKQYFDDLYCNLVDSEGEQSGSL	146

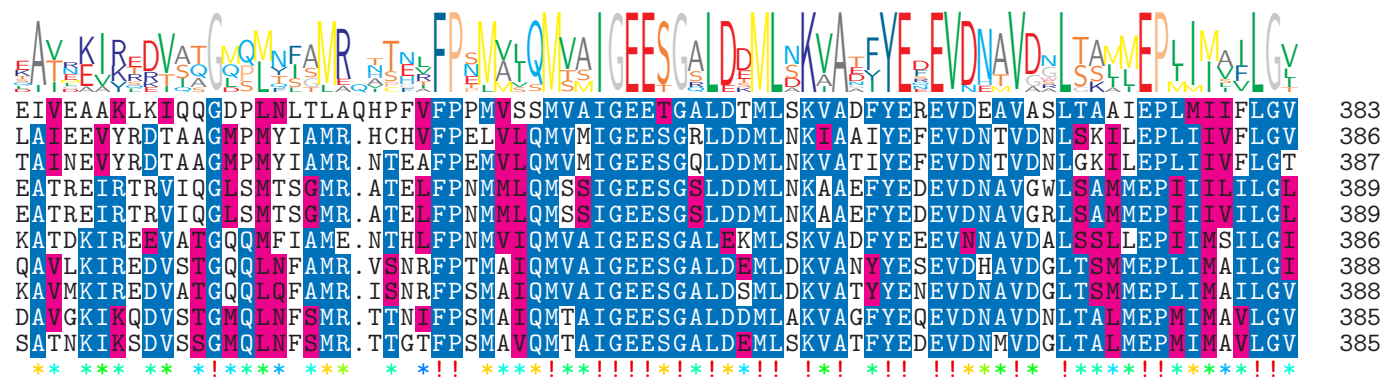
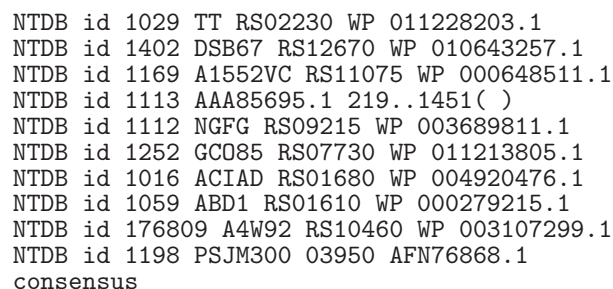
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NTDB id 1402 DSB67 RS12670 WP 010643257.1	DLILDRLASFLEKELELRGKIRSAMTYPIVVFVAVGVAYFLLTGIVPQFAQILTDLGSSELPLLTRFLIAVSDLLRAATL	227
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NTDB id 1113 AAA85695.1 219..1451()	PEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVPIPEFESMFKGFGAELPWFTQQVCLKSHVQAYSL	230
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NTDB id 1059 ABD1 RS01610 WP 000279215.1	EIMLDRVAIYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPFTQVNVNMSNWMQDYWF	229
NTDB id 176809 A4W92 RS10460 WP 003107299.1	ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFASFGADLPFTQVNVNMSKWMQYWF	226
NTDB id 1198 PSJM300 03950 AFN76868.1	ETLLDRVATYKEKTEALKAKIKKAMTYPIAVIVVAIIVSAILLIKVVPQFQSVFEGFGAELPAFTMMVINISNVLQEWL	226
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NTDB id 1059 ABD1 RS01610 WP 000279215.1
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consensus

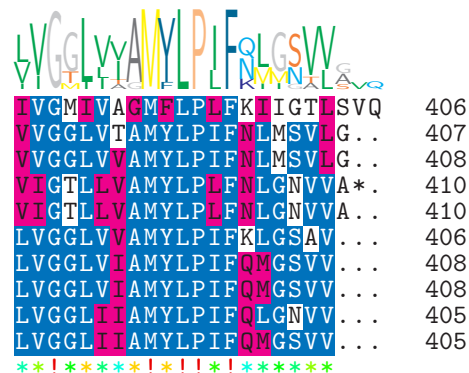
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consensus

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