

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	MAKAT.....QTLPLKNYRWKGINSSGKK.VSGQMLAISEIEVRDRLKDQHIQIKKLLKKGVSILAR.LTHRVRKSKDITI	72
NTDB id 167771 AL538 RS07090 WP 005446256.1	.MKT.....IAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVVRERLDAQHIKIKKLLKKGVSIFITK.ISHRVKGKDITV	71
NTDB id 1402 DSB67 RS12670 WP 010643257.1	.MKT.....IAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVVRERLDAQHIKIKKLLKKGVSIFITK.ISHRVKGKDITV	71
NTDB id 1113 AAA85695.1 219..1451()	.MAKNGGFSLF AKKEKR FIFEGRHSASDKLVNGEVSAFTEEEARKKLA KRGI RPLQITRV....KTSSKRKITQEDITV	74
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MAKNGGFSLF AKKEKR FIFEGRHSASDKLVNGEVSAFTEEEARKKLA KRGI RPLQITRV....KTSSKRKITQEDITV	74
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MDKN.....SPPLLT FHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGI VTNKV VVKRKP L FDR.KNKKITQADITV	71
NTDB id 1198 PSJM300 03950 AFN76868.1	.MAQK.....AIKNSVFTWEG LDRQGA K.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPMDIAL	70
NTDB id 1016 ACIAD RS01680 WP 004920476.1	MAAKK.....TQVMPVFAYEGVDRKG I.KGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVPLDIAI	73
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAVKK.....AQMMPTFA YEGVDRKG V.KGELPAKNMALAKVTLRKQGITVRNIREKRKNILEGLFKKKVVTTLDITI	73
consensus	*** * ** * ** ! * * ! * ! ** * ** * ! ** * ** * ! ** * ** ! ** *	

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	LTRQLATM LTTGVPIVQALKLVGDNHRKAEMKSI LAQITKSVEAGTPLSKAMRTASAHFDTLYVDLIVETGEMSGNLP EVF	152
NTDB id 167771 AL538 RS07090 WP 005446256.1	FTRQIATMLMTGVPIVQALKLVSENHKKAE MKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQVF	151
NTDB id 1402 DSB67 RS12670 WP 010643257.1	FTRQIATMLMTGVPIVQALKLVSENHKKAE MKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQVF	151
NTDB id 1113 AAA85695.1 219..1451()	FTRQLSTM INAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL	154
NTDB id 1112 NGFG RS09215 WP 003689811.1	FTRQLSTM IKA GLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL	154
NTDB id 1252 GC085 RS07730 WP 011213805.1	FSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHD IETGLTLAESLIKHPLYFNE LFCNLVDAGEKSGSLDIML	151
NTDB id 1198 PSJM300 03950 AFN76868.1	FTRQMATMMKAGVPL LQSFDIIGEGFDNPNMRKLVD LKQEVAAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETLL	150
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIML	153
NTDB id 1059 ABD1 RS01610 WP 000279215.1	FTRQLATMMKAGVPLVQGF EIVAEGLENPAMREVLG IKGVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETML	153
consensus	*** ! ** ! ** * ! ** ! ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *	

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	ERLATYREKSEQ LRAKVIKALIYPSMVVLVALGVSYLMLTMVIP EFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWAFI	232
NTDB id 167771 AL538 RS07090 WP 005446256.1	ERLATYREKSEQ LRAKVIKALIYPSMVVLVALGVSYLMLTKVIP EF EKMF TGFGAELPAFTQMVLNLSAWTQNWGPFTIGL	231
NTDB id 1402 DSB67 RS12670 WP 010643257.1	ERLATYREKSEQ LRAKVIKALIYPSMVVLVALGVSYLMLTRVIP EF EKMF TGFGADLPAFTQMVLNLSAWTQNWGPFTIGL	231
NTDB id 1113 AAA85695.1 219..1451()	DKLAIYKEKTQAIRKKVKTALTYPVSVI A V A IGLV FVMIFVLPAFKEVYANMGAELPALTQTVM DMSDFVSYGWMVLI	234
NTDB id 1112 NGFG RS09215 WP 003689811.1	DKLAIYKEKTQAIRKKVKTALTYPVSVI A V A IGLV FVMIFVLPAFKEVYANMGAELPALTQTVM DMSDFVSYGWMVLI	234
NTDB id 1252 GC085 RS07730 WP 011213805.1	DKVATYKEKIEI IKKKIKKALTYP I A V M V V A L L V T A G L L I Y V V P Q F E S L F K G F G A D L P A M T R A V I T M S E F M Q A Y W Y I I F G	231
NTDB id 1198 PSJM300 03950 AFN76868.1	DRVATYKEKTEAL KAKIKKAMNYP I A V V L V A V I V T A I L L I K V V P Q F Q D V F A N F G A E L P A F T L M V I G L S E A L Q A W Y V V L A	230
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFTSFGADLPAFTQLV VNM SNWMQDYWFILIL	233
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DRVAIYKEKSEL LKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFASF GADLPAFTQM VVNMSKWMQ EYWFIMII	233
consensus	*** ! ** ! ** * ! ** ! ** * ! ** ! ** * ** * ** * ** * ** * ** * ** * ** * ** * ** * ** *	

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	AIAAAIFGLKALRKNSFQIRLKT SRLGLKFPITGNVLAKASTAKFSRTLATSFAAGIPILASLKT TAKTSGNVHFETA IN	312
NTDB id 167771 AL538 RS07090 WP 005446256.1	SFVSLIISGKIMSQRSDSFRLLTARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQLAIE	311
NTDB id 1402 DSB67 RS12670 WP 010643257.1	SFVSLIISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQLAIE	311
NTDB id 1113 AAA85695.1 219..1451()	ALGFAIYRFLKLRARSIKIQRMDAILRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	314
NTDB id 1112 NGFG RS09215 WP 003689811.1	ALGFAIYGF LKLRARSIKIQRMDAILRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	314
NTDB id 1252 GC085 RS07730 WP 011213805.1	ALGGVVYSFFYAKNHSLEFAQTIDRVMLKL PVI GP ILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATD	311
NTDB id 1198 PSJM300 03950 AFN76868.1	FGVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVG DILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFERSATN	310
NTDB id 1016 ACIAD RS01680 WP 004920476.1	VIGAATAGFLEARKRSKRFRDQLDRLVLR LPIVGD LVYKAI IARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAVL	313
NTDB id 1059 ABD1 RS01610 WP 000279215.1	AIGAVIAAFLEAKRSKRFRDGLDKLALKLPIFGDLVYKAI IARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAVM	313
consensus	***** ** * ! ** * ***** ! ** * ! ** * ! ** * ! ** * ! ** * ! ** * ! ** * ! ** *	

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NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

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[illegible][illegible]

- non conserved
- similar
- $\geq 50\%$ conserved