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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    |
| ...MLCQNCCKINDST...                                                              | C           | 12    |
| ...MLCQNCNINEAT...                                                               | N           | 12    |
| ...MLCQNCCKINDST...                                                              | C           | 12    |
| ...MMFGRFTERAQKVLALAQEEALRLGHNNIGTEHILLGLVREGEGLAAKALQALGLGSEKIQKEVESLIG.....R   | L           | 70    |
| MKFENIKYPTPTLDRILEKAE EYAHQYQYGTIESAHLIAAMATTSGSIAYSLLAGMNVDDSSDLLIDL.....EDLSSH | A           | 72    |
| ....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS   | A           | 70    |
| ....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS   | A           | 70    |
| ....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS   | A           | 70    |
| ...MTDYSKLMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEFEADVRFEDYQAAAILAIGKKPKSSS  | L           | 76    |
| ...MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVTGSAVAYLTFTDFEDRIHSEEIETAAVLAMEKRPKDL  | L           | 76    |
| ...MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVPGSAVAYLTFTDFEDRIHSEEIETAAVLAMEKRPKDL  | L           | 76    |

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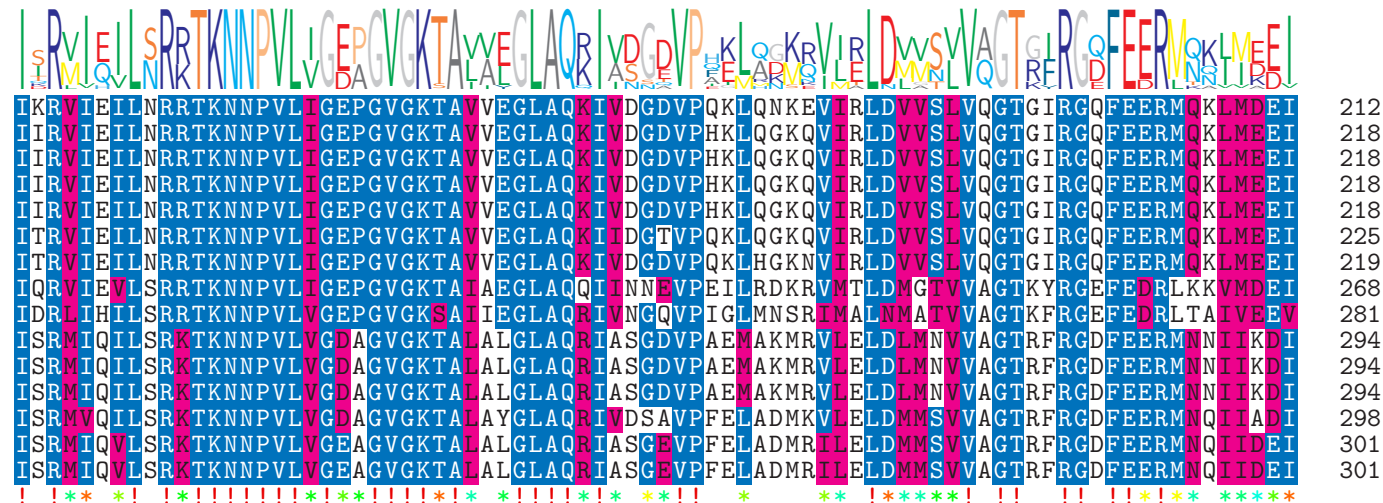
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| Sequence                                                                            | Position |
|-------------------------------------------------------------------------------------|----------|
| ....IHLYTSVNGKQKQIDLCQNCYQI...MKSCGGDEALFCAGNASNGNS.....DEPFN.PFNDIFSALQGG          | 72       |
| ....IHLYTNLNGKQKQIDLCQNCYKI...IKTDPNNSLFKGMTDLN.....NRDF.DPFGDFFNDLNNF              | 69       |
| ....IHLYTNLNGKQKQIDLCQNCYKI...IKTDPNNSLFKGMTDLN.....NRDF.DPFGDFFNDLNNF              | 69       |
| ....IHLYTNLNGKQKQIDLCQNCYKI...IKTDPNNSLFKGMTDLN.....NRDF.DPFGDFFNDLNNF              | 69       |
| ....IHLYTSVNGKQKQIDLCQNCYQI...MKSDPANSILNGLTPGYRAQ.....DRSTSPFFDDFFGDLNNF           | 73       |
| ....IHLYANVNGKQKQIDLCQNCYQI...MKTDPENGLNHLSSQ...N.....SSSINPFFDDFFGDLNNF            | 70       |
| GQEMSQTIHYTPRAKKVIELSMDEARKLGHSYVGTETHTLLGLIREGEGVAARVLNNLGVSLNKARQQVLQL.....       | 141      |
| VKVKRSTLRFSPRAFEVMTAASFIAIHNNSEAVGTEHLLYALLQVEDGFGQLLLKL.....QKINIVSLRKLEKR         | 143      |
