

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	MAKAT.....QTLPLKNYRMWKGINSNGKK.VSGQMLAISIEIVRDKLKDQHITQIKKLKKGVSVLAR.LTHRVKSKDITV	72
NTDB id 110664 ACGHCW RS02980 WP 005446256.1	.MKT.....IAPQLKNYRMWKGINSNGKK.TSGNVLAMTEVEVRERLDAQHIKIKKLKKGVSIFITK.ISHRVKGKDITV	71
NTDB id 1402 DSB67 RS12670 WP 010643257.1	.MKT.....IAPQLKNYRMWKGINSNGKK.TSGNVLAMTEVEVRERLDAQHIKIKKLKKGVSIFITK.ISHRVKGKDITV	71
NTDB id 1113 AAA85695.1 219..1451()	.MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSFAFTEEEARKKLAKRGIRPLQITRV....KTSSKRKITQEDITV	74
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSFAFTEEEARKKLAKRGIRPLQITRV....KTSSKRKITQEDITV	74
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MDKN.....SPPILTFHYQCINKAGQK.MBCDIQARSLATAKADLRKQGIVTNKVVKRRKP.FDR.KNKKITQADITV	71
NTDB id 1198 PSJM300 03950 AFN76868.1	.MAQK.....AIKNSVFTWEGLDRQCAK.IKGELSCVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPMDIAL	70
NTDB id 1016 ACIAD RS01680 WP 004920476.1	MAAKK.....TQVMPVFAFEGVDRKGCIK.LKGELPARNMALAKVTLRKQGITITIREKRKNIFEGLLKKKVKVPLDIAI	73
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAVKK.....AQMMPTFAFEGVDRKGCIK.LKGELPAKNMALAKVTLRKQGITITIREKRKNIFEGLLFKKKVTTLDTIT	73
consensus	*** * ** * **!* * * ! * !** * ** ** * !**** * **** * *	

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	LTRQLATMTTGVPIVQALKLVGDNHRKAEMKSLAQITKSVEACTPLSKAMRTASAHFDTLVVDLVETGEMSGNLPFV	152
NTDB id 110664 ACGHCW RS02980 WP 005446256.1	FTRQIATMTMTGVPIVQALKLVSENHKKAEMKSLMSVTRAVEACTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQVF	151
NTDB id 1402 DSB67 RS12670 WP 010643257.1	FTRQIATMTMTGVPIVQALKLVSENHKKAEMKSLMSVTRAVEACTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQVF	151
NTDB id 1113 AAA85695.1 219..1451()	FTRQLSTMINAGIPLMQAFDIVARGHGPNPSMTEMLMEIRGQVEQCSSLBRAFSNHPKYFDRFYCNLVAAGETGCVLESLL	154
NTDB id 1112 NGFG RS09215 WP 003689811.1	FTRQLSTMIKAGIPLMQAFDIVARGHGPNPSMTEMLMEIRGQVEQCSSLBRAFSNHPKYFDRFYCNLVAAGETGCVLESLL	154
NTDB id 1252 GC085 RS07730 WP 011213805.1	FSRQLATMIESGIPLVQAFDIVAKQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDIML	151
NTDB id 1198 PSJM300 03950 AFN76868.1	FTRQMATMMKAGVPLIQSFDITGEGFDNPNMKLVDDLKQEVAAACNSFASSIRKKPQYFDDLYCNLVDSGEQSGSLETIL	150
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FTRQLATMMKAGVPLVQAFDIVAEGLENPAMRDVVLGLKNEVEGNTFAGALRKYPPQYFDNLFCSLIESGEQSGSLEIML	153
NTDB id 1059 ABD1 RS01610 WP 000279215.1	FTRQLATMMKAGVPLVQCFEIVAEGLENPAMREVLIGIKGEVCGSIFASALRKYPPHFDNLFCSLVESGEQSGALETML	153
consensus	***!!**!!* *!*!*!!***** ** * **** * ** * ****!***** ** *!* * ** *!***!!* * *	

