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NTDB id 1029 TT RS02230 WP 011228203.1      ..............MPVYQYKARDRQGRL.VEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGLK   65
NTDB id 1169 A1552VC RS11075 WP 000648511.1 MKAT......QTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTHRVKSK   68
NTDB id 1402 DSB67 RS12670 WP 010643257.1   .MKT......IAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISHRVKGK   67
NTDB id 1112 NGFG RS09215 WP 003689811.1    .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT....SSKRKITQE   70
NTDB id 1113 AAA85695.1 219..1451( )        .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT....SSKRKITQE   70
NTDB id 1252 GCO85 RS07730 WP 011213805.1   .MDKN......SPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNKKITQA   67
NTDB id 1198 PSJM300 03950 AFN76868.1       .MAQK......AIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKIKPM   66
NTDB id 1059 ABD1 RS01610 WP 000279215.1    MAVKK......AQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKKKVTTL   69
NTDB id 1016 ACIAD RS01680 WP 004920476.1   MAAKK......TQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG....LLKKKVKPL   69
consensus                                    ***         *  *  * **** * * * * *** * *   **  !***** *  ***    *           ***
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NTDB id 1169 A1552VC RS11075 WP 000648511.1 DITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNL   148
NTDB id 1402 DSB67 RS12670 WP 010643257.1   DITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNL   147
NTDB id 1112 NGFG RS09215 WP 003689811.1    DITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL   150
NTDB id 1113 AAA85695.1 219..1451( )        DITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL   150
NTDB id 1252 GCO85 RS07730 WP 011213805.1   DITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSL   147
NTDB id 1198 PSJM300 03950 AFN76868.1       DIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSL   146
NTDB id 1059 ABD1 RS01610 WP 000279215.1    DITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEQGSTFASALRKYPQHFDNLFCSLVESGEQSGAL   149
NTDB id 1016 ACIAD RS01680 WP 004920476.1   DIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSL   149
consensus                                   !*****!!**!!* *!****!*********  **  ****** **  *****!****  **** *  *!*  ****!***!!  *!  !
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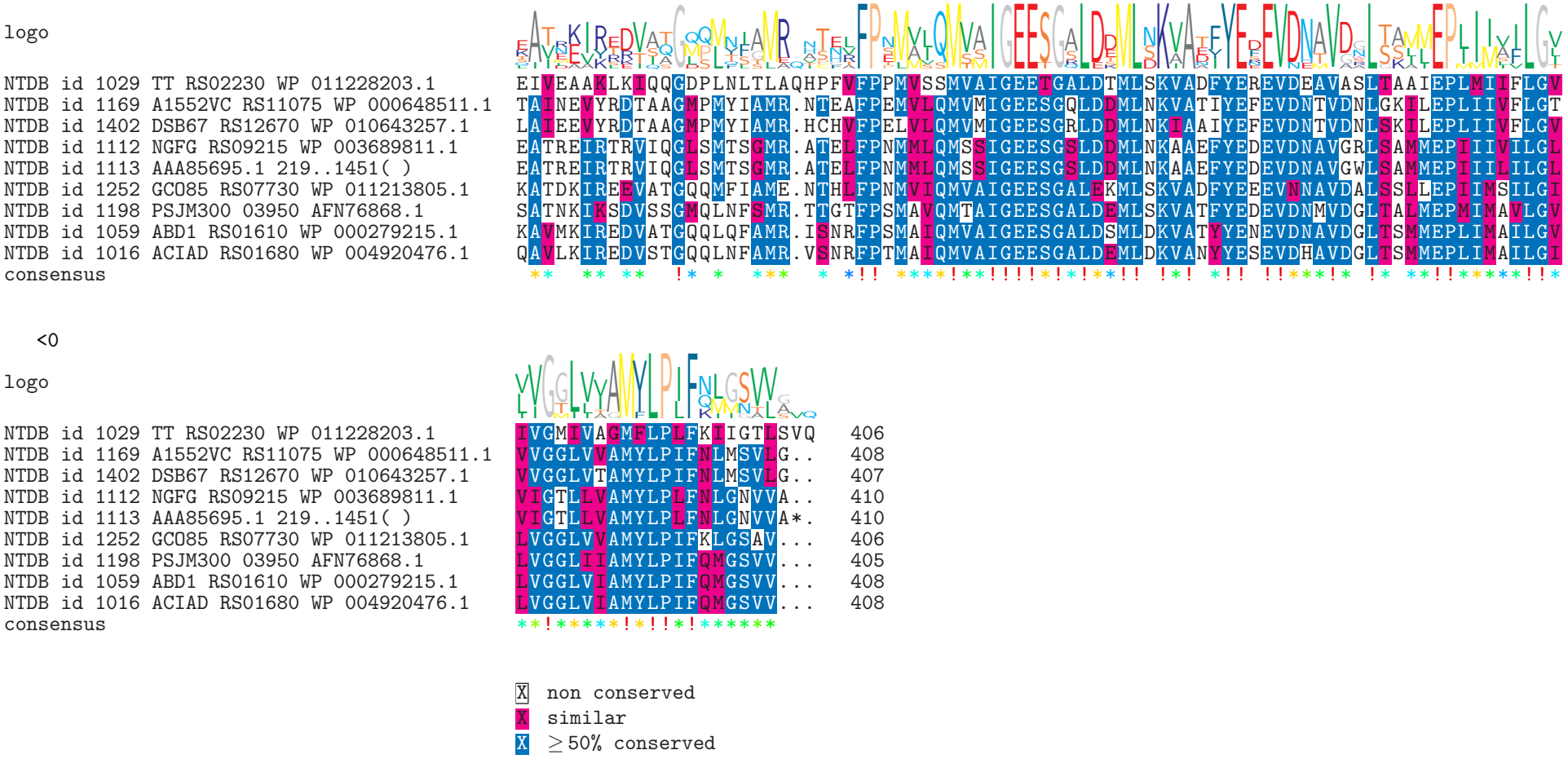


