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logo
NTDB id 1029 TT RS02230 WP 011228203.1          ................MPVYQYKARDRQG.RLVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPG   63
NTDB id 1402 DSB67 RS12670 WP 010643257.1       .........MKTIAPQLKNYRWKGINSSG.KKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITKI.....SHRVK   65
NTDB id 1169 A1552VC RS11075 WP 000648511.1     ........MKATQTLPLKNYRWKGINSNG.KKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLARL.....THRVK   66
NTDB id 1112 NGFG RS09215 WP 003689811.1        MAKN...GGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.........SKRKIT   68
NTDB id 1113 AAA85695.1 219..1451( )            MAKN...GGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.........SKRKIT   68
NTDB id 160932 CAter282 RS18365 WP 061534605.1 MATAAPRSASSARQVKEWVYLWEGKDKKG.KAVRGELRAGSETVVTVTMRRQGILVTKIKKKTFR.........SGKKIS   70
NTDB id 1252 GC085 RS07730 WP 011213805.1       .........MDKNSPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNKKIT   65
NTDB id 1198 PSJM300 03950 AFN76868.1           .........MAQKAIKNSVFTWEGLDRQG.AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKIK   64
NTDB id 1059 ABD1 RS01610 WP 000279215.1        ........MAVKKAQMMPTFAYEGVDRKG.VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL....FKKKVT   67
NTDB id 1016 ACIAD RS01680 WP 004920476.1       ........MAAKKTQVMPVFAYEGVDRKG.IKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGL....LKKKVK   67
consensus                                                   *  *  * ******* * *** *** * ** ***  ****** * ****** **   *       ****
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logo
NTDB id 1029 TT RS02230 WP 011228203.1          LKDLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFSRLYVNLVRAGETSG   142
NTDB id 1402 DSB67 RS12670 WP 010643257.1       GKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSG   145
NTDB id 1169 A1552VC RS11075 WP 000648511.1     SKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSG   146
NTDB id 1112 NGFG RS09215 WP 003689811.1        QEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGG   148
NTDB id 1113 AAA85695.1 219..1451( )            QEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGG   148
NTDB id 160932 CAter282 RS18365 WP 061534605.1 DKDISLFTRQLATMMKAGVPLLQSFDIVAKGHANPSVSKLVNEIRGDVETGTSLSQAFRKYPLYFDPLFCNLVGAGEQAG   150
NTDB id 1252 GC085 RS07730 WP 011213805.1       QADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSG   145
NTDB id 1198 PSJM300 03950 AFN76868.1           PMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSG   144
NTDB id 1059 ABD1 RS01610 WP 000279215.1        TLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSG   147
NTDB id 1016 ACIAD RS01680 WP 004920476.1       PLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSG   147
consensus                                         !*****!!**!!***!****!****** ** ** ****** ** ****!**** **** * *!* ****!***!!**!
