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NTDB id 601 KW2 RS02615 WP 021036805.1
NTDB id 281 KZH43 RS03550 WP 000882517.1
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NTDB id 243 SPR RS03635 WP 000882517.1
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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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Sequence	Position 10	Score
...MLCQNCNINEAT...	L	12
...MLCQNCCKINDST...	C	12
...MLCQNCCKINDST...	C	12
...MLCQNCCKINDST...	C	12
...MLCQNCCKINDST...	C	12
...MLCQNCNINEST...	N	12
...MLCQNCCKINEAT...	C	12
...MMFGRFTERAQKVLALAQEEALRLGHNNGTEHILLGLVREGEGLAAKALQALGLGSEKIQKEVESLIG.....R	L	70
MKFENIKYPTPTLDRILEKAE EYAHQYQYGTIESAHLIAAMATTSGSIAYSLLAGMNVDDSSDLLIDL.....EDLSSH	A	72
....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	A	70
....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	A	70
....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	A	70
...MTDYSKLMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEFEADVRFEDYQAAAILAIGKKPKSSS	S	76
...MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVTGSAVAYLTFTDFEDRIHSEEIETA AVLAMEKRPKDL S	S	76
...MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVPGSAVAYLTFTDFEDRIHSEEIETA AVLAMEKRPKDL S	S	76

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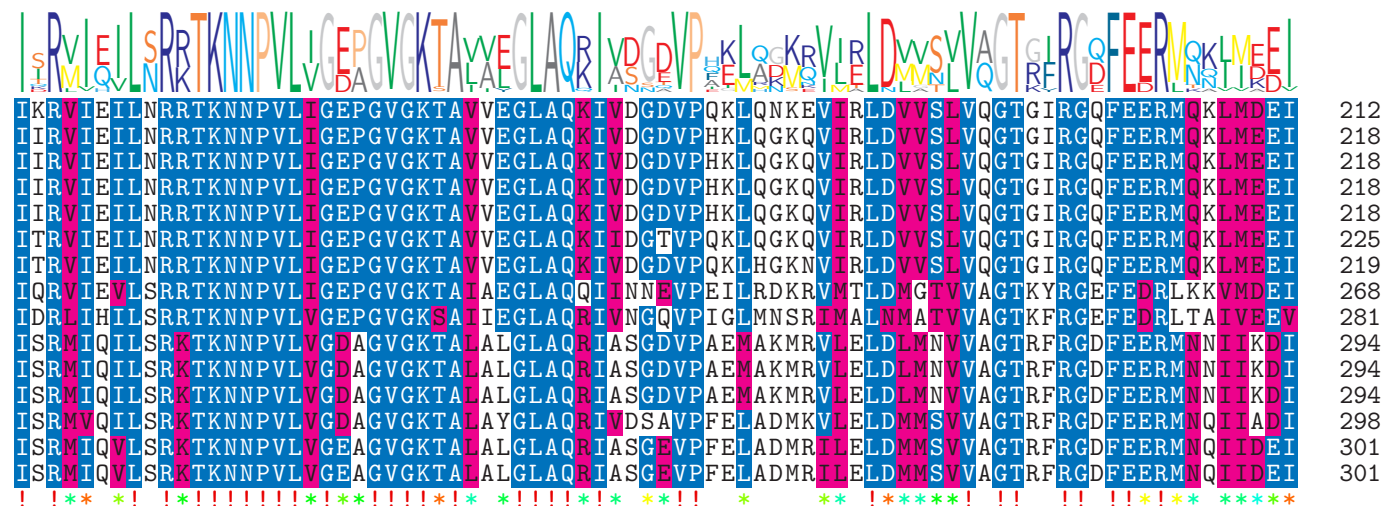
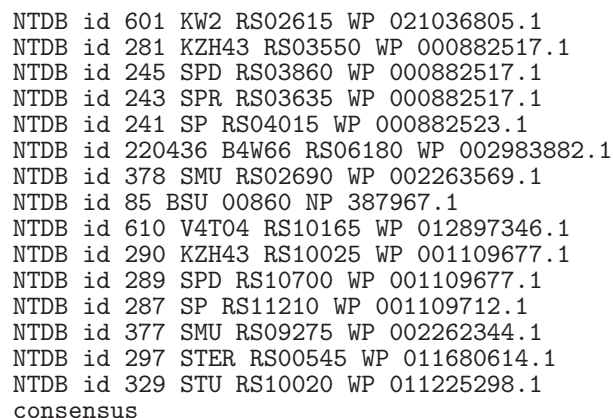
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....IHLYTNLNGKQKQIDLCQNCYKI...IKTDPNNSLFKGMTDLN.....NRDF.DPFGDFFNDLNNF	69
....IHLYTNLNGKQKQIDLCQNCYKI...IKTDPNNSLFKGMTDLN.....NRDF.DPFGDFFNDLNNF	69
....IHLYTSVNGKQKQIDLCQNCYQI...MKSDPANSILNGLTPGYRAQ.....DRSTSPFFDDFFGDLNNF	73
....IHLYANVNGKQKQIDLCQNCYQI...MKTDPENGLNHLSSQ...N.....SSSINPFFDDFFGDLNNF	70
GQEMSQTIHYTPRAKKVIELSMDEARKLGHSYVGTETIHLGLIREGEGVAARVLNNLGVSLNKARQVQLQL.....	141
VKVKRSTLRFSPRAFEVMTAASFIAHNNSEAVGTEHLLYALLQVEDGFGQLLLKL.....QKINIVSLRKLEKR	143
QDETFTFELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLIAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER	150
QDETFTFELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLIAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER	150
QDETFTFELPFSRRLQILFDEAEYVASVVHAKVLGTEHVLIAILHDSNALATRILERAGFSYEDKKDQVKIAALRRNLEER	150
N..DTIMLLEQSHALKRTLAEAAAIISQVTHAKEVGTETHVLFAMLLNPNLLATRILELVGFHAKDDGESIRLLDLRKVTERY	154
ESDIIDLRAQSPAELAMLQEAQEIASVTGAVEVGSSEHVLMAFLHLKDLMVCRLLLEVAGFYKDDSDKPRIIDLRRSLERN	156
ESDIIDLRAQSPAELAMLQEAQGIASVTGAVEVGSSEHVLMAFLHLKDLMVCRLLLEVAGFYKDDSDKPRIIDLRRSLERN	156

