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logo
NTDB id 1029 TT RS02230 WP 011228203.1        .............MPVYQYKARDRQGR.LVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGLKD   66
NTDB id 1169 A1552VC RS11075 WP 000648511.1   .....MKATQTLPLKNYRWKGINSNGK.KVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLARL.....THRVKSKD   69
NTDB id 1402 DSB67 RS12670 WP 010643257.1     ......MKTIAPQLKNYRWKGINSSGK.KTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITKI.....SHRVKGKD   68
NTDB id 1113 AAA85695.1 219..1451( )          MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.....S....SKRKITQED   71
NTDB id 1112 NGFG RS09215 WP 003689811.1      MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.....S....SKRKITQED   71
NTDB id 1252 GC085 RS07730 WP 011213805.1     ......MDKNSPPLLTFHYQGINKAGQ.KMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDRK.....NKKITQAD   68
NTDB id 1059 ABD1 RS01610 WP 000279215.1      .....MAVKKAQMMPTFAYEGVDRKGV.KIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL....FKKKVTTLD   70
NTDB id 1016 ACIAD RS01680 WP 004920476.1     .....MAAKKTQVMPVFAYEGVDRKGI.KLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGL....LKKKVKPLD   70
NTDB id 32736 TGR7 RS03890 WP 012637366.1     ........MAETQNITFQWEGLDKKGS.RVKGETTATSELLARAELRRQGINPTRVRKKPKSLFGG......KKKIVPKD   65
NTDB id 1198 PSJM300 03950 AFN76868.1         ......MAQKAIKNSVFTWEGLDRQGA.KIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFSA......GKKIKPMD   67
consensus                                               *  *  * ****** *  ** *** * ** ***  !***** * ******* *   *     ****   !

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NTDB id 1029 TT RS02230 WP 011228203.1        LAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKH.KIFSRLYVNLVRAGETSGGLD  145
NTDB id 1169 A1552VC RS11075 WP 000648511.1   ITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLP  149
NTDB id 1402 DSB67 RS12670 WP 010643257.1     ITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLS  148
NTDB id 1113 AAA85695.1 219..1451( )          ITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLE  151
NTDB id 1112 NGFG RS09215 WP 003689811.1      ITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLE  151
NTDB id 1252 GC085 RS07730 WP 011213805.1     ITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLD  148
NTDB id 1059 ABD1 RS01610 WP 000279215.1      ITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALE  150
NTDB id 1016 ACIAD RS01680 WP 004920476.1     IAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLE  150
NTDB id 32736 TGR7 RS03890 WP 012637366.1     IAVFLRQMATMMEAGVPLVQAFDIVGRGHENPSMQELILAMKSDVEGGTTFSAALGKHPKYFDDLVVNLVNAGEQAGALE  145
NTDB id 1198 PSJM300 03950 AFN76868.1         IALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLE  147
consensus                                     *****!!**!!* *!****!****** ***** ****** ** ****!**** ****** *!* ****!***!!**! !*

