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NTDB id 1402 DSB67 RS12670 WP 010643257.1	.MKTII.....APQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRRERLDAQHIKIKKKLKKGSISFITK.ISHRVKVGKDITI	71
NTDB id 168017 AL549 RS18915 WP 061058909.1	MKLKT.....HSQIKNYQWKGINAGAKK.VSGNTLALTELEVDRDKLMQHIQIKKKIKKSSVSVFTR.LSHKVKVGKDITL	72
NTDB id 1169 A1552VC RS11075 WP 000648511.1	MKATQ.....TLPLKNYRWKGINSGKK.VSGQMLAISEIEVRDKLKDQHIQIKKKLKKGSVSLAR.LTHRVRKSKDITI	72
NTDB id 1113 AAA85695.1 219..1451()	.MAKNGGFSLF AKKEKRFI FEGRHSASDKLVNGEVS AFTEEEARKKLAKRGIRPLQITRV....KTSSKRKITQEDITV	74
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MAKNGGFSLF AKKEKRFI FEGRHSASDKLVNGEVS AFTEEEARKKLAKRGIRPLQITRV....KTSSKRKITQEDITV	74
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MDKN.....SPPLILTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKKKITQADITV	71
NTDB id 1198 PSJM300 03950 AFN76868.1	.MAQK.....AIKNSVFTWGLDRQGAQ.IKGELSGVSPALVKAQLRKQGINPQKVRKKKSISLFS..AGKKIKPMDIAL	70
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAVKK.....AQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKKVVTTLDITI	73
NTDB id 1016 ACIAD RS01680 WP 004920476.1	MAAKK.....TQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKVPLDIAI	73
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NTDB id 1402 DSB67 RS12670 WP 010643257.1	FTRQLATMIMTGVPIVQALKLVSENHKKAEKMSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQVF	151
NTDB id 168017 AL549 RS18915 WP 061058909.1	LTRQLATMLTTGVPILQSLKLVDNHRKAEMKSI LANVSKAVEAGTPLSKALRSASPQFDGIYVDLVATGEQSGNLDQVF	152
NTDB id 1169 A1552VC RS11075 WP 000648511.1	LTRQLATMLTTGVPILQSLKLVDNHRKAEMKSI LAQITKSVEAGTPLSKAMRTASAHFDLTLYVDLVETGEMSGNLPEVF	152
NTDB id 1113 AAA85695.1 219..1451()	FTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL	154
NTDB id 1112 NGFG RS09215 WP 003689811.1	FTRQLSTMIAKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL	154
NTDB id 1252 GC085 RS07730 WP 011213805.1	FSRQLATMIESGPIPLVQAFDIVAKGQSNKRLKDLIETIKHD IETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDIML	151
NTDB id 1198 PSJM300 03950 AFN76868.1	FTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDL LKQEVAAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETLL	150
NTDB id 1059 ABD1 RS01610 WP 000279215.1	FTRQLATMMKAGVPLVQGFIEVAEGLNPAMREVVLG IKGEVEGGSTFASALRKYPQHFDNLFCSLVSERGEQSGALETML	153
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FTRQLATMMKAGVPLVQAFEIVAEGLNPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIML	153
consensus	***!*****! *!*!*!*!*!*!*!*!*!* * * ***** * * *****!*****! *!*!* * * *	

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NTDB id 1402 DSB67 RS12670 WP 010643257.1	ERLATYREKSEQLRRAKVIKAL IYPAMVVLVALGVSYLMLTRV IPEFEKMF TGFGADLP AFTQMVLNLSA WTTQN WGPFI GL	231
NTDB id 168017 AL549 RS18915 WP 061058909.1	ERLAFYREKNEQLRAKVIKAL IYPCMVVLVALGVSYLMLTKVIPEFRKMFTGFGAELPWFTQKVLDLSDFVQAYSSWFFI	232
NTDB id 1169 A1552VC RS11075 WP 000648511.1	ERLATYREKSEQLRRAKVIKAL IYPSMVVLVALGVSYLMLTMV IPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWAFI	232
NTDB id 1113 AAA85695.1 219..1451()	DKLAIYKEKTQAIRKKVKTALTYPVSVI AIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMS DFFVS YGWMVLI	234
NTDB id 1112 NGFG RS09215 WP 003689811.1	DKLAIYKEKTQAIRKKVKTALTYPVSVI AIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMS DFFVS YGWMVLI	234
NTDB id 1252 GC085 RS07730 WP 011213805.1	DKVATYKEKIEI IKKKIKKALTYP IAVMVVALLV TAGLLIYVVPQFESLFKGFAGADLPAMTRAVITMSEFMQAYWYIIFG	231
NTDB id 1198 PSJM300 03950 AFN76868.1	DRVATYKEKTEALKAKIKKAMNYP IAVVLVAVIVTATILLIKVVPQFQDV FANFGAELPAFTLMVIGLSEALQAWWYVVL A	230
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFAGADLP AFTQMVMVNM SKWMQ EYWFIM I	233
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLP AFTQLVNM SNWMQDYWFILIL	233
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NTDB id 1402 DSB67 RS12670 WP 010643257.1	SFVSLIISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQLAIE	311
NTDB id 168017 AL549 RS18915 WP 061058909.1	TLFSAIYLLRGLSKKSPAFRLKMSRSLSLKIPVIGGVLSKAAIAKFSRTLATSFSAGIPILTSKTTSKTAGNLHYQYAI E	312
NTDB id 1169 A1552VC RS11075 WP 000648511.1	AIAAAIFGLKALRKNSFQIRLKT SRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKT TAKTSGNVHFETAI E	312
NTDB id 1113 AAA85695.1 219..1451()	ALGFAIYRFLKLRKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	314
NTDB id 1112 NGFG RS09215 WP 003689811.1	ALGFAIYGFLKLRKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	314
NTDB id 1252 GC085 RS07730 WP 011213805.1	ALGGVVSFFYAKNHSLEFAQTI DRVMLKL PVI GP ILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATD	311
NTDB id 1198 PSJM300 03950 AFN76868.1	GFVGAAYAFKQAHTRSEKFRNWFDRI MLKVPVVGDI LYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFERSATN	310
NTDB id 1059 ABD1 RS01610 WP 000279215.1	ATGAVITAAFLEAKKRSKKFRDGLDKLALKLP IFGDLVYKAI IARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAVM	313
NTDB id 1016 ACIAD RS01680 WP 004920476.1	VIGAIIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAI IARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAVL	313
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consensus

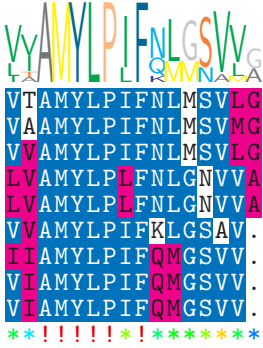


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consensus



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☒ non conserved
☒ similar
☒ ≥ 50% conserved