

logo

NTDB id 85 BSU 00860 NP 387967.1	..MMFGRFTERA QKVLALAQEEALRLGHNNIGTEHILLGLVREGEGTAAKALQALGLGSEKIQKEVESLIG.....R	70
NTDB id 610 V4T04 RS10165 WP 012897346.1	MKFENIKYTP TLDRILEKAE EYAHQYQYGTIESAHL LAA MATTSGS IAYSLLAGMNV DSSDLLIDL.....EDLSSH	72
NTDB id 290 KZH43 RS10025 WP 001109677.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHYSYVAGATLNDYPYEMDRLE.....EVALELTETDYS	70
NTDB id 289 SPD RS10700 WP 001109677.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHYSYVAGATLNDYPYEMDRLE.....EVALELTETDYS	70
NTDB id 287 SP RS11210 WP 001109712.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHYSYVAGATLNDYPYEMDRLE.....EVALELTETDYS	70
NTDB id 377 SMU RS09275 WP 002262344.1	MTDYS LKMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEF EADVRFEDYQAAA ILAIGKKPKSSS	76
NTDB id 297 STER RS00545 WP 011680614.1	MTIYSRKMQAIFHRAQLEAERFESP FLETWHVLLAMVEVTGVSAYLTFTDFEDRIHSEEIETA AVVLAMEKRPKDLS	76
NTDB id 329 STU RS10020 WP 011225298.1	MTIYSRKMQAIFHRAQLEAERFESP FLETWHVLLAMVEVPGVSAYLTFTDFEDRIHSEEIETA AVVLAMEKRPKDLS	76
NTDB id 293566 DLJ51 RS02445 WP 002960430.1		0
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	MLCQNCNINDS.....	11
NTDB id 245 SPD RS03860 WP 000882517.1	MLCQNCNINDS.....	11
NTDB id 243 SPR RS03635 WP 000882517.1	MLCQNCNINDS.....	11
NTDB id 241 SP RS04015 WP 000882523.1	MLCQNCNINDS.....	11
consensus	***	

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NTDB id 610 V4T04 RS10165 WP 012897346.1	VKVKRSTLRFSPRAEEVMTAASF LAIHNNSEAVGTEHLLYALLQVEDGFG.....LQLLKL.....QKINIV	134
NTDB id 290 KZH43 RS10025 WP 001109677.1	QDETFTTELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLVYAILHDGNALA.....TRILERAGFSYEDKKDQVKIA	141
NTDB id 289 SPD RS10700 WP 001109677.1	QDETFTTELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLVYAILHDGNALA.....TRILERAGFSYEDKKDQVKIA	141
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NTDB id 377 SMU RS09275 WP 002262344.1	N..DIMLLEQSHALKRTIAEAAAISQVTHAKEVGTEHVLFLAMLLNPNLLA.....TRILELVGFHAKDDGESIRLL	145
NTDB id 297 STER RS00545 WP 011680614.1	ESDIIDLRAQSPA LEAMLQEAQEIASVTGAVEVGS EHVLMFAFL LHKDLMV.....CRLLEVAGFQYKDDSDKPRII	147
NTDB id 329 STU RS10020 WP 011225298.1	ESDIIDLRAQSPA LEAMLQEAQGIASVTGAVEVGS EHVLMFAFL LHKDLMV.....CRLLEVAGFQYKDDSDKPRII	147
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consensus	***	

