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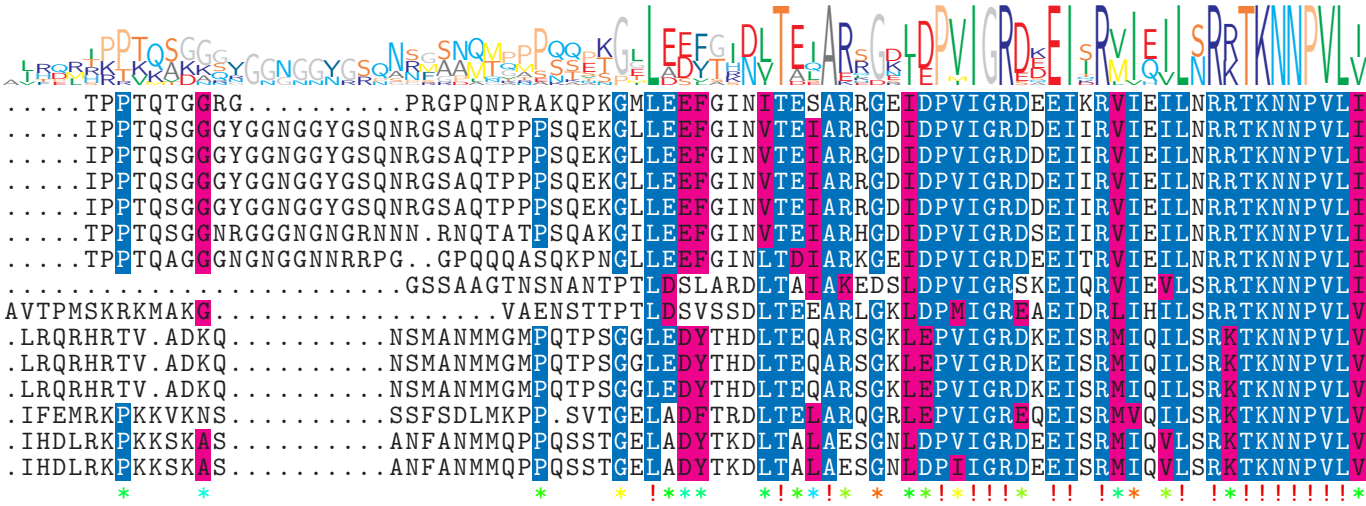
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NTDB id 610 V4T04 RS10165 WP 012897346.1	MKFENIKYTPTLDRILEKAEEYAHQYQYGTIESAHLAAMATTSGSIAYSLLAGMNVDSDDLIDL.....EDLSSHVKVKR	77
NTDB id 290 KZH43 RS10025 WP 001109677.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE.....EVALELTETDYSQDET	75
NTDB id 289 SPD RS10700 WP 001109677.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE.....EVALELTETDYSQDET	75
NTDB id 287 SP RS11210 WP 001109712.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE.....EVALELTETDYSQDET	75
NTDB id 377 SMU RS09275 WP 002262344.1	MTDYSLKMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEFEADVRFEDYQAAAILAIGKKPKSSSN..DI	79
NTDB id 297 STER RS00545 WP 011680614.1	MTIYSRKMQAIFHRAQLEAERFESPFLTWHVLLAMVEVTGSVAYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLSESDII	81
NTDB id 329 STU RS10020 WP 011225298.1	MTIYSRKMQAIFHRAQLEAERFESPFLTWHVLLAMVEVPGSVAYLTFTDFEDRIHSEEIETAAVLAMEKRPKDLSESDII	81
consensus	**.....**	

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NTDB id 610 V4T04 RS10165 WP 012897346.1	STLRFSPRAEEVMTAASFLAIHNNSEAVGTEHLLYALLQVEDGFGQLLKL.....QKINIVSLRKELEKRTGLKVPESKK	153
NTDB id 290 KZH43 RS10025 WP 001109677.1	TELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEERAGWTREDLKA	160
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NTDB id 329 STU RS10020 WP 011225298.1	DLRAQSPALEAMLQEAQGIASVTGAVEVGSEHVLMFAFLHLKDLMVCRILLEVAGFQYKDDSDKPRIIDLRRSLERNAGLSKQDLKA	166
consensus	* * * * * * * * * * * * * *	

