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NTDB id 486 SM12261 RS09375 WP 020902616.1     MDFLAVLVVILHIFIISKSYYLICKNKINIKEL.....CFFGG....YTFLVESVFELSFYFIYLDGLG..IEKFLFPL   68
NTDB id 514 SMSK321 RS10615 WP 001048129.1     MNLFGVGLVIVYFLIISHSYRLICKGQINRKEL.....YVFSA....YILLTEIVLDFPSYLLHLDDLG..IVKFLFPL   68
NTDB id 138 SP RS11430 WP 000364845.1          MDLLGFGTVIVHFLIISHSYRLICKGRINRKEL.....YVFGA....YTLLTEIVLEFSFYLLYLDKIG..IERFLFPL   68
NTDB id 249 KZH43 RS10250 WP 000362880.1       MDLFGFGTVIVHFLIISHSYHFICKGQINRKEL.....FVFGA....YTLLTEIVFDFPLYILYLDGLG..IERFLFPL   68
NTDB id 208 SPD RS10925 WP 000362880.1         MDLFGFGTVIVHFLIISHSYHFICKGQINRKEL.....FVFGA....YTLLTEIVFDFPLYILYLDGLG..IERFLFPL   68
NTDB id 174 SPR RS10405 WP 000362880.1         MDLFGFGTVIVHFLIISHSYHFICKGQINRKEL.....FVFGA....YTLLTEIVFDFPLYILYLDGLG..IERFLFPL   68
NTDB id 1081739 ACK2I7 RS08515 WP 021002245.1  MNLDKT.FIIISFIIGILSFSI.VHKKISKVKTIDFRFTLLCLC..........LFLFSSFINSINSLLAYLCLLLEPV   67
NTDB id 419 DQL23 RS10745 WP 060553298.1       MILKII.IAFFPTIIQVVSYEI.FHKKIMQSKKIDIKFIGLFFSIVFGISIISSILIEIPSFGDVISSIFHYIFLFIQPL   78
NTDB id 416 SGO RS10505 WP 012131078.1         MIFTII.LSLFPVIIQVFSYDF.FYNKINRKKKINIKLIILFWGLIMVISFLYSLFLLLPDYWKIFRDIFHYLFLLIQPL   78
consensus                                      !** *** ******!***!* ******!*****      *****     ************ ****** **   ******!*
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NTDB id 486 SM12261 RS09375 WP 020902616.1     VLYSYFR.FIKKYEKYRGVFLSLLLSLLYNSTHTFLSVTLSSIIGDDTALQYHSLFFLVVVALTYVVIVTIIRYFHLELN  147
NTDB id 514 SMSK321 RS10615 WP 001048129.1     VLYSYFR.WIKQYERDRGLFLSLLLSLLYESTHNFLSVTLSSLTGDNFVLQYYEPFFFLVTVLTYVVILKIIHYFHLDLN  147
NTDB id 138 SP RS11430 WP 000364845.1          GLYSYFR.WMKQYERDRGLFLSLLLSLLYESTHNFLSVIFSSITGDNFVLQYHFPFFFVVTVLTYFVTLKIIYYFHLELA  147
NTDB id 249 KZH43 RS10250 WP 000362880.1       GLYSYFR.WMKQYERDRGLFLSLLLSLLYESTHNFLSVTFSSITGDNFVLQYHFPFFFVVTVLTYFVTLKIIYYFHLELA  147
NTDB id 208 SPD RS10925 WP 000362880.1         GLYSYFR.WMKQYERDRGLFLSLLLSLLYESTHNFLSVTFSSITGDNFVLQYHFPFFFVVTVLTYFVTLKIIYYFHLELA  147
NTDB id 174 SPR RS10405 WP 000362880.1         GLYSYFR.WMKQYERDRGLFLSLLLSLLYESTHNFLSVTFSSITGDNFVLQYHFPFFFVVTVLTYFVTLKIIYYFHLELA  147
