

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	MAKSAARSVWNGMAKAKKMKYFWEKDSAGKMKGEYSALTEALARKRKQGLPKKRRKSKSLFETSSKKKYTK	68
NTDB id 1402 DSB67 RS12670 WP 010643257.1	MKATQTLPKKNYRWKGINNSGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLLKKSVSLLAR.LTHRVRKSK	67
NTDB id 1112 NGFG RS09215 WP 003689811.1	MKTIIAPQLKNYRWKGINNSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLLKKSISFITK.ISHRVRKSK	70
NTDB id 1113 AAA85695.1 219..1451()	MAK.....NGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQE	70
NTDB id 125978 AMD19 RS16860 WP 040107659.1	MAK.....NGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQE	78
NTDB id 1252 GC085 RS07730 WP 011213805.1	MSAARSVVKTAKTAASAEQMSPFVWEGTDRKGVK.MKGEQTARNANLLRAELRRQGITPLVVVKPKPLFGA.AGKKVSAK	67
NTDB id 1198 PSJM300 03950 AFN76868.1	MDKNSPPLLTFFHYQGINKAGQK.MEGDIQARSLAIADLRKQGIIVTNKVVKRKPFLFDR.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	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGESGVL	148
NTDB id 1402 DSB67 RS12670 WP 010643257.1	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGESGVL	147
NTDB id 1112 NGFG RS09215 WP 003689811.1	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGESGVL	150
NTDB id 1113 AAA85695.1 219..1451()	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGESGVL	150
NTDB id 125978 AMD19 RS16860 WP 040107659.1	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGESGVL	158
NTDB id 1252 GC085 RS07730 WP 011213805.1	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGESGVL	147
NTDB id 1198 PSJM300 03950 AFN76868.1	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGESGVL	146
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGESGVL	149
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGESGVL	149
consensus	DITITFTRQLATMIMKAGVPLVQAFEIVAGHNPIMRYMIMKVEGSSLSALRKHPYFDLYCNLVAGESGVL	

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	PEVFERLATYREKSEQLRRAKVIKALIYPSMVVLVALGVSYLMLTMVPIEFESMFKGFGAELPWFTQVQLKLSHWVQAVSL	228
NTDB id 1402 DSB67 RS12670 WP 010643257.1	SQVFERLATYREKSEQLRRAKVIKALIYPSMVVLVALGVSYLMLTRVPIEFEKMFTEGFGADLPFTQVQLKLSHWVQAVSL	227
NTDB id 1112 NGFG RS09215 WP 003689811.1	ESLDDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAGLVFMMIFVLPAFKEVYANMGAELPPLTQTVMDSDFVSYGW	230
NTDB id 1113 AAA85695.1 219..1451()	ESLDDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAGLVFMMIFVLPAFKEVYANMGAELPPLTQTVMDSDFVSYGW	230
NTDB id 125978 AMD19 RS16860 WP 040107659.1	ETVLDITVATYKENLEALKGKIKKALFYPMVMAMVAMLVSAILLVWVVPQFEDVFKGFGAELPAFTQMVNLSRFMVSWWW	238
NTDB id 1252 GC085 RS07730 WP 011213805.1	DIMLDKVATYKEKIEIKKKIKKALTYPVSVIAVAGLVFMMIFVLPAFKEVYANMGAELPPLTQTVMDSDFVSYGW	227
NTDB id 1198 PSJM300 03950 AFN76868.1	ETLLDRVATYKEKTEALKAKIKKAMNYPVIAVVLVAVIVTALLIKVVPQFQDVAFNFGAELPAFTLMVIGLSEALQAWWY	226
NTDB id 1016 ACIAD RS01680 WP 004920476.1	EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPFTQLVVMNSNMWDYWF	229
NTDB id 1059 ABD1 RS01610 WP 000279215.1	ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPFTQMVVMNSNMWDYWF	229
consensus	PEVFERLATYREKSEQLRRAKVIKALIYPSMVVLVALGVSYLMLTMVPIEFESMFKGFGAELPWFTQVQLKLSHWVQAVSL	

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	WAFITIAAAIFGLKALRKNSFQIRLKTSLRLKFPITGNVLAKASIAKFSRTLATSFAAGIPILASLKTAKTSGNVHFE	308
NTDB id 1402 DSB67 RS12670 WP 010643257.1	FTGLSFVSLIISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFAAGIPILASLKTAKTSGNVHFE	307
NTDB id 1112 NGFG RS09215 WP 003689811.1	MVLIALGFAIYGFLLKARSIKIQRMDAILLRMPFIFGDIVRKGTIARWGRRTATLFAAGVPLVDVLDSTAGAAGNLIYE	310
NTDB id 1113 AAA85695.1 219..1451()	MVLIALGFAIYGFLLKARSIKIQRMDAILLRMPFIFGDIVRKGTIARWGRRTATLFAAGVPLVDVLDSTAGAAGNLIYE	310
NTDB id 125978 AMD19 RS16860 WP 040107659.1	LMLFALVGAAGISVFAKRSIPAMQHGMDRLVLKVPITIGQIMHNSSIAARFARTTAVTFKAGVPLVLEALGIVAGATGNSVYE	318
NTDB id 1252 GC085 RS07730 WP 011213805.1	IIFGALGGVVSFFYAKNHSLEFAQTIIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNTIYA	307
NTDB id 1198 PSJM300 03950 AFN76868.1	VVLGAFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDIYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVER	306
NTDB id 1016 ACIAD RS01680 WP 004920476.1	ILILVIGAAIAGFLEARKRSKRFRDQLDLRLVLRPIVGDVLYKAIARIYSRTLATTFAAGVPLIDALASTAGATNNTVYE	309
NTDB id 1059 ABD1 RS01610 WP 000279215.1	IMIIAIGAVIAAFLEAKRSKRFRDGLDKLALKLPFIFGDVLYKAIARIYSRTLATTFAAGVPLIDALESTAGATNNTVYE	309
consensus	WAFITIAAAIFGLKALRKNSFQIRLKTSLRLKFPITGNVLAKASIAKFSRTLATSFAAGIPILASLKTAKTSGNVHFE	

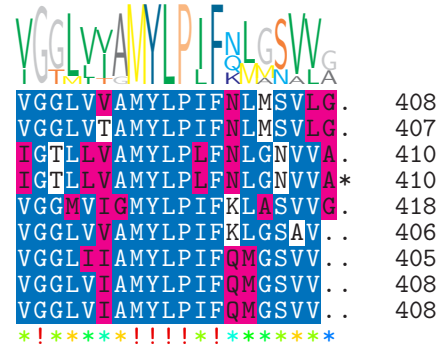
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NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

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logo



	non conserved
	similar
	$\geq 50\%$ conserved