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NTDB id 1029 TT RS02230 WP 011228203.1          ..............MPVYQYKARDRQG.RLVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGLK    65
NTDB id 1169 A1552VC RS11075 WP 000648511.1     MKAT......QTLPLKNYRWKGINSNG.KKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLARL.....THRVKSK    68
NTDB id 1402 DSB67 RS12670 WP 010643257.1       .MKT......IAPQLKNYRWKGINSSG.KKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITKI.....SHRVKGK    67
NTDB id 1112 NGFG RS09215 WP 003689811.1        .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.........SKRKITQE    70
NTDB id 1113 AAA85695.1 219..1451( )            .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.........SKRKITQE    70
NTDB id 1252 GCO85 RS07730 WP 011213805.1       .MDK......NSPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNKKITQA    67
NTDB id 25663 MFLA RS10960 WP 011480363.1       .MAA......KETKEVTYAWEGTDRKG.KRVKGEMKASGEAFVKATLRRQGINVVKISKQRFK.........SGGKITDK    63
NTDB id 1198 PSJM300 03950 AFN76868.1           .MAQ......KAIKNSVFTWEGLDRQG.AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKIKPM    66
NTDB id 1016 ACIAD RS01680 WP 004920476.1       MAAK......KTQVMPVFAYEGVDRKG.IKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGL....LKKKVKPL    69
NTDB id 1059 ABD1 RS01610 WP 000279215.1        MAVK......KAQMMPTFAYEGVDRKG.VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL....FKKKVTTL    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
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NTDB id 1113 AAA85695.1 219..1451( )            DITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL   150
NTDB id 1252 GCO85 RS07730 WP 011213805.1       DITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSL   147
NTDB id 25663 MFLA RS10960 WP 011480363.1       DVTLFTRQLATMMKAGVPLLQAFDIVGKGHSNPAVSKLLGDIKADVETGSSLSQAFRKYPLYFDNLFCNLVGAGEQAGIL   143
NTDB id 1198 PSJM300 03950 AFN76868.1           DIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSL   146
NTDB id 1016 ACIAD RS01680 WP 004920476.1       DIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSL   149
NTDB id 1059 ABD1 RS01610 WP 000279215.1        DITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGAL   149
consensus                                        !*****!!**!!***!****!****** ** ** ****** ** ****!**** **** * *!* ****!***!!**!  !
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NTDB id 1169 A1552VC RS11075 WP 000648511.1     PEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSL   228
NTDB id 1402 DSB67 RS12670 WP 010643257.1       SQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGP   227
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NTDB id 1113 AAA85695.1 219..1451( )            ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGW   230
NTDB id 1252 GCO85 RS07730 WP 011213805.1       DIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWY   227
NTDB id 25663 MFLA RS10960 WP 011480363.1       DSLLDRLATYKEKILAIKGKIKSALFYPISIIVVAFVITAVIMIFVIPAFKELFSSFGADLPAPTVMVMAISDFFVDYWW   223
NTDB id 1198 PSJM300 03950 AFN76868.1           ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWY   226
NTDB id 1016 ACIAD RS01680 WP 004920476.1       EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWF   229
NTDB id 1059 ABD1 RS01610 WP 000279215.1        ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWF   229
consensus                                        *******!***!!** ***!***!* !!*******!********** **! ! ***   *!**!!**!**** *!**** ***
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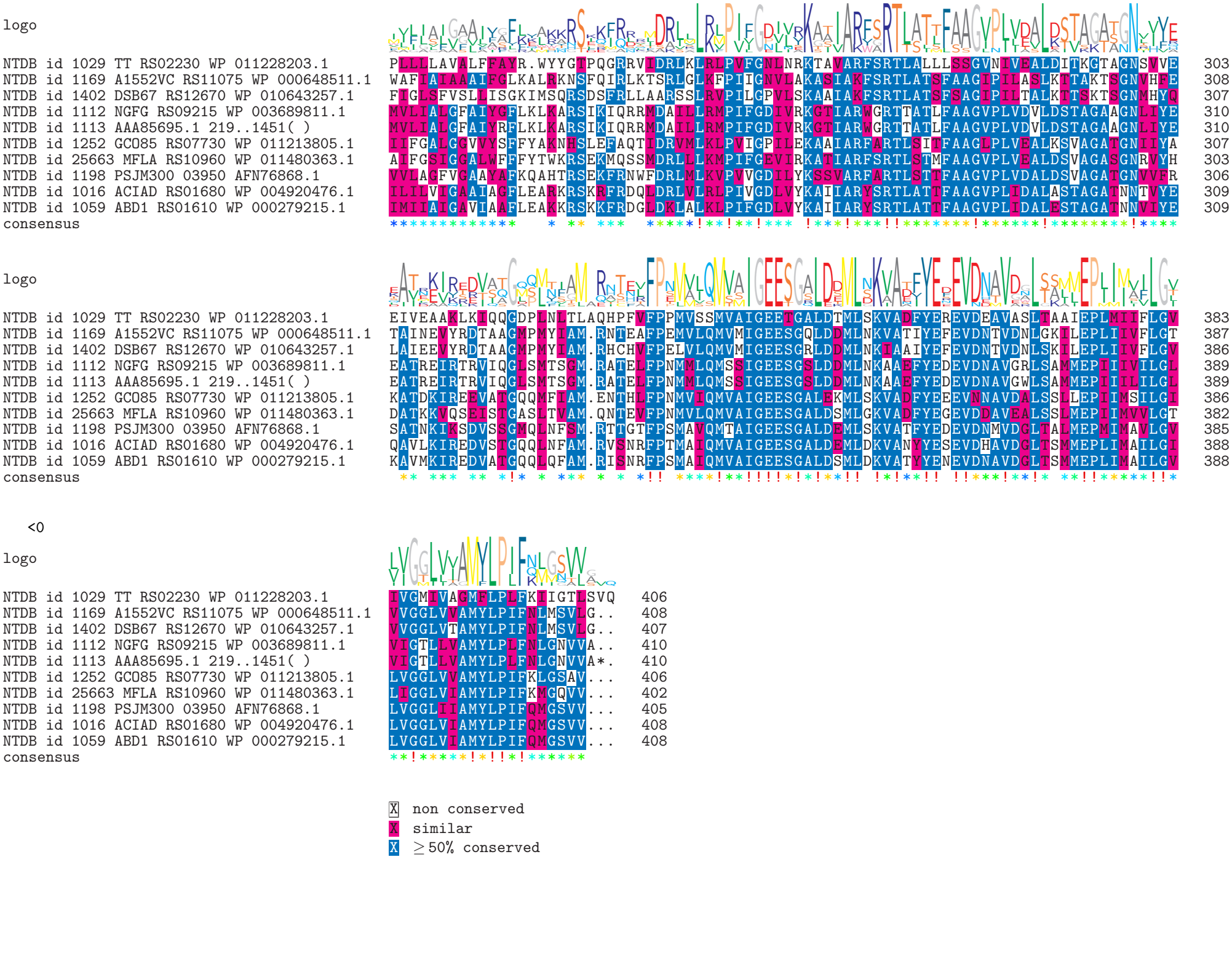
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consensus
logo
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consensus
X non conserved
X similar
X ≥ 50% conserved