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NTDB id 378 SMU RS02690 WP 002263569.1
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NTDB id 85 BSU 00860 NP 387967.1
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NTDB id 289 SPD RS10700 WP 001109677.1
NTDB id 287 SP RS11210 WP 001109712.1
NTDB id 377 SMU RS09275 WP 002262344.1
NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
consensus

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Protein	Sequence	Score
72	...TIHLYTSVNGQKKQIDLCQNCYQI...MKSGGREALFGAGNASNGNSDE.....PFNP.FNDIFSALQGQ	
70	...TIHLYANVNGQKKQIDLCQNCYQI...MKTDPENGPLNHSQNSSS.....INPFDFFGDLNNF	
69	...TIHLYTNLNGKQKIDLCQNCYKI...IKTDPNNSLFKGMTDLNNRD.....FDP.FGDFFNDLNNF	
69	...TIHLYTNLNGKQKIDLCQNCYKI...IKTDPNNSLFKGMTDLNNRD.....FDP.FGDFFNDLNNF	
69	...TIHLYTNLNGKQKIDLCQNCYKI...IKTDPNNSLFKGMTDLNNRD.....FDP.FGDFFNDLNNF	
69	...TIHLYTNLNGKQKIDLCQNCYKI...IKTDPNNSLFKGMTDLNNRD.....FDP.FGDFFNDLNNF	
146	GTEASQTVHYTPRAKKVIELSMDEARKLGHSYVGTEHILLGLIREGEGVAARVLNNLGVSLNKARQQVLQ...LLGSNE..	
146	GQEMSQTIIHYTPRAKKVIELSMDEARKLGHSYVGTEHILLGLIREGEGVAARVLNNLGVSLNKARQQVLQ...LLGSNE..	
143	VKKVRSTLRFSPRAEEVMTAASFLAIHNSEAVGTEHLYALLQVEDGFGQLKL...KQINIVSLRKELEKR	
150	QDETFTFELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER	
150	QDETFTFELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER	
150	QDETFTFELPFSRRLQVLFDEAEYVASVVHAKVLGTEHVLYAILHDSNALATRILERAGFSYEDKKDQVKIAALRRNLEER	
154	N..DITMLEQSHALKRTLAEAAAISSVTHAKEVGTEHVLFAMLLNPNLLATRILELVGFHAKDDGESIRLLDLRKVTERY	
156	ESDIIDLRAQSPAELAMLQEAQEIASVTGAVEVGSSEHVLMAFLLHKDLMVCRLLEVAGFYQKDDSDKPRIIDLRRSLERN	
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consensus

