

B. C-terminal alignment

[illegible]

			βββββ	α	α	αα	αα	αα	βββββ		α
			*▽ ▽	▲ ▽ ▲					**●●●	*	
CaFADS	84	FG-----	IDGVLVIDFT	RELSGT---S	PEK----	YVE	FLLD--TLH	AS-HVVVGA-	-----N-	FTFG---ENA	-----
1t6y	66	YA-----	RTVVLDF-FR	IKDL-TPEGF	VER-----	YLS	G-----	VS-AVVVGRL	-----D-	FRFG---KNA	-----
1coz	62	IR-----	YV DE-VIPEK--	-----	-NWEQKKQ-D	I-----	IDH	NIDVFVMG--	-----D-	D- -----	WEG K-FDFL---
1kku	83	DT-----	WE SL-QKEWK--	-----	-ETLKVL-R	H HQEKL EASDV	PKVKLLCGA-	-----DLLES	F-AVPNLWKS	EDITQI---	-----
1ej2	62	ALSENGIPAS	RYYIIPVQ--	--DI ECNAL-	WVGHIKML--	-----TP	PFD R VYSG--	-----N-	PLVQR LFS ED	-----	-----
1f9a	59	SLKD----	YDL TYYPIPIK--	--DIEFN--	-SIWVS-YVE	S-----LTP	PFDIV YSG--	-----N-	-----	-----	PLVR
1b6t/1gn8	58	ATAHL---GN	VEVVGFS DLM	-----	---ANFARN	Q-----HA-	-T-VLI RGLR	AVADFEY-E-	-----M	QLAH-MNRHL	-----
1od6	61	HL-----	AN VE-AATFS--	-----	---GLLV D-F	V-----RRV	GAQAIVKGELR	AVSDYEY-EL	QMAHLN----	-----	-----
Consensus regions								GΩ		Ψ	

		αα	βββ	βββ				α	αααα	α	ααααααα	α
				▲	▲	▽	●	●	●	●	●	
CaFADS	133	AGTADSLRQI	CQSR-LTVDV	----IDLLD	-----	-----DE-	GV-R--ISST	TVREFL-SEG	DVARANWALG	RH-----		
1t6y	109	SGNASFLR--	-KKG-VEVYE	---- I -- ED	VV -----	-----VQ-	GK-R-- VSSS	LIRNLV-QEG	RVEEIPAYLG	RY-----		
1coz	103	-----	--KDQCEV-V	-----YLP- R	-----	----- TE -	--G-- ISTT	KIKEEI----	-----	-----		
1kku	141	-----VA-	--NYGLI-CV	TRAGNDAQKF	IYESDVLWKH	RSNIHVVNW	--FANDISST	KIRRALRRQG	SIRYLPDLV	-----		
1ej2	116	-----	-----	GYEVTAPPL F	-----	-----	--YRDR YSGT	EVRRRMLDDG	DWRSLLPESV	VEVIDEINGV		
1f9a	104	VLFEERGY--	-----	--EVKR PEMF	-----	-----	N-- RKEYSGT	EIRRRMLNGE	KWEHLVPKAV	VDVIKEIKGV		
1b6t/1gn8	110	MP-----EL	ES-----	-----VFLMP	-----	----- SKEW	-SF-- ISSS	LVKEVA-HQG	---DVTHFLP	ENVHQALMAK		
1od6	107	-----RQL	Y PGL E TL--	FIL A TR Y SF	-----	----- VSS T	-----	MVKEIARYGG	DVSKLVPPAT	LRALKAKLGQ		
Consensus regions								ΦSST	QVRΨ			

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$\beta\beta\beta\beta$ $\beta\beta$ α $\alpha\alpha\alpha\alpha\alpha\alpha\alpha$ α

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CaFADS	273	DR-DA-DLYG	HDVKVEFVDH	VRAMEKFDSV	EQLLEVMAKD	VQKTRTLLAQ	DVQAHKMAPE	TYFLQAES					
1t6y/1t6x/1s4m	236	D-- FEGLY G	QRLKLEVLFK	MRDEK KFDSI	EEL KA AIQDQ	VKSARNMIDD	IINSKFEKEG	-----					
1p4m/1q9s/1nb0	91	HT FKE-DFYQ	EILNVAIVGY	LRPEK NFDSL	ES LISA IQGD	IEEAKKRLEL	PEYLKIKEDN	FFQVSK--					
1n06/1n07/1n08	101	ERQGE -DFYE	EIMRVIVLGY	IRPELN YAGL	DK LIED IHTD	IRVALN----	SMDRPSYSSY	KKDPFFKV					
Consensus regions		ΨQ ΨQ DΨYQ		ΦRQΩQΨF	L	D							