

logo

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NTDB id 601 KW2 RS02615 WP 021036805.1
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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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| Position | Sequence                                                                          | Score |
|----------|-----------------------------------------------------------------------------------|-------|
| 1        | MLCQNCNINEAT                                                                      | 12    |
| 2        | MLCQNCNINEAT                                                                      | 12    |
| 3        | MLCQNCNINEAT                                                                      | 12    |
| 4        | MLCQNCNINEAT                                                                      | 12    |
| 5        | MLCQNCNINEAT                                                                      | 12    |
| 6        | MLCQNCNINEAT                                                                      | 12    |
| 7        | MLCQNCNINEAT                                                                      | 12    |
| 8        | MLCQNCNINEAT                                                                      | 12    |
| 9        | MLCQNCNINEAT                                                                      | 12    |
| 10       | MLCQNCNINEAT                                                                      | 12    |
| 11       | MMFGRFTERA QKVLALA QEEALRLGHNNIGTEHILLGLVREGEGLAAKALQALGLGSEKIQKEVESLIG           | 70    |
| 12       | MKFENIKYPTPTLDRILEKAE EYAHQYQYGTIESAHL LAMATTSGSIAYSLLAGMNV DSSDLLIDL             | 72    |
| 13       | ....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE                    | 70    |
| 14       | ....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE                    | 70    |
| 15       | ....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE                    | 70    |
| 16       | ...MTDYS LKMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEF EADVRFEDYQAAAILAIGKKPKSSS | 76    |
| 17       | ...MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVTGSAVYLTF TDFEDRIHSEEIETA AVLAMEKRPKDLS | 76    |
| 18       | ...MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVPGSAVYLTF TDFEDRIHSEEIETA AVLAMEKRPKDLS | 76    |

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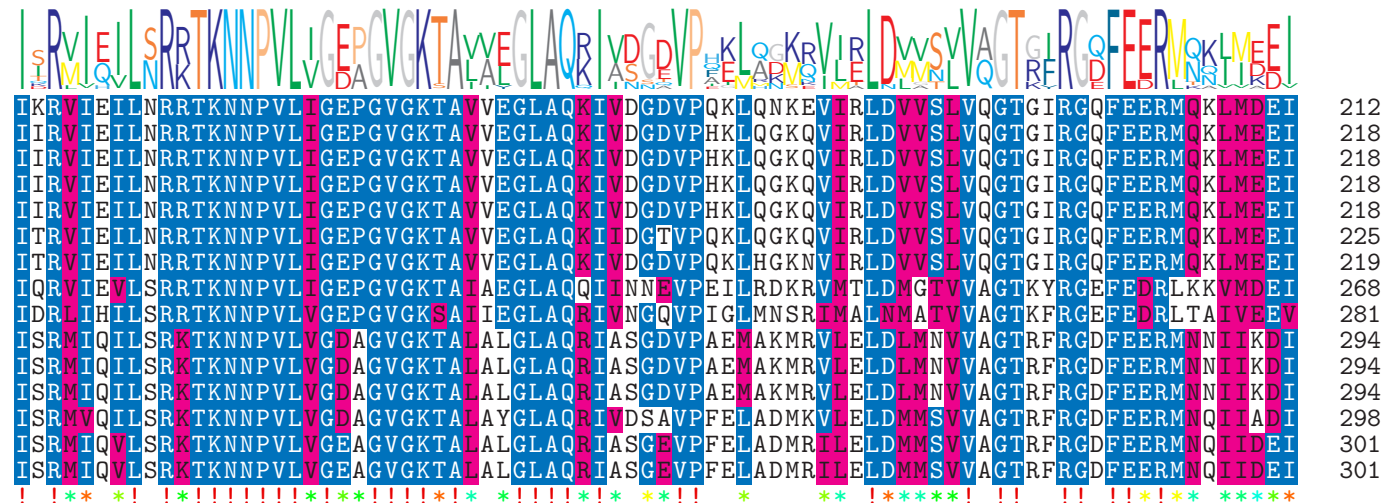
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| Sequence                                                                            | Score |
|-------------------------------------------------------------------------------------|-------|
| ....IHLYTSVNGKQKQIDLCQNCYQI...MKSCGGDEALFCAGNASNGNS.....DEPFN.PFNDIFSALQGG          | 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   |
| VKVKRSTLRFSPRAFEVMTAASFIAHNNSEAVGTETHTLLYALLQVEDGFGQLLLKL.....QKINIVSLRKETLEKR      | 143   |
| QDETFTFELPFSRRLQILFDEAEYVASVVHAKVLGTETHTVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER | 150   |
| QDETFTFELPFSRRLQILFDEAEYVASVVHAKVLGTETHTVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER | 150   |
| QDETFTFELPFSRRLQILFDEAEYVASVVHAKVLGTETHTVLYAILHDSNALATRILERAGFSYEDKKDQVKIAALRRNLEER | 150   |
| N..DTMLLEQSHALKRTLAEAAAIISQVTHAKEVGTETHTVLFAMLLNPNLLATRILELVGFHAKDDGESIRLLDLRKVTERY | 154   |
| ESDIIDLRAQSPAELAMLEAQEIASVTGAVEVGSSEHVLMAFLHLKDLMVCRLLLEVAGFYKDDSDKPRIIDLRRSLERN    | 156   |
| ESDIIDLRAQSPAELAMLEAQGIASVTGAVEVGSSEHVLMAFLHLKDLMVCRLLLEVAGFYKDDSDKPRIIDLRRSLERN    | 156   |

