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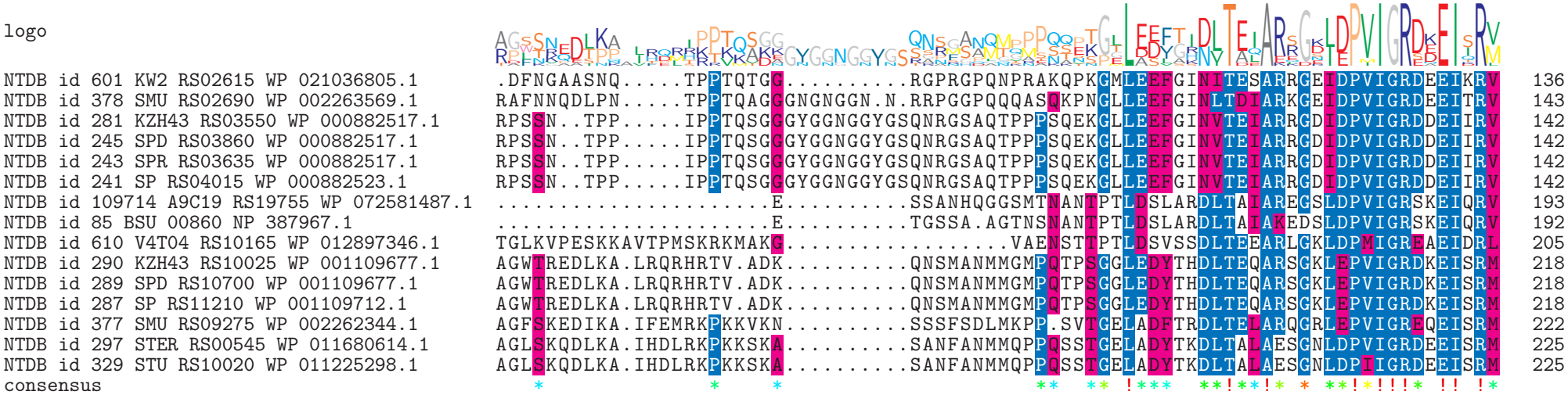


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consensus
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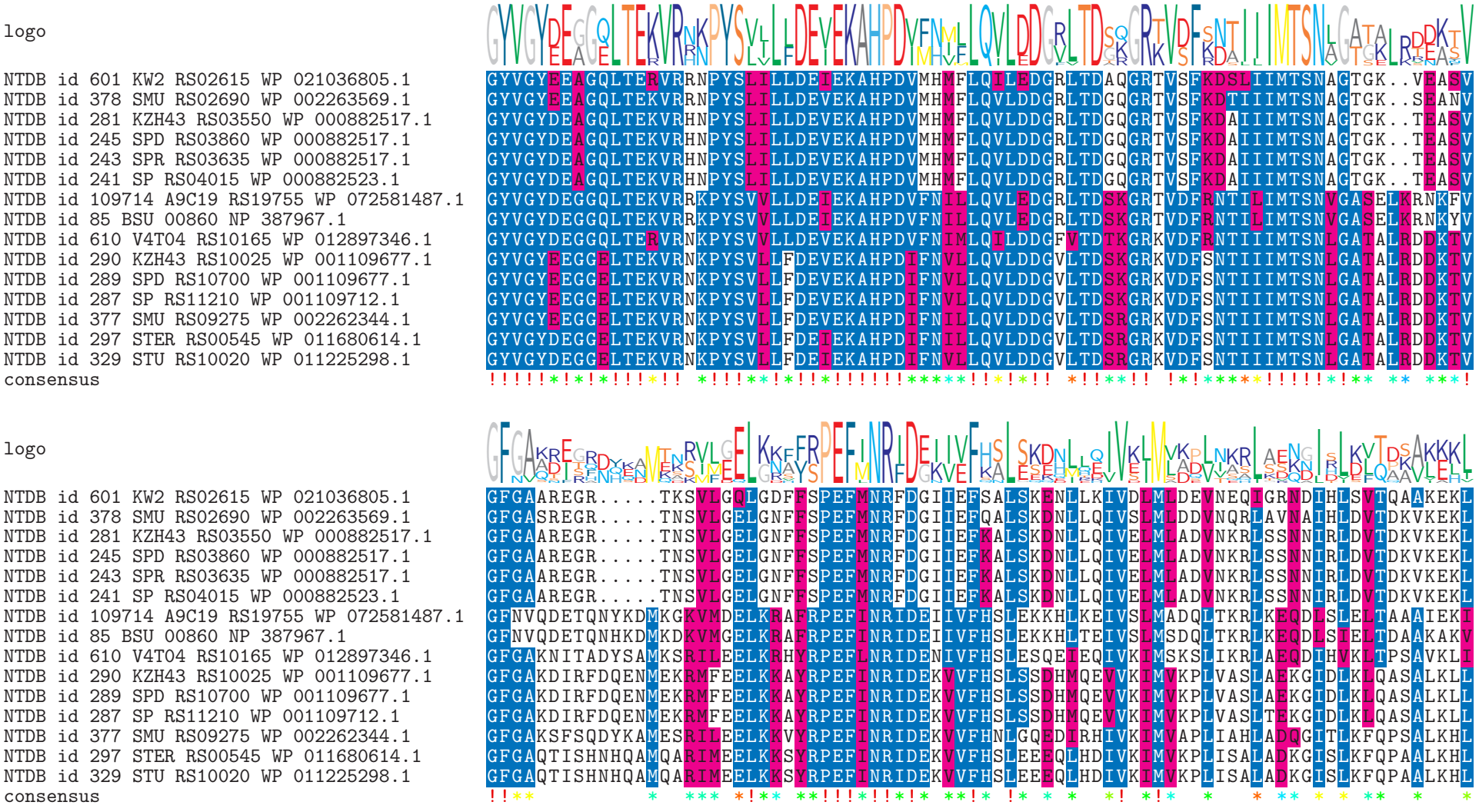


