

Sequence	Score
MDRLSIYELL SFVVPGVIMIEL <b>INFSAEYVFGKAPLITAG</b> NLSDGLLFFAIALFIGCLIHIITFWLIKRWYKKLACTPMDKMKND <b>EYITEILPDLKEIY</b>	100
.....MIEL <b>INFSAEYVFGKAPLITAG</b> NLSDGLLFFAIALFIGCLIHIITFWLIKRWYKKLACTPMDKMKND <b>EYITEILPDLKEIY</b>	82
.....MERLSIYELL SFVVLGVIMIEL <b>INFSAEYVFGKAPLITAG</b> NLSDSLLFFAIALFIGCLIHIITFRLIKRWYQKLACTPMDKMKND <b>EYITEILPHLKEIY</b>	100
.....MAAFLKGFKM <b>SKNNIFNKYPTIIHGEARG</b> .....	39
.....MSKNN <b>IFNKYPTIIHGEARG</b> .....	30
.....MSKNN <b>IFKKYPTIIHGEARG</b> .....	30
.....MDYDNENYL..IPKILL.....	24
.....MFSEIK <b>FSSLS</b> DHALAELIKMA.....	31
.....MAILNNKGEK <b>ISIDCADLIS</b> .....	30
.....MEFEDLDVVLVYFFENP.....	27
MIYYIKDLKVKGKIFENLMNKEAVEGL <b>ITFLKKA</b> <b>FEIYS</b> RENYSKYNKWFEMWKSPTSSLVFWKNYSFRCHLLFVIEKDGECLGIPASV <b>FSVLQI</b> YLADPFAP	105
.....MADMTLRQFCERYRKGD <b>FLAKDRETQIEAGWYDFCDDKALAG</b> .....	60

\* \* \* \* \*

RTNKGISVTENISNGSVFDTAYYYLEAQC...	KISQAQNFQSIYFLFRNIVTLSLFLVPVSVIFLLASF	FMNDCSLSEKITITIIIGTFVLGGLSSVIAQWFRVK	201	
RTNKGISVTENISNGSVFDTAYYYLEAQC...	KISQAQNFQSIYFLFRNIVTLSLFLVPVSVIFLLASF	FMNDCSLSEKITITIIIGTFVLGGLSSVIAQWFRVK	183	
RANKGISATENISNGSVFDTAYYYLEAQC...	KISQAQNFQSIYFLFRNIVTLSLFLVPVSVIFLLASF	FMNDCKLSGKITITIVIGTLVIGGISSVIAQWFRVK	201	
..YPRFLARKSFDDN..FTGGIPAKPVNG...	ELGQIGEPRLLAYDSR.....LGLWLSDF	FIMLDNNKPESMEDWLG.....QLKAACDRIA	114	
..YPRFLARKSFDDN..FTGGIPAKPVNG...	ELGQIGEPRLLAYDSR.....LGLWLSDF	FIMLDNNKPESMEDWLG.....QLKAACDRIA	105	
..YPRFLARKSFDDN..FTGEMPAPKVDG...	ELGQIGEPRLLAYDSR.....LGLWLSDF	FIMLDNNKPENMEDWLG.....QLKAACDRIA	105	
..AKDILVYAVLKDRQIEALEKGWIDTDG...	SIYLNFKLIELAKMFS.....CSRTTIDVMQRL	EEVNLIE.....RE	89	
..KPGVNTIKTVDEP....VVLHAPSDN...	EMVFINNCLKRRAGE.....YIHASMCKYRDL	TRKYPQWFS.....VKAPDD	99	
..GTFLVYAICSWR....EIEQVEYIS...	DYVHADNPESYKDELT.....TKEYAELKEIYEKDL	LEELKI.....TK	89	
...QLFETTESGLR....YLIGVPDSRN...	KIKNNNEIIIEFIYYQ.....NDDIVTKLIFY	YTKGTNRITY.....	84	
DTKELFVEVCNLYECLADVTVEHFEAESA	WHKLTHNETEVSKRVYSKDDDELLKYIPEFL	DTIATNKKSQKYNQIQGKIQEINKEIATLYE...	SSDYIFTE	207
LDNYRWFVKNNCPMVGPLYDDVFREFPLDEE	QRDELYFGVAIDDKRREKKYVIFTARN..DY	ENECGFNNVREVRQFINGWEDELKNEE.....	FYKAREKKRQ	156

MTDRIFGLYYAELTHNKK	219
MTDRIFGLYYAELTHNKK	201
MTDRIFGLYYAELTHHKK	219
ADDLMLNEDAAALEGWDD	132
ADDLMLNEDAAALEGWDD	123
ADDLMLNEDAAALEGWDD	123
RVDVFGYSLPYKTYINEV	108
LRGSVSKHYVDYFTKKE	116
NKQMNLNELLSLTIQNSIT	109
.IRKITYGWKEKRLSEDEE	102
YVSNLYRESAKLEQHSKQILKE	229
EMFEANNKF AEIMQRADEILWNLKED	182

- X non conserved
- X similar
- X  $\geq 50\%$  conserved