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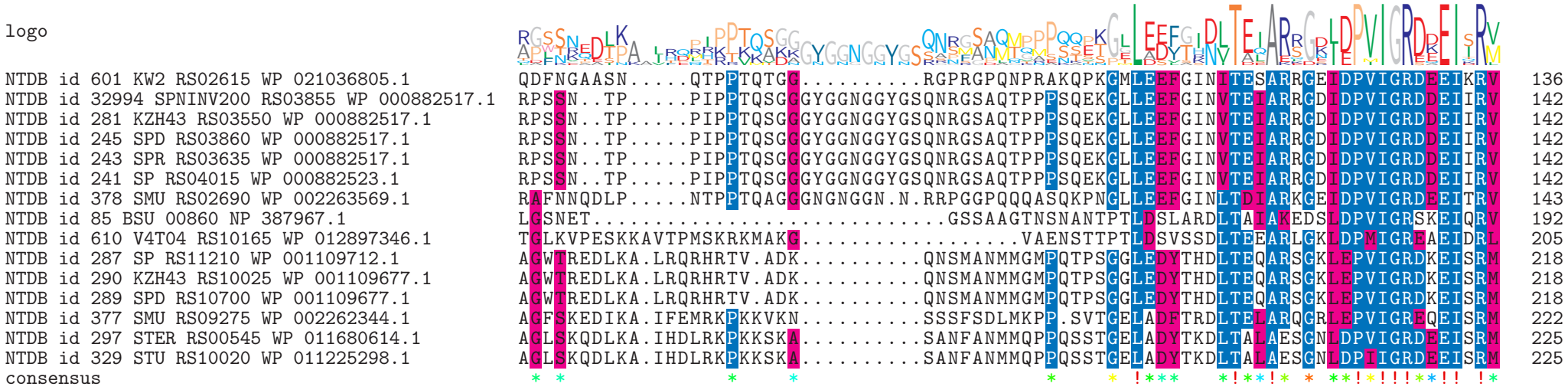


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NTDB id 290 KZH43 RS10025 WP 001109677.1        .....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE.....EVALELTETDYS  70
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consensus                                           * *  *  * ** **  *    *   *  * *  *** * * *                    *   *    *
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consensus


logo
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consensus

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consensus                                        **********  **!*!** *  *!!*!!!!!*!!!!*****!!!!  !!   !!!!*!!*!!   * ***!*******!!
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consensus                                        !*  **!**!  !  *! !***!  ** !!*  * !!!*!!!!*!!** *** *    * ***   * *       !
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NTDB id 329 STU RS10020 WP 011225298.1          ISGDIGAAVKQYKANQ.........K.....AKFPKPALVDADQIMQTLSRLSGIPVEKMTQTDSKRYLNLESELHKRVI  521
consensus                                        * **   **       *   *           *      ****  *  **   * *!*  *   *   ****  *!  *!**
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consensus                                        !!**!*  *  *!*!!** !* *  !!*!!!*!*!!!!!!!!!!** !!  *!* ** **!*!!!!*!!!*  *!*!*!!
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logo

