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NTDB id 316707 D6869 RS02775 WP 011834563.1	MLCQNCNINEA.....	11
NTDB id 601 KW2 RS02615 WP 021036805.1	MLCQNCNINEA.....	11
NTDB id 378 SMU RS02690 WP 002263569.1	MLCQNCNINEA.....	11
NTDB id 281 KZH43 RS03550 WP 000882517.1	MLCQNCNINEA.....	11
NTDB id 245 SPD RS03860 WP 000882517.1	MLCQNCNINEA.....	11
NTDB id 243 SPR RS03635 WP 000882517.1	MLCQNCNINEA.....	11
NTDB id 241 SP RS04015 WP 000882523.1	MLCQNCNINEA.....	11
NTDB id 85 BSU 00860 NP 387967.1	..MMFGRFTERAQKVLALAQEEALRLGHNNIGTEHILLGLVREGETIAAKALQALGLGSEKIQKEVESLIG.....R	70
NTDB id 610 V4T04 RS10165 WP 012897346.1	MKFENIKYTPTLDRILEKAEEYAHQYQYGTIESAHLAAMATTSGSTIAYSLLAGMNVDSDDLIDL.....EDLSSH	72
NTDB id 290 KZH43 RS10025 WP 001109677.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE.....EVALELTETDYS	70
