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NTDB id 85 BSU 00860 NP 387967.1                ..MMFGRFTERAQKVLALAQEEALRLGHNNIGTEHILLGLVREGEGIAAKALQALGLGSEKIQKEVESLIG........R   70
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NTDB id 289 SPD RS10700 WP 001109677.1          .....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE.....EVALELTETDYS   70
NTDB id 287 SP RS11210 WP 001109712.1           .....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE.....EVALELTETDYS   70
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consensus                                             **              *       * * *** ***     **
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NTDB id 329 STU RS10020 WP 011225298.1          ESDIIDLRAQSPALEAMLQEAQGIASVTGAVEVGSEHVLMAFLLHKDLMVCRLLEVAGFQYKDDSDKPRIIDLRRSLERN   156
consensus                                          ** *   * *  *  ** *       *     *******.*** * * *     **                **   **
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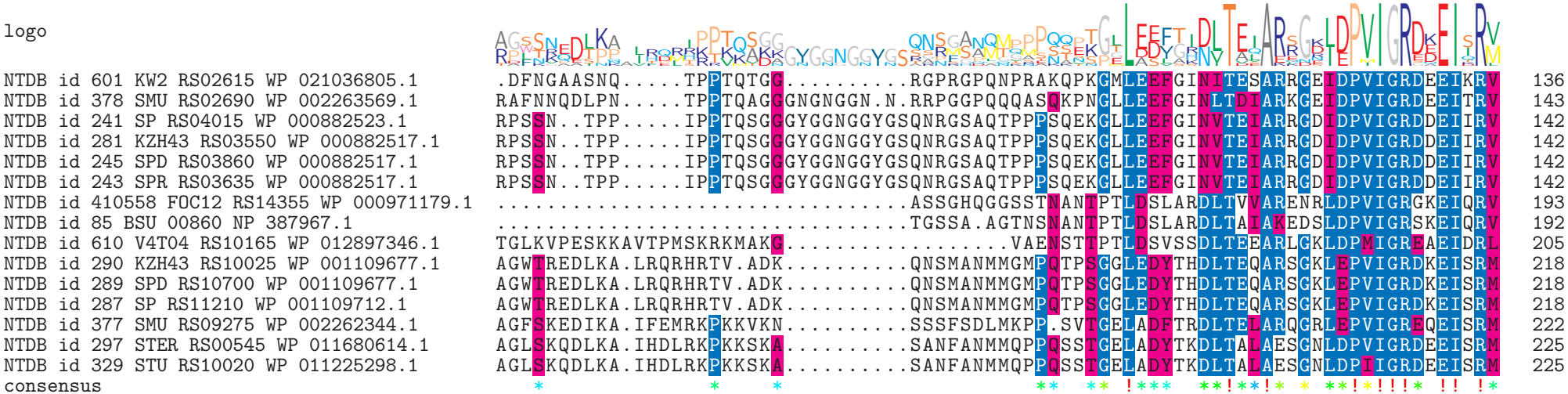
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NTDB id 297 STER RS00545 WP 011680614.1 AGLSKQDLKA.IHDLRKPKKSKA.....SANFANMMQPPQSSTGELADYTKDLTALAESGNLDPVIGRDEEISRM 225
NTDB id 329 STU RS10020 WP 011225298.1 AGLSKQDLKA.IHDLRKPKKSKA.....SANFANMMQPPQSSTGELADYTKDLTALAESGNLDPIIGRDEEISRM 225
consensus

logo
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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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NTDB id 378 SMU RS02690 WP 002263569.1       GYVGYEEAGQLTEKVRRNPYSLILLDEVEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDTIIIMTSNAGTGK..SEANV   612
NTDB id 241 SP RS04015 WP 000882523.1        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 410558 FOC12 RS14355 WP 000971179.1  GYVGYEEGGQLTEKVRRKPYSVVLLDEVEKAHPDVFNILLQVLEDGRLTDSKGRTVDFRNTIVIMTSNVGAEALKRNKHL   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                                    !!!!!*!*!*!!!*!! *!!!**!*!!*!!!!!!*****!!*!*!! *!!**!! !*!*****!!!!!*!*  ** ****
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NTDB id 601 KW2 RS02615 WP 021036805.1       GFGAAREGR.....TKSVLGQLGDFFSPEFMNRFDGIIEFSALSKENLLKIVDLMLDEVNEQIGRNDIHLSVTQAAKEKL   680
NTDB id 378 SMU RS02690 WP 002263569.1       GFGASREGR.....TNSVLGELGNFFSPEFMNRFDGIIEFQALSKDNLLQIVSLMLDDVNQRLAVNAIHLDVTDKVKEKL   687
NTDB id 241 SP RS04015 WP 000882523.1        GFGAAREGR.....TNSVLGELGNFFSPEFMNRFDGIIEFKALSKDNLLQIVELMLADVNKRLSSNNIRLDVTDKVKEKL   686
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 410558 FOC12 RS14355 WP 000971179.1  GFNVQDESRDYSDMKGKVMDELKKAFRPEFLNRIDEIIVFHMLEKKHIQEIVTLMVNQLVNRLKEQEIELHLTEGAISAI   752
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          VDLGYNPAMGARPLRRTIQENIEDSIADFYIEHPEYKQLV.ADLIDDKIVISNQTQETAETTDEEVPAE   748
NTDB id 378 SMU RS02690 WP 002263569.1          VDLGYDPKMGARPLRRTIQEHIEDAITDFYLEHPEQKELK.AIMTSNGKIVIKASNK.VETVTKATSD.   753
NTDB id 241 SP RS04015 WP 000882523.1           VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKDLK.AVMTSKGNIQIKSAKK.AEVKSSEKEK.   752
NTDB id 281 KZH43 RS03550 WP 000882517.1        VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKDLK.AVMTSKGNIQIKSAKK.AEVKSSEKEK.   752
NTDB id 245 SPD RS03860 WP 000882517.1          VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKDLK.AVMTSKGNIQIKSAKK.AEVKSSEKEK.   752
NTDB id 243 SPR RS03635 WP 000882517.1          VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKDLK.AVMTSKGNIQIKSAKK.AEVKSSEKEK.   752
NTDB id 410558 FOC12 RS14355 WP 000971179.1     ADKGFDREYGARPLRRAIQKHVEDRLSEELLKGAIEKGQKVIFDVEGESFVIHSAEKVK..........   811
NTDB id 85 BSU 00860 NP 387967.1                AEEGVDLEYGARPLRRAIQKHVEDRLSEELLRGNIHKGQHIVLDVEDGEFVVKTTAKTN..........   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