



(d)

Chain 1:	49	IKGTAPFETHANRIVGFFSKIIGELPNIEADVNTFVASHKPRGVTHDQLNNFRAGFVSYMKAHTDFAGAE
	1	11111111111111111111 222222222222222222222222222222222 222222
Chain 2:	98	CLVGGTGPLDDYLIG-----GIAEINRTFDLSPSWYVEALKYIKANHG---LSGDPA
Chain 1:	119	AAWGATLDTFFGMIF
		2222222222222222
Chain 2:	150	VEANSYIDYAINALS

(e)

Chain 1:	2	SADQISTVQASFDKVKGDVPVILYAVFKADPSIMA---KFTQFAGKDLESIKGTAPFETHANRIVGFFSK
		11111111111111111111111111111111111111111111111111111 11111 22222222222222222222
Chain 2:	33	QASASLAAAKALTEKASSLASGAANAVYSKFPYTTSQLGNPFA-----STQTGKDKCVRDIGYYLR
Chain 1:	69	IIGEL-----PN--IEADVNTFVASHKPRGVTHDQLNNFRAGFVSYMKAHTDFAGAEAAWGATLDTFFGM
		22222 22 22222222222222222222 22222222222222222222222222222222222222222222222222222
Chain 2:	94	MVTYCLVGGTGPLDDYLIGGIAEINRTFDL---SPSWYVEALKYIKANHG LSGDPAVEANSYIDYAINA
Chain 1:	132	IF
		22
Chain 2:	173	LS