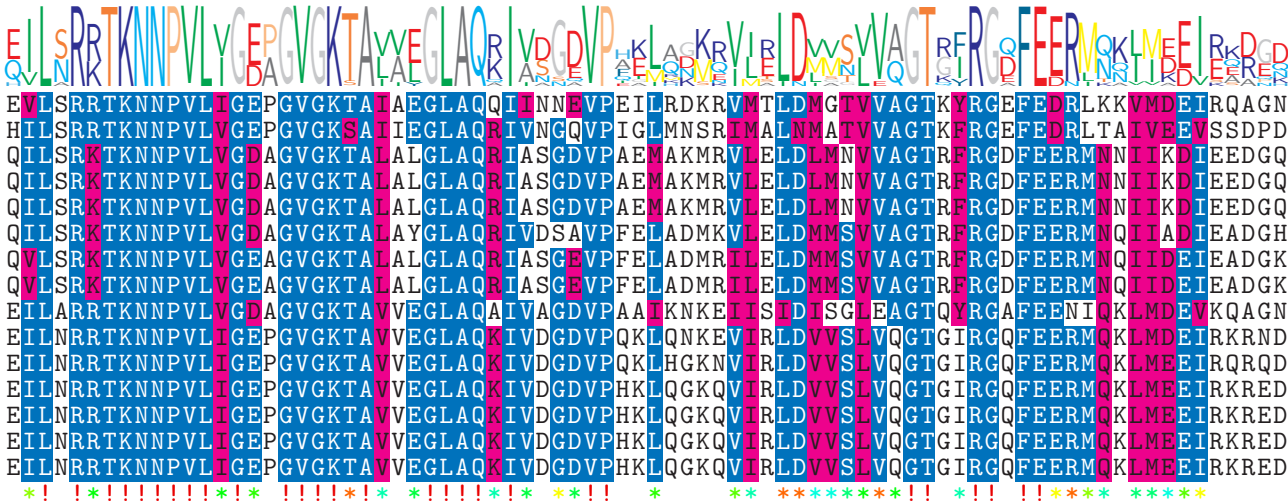
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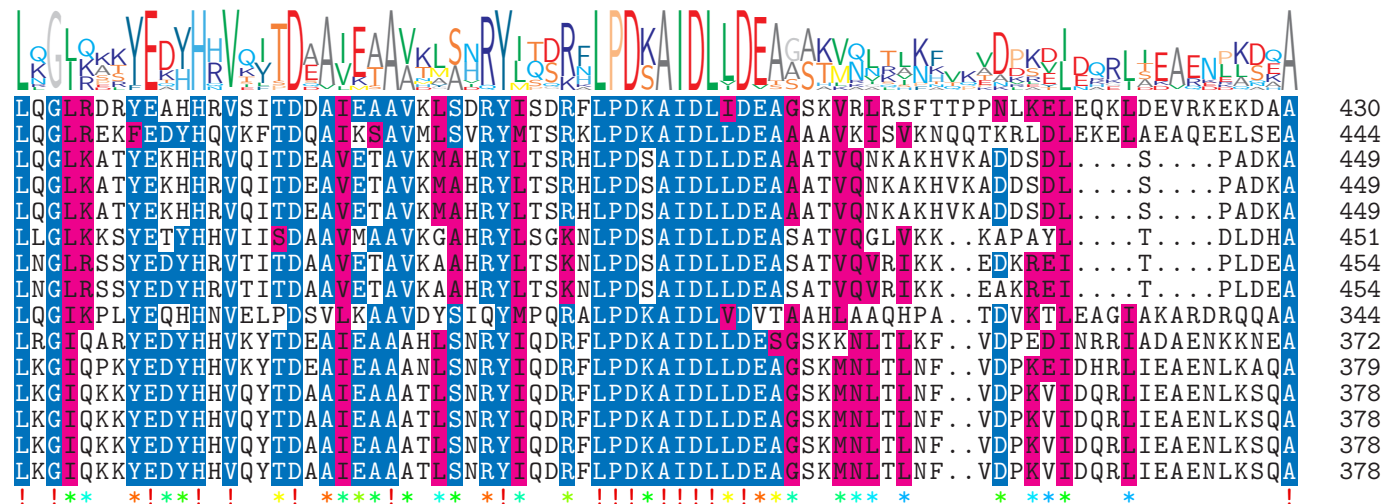
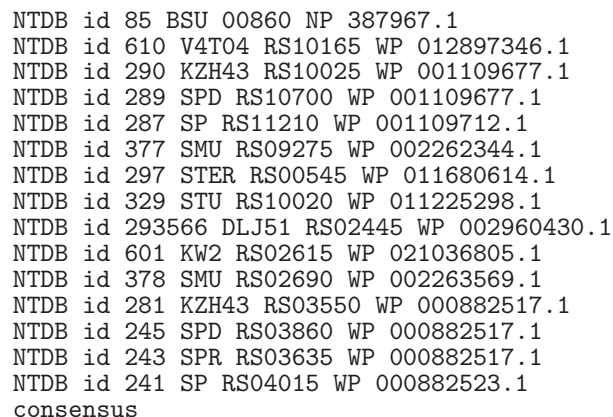
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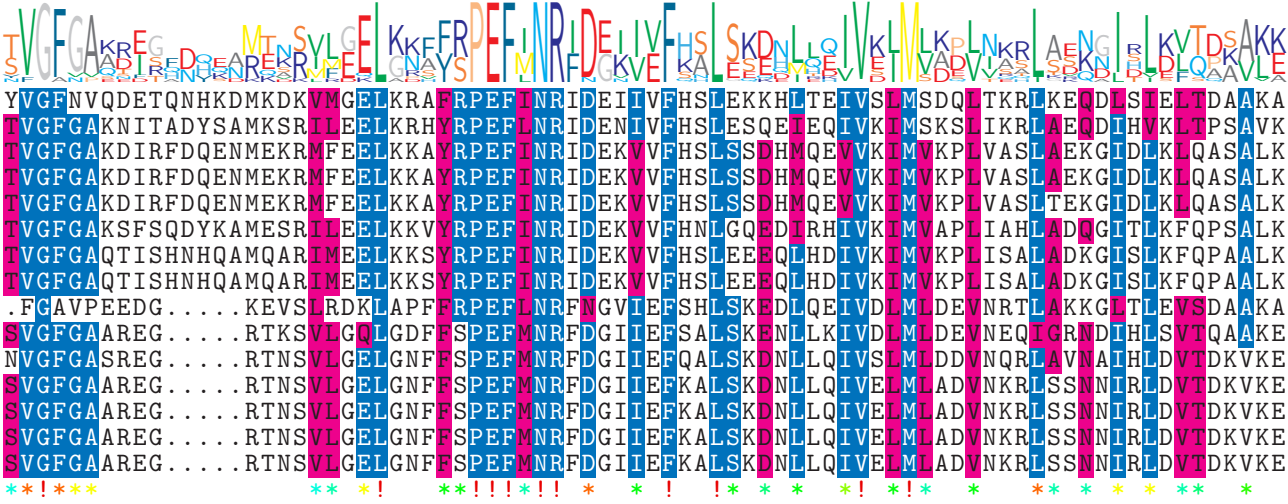
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consensus



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