

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	MAKSAARSVWNGMAKAKKMKYFWEKDSAGKMKGEYSALTEALARKRKQGLPKVRKSKSLFETSSKKKYTK	68
NTDB id 1402 DSB67 RS12670 WP 010643257.1	MKATQTLPLKNYRWKGINNSGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLLKKSVSLLAR.LTHRVRKSK	67
NTDB id 1112 NGFG RS09215 WP 003689811.1	MKTIIAPQLKNYRWKGINNSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLLKKSISFITK.ISHRVRKSK	70
NTDB id 1113 AAA85695.1 219..1451()	MAK.....NGGFSLFAKKEKRFIFEGRHSASDKLVNCEVSATFEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQE	70
NTDB id 210994 BI314 RS07535 WP 040107659.1	MAK.....NGGFSLFAKKEKRFIFEGRHSASDKLVNCEVSATFEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQE	78
NTDB id 1252 GC085 RS07730 WP 011213805.1	MSAARSVVVKTAKTAAAEQMSPFVWEGTDRKGVK.MKGEQTARNANLLRAELRRQGITPLVVVKPKPLFGA.AGKKVSAK	67
NTDB id 1198 PSJM300 03950 AFN76868.1	MDKNSPPLLTFFHYQGINKAGQK.MEGDIQARSLAIKADLRKQGIIVTNKVVKRKPFLFDR.KNKKITQA	66
NTDB id 1016 ACIAD RS01680 WP 004920476.1	MAQKAIKNSVFTWGLDRQGAQ.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPM	69
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAKKTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKVKPL	69
consensus	MAVKKAKMMPFTAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIIEKRKNILEGLFKKKVTTL	69

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGEESGVL	148
NTDB id 1402 DSB67 RS12670 WP 010643257.1	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGEESGVL	147
NTDB id 1112 NGFG RS09215 WP 003689811.1	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGEESGVL	150
NTDB id 1113 AAA85695.1 219..1451()	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGEESGVL	150
NTDB id 210994 BI314 RS07535 WP 040107659.1	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGEESGVL	158
NTDB id 1252 GC085 RS07730 WP 011213805.1	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGEESGVL	147
NTDB id 1198 PSJM300 03950 AFN76868.1	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGEESGVL	146
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGEESGVL	149
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGEESGVL	149
consensus	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGEESGVL	149

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	PEVFERLATYREKSEQLRKAVIKALIYPSMVVLVALGVSYLMLTMVPIPEFESMFKGFGAELPWFTQVQLKLSHWVQAVSL	228
NTDB id 1402 DSB67 RS12670 WP 010643257.1	SQVFERLATYREKSEQLRKAVIKALIYPSMVVLVALGVSYLMLTRVPIPEFEKMFMTGFGADLPAFTQMVLNLSAWTQNWGP	227
NTDB id 1112 NGFG RS09215 WP 003689811.1	ESLDDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFMMIFVLPAFKEVYANMGAELPLTQTVMMDSDFFVSYGW	230
NTDB id 1113 AAA85695.1 219..1451()	ESLDDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFMMIFVLPAFKEVYANMGAELPALQTVMMDSDFFVSYGW	230
NTDB id 210994 BI314 RS07535 WP 040107659.1	ETVLDITVATYKENLEALKGKIKKALFYPMVMVAVAMLVSAILLVWVVPQFEDVFKGFGAELPAFTQMIVNLSRFMVSWWW	238
NTDB id 1252 GC085 RS07730 WP 011213805.1	DIMLDKVATYKEKIEIKKKIKKALTYPVSVIAVAIGLVFMMIFVLPAFKEVYANMGAELPALQTVMMDSDFFVSYGW	227
NTDB id 1198 PSJM300 03950 AFN76868.1	ETLLDRVATYKEKTEALKAKIKKAMNYPVAVVLAIVVTAILLIKVVPQFQDVAFNFGAELPAFTLMVIGLSEALQAWWY	226
NTDB id 1016 ACIAD RS01680 WP 004920476.1	EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFAGADLPAFTQLVNVNMSNMWDYWF	229
NTDB id 1059 ABD1 RS01610 WP 000279215.1	ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFAGADLPAFTQMNVNMSKWMQEWYF	229
consensus	PEVFERLATYREKSEQLRKAVIKALIYPSMVVLVALGVSYLMLTMVPIPEFESMFKGFGAELPWFTQVQLKLSHWVQAVSL	229

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	WAFITIAAAIFGLKALRKNSFQIRLKTSLRLGKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTAKTSGNVHFE	308
NTDB id 1402 DSB67 RS12670 WP 010643257.1	FIGLSFVSLIISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFAAGIPILATLKTAKTSGNMHYQ	307
NTDB id 1112 NGFG RS09215 WP 003689811.1	MVLIALGFAIYGFLLKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRRTATLFAAGVPLVDVLDSTAGAAGNLIYE	310
NTDB id 1113 AAA85695.1 219..1451()	MVLIALGFAIYGFLLKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRRTATLFAAGVPLVDVLDSTAGAAGNLIYE	310
NTDB id 210994 BI314 RS07535 WP 040107659.1	LMLFALVGAAGISVFAKRSIPAMQHGMDRLVLKVPITIGQIMHNSSIAARFARTTAVTFKAGVPLVLEALGIVAGATGNSVYE	318
NTDB id 1252 GC085 RS07730 WP 011213805.1	IIFGALGGVVSFFYAKNHSLEFAQTIIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNTIYA	307
NTDB id 1198 PSJM300 03950 AFN76868.1	VVLGAFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDIYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVF	306
NTDB id 1016 ACIAD RS01680 WP 004920476.1	ILILVIGAAIAGFLEARKRSKRFRDQLDLRLVLRPIVGDVLYKAIARIYSRTLATTFAAGVPLIDALASTAGATNNTVYE	309
NTDB id 1059 ABD1 RS01610 WP 000279215.1	IMIIAIGAVIAAFLEAKRSKRFRDGLDKLALKLPVIGDLYKAIARIYSRTLATTFAAGVPLIDALESTAGATNNVIYE	309
consensus	WAFITIAAAIFGLKALRKNSFQIRLKTSLRLGKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTAKTSGNVHFE	309

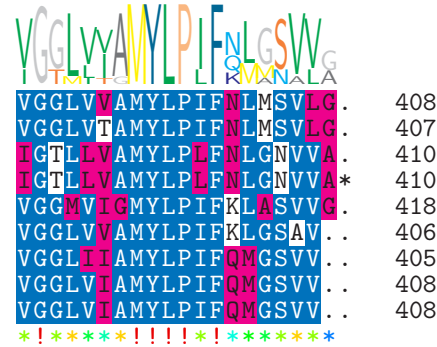
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NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

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logo



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