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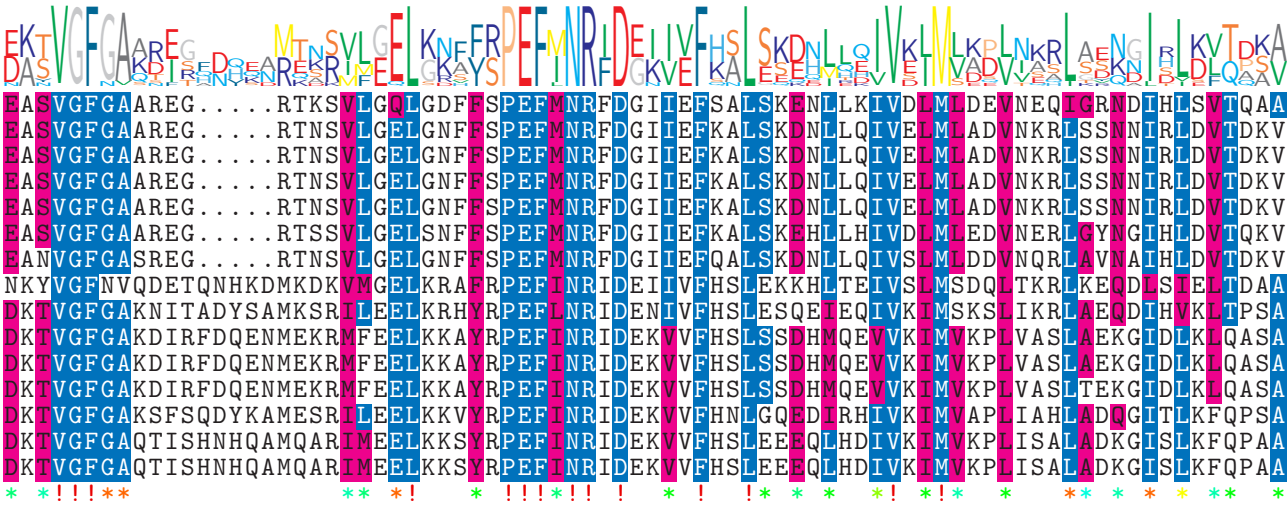
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consensus



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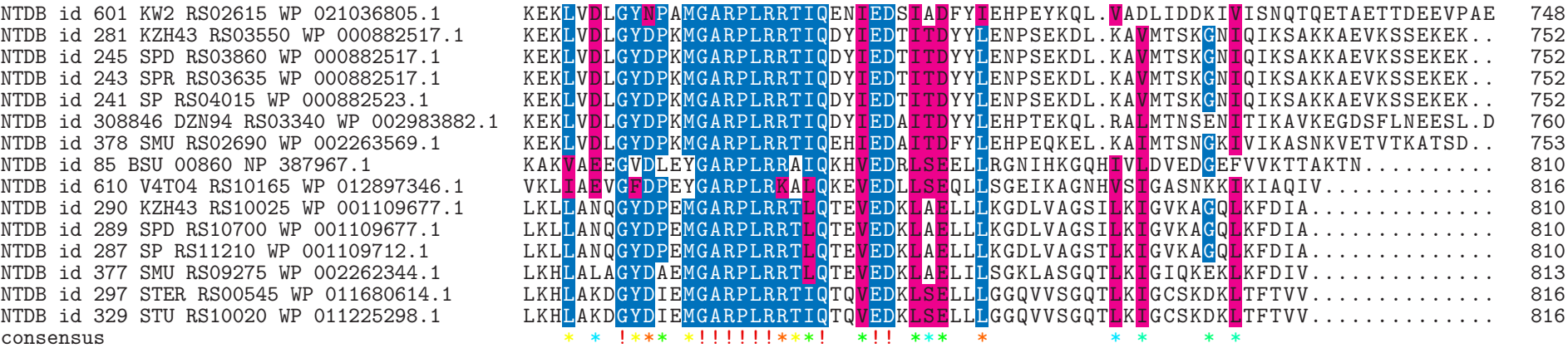
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logo



 non conserved  
 similar  
 ≥ 50% conserved