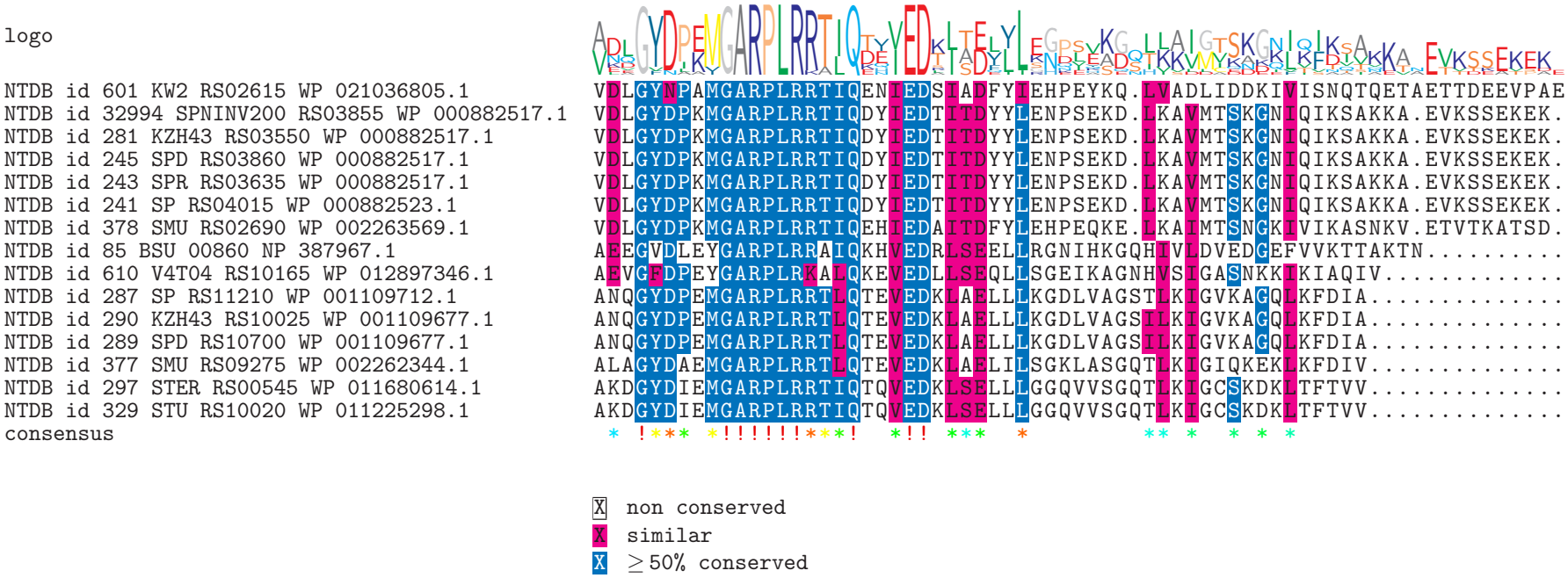


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NTDB id 32994 SPNINV200 RS03855 WP 000882517.1 GYVGYDEAGQLTEKVRHNPYSLILLDEVEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDAIIIMTSNAGTGK..TEASV   611
NTDB id 281 KZH43 RS03550 WP 000882517.1        GYVGYDEAGQLTEKVRHNPYSLILLDEVEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDAIIIMTSNAGTGK..TEASV   611
NTDB id 245 SPD RS03860 WP 000882517.1          GYVGYDEAGQLTEKVRHNPYSLILLDEVEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDAIIIMTSNAGTGK..TEASV   611
NTDB id 243 SPR RS03635 WP 000882517.1          GYVGYDEAGQLTEKVRHNPYSLILLDEVEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDAIIIMTSNAGTGK..TEASV   611
NTDB id 241 SP RS04015 WP 000882523.1           GYVGYDEAGQLTEKVRHNPYSLILLDEVEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDAIIIMTSNAGTGK..TEASV   611
NTDB id 378 SMU RS02690 WP 002263569.1          GYVGYEEAGQLTEKVRRNPYSLILLDEVEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDTIIIMTSNAGTGK..SEANV   612
NTDB id 85 BSU 00860 NP 387967.1                GYVGYDEGGQLTEKVRRKPYSVVLLDEIEKAHPDVFNILLQVLEDGRLTDSKGRTVDFRNTILIMTSNVGASELKRNKYV   671
NTDB id 610 V4T04 RS10165 WP 012897346.1        GYVGYDEGGQLTERVRNKPYSVVLLDEVEKAHPDVFNIMLQILDDGFVTDTKGRKVDFRNTIIIMTSNLGATALRDDKTV   680
NTDB id 287 SP RS11210 WP 001109712.1           GYVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTV   675
NTDB id 290 KZH43 RS10025 WP 001109677.1        GYVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTV   675
NTDB id 289 SPD RS10700 WP 001109677.1          GYVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRDDKTV   675
NTDB id 377 SMU RS09275 WP 002262344.1          GYVGYEEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNILLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTV   678
NTDB id 297 STER RS00545 WP 011680614.1         GYVGYDEGGELTEKVRNKPYSVLLFDETEKAHPDIFNILLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTV   681
NTDB id 329 STU RS10020 WP 011225298.1          GYVGYDEGGELTEKVRNKPYSVLLFDEIEKAHPDIFNVLLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRDDKTV   681
consensus                                       !!!!!*!*!*!!!*!!  !!!**!*!!*!!!!!!*  * !!*!*!! *!!  !! ! !* ***!!!!! !      * *!
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NTDB id 601 KW2 RS02615 WP 021036805.1          GFGAAREG.....RTKSVLGQLGDFFSPEFMNRFDGIIEFSALSKENLLKIVDLMLDEVNEQIGRNDIHLSVTQAAKEKL   680
NTDB id 32994 SPNINV200 RS03855 WP 000882517.1 GFGAAREG.....RTNSVLGELGNFFSPEFMNRFDGIIEFKALSKDNLLQIVELMLADVNKRLSSNNIRLDVTDKVKEKL   686
NTDB id 281 KZH43 RS03550 WP 000882517.1        GFGAAREG.....RTNSVLGELGNFFSPEFMNRFDGIIEFKALSKDNLLQIVELMLADVNKRLSSNNIRLDVTDKVKEKL   686
