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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.VSQQLAISIEIEVRDKLKDQHIQIKKLLKKGSIKLAR.....LTHRVKSK	70
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MAKNGGFSLFAKKEKRFFIEGRHSASDKLVNGEVSFAFTEEEARKKLAKRGIPLQITRVK.....T.....SSKRKITQE	70
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MAKNGGFSLFAKKEKRFFIEGRHSASDKLVNGEVSFAFTEEEARKKLAKRGIPLQITRVK.....T.....SSKRKITQE	67
NTDB id 1016 ACIAD RS01680 WP 004920476.1	.MDK.....NSPPLILTFFHYQGINKAGQK.MEGDIQARSLAIKADLRKQGIPTNKVVKKRKPLFDR.....KNKKKITQA	69
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAK.....KTQVMPVFAFEGVDRKGKIK.LKGELPARNMALAKVTLRKQGITRTIREKRKNIFEG....LLKKKVKPL	69
NTDB id 77670 HV96 RS26510 WP 003161763.1	MAVK.....KAQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGITVRNIREKRKNILEG....LFFKKVTTTL	66
NTDB id 1198 PSJM300 03950 AFN76868.1	.MAD.....KALKTSVFFVWEGTDKKGKTK.VKGELSSQNPTLVKAQLRKQGITPVKVRKKGISLLG.....AGKKIKPM	66
consensus	.MAQ.....KAIKNSVFTWGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSSISLFS.....AGKKIKPM	66

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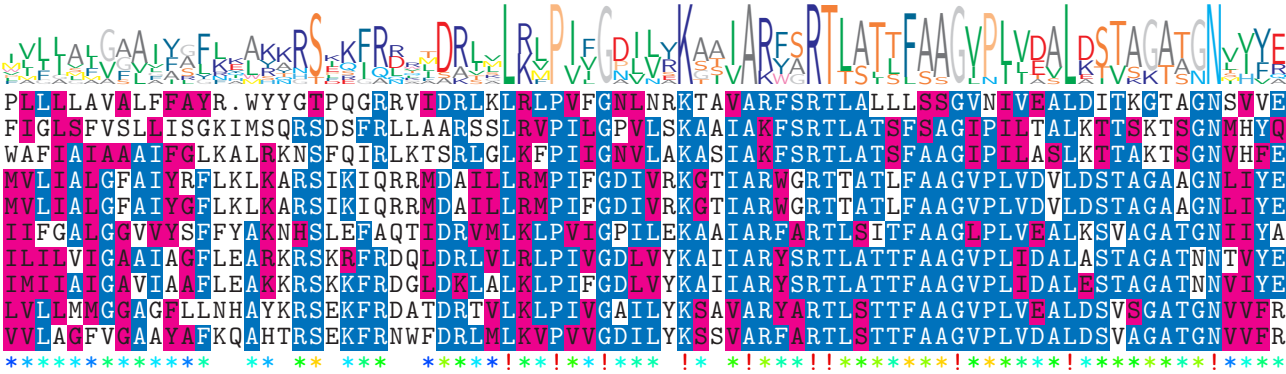
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NTDB id 1112 NGFG RS09215 WP 003689811.1	DITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL	150
NTDB id 1252 GC085 RS07730 WP 011213805.1	DITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL	147
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELCNLDVAGEKSGSL	149
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSL	149
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NTDB id 1198 PSJM300 03950 AFN76868.1	DIALFTRQMATMMKAGVPLVQAFDIIEGFDNPNMRKLVDEEIKQEVAGGNSLANSLRKKPKQYFDSLYCNLVDAGEQSGAL	146
consensus	DIALFTRQMATMMKAGVPLVQAFDIIEGFDNPNMRKLVDDLKQEVAAAGNSFASSLRKKPKQYFDDLYCNLVDAGEQSGSL	146

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NTDB id 1029 TT RS02230 WP 011228203.1	EILLDRYAYKEKTELRKIKKAMTPYVIVVAVAGVYLLTGVIPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	224
NTDB id 1402 DSB67 RS12670 WP 010643257.1	DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	227
NTDB id 1169 A1552VC RS11075 WP 000648511.1	SQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVPIPEFEKMFTEGFGADLPFTQMVNLNSAWTQNWGP	228
NTDB id 1113 AAA85695.1 219..1451()	PEVFERLATYREKSEQLRAKVIKALIYPMSVVLVALGVSYLMLTMVPIPEFESMFKGFGAELPWFTQQVVKLSHWVQAYSL	230
NTDB id 1112 NGFG RS09215 WP 003689811.1	ESLLDKLAIYKEKTQAIRKKVKKTALTYPVSVIAVAIGLVFVMMIFVLPAPFKEVYANMGAELPALTQTVMDMSDFFVSYGW	230
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NTDB id 1016 ACIAD RS01680 WP 004920476.1	DIMLDKVATYKEKIEIKKKIKKALTYPVAVMVVALLVTAGLLIYVVPQFESLFKGFAGDLPAMTRAVITMSEFMQAYWY	229
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NTDB id 77670 HV96 RS26510 WP 003161763.1	ETMLDRVAIYKEKSELLKQIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFASFGADLPFTQMVVNMSKMWQDYWF	226
NTDB id 1198 PSJM300 03950 AFN76868.1	ETLLDRVATYKEKTEALKAKIKKAMTYPIAVIVVAIIVSAILLIKVVPVQFQSVFEGFGAELPAFTQMVINISNVLQEWL	226
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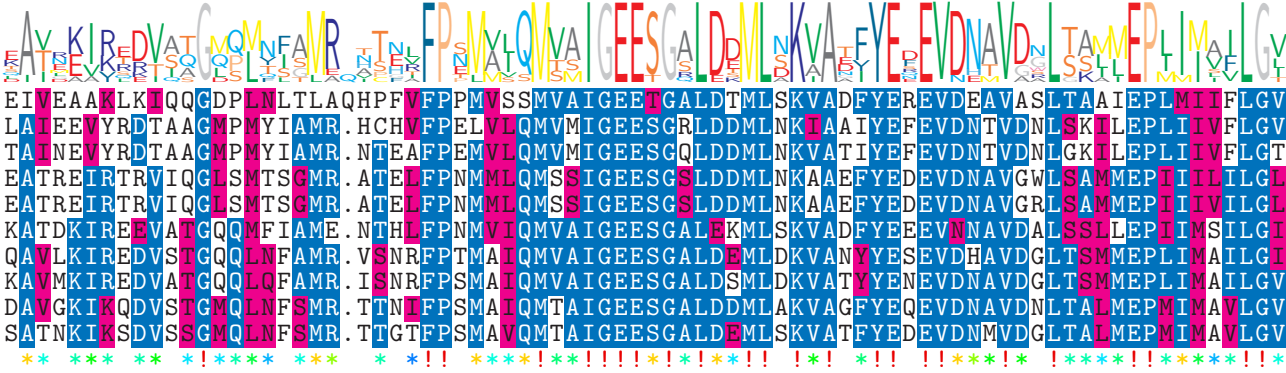
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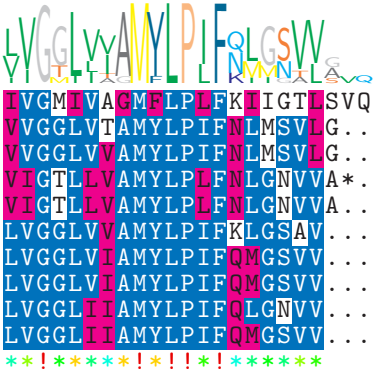


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consensus



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☒ non conserved
☒ similar
☒ ≥ 50% conserved