NTDB id 1081739 ACK2I7 RS08515 WP 021002245.1  IIYFYFY.RFKKYEKCISVFATFLTYSSVTTSETFFSVIISSVTGDKFVDRYWGLFYIFINIISLVFILKAIDYFKFNFK  146
NTDB id 419 DQL23 RS10745 WP 060553298.1       IFYKYFL.KRKKEYDNYLNLFLSFVIYLSVETSETFLSVIISSITGDYFVKQHYDIFYIIINLLSLFIILKVVDFFDFYFE  157
NTDB id 416 SGO RS10505 WP 012131078.1         IFYKYFLIKRKEYENYLNLFLSFVIYLSVETSETFLSVIISSITGDSFVKQHYDIFYIIINLLSLFIILKVVDFFDFYFE  158
consensus                                      **!*!!* **!*!******!*****************!*!!**!!**!!******* *!****************** *!****
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NTDB id 486 SM12261 RS09375 WP 020902616.1     YFDKDYLYPFLKKVFFALLLLHVVSFISDMVSTIKHLNSFGSILSSIVFISLLLTFFAMNSHKEKMEKEIALKQKKFEQK  227
NTDB id 514 SMSK321 RS10615 WP 001048129.1     YFDKDYLYPFLTKVFFALLLLHIVSFVSDMVSTIKHLNSFGSILSSIVFISLLLTFFAMNSHKDQMEKEIALKQKKFEQK  227
NTDB id 138 SP RS11430 WP 000364845.1          YFDKDYLYPFLKKVFFALLLLHIVSFVSDMVSTIKHLNSFGSILSSIVFISLLLTFFAMNSHKVQMEKEIALKQKKFEQK  227
NTDB id 249 KZH43 RS10250 WP 000362880.1       YFDEDYLYPFLKKVFFALLLLHIVSFVSDMVSTIKHLNSFGSILSSIVFISLLLTFFAMNSHKVQMEKEIALKQKKFEQK  227
NTDB id 208 SPD RS10925 WP 000362880.1         YFDEDYLYPFLKKVFFALLLLHIVSFVSDMVSTIKHLNSFGSILSSIVFISLLLTFFAMNSHKVQMEKEIALKQKKFEQK  227
NTDB id 174 SPR RS10405 WP 000362880.1         YFDEDYLYPFLKKVFFALLLLHIVSFVSDMVSTIKHLNSFGSILSSIVFISLLLTFFAMNSHKVQMEKEIALKQKKFEQK  227
NTDB id 1081739 ACK2I7 RS08515 WP 021002245.1  YFKKADFKENIVQLNFYLLFIHFLLNLSHWLSNMKNLNSFSSMIATICFLMFMSTLFYLQSIREKYEKEEQIKQKEREQL  226
NTDB id 419 DQL23 RS10745 WP 060553298.1       YYKEPIYKNDLYNVNKSYIVIHILLNISHWFSENAHLNSFASMIATIGFIMFLSTLFYLKSAREQHEKAKEIQQKKEEQR  237
NTDB id 416 SGO RS10505 WP 012131078.1         YYKEPIYKNDLYNVNKSYIVIHILLNISHWFSENAHLNSFASMIATIGFIMFLSTLFYLKSAREQYEKAKEIQQKKEEQR  238
consensus                                      !**********************!*****!***!****!!!!*!****!*!*****!*!***!*****!!*****!!**!!*
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NTDB id 514 SMSK321 RS10615 WP 001048129.1     HLQNYTDEIVGLYNEIRGFRHDYAGMLVSMQMAIDSGNLQEIDRVYNEVLVKANHKLRSDKYTYFDLNNIEDSALRSLVA  307
NTDB id 138 SP RS11430 WP 000364845.1          HLQNYTDEIVGLYNEIRGFRHDYAGMLVSMQMAIDSGNLQEIDRIYNEVLVKANHKLRSDKYTYFDLNNIEDSALRSLVA  307
NTDB id 249 KZH43 RS10250 WP 000362880.1       HLQNYTDEIVGLYNEIRGFRHDYAGMLVSMQMAIDSGNLQEIDRIYNEVLVKANHKLRSDKYTYFDLNNIEDSALRSLVA  307
