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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.TSGNVLAMTEIEVRRERLDAQHIKIKKLLKKGSIKFITK.....ISHRVKGK	68
NTDB id 1113 AAA85695.1 219..1451()	MKAT.....QTLPLKNYRWKGINSGKK.VSQQLAISEIEVRDKLKDQHIQIKKLLKKGSIKLAR.....LTHR.VKSK	70
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSATETEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	70
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSATETEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	67
NTDB id 1016 ACIAD RS01680 WP 004920476.1	.MDK.....NSPPLILT FHYQGINKAGQK.MEGDIQARS LAIAKADLRKQGI VTNKVVKRKRP L FDR.....KNKKITQA	69
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAK.....KTQVMPVFA YEGVDRKG I K.LKGELPARNMALAKVTLRKQGITRTIREKRKNIFEG....LLKKKVKPL	69
NTDB id 973332 WAF13 RS28345 WP 003094649.1	MAVK.....KAQMMPTFAYEGVDRKG V K.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKKKVTTL	66
NTDB id 1198 PSJM300 03950 AFN76868.1	.MAD.....KALKTSV FVWEGTDKKG T K.VKGELSSQNPTLVKAQLRKQG ITPVKVRKKGISLLG.....AGKKIKPM	66
consensus	.MAQ.....KAIKNSVFTWGLDRQGA K .IKGELSGVSPALVKAQLRKQGINPQKVRKKSSISLFS.....AGKKIKPM	66

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NTDB id 1402 DSB67 RS12670 WP 010643257.1	DLAIFSRQLATMLGAGLTLLQALAILERQTEENRKFREILKQVRTDVEGGMAFSEALS KH .KIFSRLYVNLVRAGETSGGL	147
NTDB id 1169 A1552VC RS11075 WP 000648511.1	DITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNL	148
NTDB id 1113 AAA85695.1 219..1451()	DITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLIVETGEMSGNL	150
NTDB id 1112 NGFG RS09215 WP 003689811.1	DITVFTRQLSTMINAGLPLMQAFEIVARGHG NPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL	150
NTDB id 1252 GC085 RS07730 WP 011213805.1	DITVFTRQLSTMIKAGLPLMQAFEIVARGHG NPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL	147
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NTDB id 1059 ABD1 RS01610 WP 000279215.1	DIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSL	149
NTDB id 973332 WAF13 RS28345 WP 003094649.1	DITIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLIESGEQSGAL	146
NTDB id 1198 PSJM300 03950 AFN76868.1	DIALFTRQMS TMM AAGVPL LQSFDI ISEGFDNPNMRKLV E EIKQEVAGGNSLANSLRKKPQYFDSLYCNLVDAGEQSGAL	146
consensus	DIALFTRQMATMMKAGVPL LQSFDI IGEF DNP NMRKLVDD LKQEVAAAGNSFASSLRKKPQYFDDLYCNLVD SGEQSGSL	146

