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logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1    ...............MKATQTLPLKNYRWKGINSNG.KKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.LTHR   64
NTDB id 1402 DSB67 RS12670 WP 010643257.1      ...............MKTIAPQLKNYRWKGINSSG.KKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.ISHR   63
NTDB id 1113 AAA85695.1 219..1451( )           .....MA....KNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRK   66
NTDB id 1112 NGFG RS09215 WP 003689811.1       .....MA....KNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRK   66
NTDB id 1198 PSJM300 03950 AFN76868.1          ...............MAQKAIKNSVFTWEGLDRQG.AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKK   62
NTDB id 1059 ABD1 RS01610 WP 000279215.1       ...............MAVKKAQMMPTFAYEGVDRKG.VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKK   65
NTDB id 1016 ACIAD RS01680 WP 004920476.1      ...............MAAKKTQVMPVFAYEGVDRKG.IKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKK   65
NTDB id 1033414 AB8808 RS06060 WP 369930572.1 MAIATASKNARAMGAARATVSALVTYDWTALDKRG.KRMKGEMQAKNASLVKAELRRQGMNPQQVKERTKPLFGS.SGKK   78
NTDB id 1252 GC085 RS07730 WP 011213805.1      ...............MDKNSPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKK   63
consensus                                                     *  *  * **** * * *** !** * *  ***  !*****    *****  *      **

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NTDB id 1169 A1552VC RS11075 WP 000648511.1    VKSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEM  144
NTDB id 1402 DSB67 RS12670 WP 010643257.1      VKGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQ  143
NTDB id 1113 AAA85695.1 219..1451( )           ITQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGET  146
NTDB id 1112 NGFG RS09215 WP 003689811.1       ITQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGET  146
NTDB id 1198 PSJM300 03950 AFN76868.1          IKPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQ  142
NTDB id 1059 ABD1 RS01610 WP 000279215.1       VTTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQ  145
NTDB id 1016 ACIAD RS01680 WP 004920476.1      VKPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQ  145
NTDB id 1033414 AB8808 RS06060 WP 369930572.1 VTARDVAIFSRQIATMMSSGVPMVQALEIITGGQKNPRFKTILLDIKTSIEGGSSLHEAMALHPVQFDELYRNLVHAGES  158
NTDB id 1252 GC085 RS07730 WP 011213805.1      ITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEK  143
consensus                                      **  !*****!!**!!* *!*!**!********  ** ****** **  ***!***  ***  * *!* ****!***!!

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NTDB id 1169 A1552VC RS11075 WP 000648511.1    SGNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQ  224
NTDB id 1402 DSB67 RS12670 WP 010643257.1      SGNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQ  223
NTDB id 1113 AAA85695.1 219..1451( )           GGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFV  226
NTDB id 1112 NGFG RS09215 WP 003689811.1       GGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFV  226
NTDB id 1198 PSJM300 03950 AFN76868.1          SGSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQ  222
NTDB id 1059 ABD1 RS01610 WP 000279215.1       SGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQ  225
NTDB id 1016 ACIAD RS01680 WP 004920476.1      SGSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQ  225
NTDB id 1033414 AB8808 RS06060 WP 369930572.1 AGVLDTVLDTVATYKERMESIKKKIKKALFYPIMVLVVALLVSMILLLFVVPVFQQTFKDAGADLPAPTQFVVSASEFMQ  238
NTDB id 1252 GC085 RS07730 WP 011213805.1      SGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQ  223
consensus                                      *! !*******!*!*!*** ** !***!* !!* !**!!**** **** !*! ! ***  *!!*!!**!* !* *!****

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NTDB id 1169 A1552VC RS11075 WP 000648511.1    AYSLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGN  304
NTDB id 1402 DSB67 RS12670 WP 010643257.1      NWGPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKITSKTSGN  303
NTDB id 1113 AAA85695.1 219..1451( )           SYGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGN  306
NTDB id 1112 NGFG RS09215 WP 003689811.1       SYGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGN  306
NTDB id 1198 PSJM300 03950 AFN76868.1          AWWYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGN  302
NTDB id 1059 ABD1 RS01610 WP 000279215.1       EYWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNN  305
NTDB id 1016 ACIAD RS01680 WP 004920476.1      DYWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNN  305
NTDB id 1033414 AB8808 RS06060 WP 369930572.1 SYWWMVIGGIVGGVAALIYFKKRSPRFAHFLERIMLRLPVMGNIMHQSAIARFARTLGVTFHAGVPLVEALEAVAGATGS  318
NTDB id 1252 GC085 RS07730 WP 011213805.1      AYWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGN  303
consensus                                       ****************  * *! ***  *****!**!**!*** ** *!***!!****!*!!*!****!********
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NTDB id 1169 A1552VC RS11075 WP 000648511.1     VHFETAINEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVF   384
NTDB id 1402 DSB67 RS12670 WP 010643257.1       MHYQLAIEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVF   383
NTDB id 1113 AAA85695.1 219..1451( )            LIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILI   386
NTDB id 1112 NGFG RS09215 WP 003689811.1        LIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVI   386
NTDB id 1198 PSJM300 03950 AFN76868.1           VVFRSATNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAV   382
NTDB id 1059 ABD1 RS01610 WP 000279215.1        VIYEKAVMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAI   385
NTDB id 1016 ACIAD RS01680 WP 004920476.1       TVYEQAVLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAI   385
NTDB id 1033414 AB8808 RS06060 WP 369930572.1  IIYGEAVMQMRDDIAVGHQLQLSMRQTGLFPNMVVQMTAIGEESGSLDAMLFKVAEFYEEEVGNAVDNLATLLEPMIMVI   398
NTDB id 1252 GC085 RS07730 WP 011213805.1       IIYAKATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSI   383
consensus                                       **** !*  ** *** !***  *!* * *!! ***!!**!!!!!! !**!! !*! *!!*!!***!* !* **!!*!***
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NTDB id 1169 A1552VC RS11075 WP 000648511.1     LGTVVGGLVVAMYLPIFNLMSVLG.   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1       LGVVVGGLVTAMYLPIFNLMSVLG.   407
NTDB id 1113 AAA85695.1 219..1451( )            LGLVIGTLLVAMYLPLFNLGNVVA*   410
NTDB id 1112 NGFG RS09215 WP 003689811.1        LGLVIGTLLVAMYLPLFNLGNVVA.   410
NTDB id 1198 PSJM300 03950 AFN76868.1           LGVLVGGLIIAMYLPIFQMGSVV..   405
NTDB id 1059 ABD1 RS01610 WP 000279215.1        LGVLVGGLVIAMYLPIFQMGSVV..   408
NTDB id 1016 ACIAD RS01680 WP 004920476.1       LGILVGGLVIAMYLPIFQMGSVV..   408
NTDB id 1033414 AB8808 RS06060 WP 369930572.1  LGVLVGGMVISLYLPIFKLAGTV..   421
NTDB id 1252 GC085 RS07730 WP 011213805.1       LGILVGGLVVAMYLPIFKLGSAV..   406
consensus                                       !!***!******!!!*!******
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X non conserved
X similar
X ≥ 50% conserved