NTDB id 208 SPD RS10925 WP 000362880.1         HLQNYTDEIVGLYNEIRGFRHDYAGMLVSMQMAIDSGNLQEIDRIYNEVLVKANHKLRSDKYTYFDLNNIEDSALRSLVA  307
NTDB id 174 SPR RS10405 WP 000362880.1         HLQNYTDEIVGLYNEIRGFRHDYAGMLVSMQMAIDSGNLQEIDRIYNEVLVKANHKLRSDKYTYFDLNNIEDSALRSLVA  307
NTDB id 1081739 ACK2I7 RS08515 WP 021002245.1  QLQKYTDEIVSLYNEIRGFRHDYGGMLASFQSAIHTGDIKEVERIYQEVLVNANLQLRSDKYTYFDLNNVGDSALRSVMT  306
NTDB id 419 DQL23 RS10745 WP 060553298.1       QLQLYTDEIVGLYNEIRGFRHDYAGMLISLQTGINSGDMKEVERIFHNVLSQANISLRSDDYTFFELNNVQDTALRSVLI  317
NTDB id 416 SGO RS10505 WP 012131078.1         QLQLYTDEIVGLYNEIRGFRHDYAGMLTSLQTGINSGDMKEVERIFHNVLSQANISLRSDDYTRFELNNVQDTALRSVLI  318
consensus                                      *!!*!!!!!!*!!!!!!!!!!!!!*!!!*!*!**!**!***!**!****!!**!!**!!!!*!!*!*!!!**!*!!!!***
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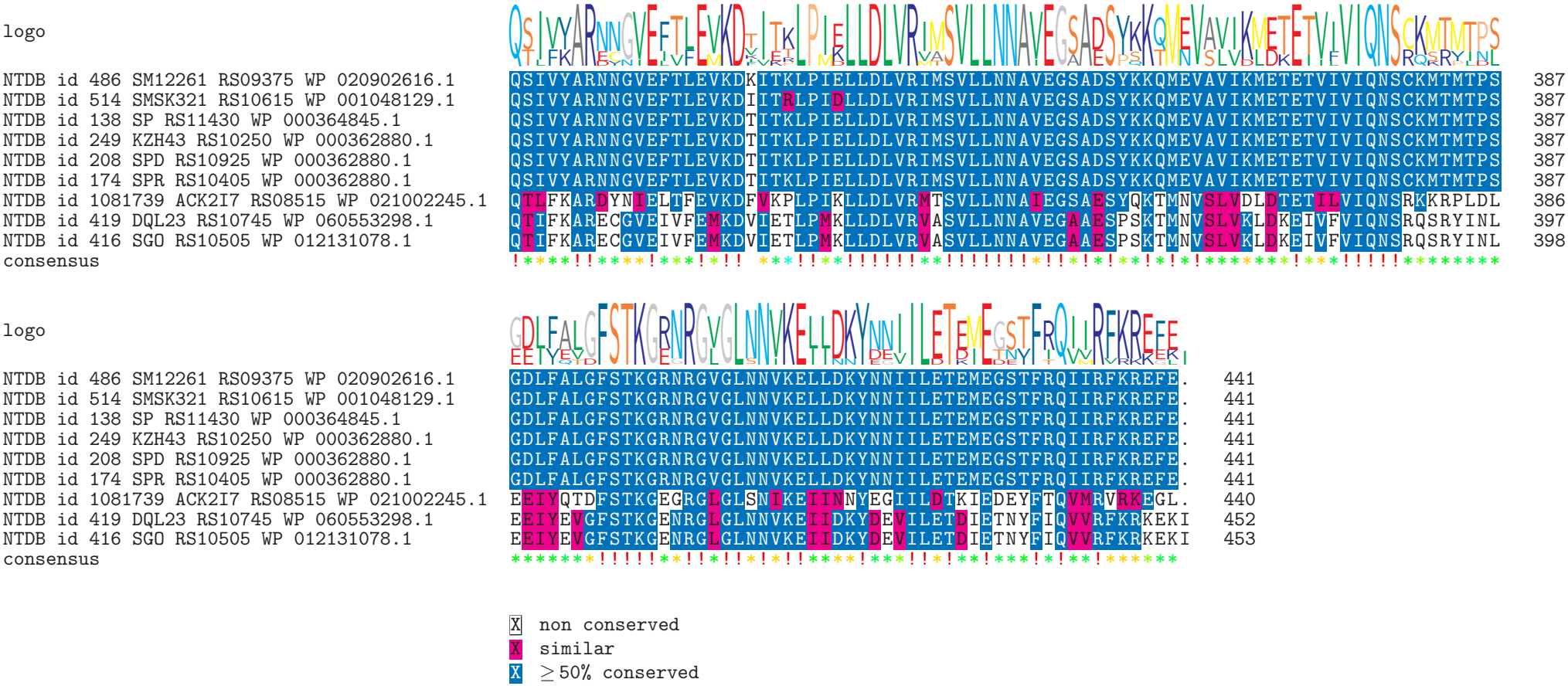
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NTDB id 514 SMSK321 RS10615 WP 001048129.1 QSIVYARNNGVEFTLEVKDIITRLPIDLLDLVRIMSVLLNNAVEGSADSYKKQMEVAVIKMETETVIVIQNSCKMTMTPS 387
NTDB id 138 SP RS11430 WP 000364845.1 QSIVYARNNGVEFTLEVKDTITKLPIELLDLVRIMSVLLNNAVEGSADSYKKQMEVAVIKMETETVIVIQNSCKMTMTPS 387
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NTDB id 1081739 ACK2I7 RS08515 WP 021002245.1 QTLFKARDYNIELTFEVKDFVKPLPIKLLDLVRMTSVLLNNAIEGSAESYQKTMNVSLVDLDTETILVIQNSRKKRPLDL 386
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NTDB id 416 SGO RS10505 WP 012131078.1 QTIFKARECGVEIVFEMKDVIETLPMKLLDLVRVASVLLNNAVEGAAESPSKTMNVSLVKLDKEIVFVIQNSRQSRYINL 398
consensus
logo
NTDB id 486 SM12261 RS09375 WP 020902616.1 GDLFALGFSTKGRNRGVGLNNVKELLDKYNNIILETEMEGSTFRQIIRFKREFE. 441
NTDB id 514 SMSK321 RS10615 WP 001048129.1 GDLFALGFSTKGRNRGVGLNNVKELLDKYNNIILETEMEGSTFRQIIRFKREFE. 441
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NTDB id 174 SPR RS10405 WP 000362880.1 GDLFALGFSTKGRNRGVGLNNVKELLDKYNNIILETEMEGSTFRQIIRFKREFE. 441
NTDB id 1081739 ACK2I7 RS08515 WP 021002245.1 EEIYQTDFSTKGEGRGLGLSNIKEIINNYEGIILDTKIEDEYFTQVMRVRKEGL. 440
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NTDB id 416 SGO RS10505 WP 012131078.1 EEIYEVGFSTKGENRGLGLNNVKEIIDKYDEVILETDIETNYFIQVVRFKRKEKI 453
consensus
X non conserved
X similar
X ≥ 50% conserved