


[illegible]



Sequence	Score
KIDRDAALAVALQFQAAAVNDLHSGDE.....	100
KINRDAALAVALQFQAAAVNDLHSGDE.....	100
KIDRDAAVAVALQFQAAAVNDLHSGDE.....	100
VFSESVAVDHGLKLAADTE.....	95
FFSEEEAQRADDLINNFADFGHDEGDATFRIKAQSYRLKKYDCHALWSMINQASLTIESVKPETFCDEDSDEDISSDSLVLVLTSLRFLNFKQNEAFAT	181
MFDYDLALQQAENLLNLVET.....	85
VFDVQEAINKARSLHIANQSPC.....	86
KFDADQALRYAVYLSGILDYQSSKLKWL.....	99
KFNTENALKIAQLFLEA.....	95
KDFDGKALEL.....	89
EFENDAGDKIWLEYNKVSVGGETTYFVKNVEVELNTEEFMNLFF.....	129
KLATDEDKEKHDKQEVIIKSGLN.....	116
RFVEKCFQNY.....	63
WFVVNDETGALSGKYGSVYTESGWYICNESGEKIENKLTENQISSIRVAMDRGDTATYSWEFDD.....	162
YFVKEDNLYKLVQVTFDKIFFGKLYELKRQLSQKKQ.....	126

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logo

Acr00072	type I-E, I-F	.....	100
Acr00074	type I-F	.....	100
Acr00073	type I-F	.....	100
Acr00075	type I-F	.....	95
Acr00083	type I-F	LTQYYTVSEGLTVEDLLDYSLLDYPNFDHDESGKTYNLMENIAQRYYTECIKVVMDYFRDAHKELPDVIRSEEITSMILQPMKLPIMAN	270
Acr00077	type I-F	.....	85
Acr00078	type I-F	.....	86
Acr00079	type I-F	.....	99
Acr00081	type I-F	.....	95
Acr00080	type I-F	.....	89
Acr00024	type I-D	.....	129
Acr00159	type II-A	.....	116
Acr00064	type I-E	.....	63
Acr00125	type I-F	.....	162
Acr00008	type I-D	.....	126
consensus			

- ⓧ non conserved
- ⓧ similar
- ⓧ ≥ 50% conserved