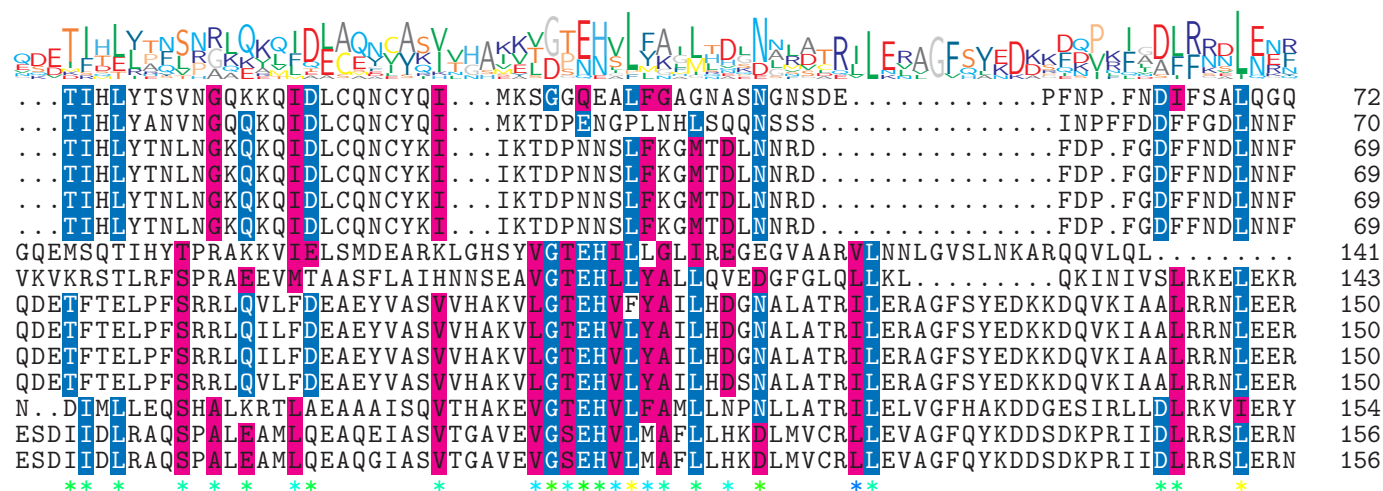
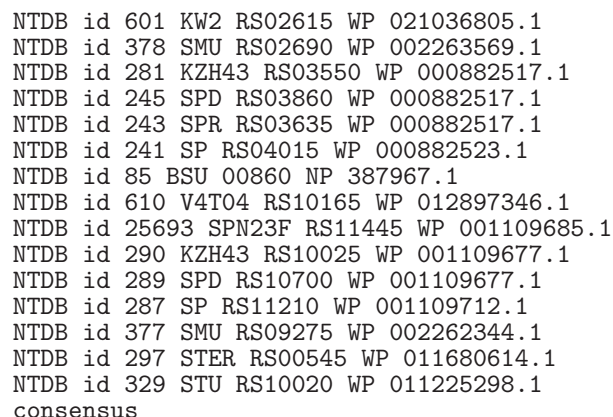


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consensus

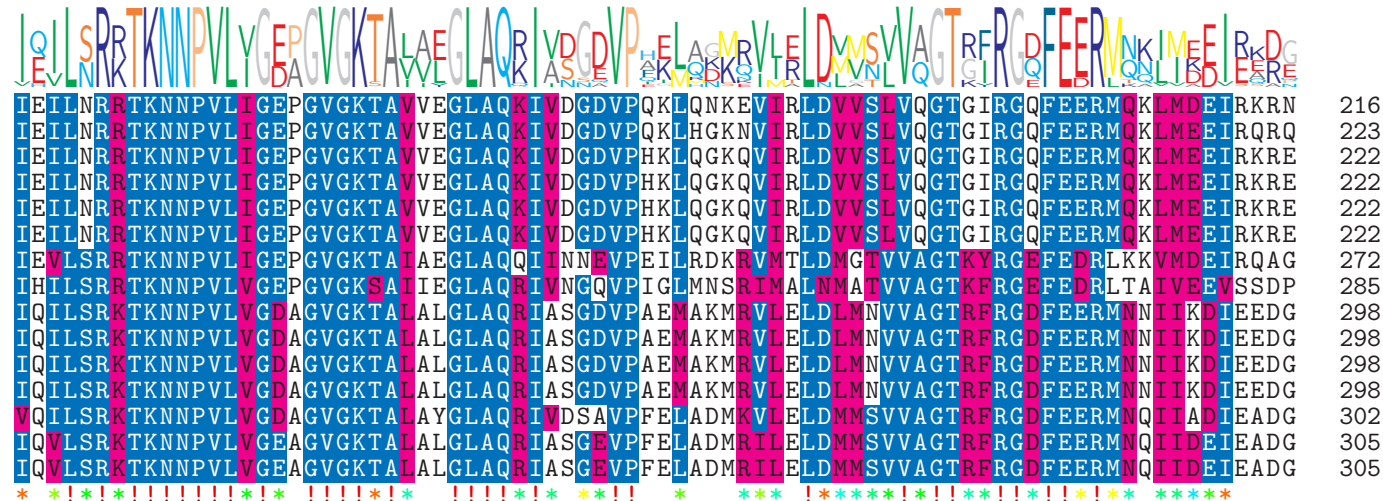
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consensus

