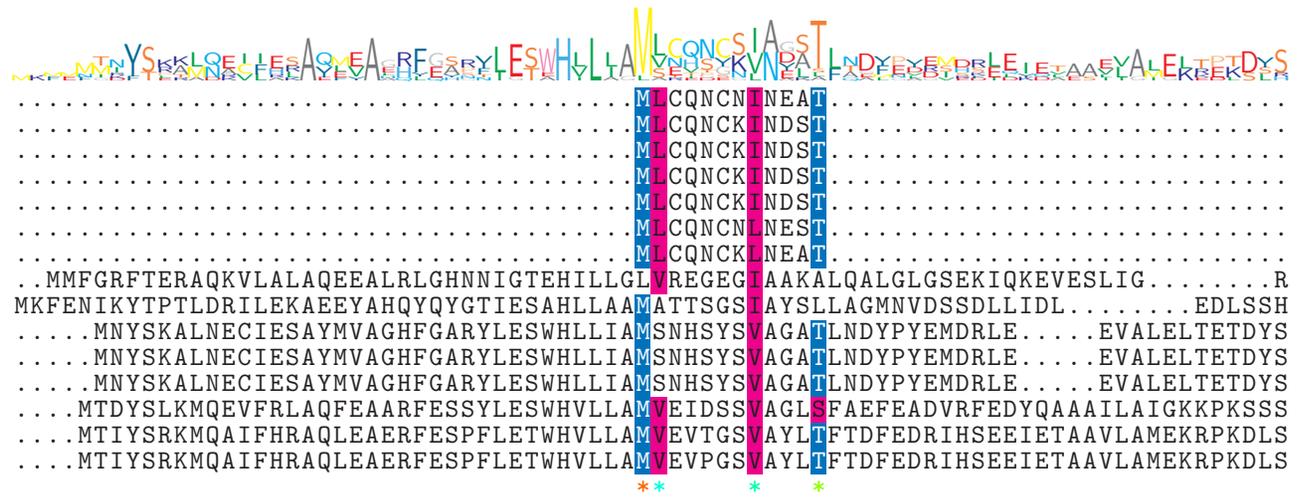


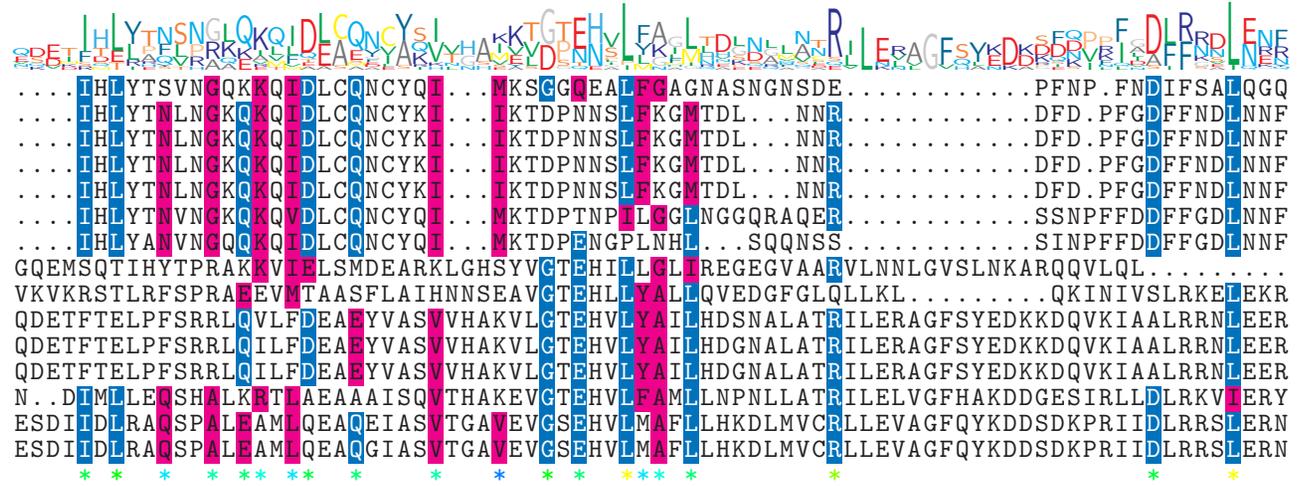
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 NTDB id 289 SPD RS10700 WP 001109677.1
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 NTDB id 329 STU RS10020 WP 011225298.1
 consensus



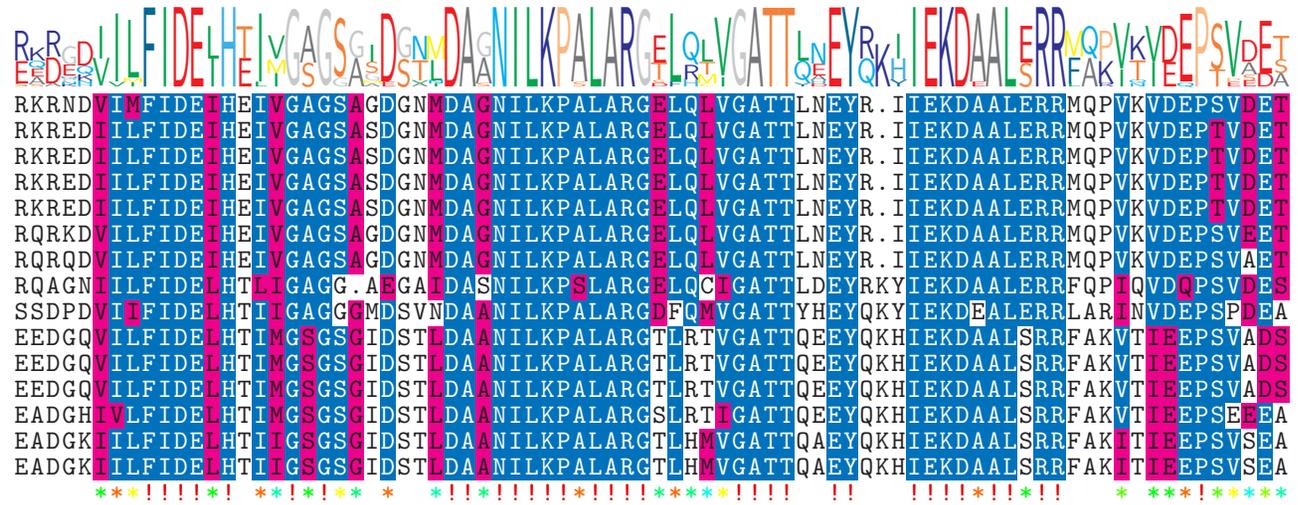
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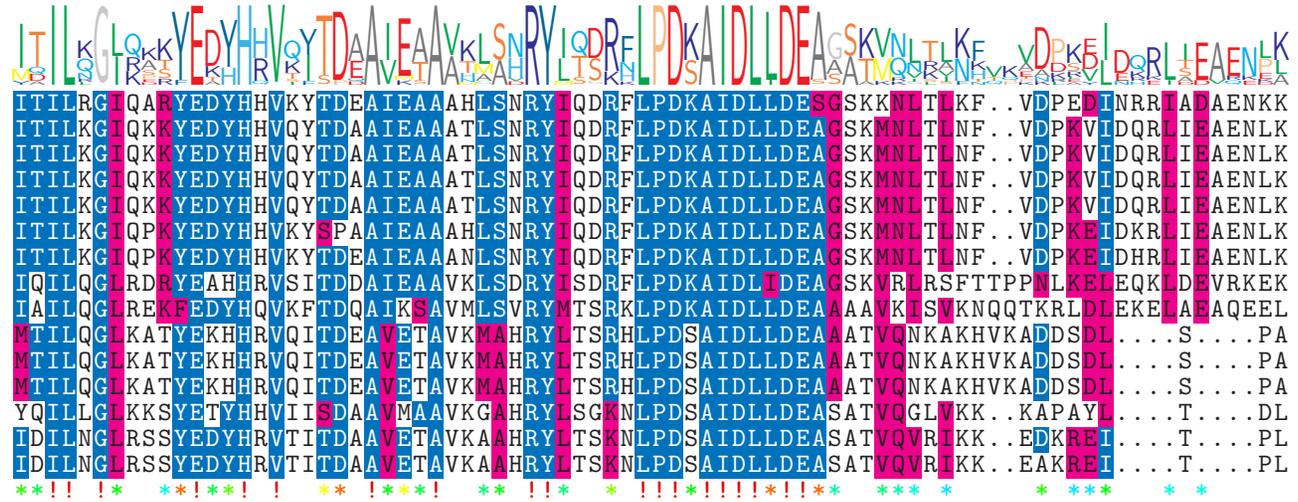
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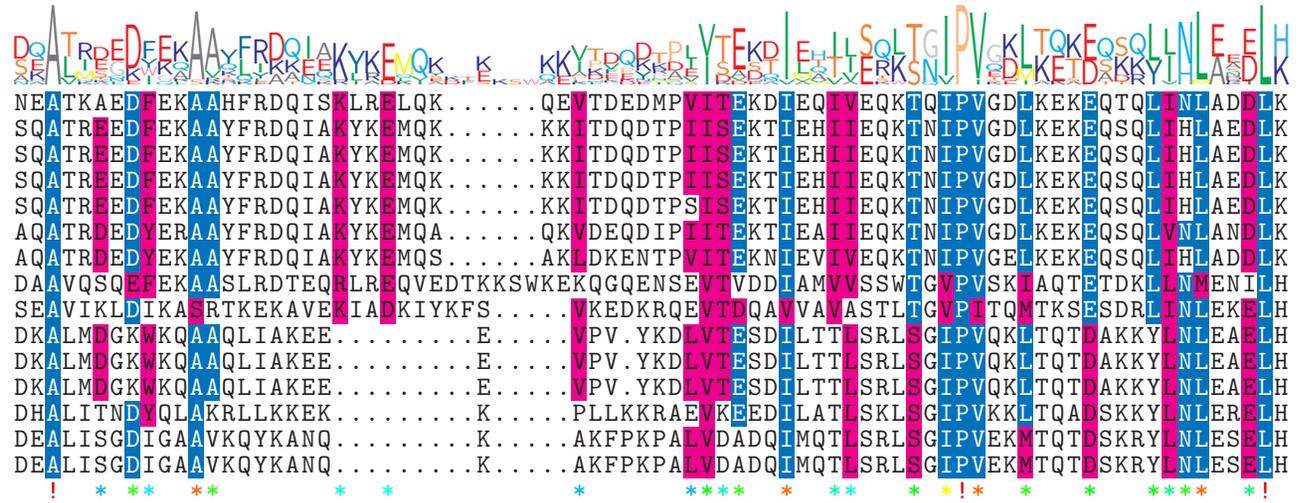
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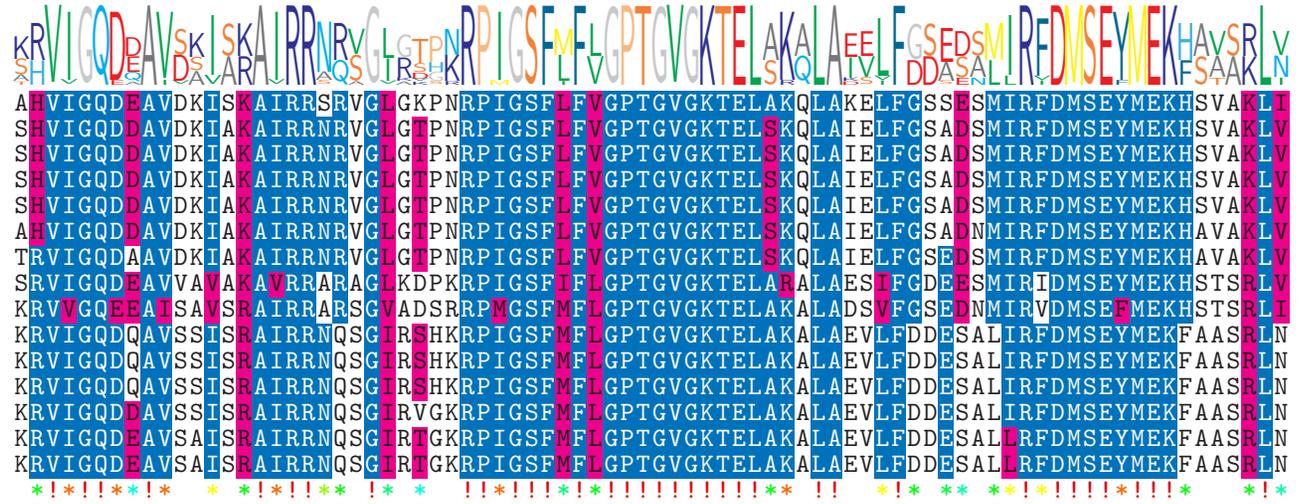