NTDB id 245 SPD RS03860 WP 000882517.1          GFGAAREG.....RTNSVLGELGNFFSPEFMNRFDGIIEFKALSKDNLLQIVELMLADVNKRLSSNNIRLDVTDKVKEKL   686
NTDB id 243 SPR RS03635 WP 000882517.1          GFGAAREG.....RTNSVLGELGNFFSPEFMNRFDGIIEFKALSKDNLLQIVELMLADVNKRLSSNNIRLDVTDKVKEKL   686
NTDB id 241 SP RS04015 WP 000882523.1           GFGAAREG.....RTNSVLGELGNFFSPEFMNRFDGIIEFKALSKDNLLQIVELMLADVNKRLSSNNIRLDVTDKVKEKL   686
NTDB id 378 SMU RS02690 WP 002263569.1          GFGASREG.....RTNSVLGELGNFFSPEFMNRFDGIIEFQALSKDNLLQIVSLMLDDVNQRLAVNAIHLDVTDKVKEKL   687
NTDB id 85 BSU 00860 NP 387967.1                GFNVQDETQNHKDMKDKVMGELKRAFRPEFINRIDEIIVFHSLEKKHLTEIVSLMSDQLTKRLKEQDLSIELTDAAKAKV   751
NTDB id 610 V4T04 RS10165 WP 012897346.1        GFGAKNITADYSAMKSRILEELKRHYRPEFLNRIDENIVFHSLESQEIEQIVKIMSKSLIKRLAEQDIHVKLTPSAVKLI   760
NTDB id 287 SP RS11210 WP 001109712.1           GFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLTEKGIDLKLQASALKLL   755
NTDB id 290 KZH43 RS10025 WP 001109677.1        GFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLAEKGIDLKLQASALKLL   755
NTDB id 289 SPD RS10700 WP 001109677.1          GFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSSDHMQEVVKIMVKPLVASLAEKGIDLKLQASALKLL   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 VDLGYNPAMGARPLRRTIQENIEDSIADFYIEHPEYKQ.LVADLIDDKIVISNQTQETAETTDEEVPAE 748
NTDB id 32994 SPNINV200 RS03855 WP 000882517.1 VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKD.LKAVMTSKGNIQIKSAKKA.EVKSSEKEK. 752
NTDB id 281 KZH43 RS03550 WP 000882517.1 VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKD.LKAVMTSKGNIQIKSAKKA.EVKSSEKEK. 752
NTDB id 245 SPD RS03860 WP 000882517.1 VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKD.LKAVMTSKGNIQIKSAKKA.EVKSSEKEK. 752
NTDB id 243 SPR RS03635 WP 000882517.1 VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKD.LKAVMTSKGNIQIKSAKKA.EVKSSEKEK. 752
NTDB id 241 SP RS04015 WP 000882523.1 VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKD.LKAVMTSKGNIQIKSAKKA.EVKSSEKEK. 752
NTDB id 378 SMU RS02690 WP 002263569.1 VDLGYDPKMGARPLRRTIQEHIEDAITDFYLEHPEQKE.LKAIMTSNGKIVIKASNKV.ETVTKATSD. 753
NTDB id 85 BSU 00860 NP 387967.1 AEEGVDLEYGARPLRRAIQKHVEDRLSEELLRGNIHKGQHIVLDVEDGEFVVKTTAKTN..... 810
NTDB id 610 V4T04 RS10165 WP 012897346.1 AEVGFDPEYGARPLRKALQKEVEDLLSEQLLSGEIKAGNHVSIGASNKKIKIAQIV..... 816
NTDB id 287 SP RS11210 WP 001109712.1 ANQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSTLKIGVKAGQLKFDIA..... 810
NTDB id 290 KZH43 RS10025 WP 001109677.1 ANQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA..... 810
NTDB id 289 SPD RS10700 WP 001109677.1 ANQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA..... 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
non conserved
similar
≥ 50% conserved