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| Sequence                                                                           | Score |
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| GVVGYEEAGQLTEKVRNKPYSVLLFDEVEKAHPDVMHMFLLQVLDGRLTDAQGRTVSFKDTIIIMTSNAGTGK..SEANV   | 612   |
| GVVGYDEAGQLTEKVRHNKPYSVLLFDEVEKAHPDVMHMFLLQVLDGRLTDAQGRTVSFKDAIIIMTSNAGTGK..TEASV  | 611   |
| GVVGYDEAGQLTEKVRHNKPYSVLLFDEVEKAHPDVMHMFLLQVLDGRLTDAQGRTVSFKDAIIIMTSNAGTGK..TEASV  | 611   |
| GVVGYDEAGQLTEKVRHNKPYSVLLFDEVEKAHPDVMHMFLLQVLDGRLTDAQGRTVSFKDAIIIMTSNAGTGK..TEASV  | 611   |
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| GVVGYDEGGQLTEKVRNKPYSVLLFDEVEKAHPDVFNILLQVLEDGRLTDSKGRVTDFRNTILIMTSNVGASELKRNKYV   | 671   |
| GVVGYDEGGQLTEKVRNKPYSVLLFDEVEKAHPDVFNIMLLQVLDGDFVTDTKGRKVDFRNTIIIMTSNGLGATALRDDKTV | 680   |
| GVVGYEEGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDGVLTDVSKGRKVDFSNTIIIMTSNGLGATALRDDKTV   | 675   |
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| GVVGYDEGELTEKVRNKPYSVLLFDETEKAHPDIFNVLLQVLDGVLTDVSRGRKVDFSNTIIIMTSNGLGATALRDDKTV   | 681   |
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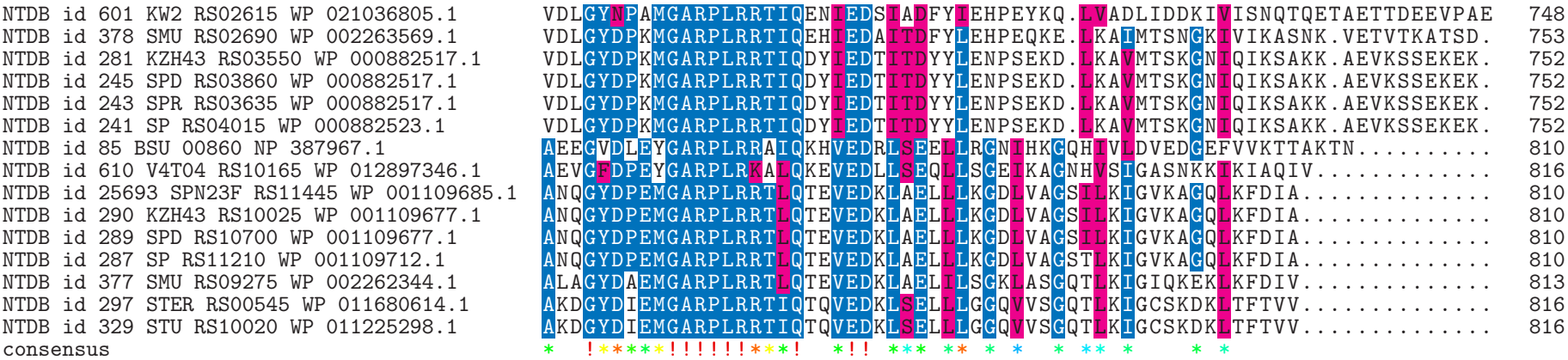
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| Sequence                               | Position |
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| GFGAAREG . . . . . RTNSVL GELGNFFS     | 686      |
| GFNVQDETQNHKDKDKVMGELKRAFRPEFINRIDEI   | 751      |
| GFGAKNITADYSAMKSRILEELKRHRVPEFINRIDEIN | 760      |
| GFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEK  | 755      |
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| GFGAKSFSQDYKAMESRILEELKKVYRPEFINRIDEK  | 758      |
| GFGAQTISHNHQAMQARIMEELKKSYPPEFINRIDEK  | 761      |
| GFGAQTISHNHQAMQARIMEELKKSYPPEFINRIDEK  | 761      |

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logo



  non conserved  
  similar  
  ≥ 50% conserved