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consensus



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consensus



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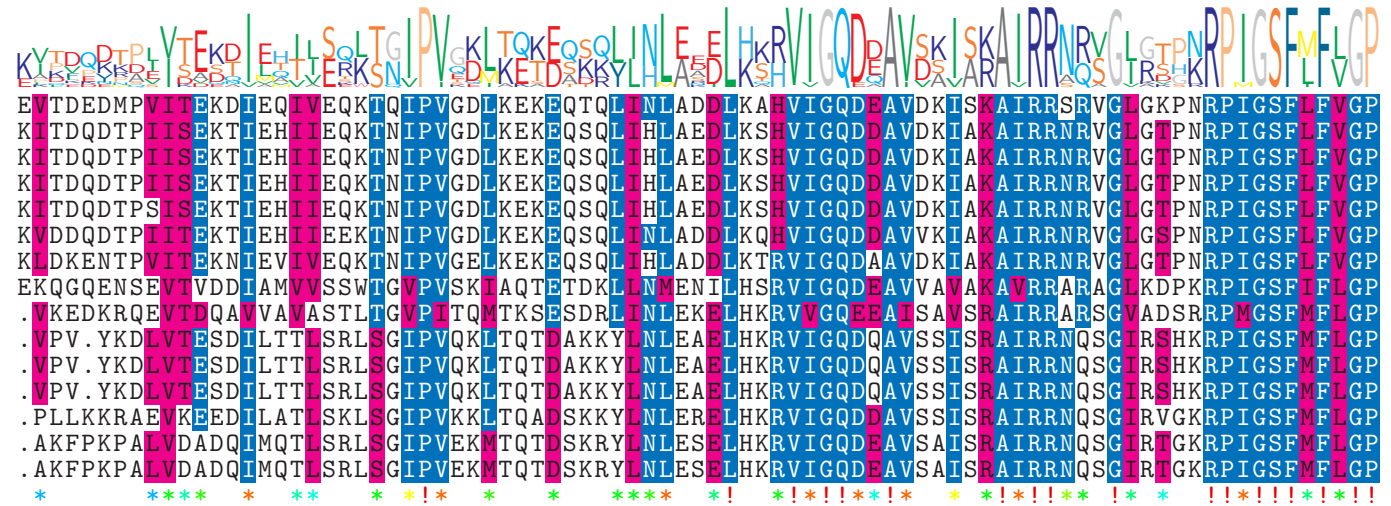


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consensus

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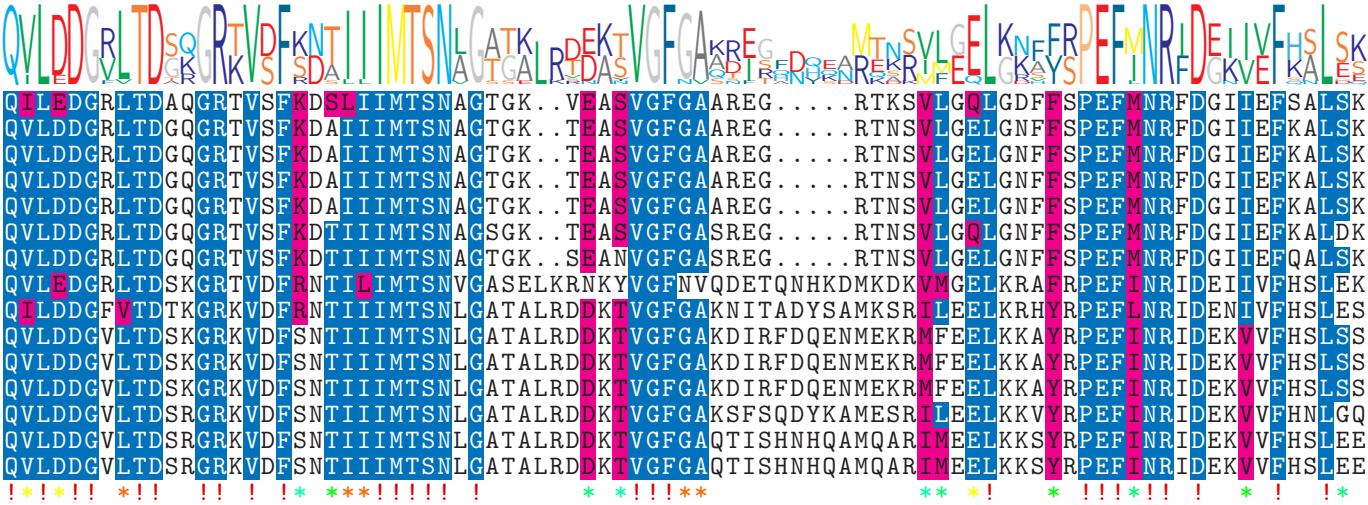
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consensus



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consensus



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consensus		

- X non conserved
- X similar
- X ≥ 50% conserved