logo

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NTDB id 1113 AAA85695.1 219..1451( )  ..........MAKNGGFS...LFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT   61
NTDB id 1112 NGFG RS09215 WP 003689811.1  ..........MAKNGGFS...LFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT   61
NTDB id 1058893 ACFCQI RS12330 WP 395117093.1  MATATATAKARADKTRALGAQRAEVSQLTTYEWVALDKRG.KRMKGDMPAKNASLVKAELRRQGMNPQTVRERAKPLFGA   79
NTDB id 1252 GCO85 RS07730 WP 011213805.1  ....................MDKNSPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR   59
NTDB id 1198 PSJM300 03950 AFN76868.1  ....................MAQKAIKNSVFTWEGLDRQG.AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS.   58
NTDB id 1016 ACIAD RS01680 WP 004920476.1  ....................MAAKKTQVMPVFAYEGVDRKG.IKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG   60
NTDB id 1059 ABD1 RS01610 WP 000279215.1  ....................MAVKKAQMMPTFAYEGVDRKG.VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG   60
consensus                                  *   *   * *******  *   ***!** *** ****   !***!* *   **** * **
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NTDB id 1113 AAA85695.1 219..1451( )  SSKRKITQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLV   141
NTDB id 1112 NGFG RS09215 WP 003689811.1  SSKRKITQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLV   141
NTDB id 1058893 ACFCQI RS12330 WP 395117093.1  .SGSTIKPGDVAIFSRQIATMMASGVPMVQSFDIIADGQKNVRFKNVLLDVKQNIEGGASLHEAIGRYPVQFDELYCNLV   158
NTDB id 1252 GCO85 RS07730 WP 011213805.1  .KNKKITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLV   138
NTDB id 1198 PSJM300 03950 AFN76868.1  .AGKKIKPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLV   137
NTDB id 1016 ACIAD RS01680 WP 004920476.1  LLKKKVKPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLI   140
NTDB id 1059 ABD1 RS01610 WP 000279215.1  LFKKKVTTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLV   140
consensus                                   *****  !***!*!!**!!***!*!**!*!*!***!  !* *********** ****! *** ** *  ! *!* **!*!*
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NTDB id 1113 AAA85695.1 219..1451( )  AAGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDM   221
NTDB id 1112 NGFG RS09215 WP 003689811.1  AAGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDM   221
NTDB id 1058893 ACFCQI RS12330 WP 395117093.1  HAGETSGVLDTVLDTVATYKERTEAIKKKIKKALFYPMMVLAVVFIVILIMLLFVVPVFAKTFQDAGAQLPAPTQFLVDA   238
NTDB id 1252 GCO85 RS07730 WP 011213805.1  DAGEKSGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITM   218
NTDB id 1198 PSJM300 03950 AFN76868.1  DSGEQSGSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGL   217
NTDB id 1016 ACIAD RS01680 WP 004920476.1  ESGEQSGSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNM   220
NTDB id 1059 ABD1 RS01610 WP 000279215.1  ESGEQSGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNM   220
consensus                                  **!!  *!  !***!!**!*!!!*******!*!*!* !!**!**!*****  *****!*!  !  ****  *!!*!!*  !*  **  *
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NTDB id 1113 AAA85695.1 219..1451( )  SDFFVSYGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTA   301
NTDB id 1112 NGFG RS09215 WP 003689811.1  SDFFVSYGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTA   301
NTDB id 1058893 ACFCQI RS12330 WP 395117093.1  SEFMQGYWYIVVGIIVGSIAAIVIGKKRSPKFAHFLDRLALKMPVMGDIVRNSAIARFARTLGVTFRAGVPLVEALDAVA   318
NTDB id 1252 GCO85 RS07730 WP 011213805.1  SEFMQAYWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVA   298
NTDB id 1198 PSJM300 03950 AFN76868.1  SEALQAWWYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVA   297
NTDB id 1016 ACIAD RS01680 WP 004920476.1  SNWMQDYWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTA   300
NTDB id 1059 ABD1 RS01610 WP 000279215.1  SKWMQEYWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTA   300
consensus                                  !**** ***************** ** *! **    *!***!**!**!*** ** *!!**!!****!*!!*!!***!***!
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NTDB id 1113 AAA85695.1 219..1451( )    GAAGNLIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEP   381
NTDB id 1112 NGFG RS09215 WP 003689811.1 GAAGNLIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEP   381
NTDB id 1058893 ACFCQI RS12330 WP 395117093.1 GATGSIVYGDAVRQMRDDISVGHQLQLAMKQTGLFPNMVVQMTGIGEESGSLDSMLFKVAEFYEEEVSNAVDTLSTLLEP   398
NTDB id 1252 GCO85 RS07730 WP 011213805.1 GATGNIIYAKATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEP   378
NTDB id 1198 PSJM300 03950 AFN76868.1 GATGNVVFRSATNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEP   377
NTDB id 1016 ACIAD RS01680 WP 004920476.1 GATNNTVYEQAVLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEP   380
NTDB id 1059 ABD1 RS01610 WP 000279215.1 GATNNVIYEKAVMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEP   380
consensus                               !!********  !*  *******  *!  ***  *!*  *  *!!*!**!!**!!!!!!*!**!!  !*!**!!*!!***!**!****!!
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NTDB id 1113 AAA85695.1 219..1451( )    IIILILGLVIGTLLVAMYLPLFNLGNVVA*   410
NTDB id 1112 NGFG RS09215 WP 003689811.1 IIIVILGLVIGTLLVAMYLPLFNLGNVVA.   410
NTDB id 1058893 ACFCQI RS12330 WP 395117093.1 LIMVVLGTLVGGIVIALYLPIFKLAGTF..   426
NTDB id 1252 GCO85 RS07730 WP 011213805.1 IIMSILGILVGGLVVAMYLPIFKLGSAV..   406
NTDB id 1198 PSJM300 03950 AFN76868.1 MIMAVLGVLVGGLIIAMYLPIFQMGSVV..   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1 LIMAILGILVGGLVIAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1 LIMAILGVLVGGLVIAMYLPIFQMGSVV..   408
consensus                               *!*  *!!***!****!*!!!*!*******
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X non conserved
X similar
X ≥ 50% conserved