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consensus

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logo

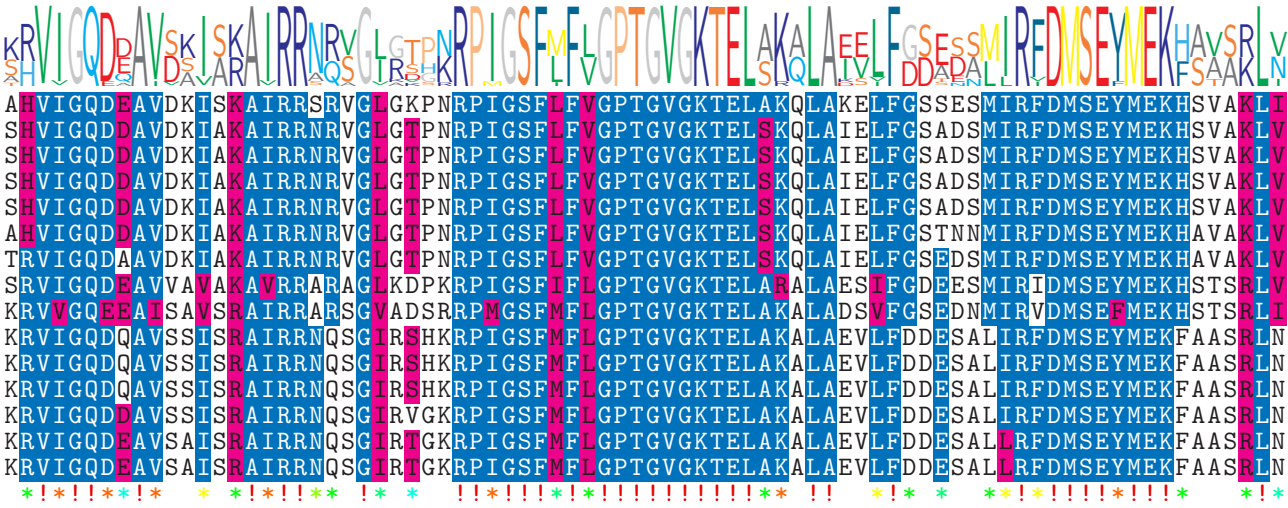
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consensus					