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 consensus



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 consensus

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 GAPPGYVGYEAGQLTEKVRNHPYSLLLLDEVEKAHPDVMHMFLLQVLEDDGRLTDGQGRTVSEFKDAIIIMTSNAGTGK..T 607
 GAPPGYVGYEAGQLTEKVRNHPYSLLLLDEVEKAHPDVMHMFLLQVLEDDGRLTDGQGRTVSEFKDAIIIMTSNAGTGK..T 607
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 GAPPGYVGYEAGQLTEKVRNHPYSLLLLDEVEKAHPDVMHMFLLQVLEDDGRLTDGQGRTVSEFKDTIIIMTSNAGTGK..S 614
 GAPPGYVGYEAGQLTEKVRNHPYSLLLLDEVEKAHPDVMHMFLLQVLEDDGRLTDGQGRTVSEFKDTIIIMTSNAGTGK..S 608
 GSPPGYVGYDEGGQLTEKVRNHPYSVLLLEVEKAHPDVFNMLLQVLEDDGRLTDSKGRTVDFRNTIILIMTSNVGASELKR 667
 GAPPGYVGYDEGGQLTEKVRNHPYSVLLLEVEKAHPDVFNMLLQVLEDDGRLTDSKGRKVDFSNTIIIMTSNLAGATALRD 676
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 consensus

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 EASVGFGAAREG.....RTNSVLGELGNFFSPEFMNRFDGIIEFKALSNDLLQIVELMLADV NKR LSSNNIRLDVTDKV 682
 EASVGFGAAREG.....RTNSVLGELGNFFSPEFMNRFDGIIEFKALSNDLLQIVELMLADV NKR LSSNNIRLDVTDKV 682
 EASVGFGAAREG.....RTNSVLGELGNFFSPEFMNRFDGIIEFKALSNDLLQIVELMLADV NKR LSSNNIRLDVTDKV 682
 EASVGFGAAREG.....RTSSVLGELSNFFSPEFMNRFDGIIEFKALSNDLLHIVDMLLEDV NKR LSYNGIHLDVTDKV 689
 EANVGFGASREG.....RTNSVLGELGNFFSPEFMNRFDGIIEFQALSNDLLQIVSELMLDDV NQR LAVNAIHLDVTDKV 683
 NKYVGFNVQDETQNHKDMKDKVMGELKRAFRPEFINRIDEIVFHSLEKKHTEIVSLSMSDQLTKRLEQDLSIELTDAA 747
 DKTVGFGAKNITADYSAMKSRILEELKRHYRPEFINRIDEIVFHSLESQETEQIVKIMSKSLIKRLAEQDTHVKLTPSA 756
 DKTVGFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSDDHMQEIVKIMVKPLIVASLAEKGDILKIQASA 751
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 consensus



[X] non conserved
 [X] similar
 [X] ≥ 50% conserved