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logo
NTDB id 1029 TT RS02230 WP 011228203.1        ................MPVYQYKARDRQ.GRLVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGP   62
NTDB id 1402 DSB67 RS12670 WP 010643257.1     ....MKT......IAPQLKNYRWKGINSS.GKKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISHRV   64
NTDB id 1169 A1552VC RS11075 WP 000648511.1   ...MKAT......QTLPLKNYRWKGINSN.GKKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTHRV   65
NTDB id 1112 NGFG RS09215 WP 003689811.1      ....MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.........SKRKI   67
NTDB id 1113 AAA85695.1 219..1451( )          ....MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.........SKRKI   67
NTDB id 251309 CRN81 RS17810 WP 011137374.1  MATTAAKK......ANPGYIWEWEGKDKS.GKMIRGELRAESEAVAKTQLRRQGINVAKIRRRRSG.........FGKKI   64
NTDB id 1252 GC085 RS07730 WP 011213805.1     ....MDKN......SPPLLTFHYQGINKA.GQKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNKKI   64
NTDB id 1198 PSJM300 03950 AFN76868.1         ....MAQK......AIKNSVFTWEGLDRQ.GAKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKI   63
NTDB id 1016 ACIAD RS01680 WP 004920476.1     ...MAAKK......TQVMPVFAYEGVDRK.GIKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGL....LKKKV   66
NTDB id 1059 ABD1 RS01610 WP 000279215.1      ...MAVKK......AQMMPTFAYEGVDRK.GVKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL....FKKKV   66
consensus                                        ***        *  *  * ******  **** *** * ******  !***** * ****** **          ***

logo
NTDB id 1029 TT RS02230 WP 011228203.1        GLKDLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFSRLYVNLVRAGETS   141
NTDB id 1402 DSB67 RS12670 WP 010643257.1     KGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQS   144
NTDB id 1169 A1552VC RS11075 WP 000648511.1   KSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMS   145
NTDB id 1112 NGFG RS09215 WP 003689811.1      TQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETG   147
NTDB id 1113 AAA85695.1 219..1451( )          TQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETG   147
NTDB id 251309 CRN81 RS17810 WP 011137374.1  TEKDITLFTRQLSTMMRAGVPLLQAFDIAAKGHSNPAVTRMLLEVRADVETGLSLAEAFRKRPLYFDKLFCNIIAAGEAG   144
NTDB id 1252 GC085 RS07730 WP 011213805.1     TQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKS   144
NTDB id 1198 PSJM300 03950 AFN76868.1         KPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQS   143
NTDB id 1016 ACIAD RS01680 WP 004920476.1     KPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQS   146
NTDB id 1059 ABD1 RS01610 WP 000279215.1      TTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQS   146
consensus                                     *  !*****!!**!!***!****!****** ** ** ****** ** ****!***  **** * *!* ********!! *

