

logo

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.....QTLPLKNYRWKGINSSGKK.VSQQLAISIEIEVRDKLKDQHIQIKKLLKKGSIKLAR.....LTHRVKSK	70
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MAKNGGFSLFAKKEKRFFIEGRHSASDKLVNGEVSATETEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	70
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MAKNGGFSLFAKKEKRFFIEGRHSASDKLVNGEVSATETEEEARKKLAKRGIRPLQITRVK.....T.....SSKRKITQE	67
NTDB id 1016 ACIAD RS01680 WP 004920476.1	.MDK.....NSPPLILTFFHYQGINKAGQK.MEGDIQARS LAIAKADLRKQGI VTNKVVKRKPFLFDR.....KNKKKITQA	69
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAK.....KTQVMPVFAFEGVDRKGKIK.LKGELPARNMALAKVTLRKQGITRTIREKRKNIFEG....LLKKKVKPL	69
NTDB id 414409 GQS72 RS29310 WP 003161763.1	MAVK.....KAQMMPTFAYEGVDRKGKIK.LKGELPAKNMALAKVTLRKQGITVRNIREKRKNILEG....LFFKKVTTTL	66
NTDB id 1198 PSJM300 03950 AFN76868.1	.MAD.....KALKTSVFFVWEGTDKKGKTK.VKGELSSQNPTLVKAQLRKQGITPVKVRKKGISLLG.....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 414409 GQS72 RS29310 WP 003161763.1	DITIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLIESGEQSGAL	146
NTDB id 1198 PSJM300 03950 AFN76868.1	DIALFTRQMATMMKAGVPLVQAFDIISSEGFNDPNMNRKLVVEIKQEVAGGNSLANSLRKKPKQYFDSLYCNLVDAGEQSGAL	146
consensus	DIALFTRQMATMMKAGVPLVQAFDIISSEGFNDPNMNRKLVDDLKQEVAAAGNSFASSLRKKPKQYFDDLYCNLVDAGEQSGSL	146

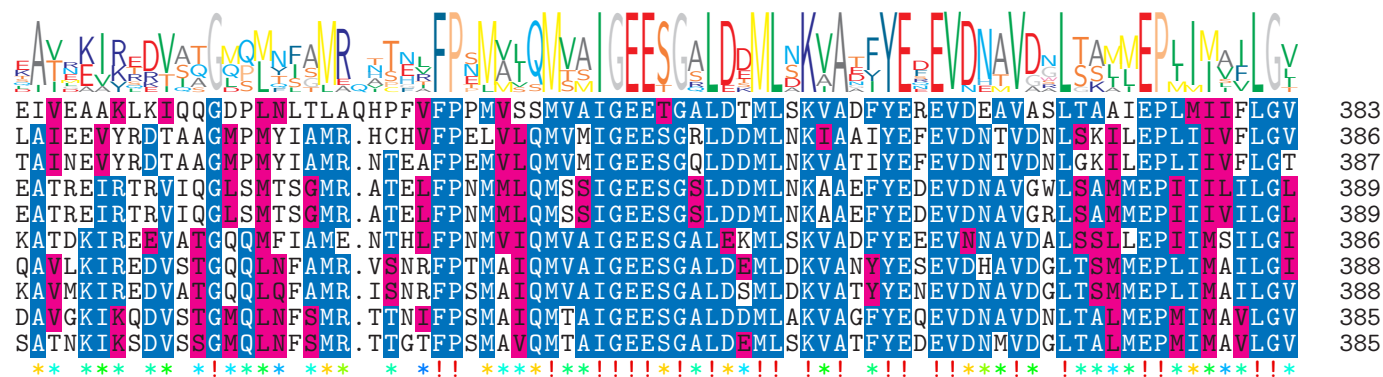
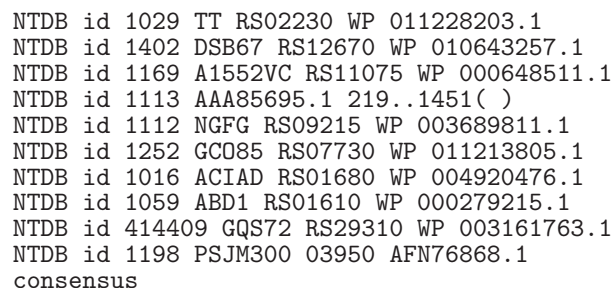
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NTDB id 1029 TT RS02230 WP 011228203.1	EILLDRYAYKYEKTELRKIKKAMTPYVIVVAVAGVYLLTGVIPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	224
NTDB id 1402 DSB67 RS12670 WP 010643257.1	DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	227
NTDB id 1169 A1552VC RS11075 WP 000648511.1	SQVFERLATYREKSEQLRAKVIKALIYPMAMVVLVALGVSYLMLTRVPIPEFEKMFMTGFGADLPFTQMVNLNSAWTQNWGP	228
NTDB id 1113 AAA85695.1 219..1451()	PEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVPIPEFESMFKGFGAELPWFTQQVCLKSHVQAYSL	230
NTDB id 1112 NGFG RS09215 WP 003689811.1	ESLLDKLAIYKEKTQAIRKKVKKTALTYPVSVIAVAIGLVFVMMIFVLPAPFKEVYANMGAELPALTQTVMDMSDFFVSYGW	230
NTDB id 1252 GC085 RS07730 WP 011213805.1	ESLLDKLAIYKEKTQAIRKKVKKTALTYPVSVIAVAIGLVFVMMIFVLPAPFKEVYANMGAELPALTQTVMDMSDFFVSYGW	227
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DIMLDKVATYKEKIEIKKKIKKALTYPYIAVMVVALLVTAGLLIYVVPQFESLFKGFAGDLPAMTRAVITMSEFMQAYWY	229
NTDB id 1059 ABD1 RS01610 WP 000279215.1	EIMLDRVAIYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPFTQVNVNMSNMWQDYWF	229
NTDB id 414409 GQS72 RS29310 WP 003161763.1	ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFASFGADLPFTQMVVNMSKMWQDYWF	226
NTDB id 1198 PSJM300 03950 AFN76868.1	ETLLDRVATYKEKTEALKAKIKKAMTYPIAVIVVAIIVSAILLIKVVPVQFQSVFEGFGAELPAFTQMVINISNVLQEWL	226
consensus	ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVVLVAVIVTAILLIKVVPVQFQDVVFANFGAELPAFTLMVIGLSEALQAWWY	226

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consensus

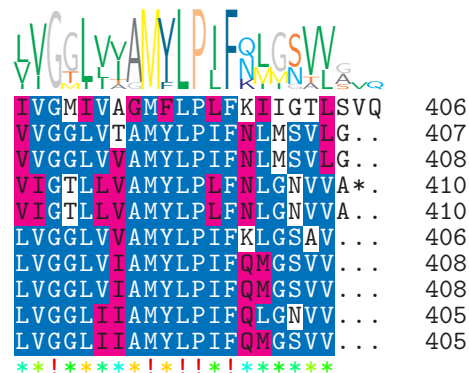
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NTDB id 414409 GQS72 RS29310 WP 003161763.1
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consensus

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