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consensus                                    !!**!*  * *!*!!** !* * *!!*!!!*!*!!!!!!!!!!**!!* *!* ** **!*!!!!*!!!*  **!*!*!!
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logo
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NTDB id 378 SMU RS02690 WP 002263569.1 GYVGYEEAGQLTEKVRRNPYSLILLDEVEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDTIIIMTSNAGTGK..SEANV 612
NTDB id 281 KZH43 RS03550 WP 000882517.1 GYVGYDEAGQLTEKVRHNPYSLILLDEVEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDAIIIMTSNAGTGK..TEASV 611
NTDB id 245 SPD RS03860 WP 000882517.1 GYVGYDEAGQLTEKVRHNPYSLILLDEVEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDAIIIMTSNAGTGK..TEASV 611
NTDB id 243 SPR RS03635 WP 000882517.1 GYVGYDEAGQLTEKVRHNPYSLILLDEVEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDAIIIMTSNAGTGK..TEASV 611
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NTDB id 109714 A9C19 RS19755 WP 072581487.1 GYVGYDEGGQLTEKVRRKPYSVVLLDEIEKAHPDVFNILLQVLEDGRLTDSKGRTVDFRNTILIMTSNVGASELKRNKFV 672
NTDB id 85 BSU 00860 NP 387967.1 GYVGYDEGGQLTEKVRRKPYSVVLLDEIEKAHPDVFNILLQVLEDGRLTDSKGRTVDFRNTILIMTSNVGASELKRNKYV 671
NTDB id 610 V4T04 RS10165 WP 012897346.1 GYVGYDEGGQLTERVRNKPYSVVLLDEVEKAHPDVFNIMLQILDDGFVTDTKGRKVDFRNTIIIMTSNLGATALRDDKTV 680
NTDB id 290 KZH43 RS10025 WP 001109677.1 GYVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTV 675
NTDB id 289 SPD RS10700 WP 001109677.1 GYVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTV 675
NTDB id 287 SP RS11210 WP 001109712.1 GYVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTV 675
NTDB id 377 SMU RS09275 WP 002262344.1 GYVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNILLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTV 678
NTDB id 297 STER RS00545 WP 011680614.1 GYVGYDEGGELTEKVRNKPYSVLLFDEIEKAHPDIFNILLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTV 681
NTDB id 329 STU RS10020 WP 011225298.1 GYVGYDEGGELTEKVRNKPYSVLLFDEIEKAHPDIFNVLLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTV 681
consensus
logo
NTDB id 601 KW2 RS02615 WP 021036805.1 GFGAAREGR.....TKSVLGQLGDFFSPEFMNRFDGIIEFSALSKENLLKIVDLMLDEVNEQIGRNDIHLSVTQAAKEKL 680
NTDB id 378 SMU RS02690 WP 002263569.1 GFGASREGR.....TNSVLGELGNFFSPEFMNRFDGIIEFQALSKDNLLQIVSLMLDDVNQRLAVNAIHLDVTDKVKEKL 687
NTDB id 281 KZH43 RS03550 WP 000882517.1 GFGAAREGR.....TNSVLGELGNFFSPEFMNRFDGIIEFKALSKDNLLQIVELMLADVNKRLSSNNIRLDVTDKVKEKL 686
NTDB id 245 SPD RS03860 WP 000882517.1 GFGAAREGR.....TNSVLGELGNFFSPEFMNRFDGIIEFKALSKDNLLQIVELMLADVNKRLSSNNIRLDVTDKVKEKL 686
NTDB id 243 SPR RS03635 WP 000882517.1 GFGAAREGR.....TNSVLGELGNFFSPEFMNRFDGIIEFKALSKDNLLQIVELMLADVNKRLSSNNIRLDVTDKVKEKL 686
NTDB id 241 SP RS04015 WP 000882523.1 GFGAAREGR.....TNSVLGELGNFFSPEFMNRFDGIIEFKALSKDNLLQIVELMLADVNKRLSSNNIRLDVTDKVKEKL 686
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NTDB id 85 BSU 00860 NP 387967.1 GFNVQDETQNHKDMKDKVMGELKRAFRPEFINRIDEIIVFHSLEKKHLTEIVSLMSDQLTKRLKEQDLSIELTDAAKAKV 751
NTDB id 610 V4T04 RS10165 WP 012897346.1 GFGAKNITADYSAMKSRILEELKRHYRPEFLNRIDENIVFHSLESQEIEQIVKIMSKSLIKRLAEQDIHVKLTPSAVKLI 760
NTDB id 290 KZH43 RS10025 WP 001109677.1 GFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLAEKGIDLKLQASALKLL 755
NTDB id 289 SPD RS10700 WP 001109677.1 GFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLAEKGIDLKLQASALKLL 755
NTDB id 287 SP RS11210 WP 001109712.1 GFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLTEKGIDLKLQASALKLL 755
NTDB id 377 SMU RS09275 WP 002262344.1 GFGAKSFSQDYKAMESRILEELKKVYRPEFINRIDEKVVFHNLGQEDIRHIVKIMVAPLIAHLADQGITLKFQPSALKHL 758
NTDB id 297 STER RS00545 WP 011680614.1 GFGAQTISHNHQAMQARIMEELKKSYRPEFINRIDEKVVFHSLEEEQLHDIVKIMVKPLISALADKGISLKFQPAALKHL 761
NTDB id 329 STU RS10020 WP 011225298.1 GFGAQTISHNHQAMQARIMEELKKSYRPEFINRIDEKVVFHSLEEEQLHDIVKIMVKPLISALADKGISLKFQPAALKHL 761
consensus