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	ERLATYREKSEQLRRAKVIKALITPSMVVLVALGVSYLMITMVIPEFESMFKGFGAELPWFTQVVLKLSHWVQAYSLWAFI	232
NTDB id 110664 ACGHCW RS02980 WP 005446256.1	ERLATYREKSEQLRRAKVIKALITPAMVVLVALGVSYLMITMVIPEFEKMFTEGFGAELPAFTQVVLNLSAWTQNWGPFTGL	231
NTDB id 1402 DSB67 RS12670 WP 010643257.1	ERLATYREKSEQLRRAKVIKALITPAMVVLVALGVSYLMITMVIPEFEKMFTEGFGADLPAFTQVVLNLSAWTQNWGPFTGL	231
NTDB id 1113 AAA85695.1 219..1451()	DKLATYKEKTAIRKKVKTALTYPVSVIATAICLVFVMMIFVLPAPKEVYANMGAELPPLTQCTVMDMSDFVSYGWMVLI	234
NTDB id 1112 NGFG RS09215 WP 003689811.1	DKLATYKEKTAIRKKVKTALTYPVSVIATAICLVFVMMIFVLPAPKEVYANMGAELPPLTQCTVMDMSDFVSYGWMVLI	234
NTDB id 1252 GC085 RS07730 WP 011213805.1	DKVATYKEKTEIKKKTKKALTYPPIAVMVVALLVTAGLLIYVVPQFESLFKGFADLPAMTRAVITMSEFMQAYWYIIFG	231
NTDB id 1198 PSJM300 03950 AFN76868.1	DRVATYKEKTEALKAKIKKANYPPIAVVIVAVIVTATLLIKVVPQFQDVFAFAGAELPAFTLMVIGLSEALQAWYVVVLA	230
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFAGADLPAFTQVVLNMSNWMQDYWFILIL	233
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DRVATYKEKSELKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFASFAGADLPAFTQVVLNMSKWMQDYWFIMII	233
consensus	***!!**!!** * * !***!* !! !***!!***** ** *!* * ** *!*** * ****	

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	ALGAAIYSFLAKKRSLKFRDRRLRYPIGLDKAARLARSRTLATIFAAGYPLVDALKSTAGATGNLYEAT	312
NTDB id 110664 ACGHCW RS02980 WP 005446256.1	SFVSLIISGKIMSQRSDSFRLLTARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKITTSKTSGNMHYQLATE	311
NTDB id 1402 DSB67 RS12670 WP 010643257.1	SFVSLIISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKITTSKTSGNMHYQLATE	311
NTDB id 1113 AAA85695.1 219..1451()	ALGFAIYRFLKLRKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAAGNLIYEEATR	314
NTDB id 1112 NGFG RS09215 WP 003689811.1	ALGFAIYRFLKLRKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAAGNLIYEEATR	314
NTDB id 1252 GC085 RS07730 WP 011213805.1	ALGGVVSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGPLVEALKSVAGATGNIIYAKATD	311
NTDB id 1198 PSJM300 03950 AFN76868.1	GFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDIYKSSVARFARTLSITFAAGVPLVDALDSVAGATGNVVERSATN	310
NTDB id 1016 ACIAD RS01680 WP 004920476.1	VIGAAIACFLEAKRKRFRDQLDRLVLRPIVGDIVYKAIARIYSRTLATIFAAGVPLIDALASTAGATNNTVYEQAVL	313
NTDB id 1059 ABD1 RS01610 WP 000279215.1	ALGAVIAAFLEAKRKRFRDGLDKLALKLPVIGDIVYKAIARIYSRTLATIFAAGVPLIDALESTAGATNNVIYEKAVM	313
consensus	***** ** *!* ** * ****!***!!**!!** *!* * ****!***!!**!!** *!* ****!*	

logo

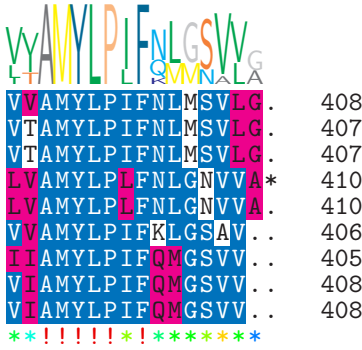
NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 110664 ACGHCW RS02980 WP 005446256.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1113 AAA85695.1 219..1451()
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus



<0

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 110664 ACGHCW RS02980 WP 005446256.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1113 AAA85695.1 219..1451()
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus



 non conserved
 similar
 ≥ 50% conserved