



Sequence	Position
MLCQNCKINEA	11
MLCQNCKINDS	11
MLCQNCKINDS	11
MLCQNCKINDS	11
MLCQNCKINDS	11
MMFGRFTERAQKVLALAQEEALRLGHNNIGTEHILLGLVREGEGLAAKALQALGLGSEKIQKEVESLIG	70
MKFENIKYTPTLDRILEKAEEYAHHQYQYGTIESAHLAAMATTSGSIAYSLLAGMNVDSDDLIDL	72
....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE	70
....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE	70
....MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLE	70
...MTDYSCLKMQEVFRLAQFEAAARFESSYLESWHVLLAMVEIDS	76
...MTDYSCLKMQEVFRLAQFEAAARFESSYLESWHVLLAMVEIDS	76
...MTIYSRKMQAIFHRAQLEAERFESPFLTWHVLLAMVEVPG	76
...MTIYSRKMQAIFHRAQLEAERFESPFLTWHVLLAMVEVPG	76

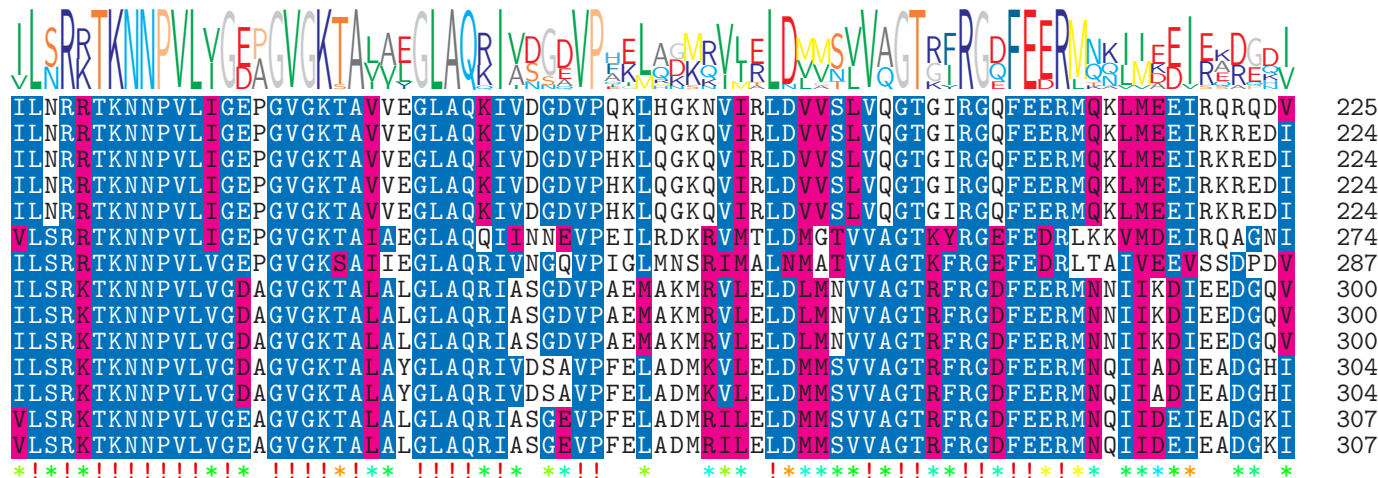
Conservation scores: ** * * * * * * * * * *

[illegible]