logo
NTDB id 1029 TT RS02230 WP 011228203.1        GGLDLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRA   221
NTDB id 1402 DSB67 RS12670 WP 010643257.1     GNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQN   224
NTDB id 1169 A1552VC RS11075 WP 000648511.1   GNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQA   225
NTDB id 1112 NGFG RS09215 WP 003689811.1      GVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVS   227
NTDB id 1113 AAA85695.1 219..1451( )          GVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVS   227
NTDB id 251309 CRN81 RS17810 WP 011137374.1  GVLDTLLDKLATYKEKVMAIKSKIKSAMIYPSAIVGTAFIITAVIMIYVIPAFKDLFSSFGANLPAPTLFVIWLSDQFVH   224
NTDB id 1252 GC085 RS07730 WP 011213805.1     GSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQA   224
NTDB id 1198 PSJM300 03950 AFN76868.1         GSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQA   223
NTDB id 1016 ACIAD RS01680 WP 004920476.1     GSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQD   226
NTDB id 1059 ABD1 RS01610 WP 000279215.1      GALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQE   226
consensus                                     ! !*******!***!!** ** !***!* !!* ****!********* **! ! ***  *!**!!**!* ** *!****
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logo
NTDB id 1029 TT RS02230 WP 011228203.1        ATLPLLLLAVALFFAYR.WYYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNS   300
NTDB id 1402 DSB67 RS12670 WP 010643257.1     WGPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNM   304
NTDB id 1169 A1552VC RS11075 WP 000648511.1   YSLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNV   305
NTDB id 1112 NGFG RS09215 WP 003689811.1      YGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNL   307
NTDB id 1113 AAA85695.1 219..1451( )          YGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNL   307
NTDB id 251309 CRN81 RS17810 WP 011137374.1   FWWLIFGTLFGAIFAFFYAFKRTPKMQEQMDRILLRLPVIGDIIRKATIARWARTLSTLFSAGVPLVEALDSVGGAAGNQ   304
NTDB id 1252 GC085 RS07730 WP 011213805.1     YWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNI   304
NTDB id 1198 PSJM300 03950 AFN76868.1         WWYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNV   303
NTDB id 1016 ACIAD RS01680 WP 004920476.1     YWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNT   306
NTDB id 1059 ABD1 RS01610 WP 000279215.1      YWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNV   306
consensus                                     ***************  ** ** ***  ****!**!**!***  !***!***!!*******!******!********!*

logo
NTDB id 1029 TT RS02230 WP 011228203.1        VVEEIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAIEPLMIIF   380
NTDB id 1402 DSB67 RS12670 WP 010643257.1     HYQLAIEEVYRDTAAGMPMYIAM.RHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVF   383
NTDB id 1169 A1552VC RS11075 WP 000648511.1   HFETAINEVYRDTAAGMPMYIAM.RNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVF   384
NTDB id 1112 NGFG RS09215 WP 003689811.1      IYEEATREIRTRVIQGLSMTSGM.RATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVI   386
NTDB id 1113 AAA85695.1 219..1451( )          IYEEATREIRTRVIQGLSMTSGM.RATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILI   386
NTDB id 251309 CRN81 RS17810 WP 011137374.1   VYAEATRRIQADVSTGSSLNYSM.QRTDLFPNMVLQMTSIGEESGSLDQMLDKVADFYEEEVDNAVAALSSLLEPAIMVI   383
NTDB id 1252 GC085 RS07730 WP 011213805.1     IYAKATDKIREEVATGQQMFIAM.ENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSI   383
NTDB id 1198 PSJM300 03950 AFN76868.1         VFRSATNKIKSDVSSGMQLNFSM.RTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAV   382
NTDB id 1016 ACIAD RS01680 WP 004920476.1     VYEQAVLKIREDVSTGQQLNFAM.RVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAI   385
NTDB id 1059 ABD1 RS01610 WP 000279215.1      IYEKAVMKIREDVATGQQLQFAM.RISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAI   385
consensus                                     *** ** *** ** *!* ** ** * * *!! ****!**!!!!*!*!**!! !*!**!!*!!***!**!* **!!*****

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logo
NTDB id 1029 TT RS02230 WP 011228203.1        LGVIVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1402 DSB67 RS12670 WP 010643257.1     LGVVVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1   LGTVVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1112 NGFG RS09215 WP 003689811.1      LGLVIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1113 AAA85695.1 219..1451( )          LGLVIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 251309 CRN81 RS17810 WP 011137374.1   LGILIGGLVIAMYMPIFKMGQVVG..   407
NTDB id 1252 GC085 RS07730 WP 011213805.1     LGILVGGLVVAMYLPIFKLGSAV...   406
NTDB id 1198 PSJM300 03950 AFN76868.1         LGVLVGGLIIAMYLPIFQMGSVV...   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1     LGILVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1      LGVLVGGLVIAMYLPIFQMGSVV...   408
consensus                                     !!***!*****!**!*!******
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X non conserved

X similar

X ≥ 50% conserved