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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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Sequence	Position 10
...MLCQNCNINEAT...	12
...MLCQNCNKINDST...	12
...MLCQNCNKINDST...	12
...MLCQNCNKINDST...	12
...MLCQNCNKINDST...	12
...MLCQNCNINEST...	12
...MLCQNCNKINEAT...	12
...MMFGRFTERAQKVLALAQEEALRLGHNNIGTEHILLGLVREGEGLAAKALQALGLGSEKIQKEVESLIG.....R	70
MKFENIKYPTPTLDRILEKAE EYAHQYQYGTIESAHLIAAMATTSGSIAYSLLAGMNVDDSSDLLIDL.....EDLSSH	72
....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	70
....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	70
....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE....EVALELTETDYS	70
...MTDYSKMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSSVAGLSFAEFEADVRFEDYQAAAILAIGKKPKSSS	76
...MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVTGSVAYLTFDTDFEDRIHSEEIETA AVLAMEKRPKDL S	76
...MTIYSRKMQAIFHRAQLEAERFESPFLETWHVLLAMVEVPGSVAYLTFDTDFEDRIHSEEIETA AVLAMEKRPKDL S	76

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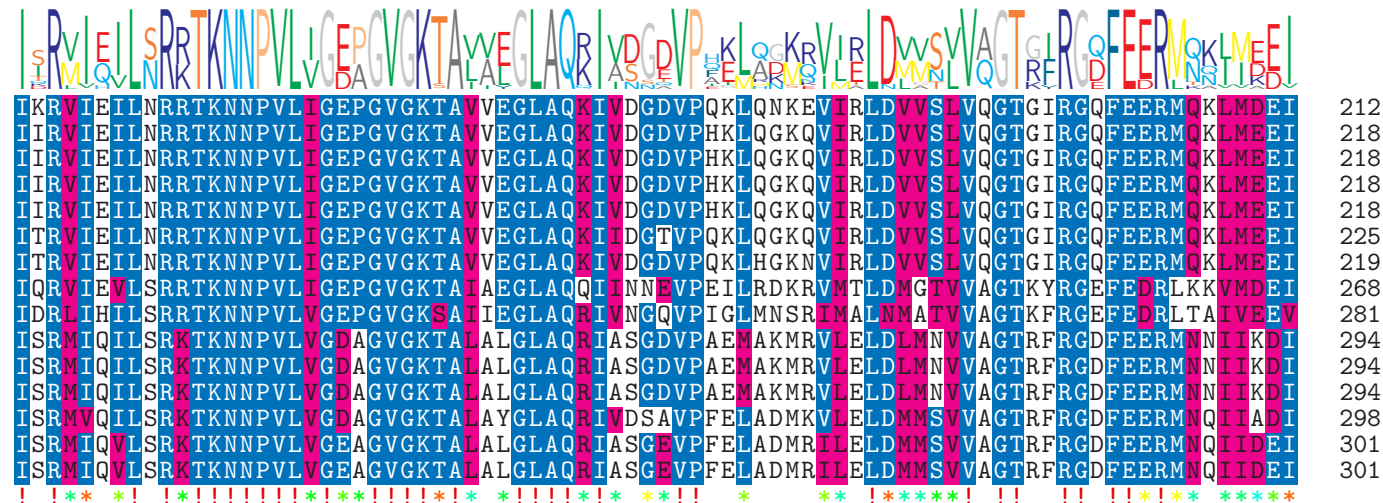
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....IHLYTNLNGKQKQIDLCQNCYKI...IKTDPNNSLFKGMTDLN.....NRDF.DPFGDFFNDLNNF	69
....IHLYTNLNGKQKQIDLCQNCYKI...IKTDPNNSLFKGMTDLN.....NRDF.DPFGDFFNDLNNF	69
....IHLYTSVNGKQKQIDLCQNCYQI...MKSDPANSILNGLTPGYRAQ.....DRSTSPFFDDFFGDLNNF	73
....IHLYANVNGKQKQIDLCQNCYQI...MKTDPENGLNHLSSQ...N.....SSSINPFFDDFFGDLNNF	70
GQEMSQTIHYTPRAKKVIELSMDEARKLGHSYVGTETHTLLGLIREGEGVAARVLNNLGVSLNKARQQVLQL.....	141
VKVKRSTLRFSPRAFEVMTAASFIAIHNNSEAVGTEHLLYALLQVEDGFGQLLLKL.....QKINIVSLRKELK	143
QDETFTLFPFSRRLQILFDEAEYVASVVHAKVLGTETHTVLYAILHDGNALATRILERAGFSYEDKKQVKIAALRRNLEER	150
QDETFTLFPFSRRLQILFDEAEYVASVVHAKVLGTETHTVLYAILHDGNALATRILERAGFSYEDKKQVKIAALRRNLEER	150
QDETFTLFPFSRRLQILFDEAEYVASVVHAKVLGTETHTVLYAILHDSNALATRILERAGFSYEDKKQVKIAALRRNLEER	150
N..DTMLLEQSHALKRTLAEAAAIISQVTHAKEVGTETHTVLFAMLLNPNLLATRILELVGFHAKDDGESIRLLDLRKVTERY	154
ESDIIDLRAQSPAELAMLEAQEIASVTGAVEVGSHEVLMAFLLHKDLMVCRLLLEVAGFYKDDSDKPRIIDLRRSLERN	156
ESDIIDLRAQSPAELAMLEAQGIASVTGAVEVGSHEVLMAFLLHKDLMVCRLLLEVAGFYKDDSDKPRIIDLRRSLERN	156