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NTDB id 1402 DSB67 RS12670 WP 010643257.1   SQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGP   227
NTDB id 1112 NGFG RS09215 WP 003689811.1    ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGW   230
NTDB id 1113 AAA85695.1 219..1451( )        ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGW   230
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NTDB id 1198 PSJM300 03950 AFN76868.1       ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTATLLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWY   226
NTDB id 1059 ABD1 RS01610 WP 000279215.1    ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWF   229
NTDB id 1016 ACIAD RS01680 WP 004920476.1   EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWF   229
consensus                                   * *****!***!!** ** !***!* !!* !***!********** **! ! ***  *!**!!**!* ** *!**** * *
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NTDB id 1112 NGFG RS09215 WP 003689811.1    MVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE   310
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NTDB id 1198 PSJM300 03950 AFN76868.1       VVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFR   306
NTDB id 1059 ABD1 RS01610 WP 000279215.1    IMITAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYE   309
NTDB id 1016 ACIAD RS01680 WP 004920476.1   ILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYE   309
consensus                                   ************    * ** ***  ****!**!**!*** !* *!***!!*******!******!*********!****
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NTDB id 1402 DSB67 RS12670 WP 010643257.1 LAIEEVYRDTAAGMPMYIAMR.HCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGV 386
NTDB id 1112 NGFG RS09215 WP 003689811.1 EATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGL 389
NTDB id 1113 AAA85695.1 219..1451( ) EATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGL 389
NTDB id 1252 GCO85 RS07730 WP 011213805.1 KATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGI 386
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NTDB id 1059 ABD1 RS01610 WP 000279215.1 KAVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGV 388
NTDB id 1016 ACIAD RS01680 WP 004920476.1 QAVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGI 388
consensus
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NTDB id 1029 TT RS02230 WP 011228203.1 IVGMIVAGMFLPLFKIIGTLSVQ 406
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consensus
X non conserved
X similar
X ≥ 50% conserved