




[illegible]

Sequence	Score
KLNMPPFYAYYDMFKKQQLLKWLNKNRNDVIGGTGRMYTASGNY...IANAYLEVALESSSLGSGSYMLQMRFKDYSGKGQEPISGRQNRLEWIENNLENIR	183
KLNMPPFYAYYDMFKKQLLINWLNKNRNDVIGGTGRMYTASGNY...IANAYLEVALESSSLGSGSYMIQMRFKDYSGKGQEPISGRKNRLEWIENNLENIR	183
KMNMPFYAYYDMFKKQQLLKWLNKNRNDVIGGTGRMYTASGNY...IANAYLEVALESSSLGSGSYMLQMRFKDYSGKGQEPISGRQNRLEWIENNLENIR	183
DYAAAQYVAWEASEDNS..IESIEAN.LEFIKDEGAKFNTENALK..IAQLFLEA.....	95
DYAAAQYVAWEASEDNS..IESIEAN.LEFIKDEGAKFNTENALK..IAQLFLEA.....	91
NYITETFEWWEFEN....QYLEFE.LDYVVKDEKIFVLEMHF.....WRKIRK.....	96
NYITETFEWWEFEN....QYLEFE.LDYVVKDEKIFVLEMHF.....WRKIRKLE.....	98
NIYTDTYEWWEFNN....QYLELE.IDYYRQNDKIYLLLEHF.....WRKVKK.....	103
DLMTSSELLGQLGKNYSDDIENLITGRELITFAYDLFLKIKELIN.VKYINLETCQNEPKLISFYQNFQFKMLESLSSEEGLKVMIMELK.....	193
NIFNGEFYGFEDS....YKNKDEKIEVITKVIKLFKYENGELK.LLGIKFEKSINKIS.....	116
QVTATLESVIEAGDINTKWFVNDETGALSGKYGSVYTESGWYICNESGEKENKLTENQISSIRVAMDRGDTATYSWEFDD.....	162
.WMIIGKELYENEVGNVYHAQFIVVKYKKIIVSVSFYFVKEDNIYK....LVQVTFDKIFFGKLYELKRQLSQKKQ.....	126
IHFQSSGISVSLSSPLNSPIFLRRFSACSVGFEEIPTALQRIIRS...VYTAKLLEDE.....	106
KTWDAKWAKLENGR.....MASEINPGEFFIA.....	81

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