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consensus

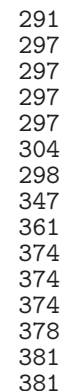
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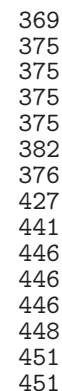
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logo

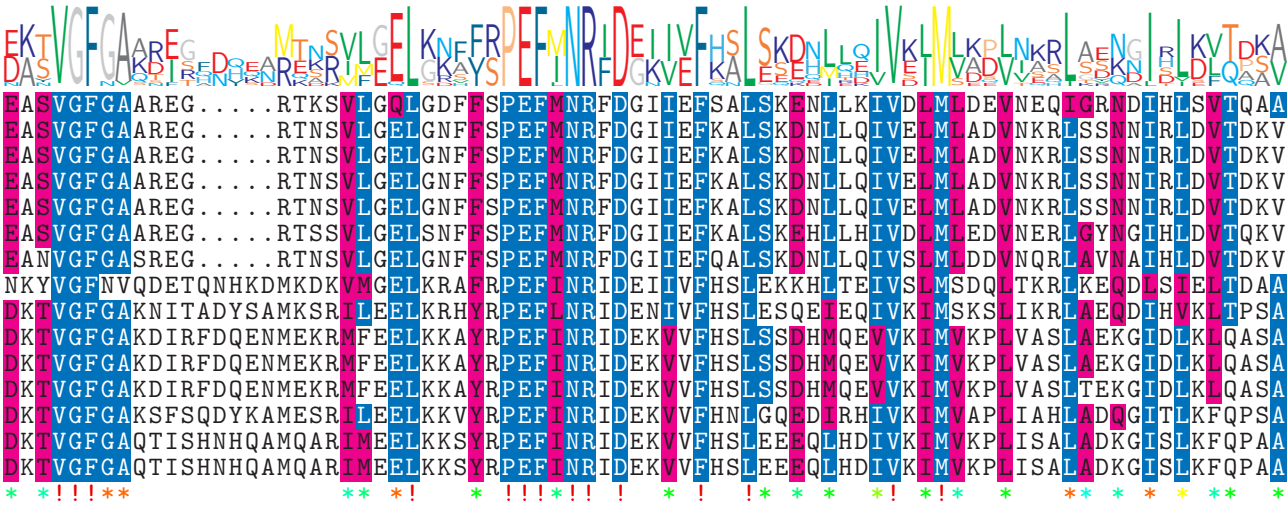
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consensus



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logo



☐ non conserved
☒ similar
☒ ≥ 50% conserved