

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	MAKSAARSVWNGMAKAKKMKYFWEKDSAGKMKGEYSALTEALARKRKQGLPKVRKSKSLFETSSKKKYTK	68
NTDB id 1402 DSB67 RS12670 WP 010643257.1	MKATQTLPKKNYRWKGINNSGKK.VSGQMLAISEIEVRDKLKDQHIQIKKKLKGVSVLLAR.LTHRVRKSK	67
NTDB id 1112 NGFG RS09215 WP 003689811.1	MKTIIAPQLKNYRWKGINNSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKKLKGVSISFITK.ISHRVRKSK	70
NTDB id 1113 AAA85695.1 219..1451()	MAK.....NGGFSLFAKKEKRFIFEGRHSASDKLVNCEVSATFEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQE	70
NTDB id 126232 AMD06 RS05690 WP 040107659.1	MAK.....NGGFSLFAKKEKRFIFEGRHSASDKLVNCEVSATFEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQE	78
NTDB id 1252 GC085 RS07730 WP 011213805.1	MSAARSVVKTAKTAASAEQMSPFVWEGTDKRGVK.MKGEQTARNANLLRAELRRQGITPLVVVKPKPLFGA.AGKKVSAK	67
NTDB id 1198 PSJM300 03950 AFN76868.1	MDKNSPPLLTFFHYQGINKAGQK.MEGDIQARSLAIADLRKQGIIVTNKVVKKKRPLFDR.KNKKITQA	66
NTDB id 1016 ACIAD RS01680 WP 004920476.1	MAQKAIKNSVFTWGLDRQGAQ.IKGELSGVSPALVKAQLRKQGINPQKVRKKSSISLFS..AGKKIKPM	69
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAKKTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKVKPL	69
consensus	MAVKKAKQMPPTFAYEGVDRKGIVK.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 126232 AMD06 RS05690 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	PEVFERLATYREKSEQLRKAVIKALIYPSMVVLVALGVSYLMLTMVPIPEFESMFKGFGAELPWFTQVVLKLSHWVQAVSL	228
NTDB id 1402 DSB67 RS12670 WP 010643257.1	SQVFERLATYREKSEQLRKAVIKALIYPSMVVLVALGVSYLMLTRVPIPEFEKMFMTGFGADLPAFTQMVLNLSAWTQNWGP	227
NTDB id 1112 NGFG RS09215 WP 003689811.1	ESLDDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAGLVFVMMIFVLPAPFKEVYANMGAELPLTQTVMMDSDFFVSYGW	230
NTDB id 1113 AAA85695.1 219..1451()	ESLDDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAGLVFVMMIFVLPAPFKEVYANMGAELPALQTVMMDSDFFVSYGW	230
NTDB id 126232 AMD06 RS05690 WP 040107659.1	ETVLDITVATYKENLEALKGKIKKALFYPMVMAMVAMLVSAILLVWVVPQFEDVFKGFGAELPAFTQMIVNLSRFMVSWWW	238
NTDB id 1252 GC085 RS07730 WP 011213805.1	DIMLDKVATYKEKIEIKKKIKKALTYPVSVIAVAGLVFVMMIFVLPAPFKEVYANMGAELPALQTVMMDSDFFVSYGW	227
NTDB id 1198 PSJM300 03950 AFN76868.1	ETLLDRVATYKEKTEALKAKIKKAMNYPVAVVAVIVTATILLIKVVPQFQDVAFNFGAELPAFTLMVIGLSEALQAWWY	226
NTDB id 1016 ACIAD RS01680 WP 004920476.1	EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFAGADLPAFTQLVNVNMSNMWDYWF	229
NTDB id 1059 ABD1 RS01610 WP 000279215.1	ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFAGADLPAFTQMNVNMSKWMQEWYF	229
consensus	PEVFERLATYREKSEQLRKAVIKALIYPSMVVLVALGVSYLMLTMVPIPEFESMFKGFGAELPWFTQVVLKLSHWVQAVSL	

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	WAFITIAAAIFGLKALRKNSFQIRLKTSLRLGKFPITGNVLAKASIAKFSRTLATSFAAGIPILASLKTAKTSGNVHFE	308
NTDB id 1402 DSB67 RS12670 WP 010643257.1	FIGLSFVSLIISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFAAGIPILATLKTAKTSGNMHYQ	307
NTDB id 1112 NGFG RS09215 WP 003689811.1	MVLIALGFAIYGFLLKARSIKIQRMDAILLRMPFIFGDIVRKGTIARWGRRTATLFAAGVPLVDVLDSTAGAAGNLIYE	310
NTDB id 1113 AAA85695.1 219..1451()	MVLIALGFAIYGFLLKARSIKIQRMDAILLRMPFIFGDIVRKGTIARWGRRTATLFAAGVPLVDVLDSTAGAAGNLIYE	310
NTDB id 126232 AMD06 RS05690 WP 040107659.1	LMLFALVGAAGISFYAYKRSPAMQHGMDRLVLKVPITIGQIMHNSSIAARFARTTAVTFKAGVPLVLEALGIVAGATGNSVYE	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	IMIIAIGAVIAAFLEAKRSKRFRDGLDKLALKLPFIFGDVLYKAIARIYSRTLATTFAAGVPLIDALESTAGATNNVIYE	309
consensus	WAFITIAAAIFGLKALRKNSFQIRLKTSLRLGKFPITGNVLAKASIAKFSRTLATSFAAGIPILASLKTAKTSGNVHFE	

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NTDB id 126232 AMD06 RS05690 WP 040107659.1
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

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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