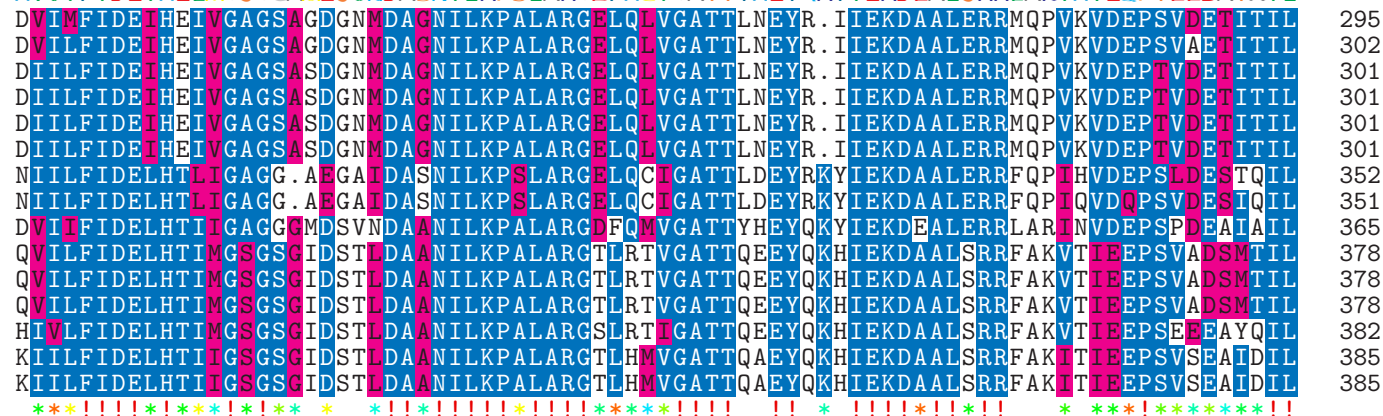
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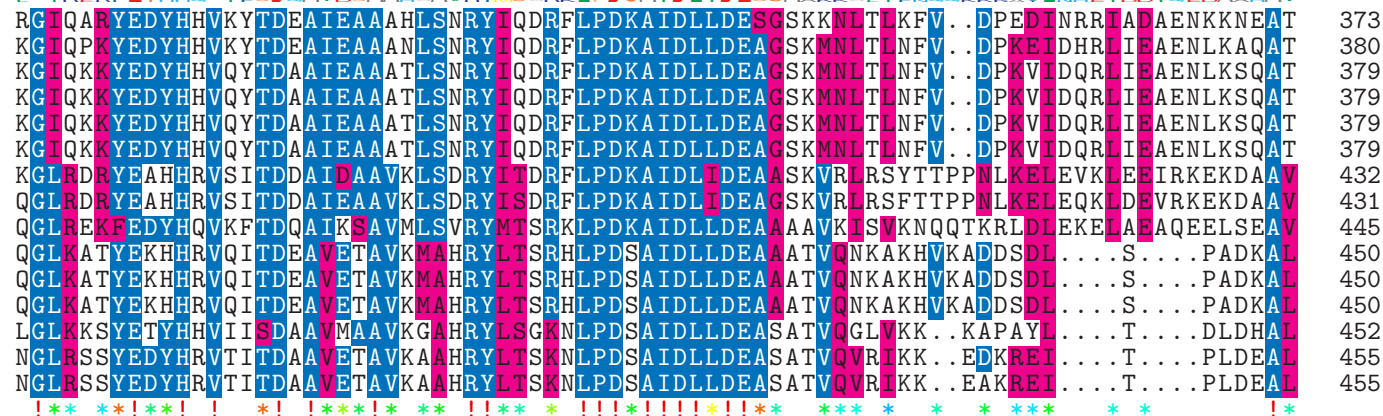
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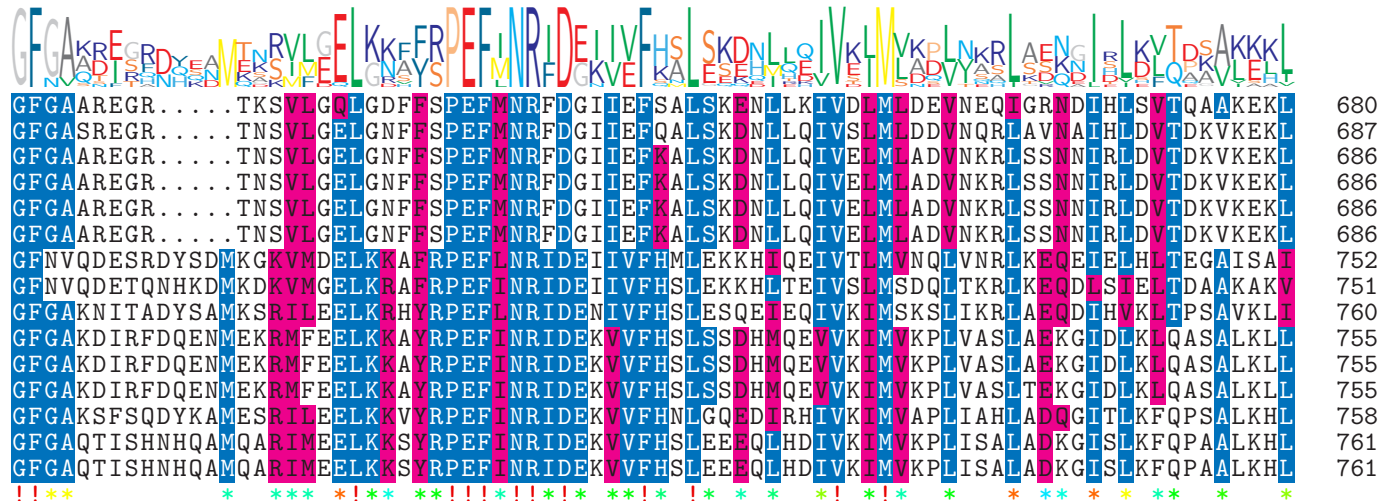
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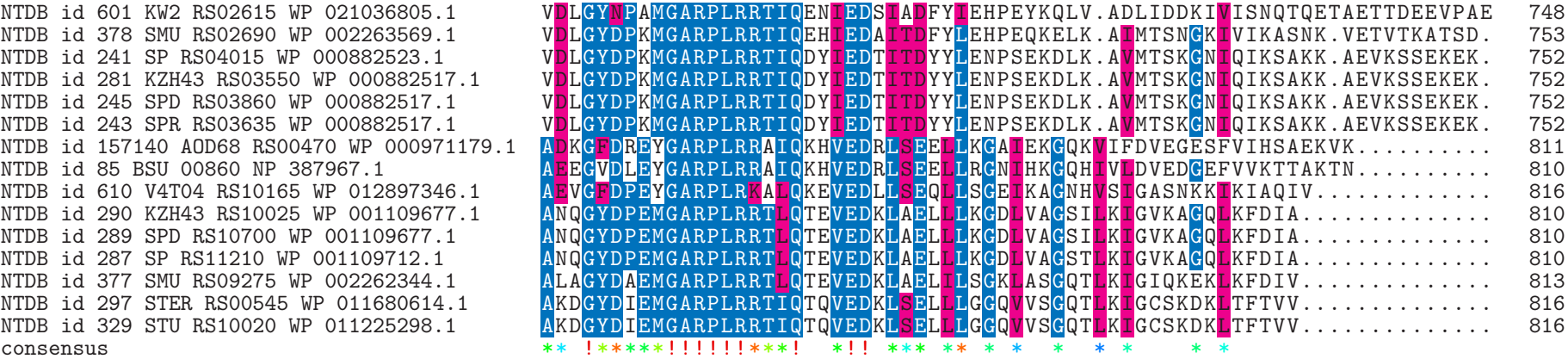
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logo



non conserved
 similar
 ≥ 50% conserved