

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	MAKSAARSVWNGMAKAKKMKYFWEKDSAGKMKGEYSALTEALARKRKQGLPKVRKSKSLFETSSKKKYTK	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.....NGGFSLFAKKEKRFIFEGRHSASDKLVNCEVSATFEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQE	70
NTDB id 148850 AB890 RS16435 WP 040107659.1	MAK.....NGGFSLFAKKEKRFIFEGRHSASDKLVNCEVSATFEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQE	78
NTDB id 1252 GC085 RS07730 WP 011213805.1	MSAARSVVVTKTAASAEQMSPFVWEGTDRKGVK.MKGEQTARNANLLRAELRRQGITPLVVKVKPKPLFGA.AGKKVSAK	67
NTDB id 1198 PSJM300 03950 AFN76868.1	MDKNSPPLLTFFHYQGINKAGQK.MEGDIQARSLAIADLRKQGIIVTNKVVKKKRPLFDR.KNKKITQA	66
NTDB id 1016 ACIAD RS01680 WP 004920476.1	MAQKAIKNSVFTWEGLDKRGQAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPM	69
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAKKTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKVKPL	69
consensus	MAVKKAQMMPTFAYEGVDRKGVK.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 148850 AB890 RS16435 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	PEVFERLATYREKSEQLRRAKVIKALIYPSMVVLVALGVSYLMLTMVPIPEFESMFKGFGAELPWFTQVQLKLSHWVQAVSL	228
NTDB id 1402 DSB67 RS12670 WP 010643257.1	SQVFERLATYREKSEQLRRAKVIKALIYPSMVVLVALGVSYLMLTRVPIPEFEKMFMTGFGADLPAFTQMVLNLSAWTQNWGP	227
NTDB id 1112 NGFG RS09215 WP 003689811.1	ESLDDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAGLVFMMIFVLPAFKEVYANMGAELPPLTQTVMMDSDFFVSYGW	230
NTDB id 1113 AAA85695.1 219..1451()	ESLDDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAGLVFMMIFVLPAFKEVYANMGAELPALTQTVMMDSDFFVSYGW	230
NTDB id 148850 AB890 RS16435 WP 040107659.1	ETVLDITVATYKENLEALKGKIKKALFYPMVMAMVAMLVSAILLVWVVPQFEDVFKGFGAELPAFTQMIVNLSRFMVSWWW	238
NTDB id 1252 GC085 RS07730 WP 011213805.1	DIMLDKVATYKEKIEIKKKIKKALTYPVSVIAVAGLVFMMIFVLPAFKEVYANMGAELPALTQTVMMDSDFFVSYGW	227
NTDB id 1198 PSJM300 03950 AFN76868.1	ETLLDRVATYKEKTEALKAKIKKAMNYPVIAVVLVAVIVTALLIKVVPQFQDVAFNFGAELPAFTLMVIGLSEALQAWWY	226
NTDB id 1016 ACIAD RS01680 WP 004920476.1	EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFAGADLPAFTQLVNVNMSNMWDYWF	229
NTDB id 1059 ABD1 RS01610 WP 000279215.1	ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFAGADLPAFTQMNVNMSKWMQEWYF	229
consensus	PEVFERLATYREKSEQLRRAKVIKALIYPSMVVLVALGVSYLMLTMVPIPEFESMFKGFGAELPWFTQVQLKLSHWVQAVSL	

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	WAFITIAAAIFGLKALRKNSFQIRLKTSLRLKFPITGNVLAKASIAKFSRTLATSFAAGIPILASLKTAKTSGNVHFE	308
NTDB id 1402 DSB67 RS12670 WP 010643257.1	FTGLSFVSLIISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFAAGIPILTALKTTSTSGNMHYQ	307
NTDB id 1112 NGFG RS09215 WP 003689811.1	MVLIALGFAIYGFLLKARSIKIQRMDAILLRMPFIFGDIVRKGTIARWGRRTATLFAAGVPLVDVLDSTAGAAGNLIYE	310
NTDB id 1113 AAA85695.1 219..1451()	MVLIALGFAIYGFLLKARSIKIQRMDAILLRMPFIFGDIVRKGTIARWGRRTATLFAAGVPLVDVLDSTAGAAGNLIYE	310
NTDB id 148850 AB890 RS16435 WP 040107659.1	LMLFALVGAAGISFYAYKRSPAMQHGMDRLVLKVPITIGQIMHNSSIAFARTTAVTFKAGVPLVLEALGIVAGATGNSVYE	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	IMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPFIFGDLVYKAIARIYSRTLATTFAAGVPLIDALESTAGATNNVIYE	309
consensus	WAFITIAAAIFGLKALRKNSFQIRLKTSLRLKFPITGNVLAKASIAKFSRTLATSFAAGIPILASLKTAKTSGNVHFE	

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NTDB id 148850 AB890 RS16435 WP 040107659.1
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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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Sequence	Position
T A I N E V Y R D T A A G M P M Y I A M R N T E A F P E M V L Q M V M I G E E S Q L D D M L N K V A T I Y E F E V D N T V D N L G K I L E P L I I V F L G T V	388
L A I E E V Y R D T A A G M P M Y I A M R H C H V F P E L V L Q M V M I G E E S G R L D D M L N K T A A I Y E F E V D N T V D N L S K I L E P L I I V F L G V V	387
E A T R E I R T R V I Q L S M T S G M R A T E L F P N M M L Q M S S I G E E S C S L D D M L N K A A E F Y E D E V D N A V G R L S A M M E P I I V I L G L V	390
E A T R E I R T R V I Q L S M T S G M R A T E L F P N M M L Q M S S I G E E S C S L D D M L N K A A E F Y E D E V D N A V G W L S A M M E P I I I L I L G L V	390
K A V L R M R E D V S V G Y P V N V A M K Q V N L F P H M V V Q M T A I G E E A G A L D A M L F K V A E Y F E Q E V N N A V D A L S S L I E P L I M V F I G T I	398
K A T D K I R E E V A T G Q Q M F I A M E N T H L F P N M V I Q M V A I G E E S G A L E K M L S K V A D F Y E E E V N N A V D A L S S L I E P I I M S I L G I L	387
S A T N K I K S D V S S G M Q L N F S M R T T G T F P S M A V Q M T A I G E E S G A L D E M L S K V A T F Y E D E V D N M V D G L T A L M E P M I M A V L G V L	386
Q A V L K I R E D V S T G Q Q L N F A M R T V S N R F P T M A I Q M V A I G E E S G A L D E M L D K V A N Y Y E S E V D H A V D G L T S M M E P L I M A I L G I L	389
K A V M K I R E D V A T G Q Q L Q F A M R I S N R F P S M A I Q M V A I G E E S G A L D M L D K V A T Y Y E N E V D N A V D G L T S M M E P L I M A I L G V L	389

[illegible]

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