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NTDB id 1029 TT RS02230 WP 011228203.1        LILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATLP  225
NTDB id 1169 A1552VC RS11075 WP 000648511.1   EVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSLW  229
NTDB id 1402 DSB67 RS12670 WP 010643257.1     QVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGPF  228
NTDB id 1113 AAA85695.1 219..1451( )          SLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWM  231
NTDB id 1112 NGFG RS09215 WP 003689811.1      SLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWM  231
NTDB id 1252 GC085 RS07730 WP 011213805.1     IMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYI  228
NTDB id 1059 ABD1 RS01610 WP 000279215.1      TMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWFI  230
NTDB id 1016 ACIAD RS01680 WP 004920476.1     IMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWFI  230
NTDB id 32736 TGR7 RS03890 WP 012637366.1     TLLDKIATYKEKTESLKAKIKKALFYPTAVLVVAFIVTAILLIFVVPQFQDLFQGFGADLPVFTQFVIGISEFFQSYWWA  225
NTDB id 1198 PSJM300 03950 AFN76868.1         TLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWYV  227
consensus                                     ******!***!!** ***!***!* !!* !***!********* **! ! ***  *!**!!**!* ** *!**** ****
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NTDB id 1029 TT RS02230 WP 011228203.1        LLLLAVALFFAYR.WYYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSVVEE   304
NTDB id 1169 A1552VC RS11075 WP 000648511.1   AFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFET   309
NTDB id 1402 DSB67 RS12670 WP 010643257.1     IGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQL   308
NTDB id 1113 AAA85695.1 219..1451( )          VLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEE   311
NTDB id 1112 NGFG RS09215 WP 003689811.1      VLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEE   311
NTDB id 1252 GC085 RS07730 WP 011213805.1     IFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAK   308
NTDB id 1059 ABD1 RS01610 WP 000279215.1      MIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEK   310
NTDB id 1016 ACIAD RS01680 WP 004920476.1     LILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQ   310
NTDB id 32736 TGR7 RS03890 WP 012637366.1     IFGGLIGAVVLFKQAHLRSPGFRRWLDLMSLKIPVIGELLRKASIARFARTLSTMFAAGVPLVEAMESVAGATGNALYRE   305
NTDB id 1198 PSJM300 03950 AFN76868.1         VLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFRS   307
consensus                                     ************ ** ** ***  *****!**!**!*** !***!***!!*******!*****************!****

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NTDB id 1029 TT RS02230 WP 011228203.1        IVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLIAAIEPLMIIFLGVI   384
NTDB id 1169 A1552VC RS11075 WP 000648511.1   AINEVYRDTAAGMPMYIAM.RNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGTV   388
NTDB id 1402 DSB67 RS12670 WP 010643257.1     AIEEVYRDTAAGMPMYIAM.RHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVV   387
NTDB id 1113 AAA85695.1 219..1451( )          ATREIRTRVIQGLSMTSGM.RATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLV   390
NTDB id 1112 NGFG RS09215 WP 003689811.1      ATREIRTRVIQGLSMTSGM.RATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLV   390
NTDB id 1252 GC085 RS07730 WP 011213805.1     ATDKIREEVATGQQMFIAM.ENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGIL   387
NTDB id 1059 ABD1 RS01610 WP 000279215.1      AVMKIREDVATGQQLQFAM.RISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGVL   389
NTDB id 1016 ACIAD RS01680 WP 004920476.1     AVLKIREDVSTGQQLNFAM.RVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGIL   389
NTDB id 32736 TGR7 RS03890 WP 012637366.1     ATLRIRDETAAGTQLQAAM.RNTALFPNMVVQMVAIGEESGALDDMLDKVADFYEEEVDNMVDSLSSLMEPMIMAFLGVV   384
NTDB id 1198 PSJM300 03950 AFN76868.1         ATNKIKSDVSSGMQLNFSM.RTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVL   386
consensus                                     ** *** *** !**** ** * * *!! ****!**!!!!*!*!**!! !*!**!!*!!***!* !* **!!*****!!**

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NTDB id 1029 TT RS02230 WP 011228203.1        VGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1169 A1552VC RS11075 WP 000648511.1   VGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1     VGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1113 AAA85695.1 219..1451( )          IGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1112 NGFG RS09215 WP 003689811.1      IGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1252 GC085 RS07730 WP 011213805.1     VGGLVVAMYLPIFKLGSAV...   406
NTDB id 1059 ABD1 RS01610 WP 000279215.1      VGGLVIAMYLPIFQMGSVV...   408
NTDB id 1016 ACIAD RS01680 WP 004920476.1     VGGLVIAMYLPIFQMGSVV...   408
NTDB id 32736 TGR7 RS03890 WP 012637366.1     VGGLVIAMYLPIFQLGAVV...   403
NTDB id 1198 PSJM300 03950 AFN76868.1         VGGLIIAMYLPIFQMGSVV...   405
consensus                                     *!******!*!!*!******
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X non conserved

X similar

X ≥ 50% conserved