

A

Transmembrane spanning region 1

CfTX-1	64	QSGDPAKIASGCLDILVGISSVLKD-----FAKFSPIFSILSLVVGLFSGTKAEESVGSVVKKAVQEQS	127
CfTX-2	64	QSGDPASIASGCLDILVGISSVLKD-----FAKFSPVFSILSLVVGLFSGTKAEESVSSVVKAIQEQS	127
CqTX-A	64	QSGDPAKIASGCLDILVGISSVLKD-----FAKFSPIFSILSMVVGLFSGTKAEESVGSVVKKVQEQS	127
CrTX-1	65	NSGDATKIISGCLDIVAGIATTFGGPVGMGIGAVASFVSSILSL----FTGSSAKNSVAAVIDRALSKHR	130
CaTX-1	71	KSGDPFDVASGCLDIIVASVATTFGGPYGIAIGAVASLISSILSL----FSGNSMGSAIKQVIDDAFKKYR	136

MEME - Motif 2

B

