

logo

Sequence	Score
DGAWITCVSD.....VPTFLPKGCTAGTPTGGAITSL	149
DGLWKCTSD.....QDEQFIPKGCSCS.....	150
DGEWSCAST.....LDAKYKPGKCS.....	139
DGLWDCTSD.....LDSRYKPGKCL.....	141
SVKWF CGQPVTTRADDDTVADA..KDGKEIDTKHLPSTCRDKASDAK....	166
SVKWF CGQPVTTRTGDNDDTVA..DANNAIDTKHLPSTCRDESSAT.....	164
GVTWTTTCKGT.....DASLFPANFCGSVTQ.....	149
ISTWTCAPGAAN.....GIETRLPTSCQ*.....	153
ATDWCASAAKETADKRFGTGSVAVGTLPAKYAPSECK.....	188
PIMWTCYAQNKAQAASSVAPS...GTMSLAAKYAPAECR.....	168
QLKWTCSSA.....I.NTKYLPACERNSGT.....	141
AVTWKCTTT.....S.DKKYVPSECRG.....	147
DVTWTCCTGG.....TLLAKYRPASCRP.....	136
DVTWTCCTGG.....TLLAKYRPASCRP.....	136

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