| QDETFTLFPFSRRLQILFDEAEYVASVVHAKVLGTETHTVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER  | 150      |
| QDETFTLFPFSRRLQILFDEAEYVASVVHAKVLGTETHTVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER  | 150      |
| QDETFTLFPFSRRLQILFDEAEYVASVVHAKVLGTETHTVLYAILHDSNALATRILERAGFSYEDKKDQVKIAALRRNLEER  | 150      |
| N..DTIMLLEQSHALKRTLAEEAAISQVTHAKEVGTETHTVLFAMLLNPNLLATRILELVGFHAKDDGESIRLLDLRKVTERY | 154      |
| ESDIIDLRAQSPAELAMLEAQEIASVTGAVEVGSHEVLMAFLLHKDLMVCRLLLEVAGFYKDDSDKPRIIDLRRSLERN     | 156      |
| ESDIIDLRAQSPAELAMLEAQGIASVTGAVEVGSHEVLMAFLLHKDLMVCRLLLEVAGFYKDDSDKPRIIDLRRSLERN     | 156      |

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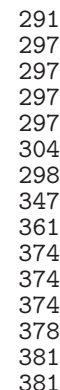
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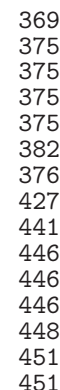
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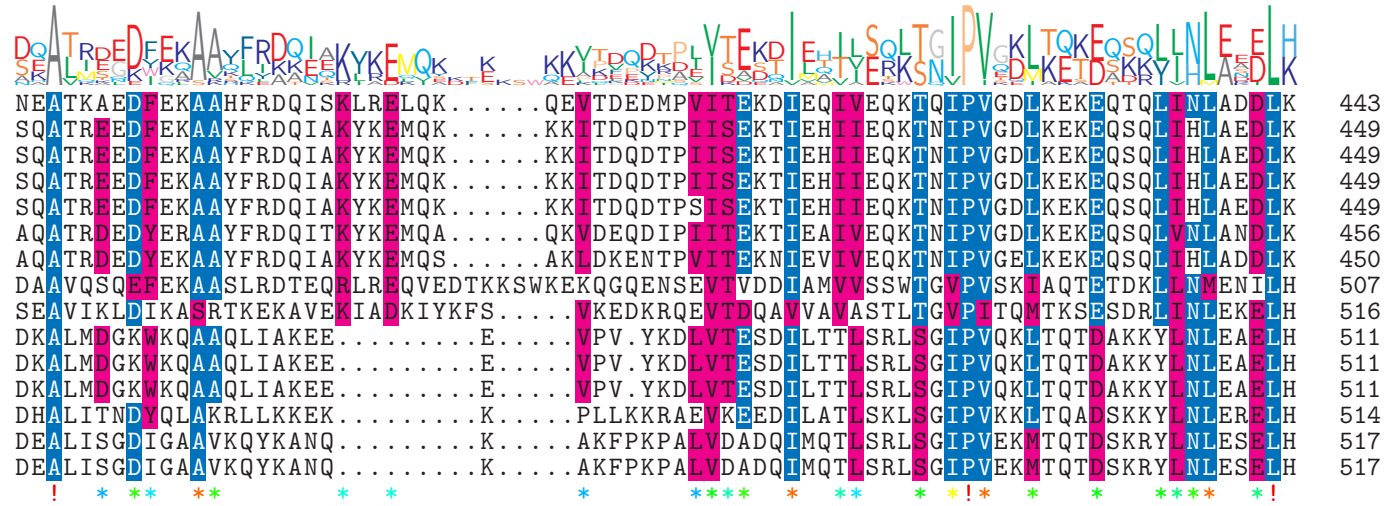




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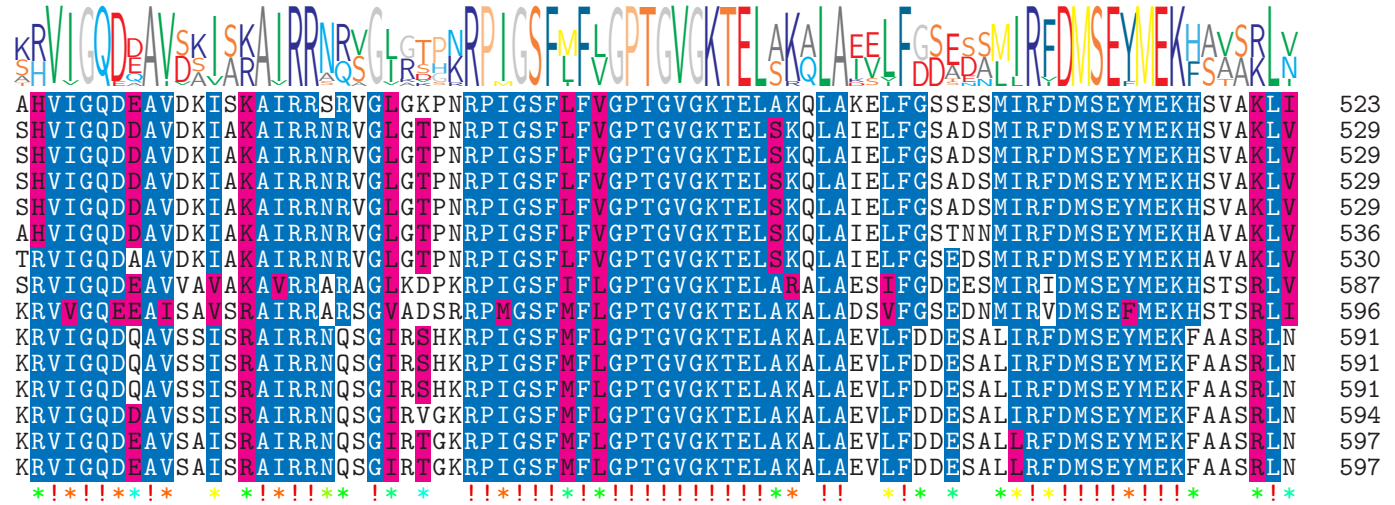
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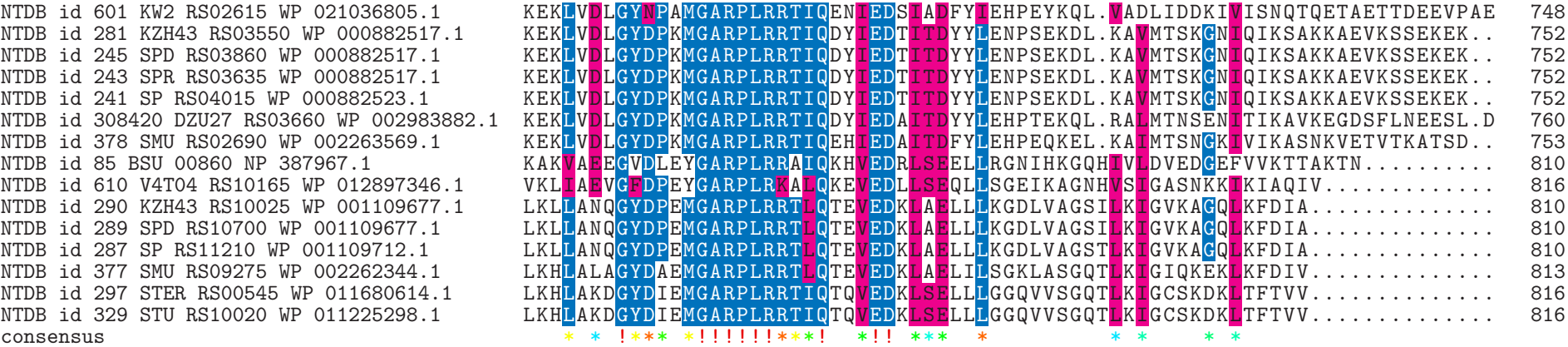
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logo



X non conserved  
! similar  
X ≥ 50% conserved