logo

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NTDB id 1402 DSB67 RS12670 WP 010643257.1   .MKTI......APQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITKI.....SHRVKGK    67
NTDB id 1169 A1552VC RS11075 WP 000648511.1 MKATQ......TLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLARL.....THRVKSK    68
NTDB id 1112 NGFG RS09215 WP 003689811.1    .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TS....SKRKITQE    70
NTDB id 1113 AAA85695.1 219..1451( )        .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TS....SKRKITQE    70
NTDB id 1252 GCO85 RS07730 WP 011213805.1   .MDKN......SPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDRK.....NKKITQA    67
NTDB id 1016 ACIAD RS01680 WP 004920476.1   MAAKK......TQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGL....LKKKVKPL    69
NTDB id 1059 ABD1 RS01610 WP 000279215.1    MAVKK......AQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL....FKKKVTTL    69
NTDB id 304235 PLA107 RS28275 WP 005745480.1 .MASK......AVKVSVYTWEGVDKKGGK.LSGEVSGHNLALVKAQLRKQGINFTKVRKKPVSIFGK......GKKIKPL    66
NTDB id 1198 PSJM300 03950 AFN76868.1       .MAQK......AIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFSA......GKKIKPM    66
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NTDB id 1169 A1552VC RS11075 WP 000648511.1 DITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNL   148
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NTDB id 1113 AAA85695.1 219..1451( )        DITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL   150
NTDB id 1252 GCO85 RS07730 WP 011213805.1   DITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSL   147
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NTDB id 304235 PLA107 RS28275 WP 005745480.1 DIAFFSRQMATMMKAGVPLLQSFDIIAEGAENPNMRALVGSLKQEVSAGNSFATALRQKPEYFDDLFCNLVDAGEQAGAL   146
NTDB id 1198 PSJM300 03950 AFN76868.1       DIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSL   146
consensus                                    !*****!!**!!***!****!********* *** ****** ** ****!***  **** * *!* ****!***!!**! !
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NTDB id 1402 DSB67 RS12670 WP 010643257.1   SQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGP   227
NTDB id 1169 A1552VC RS11075 WP 000648511.1 PEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSL   228
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NTDB id 1113 AAA85695.1 219..1451( )        ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGW   230
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NTDB id 1016 ACIAD RS01680 WP 004920476.1   EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWF   229
NTDB id 1059 ABD1 RS01610 WP 000279215.1    ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWF   229
NTDB id 304235 PLA107 RS28275 WP 005745480.1 ESLLDRVASYKEKTEKLKAKIKKAMTYPIAVLIVAIIVSGILLIKVVPQFQSVFAGFGAELPAFTLMVIGLSDIVQKWWL   226
NTDB id 1198 PSJM300 03950 AFN76868.1       ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWY   226
consensus                                    *******!***!!** ***!***!**!!* !***!************! ! **** *!**!!**!**** *!**** ***
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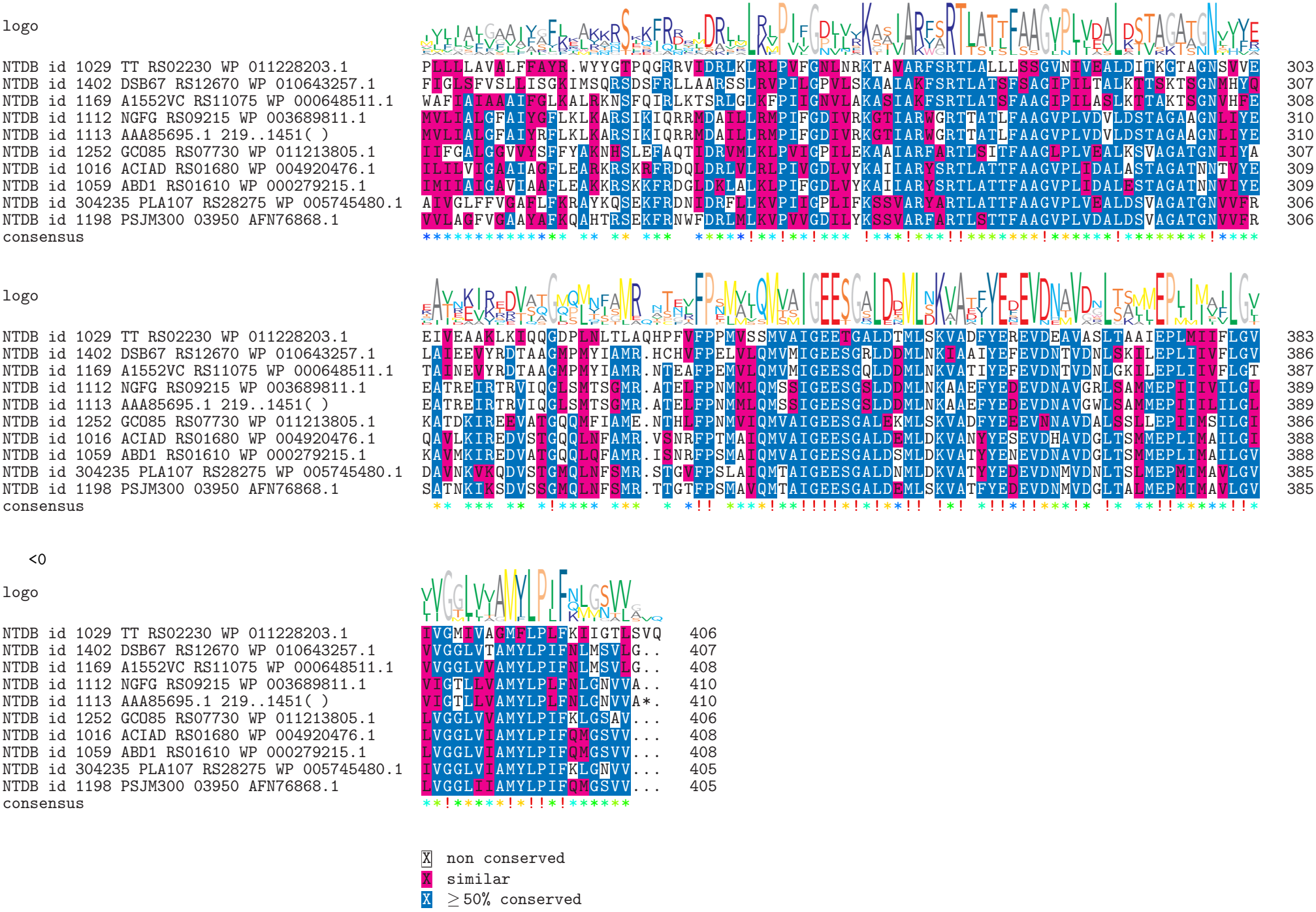
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consensus
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consensus
X non conserved
X similar
X ≥ 50% conserved