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NTDB id 601 KW2 RS02615 WP 021036805.1
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NTDB id 290 KZH43 RS10025 WP 001109677.1
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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Position	Sequence	Score
1	MLCQNCNINEAT	12
2	MLCQNCNKINDST	12
3	MLCQNCNKINDST	12
4	MLCQNCNKINDST	12
5	MLCQNCNKINDST	12
6	MLCQNCNINEAT	12
7	MLCQNCNKINDST	12
8	MMFGRFTERA QKVLALAQEEALRLGHNNGTEHILLGLVREGEGLAAKALQALGLGSEKIQKEVESLIG	70
9	MKFENIKYPTPTLDRILEKAE EYAHQYQYGTIESAHLIAAMATTSGSIAYSLLAGMNV DSSDLLIDL	72
10	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	70
11	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	70
12	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	70
13	...MTDYSKLMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEF EADVRFEDYQAAAILAIGKKPKSSS	76
14	...MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVTGSAVYLTFTDFEDRIHSEEIETA AVLAMEKRPKDLS	76
15	...MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVPGSAVYLTFTDFEDRIHSEEIETA AVLAMEKRPKDLS	76

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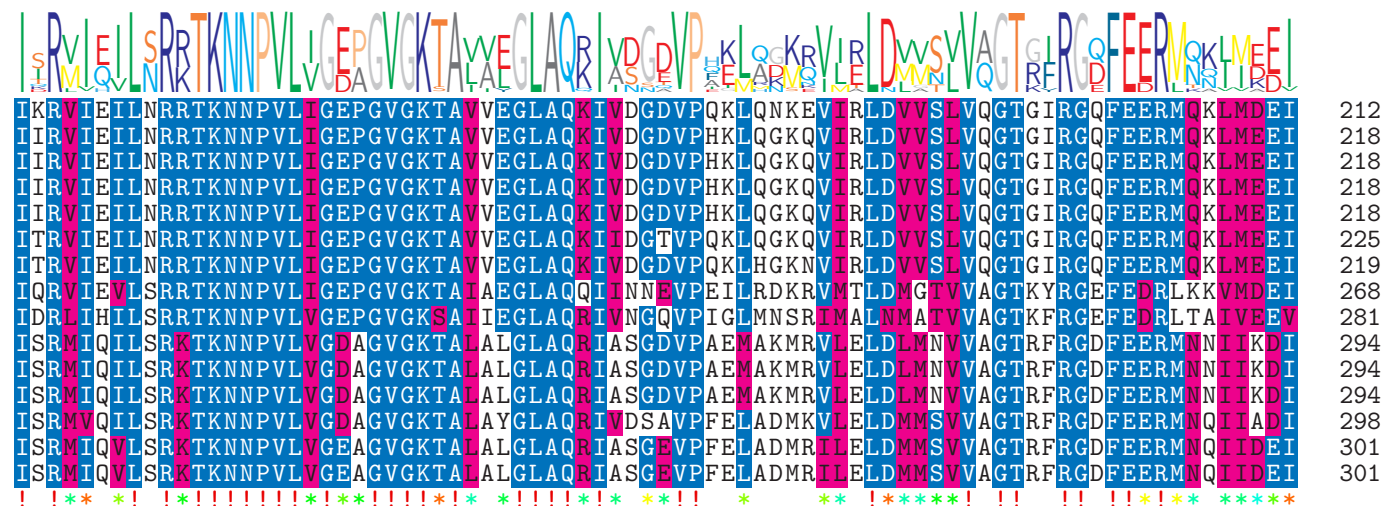
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Sequence	Score
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....IHLYTNLNGKQKQIDLCQNCYKI...IKTDPNNSLFKGMTDLN.....NRDF.DPFGDFFNDLNNF	69
....IHLYTNLNGKQKQIDLCQNCYKI...IKTDPNNSLFKGMTDLN.....NRDF.DPFGDFFNDLNNF	69
....IHLYTSVNGKQKQIDLCQNCYQI...MKSDPANSILNGLTPGYRAQ.....DRSTSPFFDDFFGDLNNF	73
....IHLYANVNGKQKQIDLCQNCYQI...MKTDPENGLNHLSSQ...N.....SSSINPFFDDFFGDLNNF	70
GQEMSQTIHYTPRAKKVIELSMDEARKLGHSYVGTETHTLLGLIREGEGVAARVLNNLGVSLNKARQQVLQL.....	141
VKVKRSTLRFSPRAFEVMTAASFIAIHNNSEAVGTETHTLLYALLQVEDGFGQLLLKL.....QKINIVSLRKETLEKR	143
QDETFTFELPFSRRLQILFDEAEYVASVVHAKVLGTETHTVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER	150
QDETFTFELPFSRRLQILFDEAEYVASVVHAKVLGTETHTVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER	150
QDETFTFELPFSRRLQILFDEAEYVASVVHAKVLGTETHTVLYAILHDSNALATRILERAGFSYEDKKDQVKIAALRRNLEER	150
N..DTMLLEQSHALKRTLAEAAAIISQVTHAKEVGTETHTVLFAMLLNPNLLATRILELVGFHAKDDGESIRLLDLRKVTERY	154
ESDIIDLRAQSPAELAMLEAQEIASVTGAVEVGSSEHVLMAFLHLKDLMVCRLLLEVAGFYKDDSDKPRIIDLRRSLERN	156
ESDIIDLRAQSPAELAMLEAQGIASVTGAVEVGSSEHVLMAFLHLKDLMVCRLLLEVAGFYKDDSDKPRIIDLRRSLERN	156

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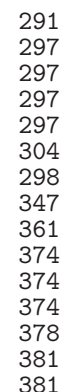
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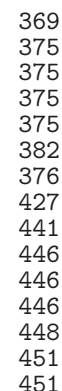
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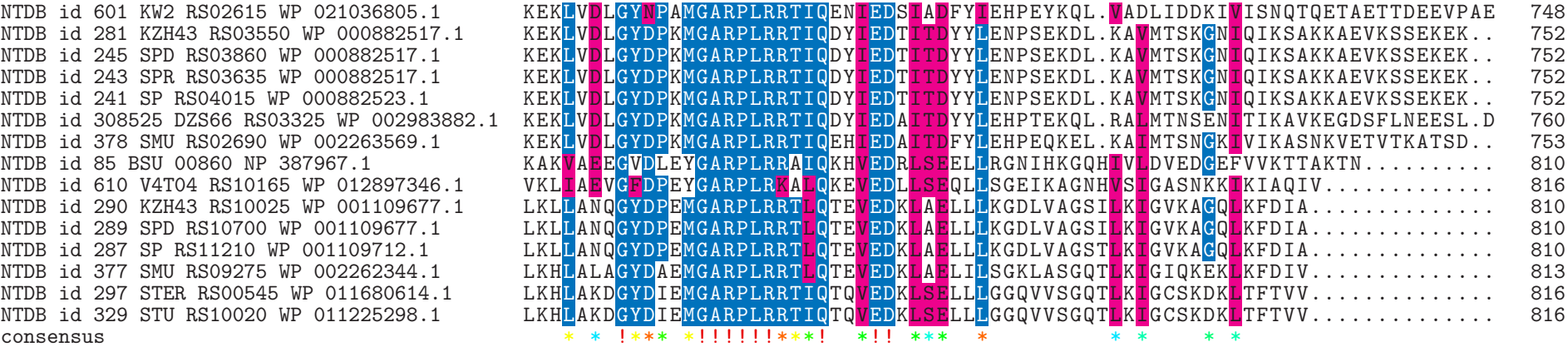
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X non conserved
! similar
X ≥ 50% conserved