NTDB id 289 SPD RS10700 WP 001109677.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE.....EVALELTETDYS	70
NTDB id 287 SP RS11210 WP 001109712.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE.....EVALELTETDYS	70
NTDB id 377 SMU RS09275 WP 002262344.1	MTDYSLKMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEFEADVRFEDYQAAAILAIGKKPKSSS	76
NTDB id 297 STER RS00545 WP 011680614.1	MTIYSRKMQAIFHRAQLEAERFESPFLLETWHVLLAMVEVTGSVAYLTFTDFEDRIHSEEIETA AVLAMEKRPKDLS	76
NTDB id 329 STU RS10020 WP 011225298.1	MTIYSRKMQAIFHRAQLEAERFESPFLLETWHVLLAMVEVPGSVAYLTFTDFEDRIHSEEIETA AVLAMEKRPKDLS	76
consensus	MLCQNCNINEA.....	

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NTDB id 378 SMU RS02690 WP 002263569.1	...TIHLYANVNGQKKQIDLCQNCYQ...IMKTDPENGPLNHLISQNSSS.....INPFFDDFFGDLNNF	70
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NTDB id 85 BSU 00860 NP 387967.1	GQEMSQTIHYTPRAKKVIELSMDEARKLGHSYVGTETIHLGLIREGEGVAARVLNNLGVSLNKAQQVLQL.....	141
NTDB id 610 V4T04 RS10165 WP 012897346.1	VKVKRSTLRFSPRAEEVMTAASFLAIHNNSEAVGTEHLLYALLQVEDGFGLQLLKL.....QKINIVSLRKELEKR	143
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NTDB id 289 SPD RS10700 WP 001109677.1	QDETFTTELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER	150
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NTDB id 297 STER RS00545 WP 011680614.1	ESDIIDLRAQSPALEAMLQEAQEIASVTGAVEVGESEHVLMAFLLHKDLMVCRLLEVAGFYKDDSDKPRIIDLRRSLERN	156
NTDB id 329 STU RS10020 WP 011225298.1	ESDIIDLRAQSPALEAMLQEAQGIASVTGAVEVGESEHVLMAFLLHKDLMVCRLLEVAGFYKDDSDKPRIIDLRRSLERN	156
consensus	...TIHLYTSVNGQKKQIDLCQNCYQ...IMKSGGQEAALFGAGNASNGNSDEP.....FNP.FNDIFSALQGG	