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consensus					



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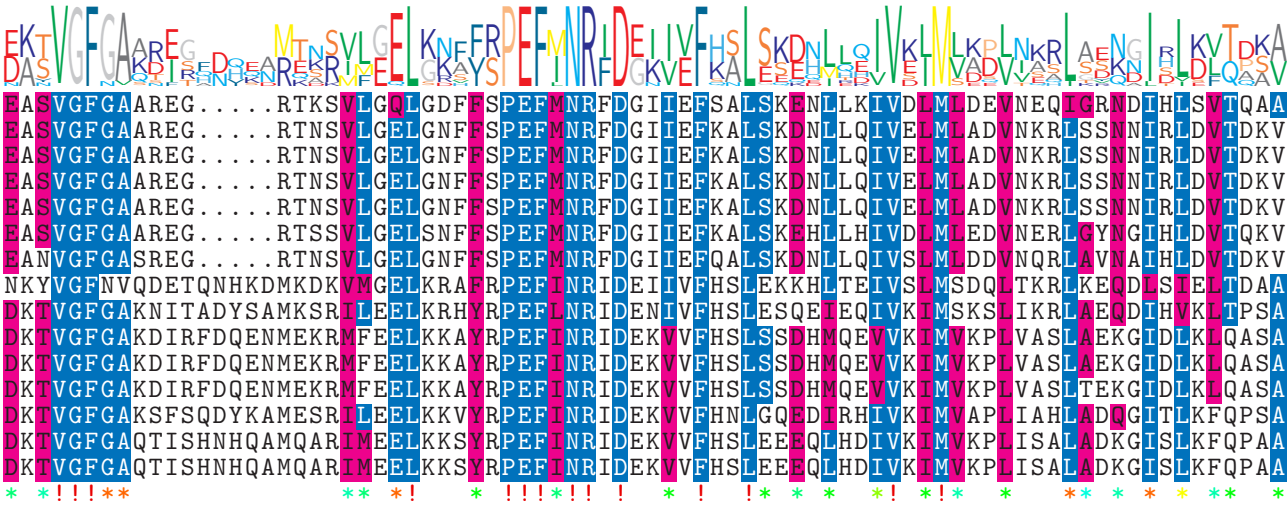
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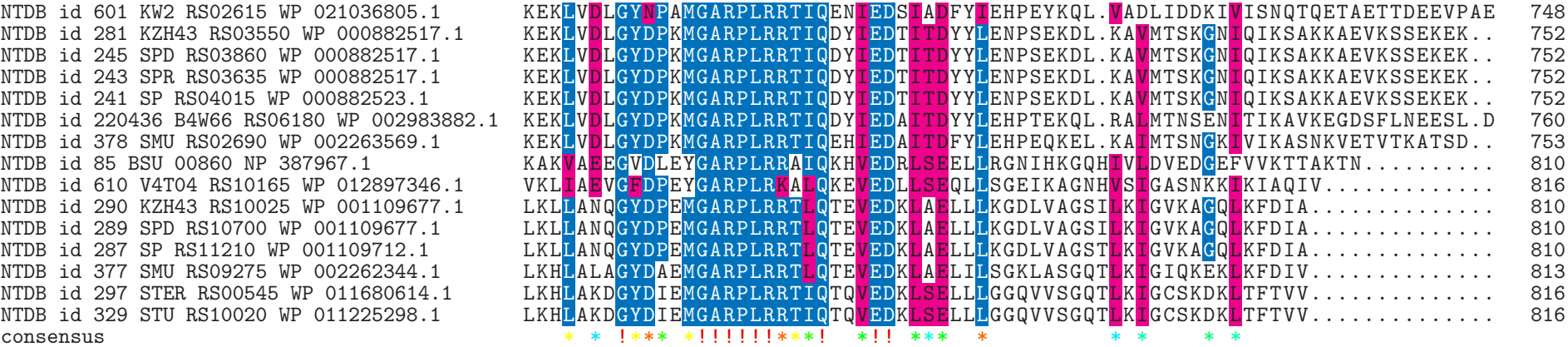
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consensus



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logo



☒ non conserved
☒ similar
☒ ≥ 50% conserved