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NTDB id 601 KW2 RS02615 WP 021036805.1        VDLGYNPAMGARPLRRTIQENIEDSIADFYIEHPEYKQLVA.DLIDDKIVISNQTQETAETTDEEVPAE   748
NTDB id 378 SMU RS02690 WP 002263569.1        VDLGYDPKMGARPLRRTIQEHIEDAITDFYLEHPEQKELKA.IMTSNGKIVIKASNK.VETVTKATSD.   753
NTDB id 281 KZH43 RS03550 WP 000882517.1      VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKDLKA.VMTSKGNIQIKSAKK.AEVKSSEKEK.   752
NTDB id 245 SPD RS03860 WP 000882517.1        VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKDLKA.VMTSKGNIQIKSAKK.AEVKSSEKEK.   752
NTDB id 243 SPR RS03635 WP 000882517.1        VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKDLKA.VMTSKGNIQIKSAKK.AEVKSSEKEK.   752
NTDB id 241 SP RS04015 WP 000882523.1         VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKDLKA.VMTSKGNIQIKSAKK.AEVKSSEKEK.   752
NTDB id 109714 A9C19 RS19755 WP 072581487.1   AEEGVDLEYGARPLRRSIQKNVEDRLSEELLRGNIHKGQKIVLDVENNEFVVKTTAT......EAVN..   813
NTDB id 85 BSU 00860 NP 387967.1              AEEGVDLEYGARPLRRAIQKHVEDRLSEELLRGNIHKGQHIVLDVEDGEFVVKTTAK......TN....   810
NTDB id 610 V4T04 RS10165 WP 012897346.1      AEVGFDPEYGARPLRKALQKEVEDLLSEQLLSGEIKAGNHVSIGASNKKIKIAQIV.............   816
NTDB id 290 KZH43 RS10025 WP 001109677.1      ANQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA..............   810
NTDB id 289 SPD RS10700 WP 001109677.1        ANQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA..............   810
NTDB id 287 SP RS11210 WP 001109712.1         ANQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSTLKIGVKAGQLKFDIA..............   810
NTDB id 377 SMU RS09275 WP 002262344.1        ALAGYDAEMGARPLRRTLQTEVEDKLAELILSGKLASGQTLKIGIQKEKLKFDIV..............   813
NTDB id 297 STER RS00545 WP 011680614.1       AKDGYDIEMGARPLRRTIQTQVEDKLSELLLGGQVVSGQTLKIGCSKDKLTFTVV..............   816
NTDB id 329 STU RS10020 WP 011225298.1        AKDGYDIEMGARPLRRTIQTQVEDKLSELLLGGQVVSGQTLKIGCSKDKLTFTVV..............   816
consensus                                     ** !*****!!!!!!***!  *!! *** ** * *  *  * * *    * *
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X non conserved

X similar

X ≥ 50% conserved