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logo
NTDB id 1029 TT RS02230 WP 011228203.1          GLDLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAA   222
NTDB id 1402 DSB67 RS12670 WP 010643257.1       NLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNW   225
NTDB id 1169 A1552VC RS11075 WP 000648511.1     NLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAY   226
NTDB id 1112 NGFG RS09215 WP 003689811.1        VLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSY   228
NTDB id 1113 AAA85695.1 219..1451( )            VLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSY   228
NTDB id 160932 CAter282 RS18365 WP 061534605.1 ILEDLLERLAIYKEKTLAIKAKIKSAMFYPVSILAVAFIVTAVIMIWVVPAFKQVFSSFGADLPGPTLVVMAISDFVVAN   230
NTDB id 1252 GC085 RS07730 WP 011213805.1       SLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAY   225
NTDB id 1198 PSJM300 03950 AFN76868.1           SLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAW   224
NTDB id 1059 ABD1 RS01610 WP 000279215.1        ALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEY   227
NTDB id 1016 ACIAD RS01680 WP 004920476.1       SLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDY   227
consensus                                        !* *****! **!!** ***!***!* !!******!********* **! ! ***  *!**!!**!**** *!******
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logo
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NTDB id 1029 TT RS02230 WP 011228203.1          TLPLLLLAVALFFAYR.WYYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSV   301
NTDB id 1402 DSB67 RS12670 WP 010643257.1       GPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMH   305
NTDB id 1169 A1552VC RS11075 WP 000648511.1     SLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVH   306
NTDB id 1112 NGFG RS09215 WP 003689811.1        GWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLI   308
NTDB id 1113 AAA85695.1 219..1451( )            GWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLI   308
NTDB id 160932 CAter282 RS18365 WP 061534605.1  WYIIFGGLFAALYLFFQSWRRSLKVQRFMDQLLLKAPIFGPVIRKATIARWTRTLATMFAAGVPLVESLDSVGGAAGNAV   310
NTDB id 1252 GCO85 RS07730 WP 011213805.1       WYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNII   305
NTDB id 1198 PSJM300 03950 AFN76868.1           WYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVV   304
NTDB id 1059 ABD1 RS01610 WP 000279215.1        WFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVI   307
NTDB id 1016 ACIAD RS01680 WP 004920476.1       WFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTV   307
consensus                                       **************   * **  ***   ****!**!**!***  !***!***!!*******!******!********!**
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logo
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NTDB id 1029 TT RS02230 WP 011228203.1          VEEIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLIAAIEPLMIIFL   381
NTDB id 1402 DSB67 RS12670 WP 010643257.1       YQLAIEEVYRDTAAGMPMYIAM.RHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFL   384
NTDB id 1169 A1552VC RS11075 WP 000648511.1     FETAINEVYRDTAAGMPMYIAM.RNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFL   385
NTDB id 1112 NGFG RS09215 WP 003689811.1        YEEATREIRTRVIQGLSMTSGM.RATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVIL   387
NTDB id 1113 AAA85695.1 219..1451( )            YEEATREIRTRVIQGLSMTSGM.RATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILIL   387
NTDB id 160932 CAter282 RS18365 WP 061534605.1  YLDATKKIQSEVSTGTSLTAAM.ENADVFPNMVTQMVSIGEESGSLDQMLGKVADFYEAEVDDAVASLSSLMEPLIMVIL   389
NTDB id 1252 GCO85 RS07730 WP 011213805.1       YAKATDKIREEVATGQQMFIAM.ENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSIL   384
NTDB id 1198 PSJM300 03950 AFN76868.1           FRSATNKIKSDVSSGMQLNFSM.RTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVL   383
NTDB id 1059 ABD1 RS01610 WP 000279215.1        YEKAVMKIREDVATGQQLQFAM.RISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAIL   386
NTDB id 1016 ACIAD RS01680 WP 004920476.1       YEQAVLKIREDVSTGQQLNFAM.RVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAIL   386
consensus                                       ** ** *** ** *!* *  ** * * *!! ****!**!!!!*!*!**!! !*!**!! !!***!* !* **!!******!
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logo
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NTDB id 1029 TT RS02230 WP 011228203.1          GVIVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1402 DSB67 RS12670 WP 010643257.1       GVVVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1     GTVVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1112 NGFG RS09215 WP 003689811.1        GLVIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1113 AAA85695.1 219..1451( )            GLVIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 160932 CAter282 RS18365 WP 061534605.1  GVLIGGLVIAMYLPIFKLGSVV...   411
NTDB id 1252 GCO85 RS07730 WP 011213805.1       GILVGGLVVAMYLPIFKLGSAV...   406
NTDB id 1198 PSJM300 03950 AFN76868.1           GVLVGGLIIAMYLPIFQMGSVV...   405
NTDB id 1059 ABD1 RS01610 WP 000279215.1        GVLVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1016 ACIAD RS01680 WP 004920476.1       GILVGGLVIAMYLPIFQMGSVV...   408
consensus                                       !***!*****!*!!*!******
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X non conserved

X similar

X $\geq$ 50% conserved