Sequence	Score
NFR ^{NEAGSSN} ^{DLKA} LPPTQAGGGNGNGGN.N.RRPGGPQQQAS ^{QKPN} GLLEEF ^{GINLTD} IARKGE ^{TD} DPVIGRDEE ^{IT} RVIE	145
NFRPSS ^{SN} .TTP.IPPTQSGGGYGGNGGYGSQNRGSAQTP ^{PPS} SQEKGLLEEF ^{GINVTE} IARRGD ^{TD} DPVIGRDEE ^{IT} RVIE	144
NFRPSS ^{SN} .TTP.IPPTQSGGGYGGNGGYGSQNRGSAQTP ^{PPS} SQEKGLLEEF ^{GINVTE} IARRGD ^{TD} DPVIGRDEE ^{IT} RVIE	144
NFRPSS ^{SN} .TTP.IPPTQSGGGYGGNGGYGSQNRGSAQTP ^{PPS} SQEKGLLEEF ^{GINVTE} IARRGD ^{TD} DPVIGRDEE ^{IT} RVIE	144
NFRPSS ^{SN} .TTP.IPPTQSGGGYGGNGGYGSQNRGSAQTP ^{PPS} SQEKGLLEEF ^{GINVTE} IARRGD ^{TD} DPVIGRDEE ^{IT} RVIE	144
. . LGSNET. GSSAAGTNS ^{NANT} TPLDSLARD ^{LTALAK} EDSLDPVIGR ^{SK} EITQ ^{RV} IE	194
KRTGLKV ^{PE} SKKA ^{VTPMS} K ^{RRKM} AKG. VAEN ST TPLDSV ^{SS} DLTBEAR ^{LCK} LDP ^{MIGR} EAEIDRL ^{LIH}	207
ERAGW ^{TRED} DLKA ^{LRQRHRTV} ADKQNSMANMMGM ^{PQTPS} GGLEDYTH ^{DLTEQARS} CKLE ^{PVIGRDK} EIS ^{SRMI} Q	220
ERAGW ^{TRED} DLKA ^{LRQRHRTV} ADKQNSMANMMGM ^{PQTPS} GGLEDYTH ^{DLTEQARS} CKLE ^{PVIGRDK} EIS ^{SRMI} Q	220
ERAGW ^{TRED} DLKA ^{LRQRHRTV} ADKQNSMANMMGM ^{PQTPS} GGLEDYTH ^{DLTEQARS} CKLE ^{PVIGRDK} EIS ^{SRMI} Q	220
RYAGFSKEDIKA ^{IFEMR} KPKK. VKNSSFS ^{FDLMKPP} .SVT ^{GELADFT} RD ^{DLTELARQ} GRLE ^{PVIGREQ} EIS ^{SRMV} Q	224
RYAGFSKEDIKA ^{IFEMR} KPKK. VKNSSFS ^{FDLMKPP} .SVT ^{GELADFT} RD ^{DLTELARQ} GRLE ^{PVIGREQ} EIS ^{SRMV} Q	224
RNAGLSKQ ^{DLKA} .I ^{HDLR} KPKK. SKASANFANMMQ ^{PPQS} ST ^{GELADYTK} DL ^{TALAES} CN ^{LDPI} GRDEE ^{IS} SRMIQ	227
RNAGLSKQ ^{DLKA} .I ^{HDLR} KPKK. SKASANFANMMQ ^{PPQS} ST ^{GELADYTK} DL ^{TALAES} CN ^{LDPI} GRDEE ^{IS} SRMIQ	227

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NTDB id 378 SMU RS02690 WP 002263569.1
 NTDB id 241 SP RS04015 WP 000882523.1
 NTDB id 281 KZH43 RS03550 WP 000882517.1
 NTDB id 245 SPD RS03860 WP 000882517.1
 NTDB id 243 SPR RS03635 WP 000882517.1
 NTDB id 85 BSU 00860 NP 387967.1
 NTDB id 610 V4T04 RS10165 WP 012897346.1
 NTDB id 287 SP RS11210 WP 001109712.1
 NTDB id 290 KZH43 RS10025 WP 001109677.1
 NTDB id 289 SPD RS10700 WP 001109677.1
 NTDB id 1020641 ABVF41 RS09445 WP 002262344.1
 NTDB id 377 SMU RS09275 WP 002262344.1
 NTDB id 329 STU RS10020 WP 011225298.1
 NTDB id 297 STER RS00545 WP 011680614.1
 consensus



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