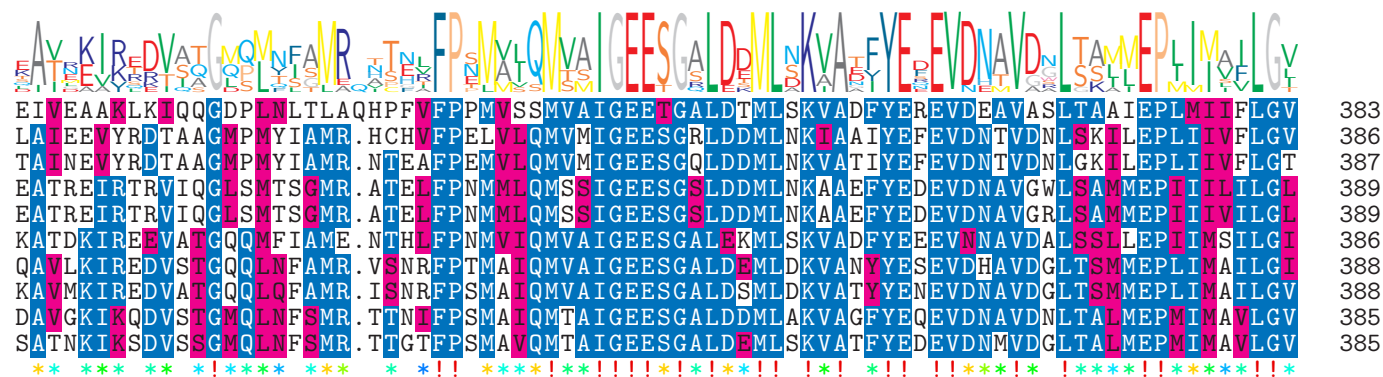
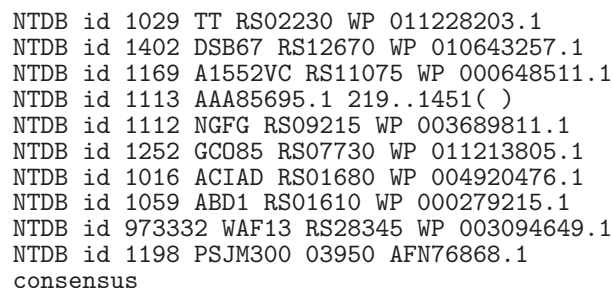
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NTDB id 1402 DSB67 RS12670 WP 010643257.1	DLILDRLASFLEKELELRGKIRSAMTYPIVVFVAVGVAYFLLTGIVPQFAQILTDLGSSELPLLTRFLI AVSDLLRAATL	227
NTDB id 1169 A1552VC RS11075 WP 000648511.1	SQVFERLATYREKSEQLRAKVIKALIYPAMVV LVALGVSYLMLTRV IPEFEKMF TGF GADLP AFTQMV LNL SAWTQNWGP	228
NTDB id 1113 AAA85695.1 219..1451()	PEVFERLATYREKSEQLRAKVIKALIYPMSVV LVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSL	230
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NTDB id 1252 GC085 RS07730 WP 011213805.1	ESLLDKLAIYKEKTQAIRKKVK TALTYPVS VIAVAIGLVFMMIFVLP AFKEVYANMGAELPALTQTVM DMSDFVSYGW	227
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DIMLDKVATYKEKIEIKKKIKKALTYP IAVMVVALLVTAGLLIYVVPQFESLFKGF GADLPAMTRAVITMSEFMQAYWY	229
NTDB id 1059 ABD1 RS01610 WP 000279215.1	EIMLDRVAIYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLP AFTQLV VNMNSNMWQDYWF	229
NTDB id 973332 WAF13 RS28345 WP 003094649.1	ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPV FQDLFASFGADLP AFTQMV VNMNSNMWQDYWF	226
NTDB id 1198 PSJM300 03950 AFN76868.1	ETLLDRVATYKEKTEALKAKIKKAMTYPIAVIVVAIIVSA ILLIKVVPQFQSVFEGFGAELPAFTMMVINISNVLQEWL	226
consensus	ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVVLVAVIVTA ILLIKVVPQFQDV FANFGAELPAFTLMVIGLSEALQAWWY	226

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consensus

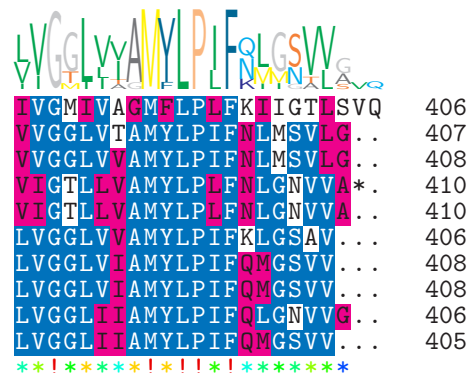
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NTDB id 973332 WAF13 RS28345 WP 003094649.1
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consensus

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