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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.....IAPQLKNYRWKKGINSNGKK.TSGNVLAMTEIEVRRERLDAQHIKIKKLLKKGSIKFITK.....ISHRVKGK	68
NTDB id 1113 AAA85695.1 219..1451()	MKAT.....QTLPLKNYRWKKGINSNGKK.VSQMLAISEIEVRDKLKDQHIQIKKLLKKGSIKLAR.....LTHRVKSK	70
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MAKNGGFSLF AKKEKR FIFEGRHSASDKLVNGEVS AFTEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	70
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MAKNGGFSLF AKKEKR FIFEGRHSASDKLVNGEVS AFTEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	67
NTDB id 1016 ACIAD RS01680 WP 004920476.1	.MDK.....NSPPLILT FHYQGINKAGQK.MEGDIQARS LAIAKADLRKQGIVTNKVVKRKPFLFDR.....KNKKKITQA	69
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAK.....KTQVMPV FAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITRTIREKRKNIFEG....LLKKKVKPL	69
NTDB id 382898 FZE14 RS27165 WP 003094649.1	MAVK.....KAQMMPT FAYEGVDRKGIVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFFKKVTTTL	66
NTDB id 1198 PSJM300 03950 AFN76868.1	.MAD.....KALKTSV FVWEGTDKKGKTK.VKGELSSQNPTLVKAQLRKQGITPVKVRKKGISLLG.....AGKKIKPM	66
consensus	.MAQ.....KAIKNSV FTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSSISLFS.....AGKKIKPM	66

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NTDB id 1402 DSB67 RS12670 WP 010643257.1	DLAIFSRQLATMLGAGLTLLQALATILERQTEENRKFREILKQVRTDVEGGMAFSEALS KH.KIFSRLYVNLVRAGETSGGL	147
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 1059 ABD1 RS01610 WP 000279215.1	DIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSL	149
NTDB id 382898 FZE14 RS27165 WP 003094649.1	DITIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLIESGEQSGAL	146
NTDB id 1198 PSJM300 03950 AFN76868.1	DIALFTRQMATMMKAGVPLVQAFDIISSEGFNDPNMNRKLVVEIKQEVAGGNSLANSLRKKPKQYFDSLYCNLVDAGEQSGAL	146
consensus	DIALFTRQMATMMKAGVPLVQAFDIISSEGFNDPNMNRKLVDDLKQEVAAAGNSFASSLRKKPKQYFDDLYCNLVDAGEQSGSL	146

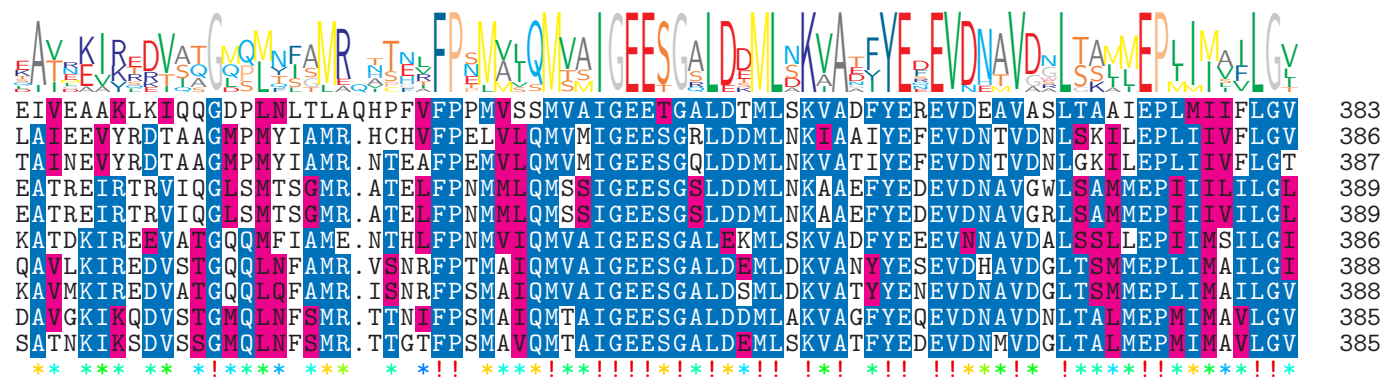
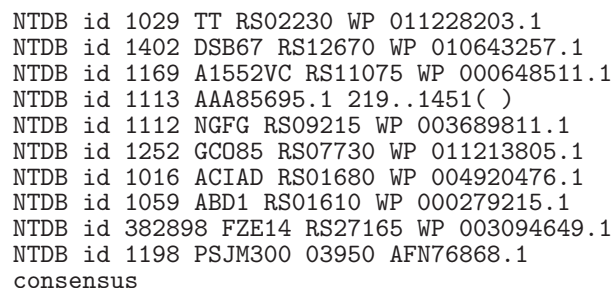
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NTDB id 1029 TT RS02230 WP 011228203.1	EILDRYAYKEKTELRKIKKAMYPVIVVAVAGVYLLLVWPFFQSVAGFAGELPAETQVIMSDMAYWL	224
NTDB id 1402 DSB67 RS12670 WP 010643257.1	DLILDRLASFLEKELELRGKIRSAMTYPIVVFVAVGVAYFLLTGIVPQFAQILTDLGSSELPLLTRFLI AVSDLLRAATL	227
NTDB id 1169 A1552VC RS11075 WP 000648511.1	SQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVPIPEFEKMF TFGADLPFTQMVNLNSAWTQNWGP	228
NTDB id 1113 AAA85695.1 219..1451()	PEVFERLATYREKSEQLRAKVIKALIYPMSVVLVALGVSYLMLTMVPIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSL	230
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NTDB id 1059 ABD1 RS01610 WP 000279215.1	EIMLDRVAIYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPFTQVLVNMNSNMWQDYWF	229
NTDB id 382898 FZE14 RS27165 WP 003094649.1	ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPV FQDLFASFGADLPFTQMVVNMNSKMWQDYWF	226
NTDB id 1198 PSJM300 03950 AFN76868.1	ETLLDRVATYKEKTEALKAKIKKAMTYPIAVIVVAIIVSAILLIKVVPQFQSVFEGFGAELPAFTMMVINISNVLQEWL	226
consensus	ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVVLVAVIVTAILLIKVVPQFQDV FANFGAELPAFTLMVIGLSEALQAWWY	226

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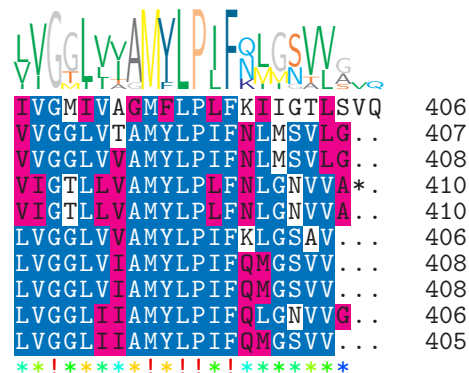
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consensus

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