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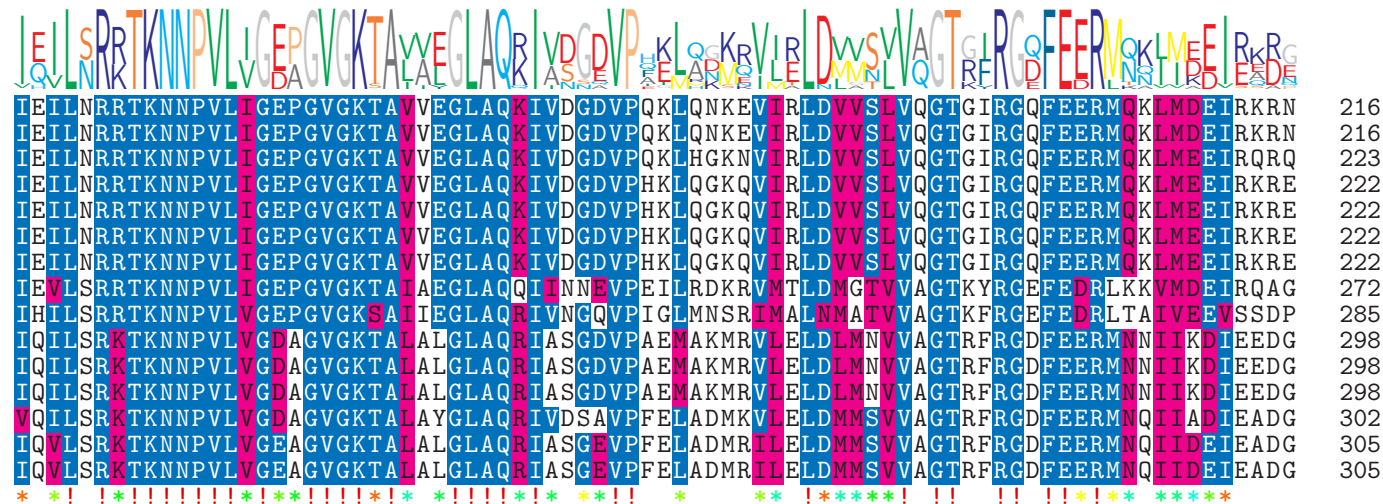
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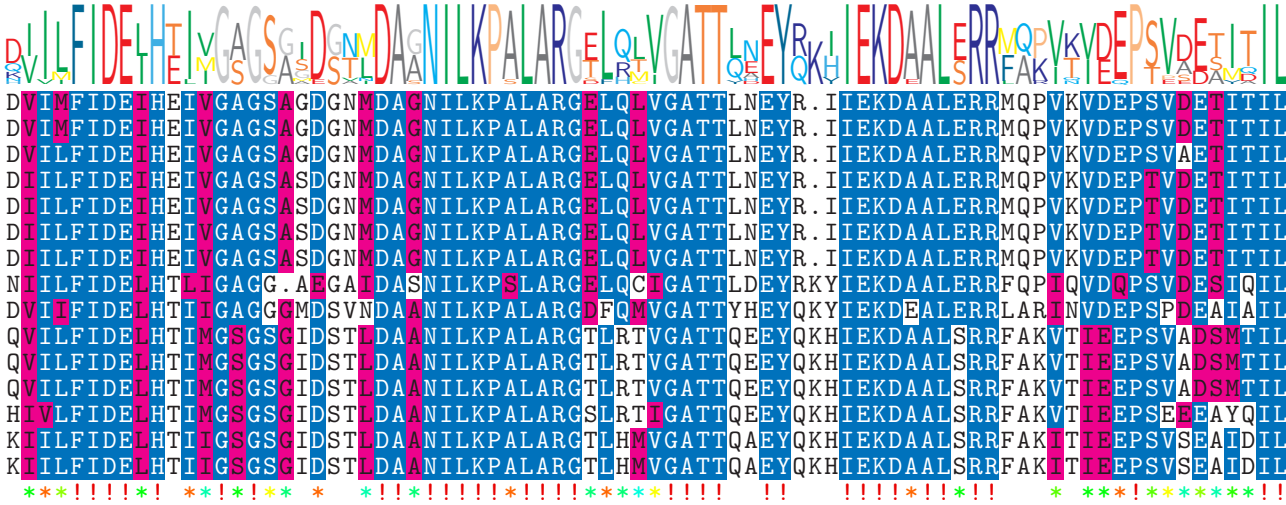
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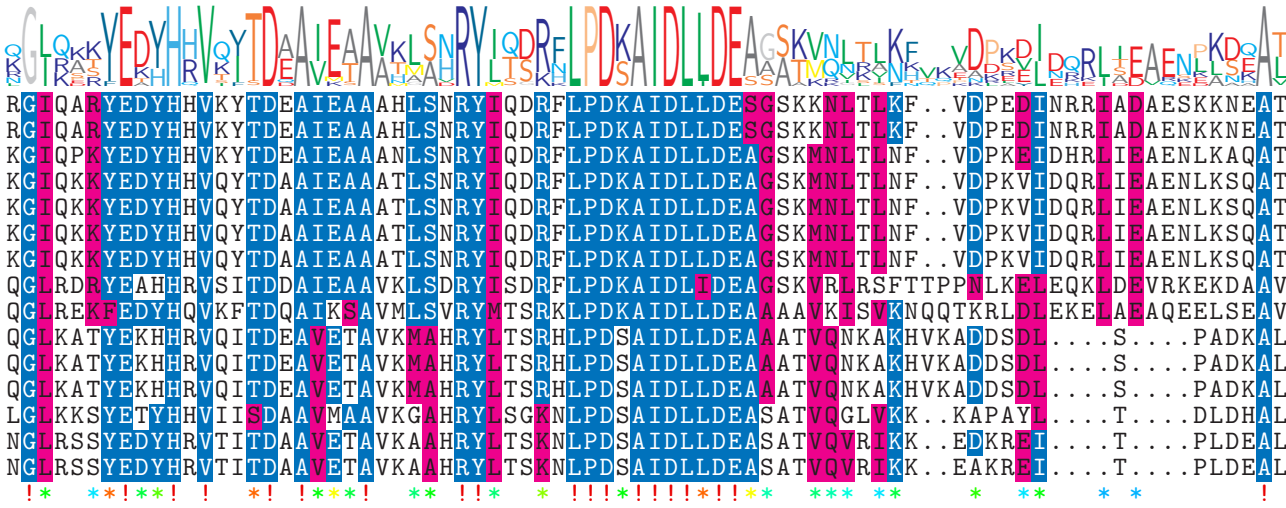
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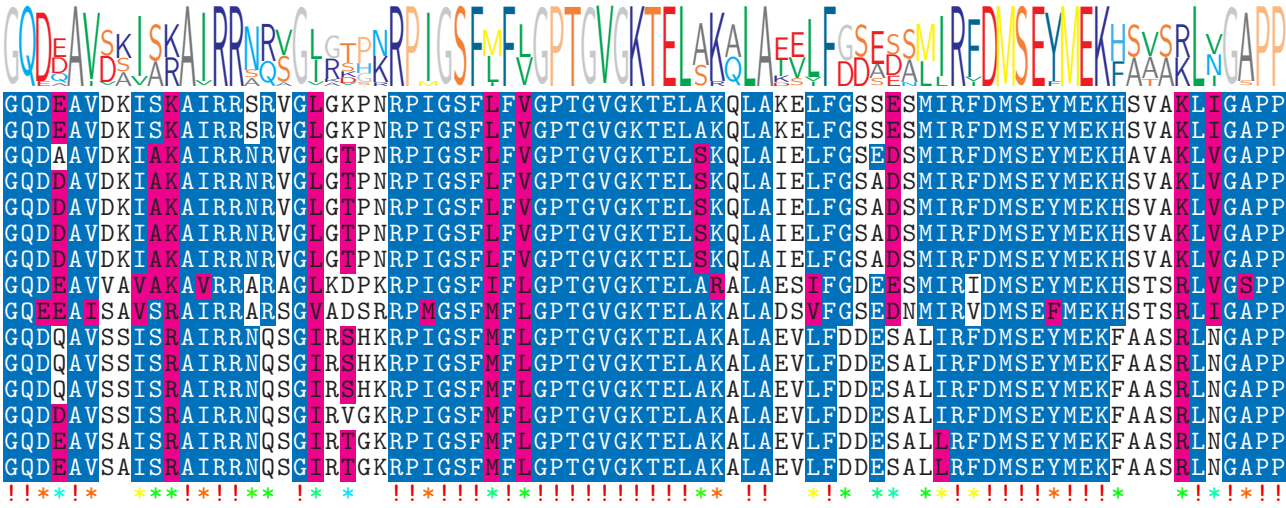
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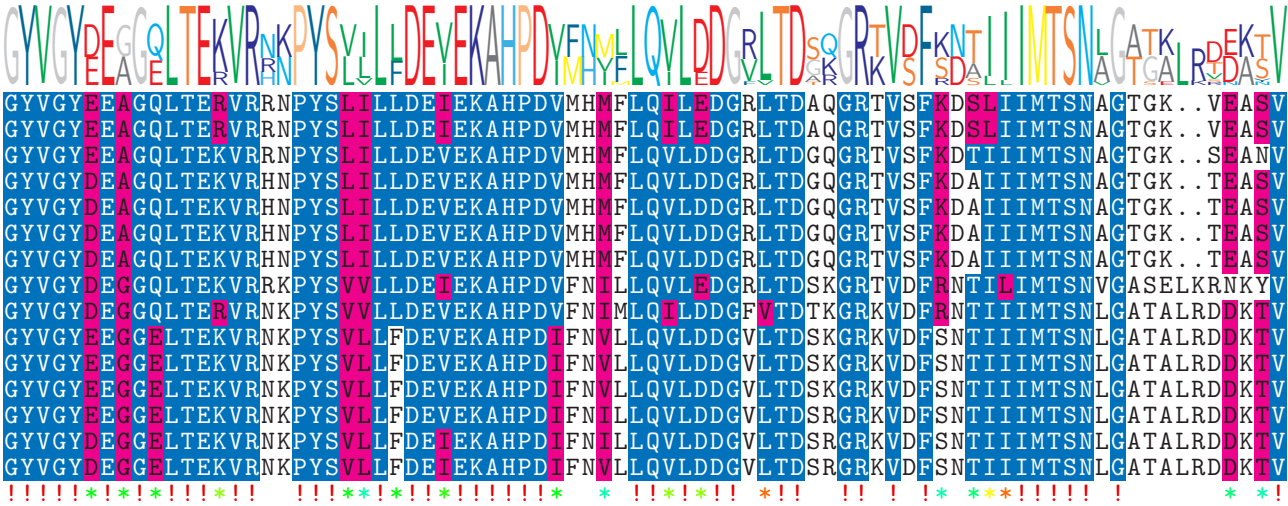
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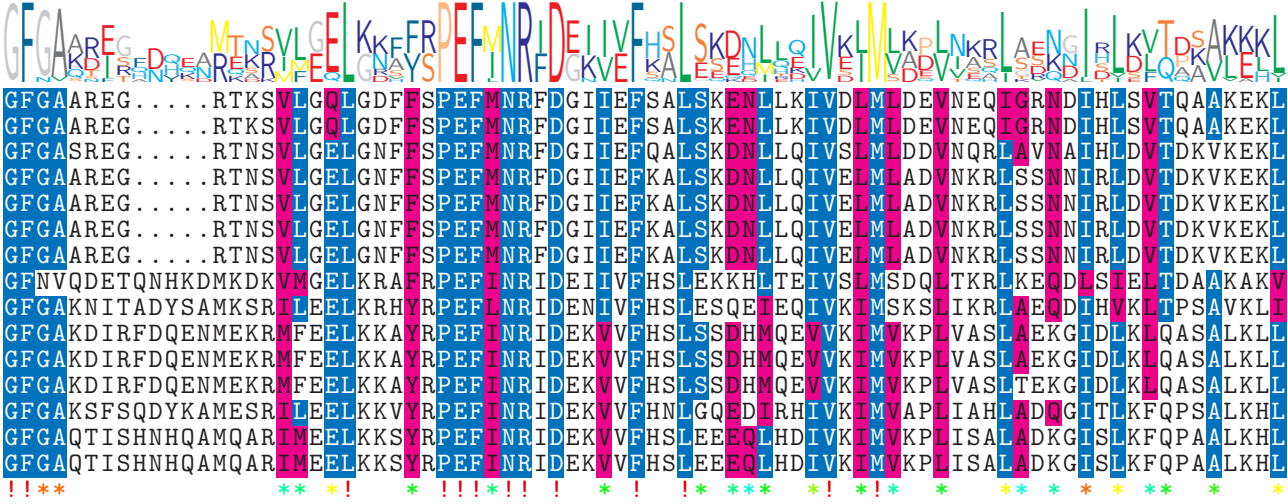
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consensus



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consensus



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X non conserved
X similar
X ≥ 50% conserved