

Supplementary material

Supplementary Table S1

Analysis of interfaces in the CA CTD crystal structure.

		Structure 1				Structure 2						* Interface area, Å ²	
Id	No.	Chain	iNat	iNres	Surface Å ²	Chain	Symmetry op-n	Sym.ID	iNat	iNres	Surface Å ²		
1	1	C	72	16	6125	B	x-1,y+1,z	1_465	71	19	6187	713.3	
	2	B	64	16	6187	C	x,y-1,z	1_545	67	20	6125	686.2	
	<i>Average:</i>												699.8
2	3	D	47	18	5069	B	x,y,z	1_555	52	19	6187	521.6	
	4	C	44	18	6125	A	x,y,z	1_555	51	19	5830	490.6	
	<i>Average:</i>												506.1
3	5	B	46	15	6187	A	x,y,z	1_555	41	16	5830	428.6	
4	6	A	34	12	5830	D	x,y-1,z+1	1_546	36	12	5069	307.7	
5	7	D	28	9	5069	A	x,y,z-1	1_554	29	12	5830	277.7	
	8	A	27	8	5830	D	x-1,y,z+1	1_456	31	10	5069	267.4	
<i>Average:</i>												272.5	
6	9	D	28	13	5069	C	x,y,z	1_555	27	9	6125	265.1	
7	10	C	22	6	6125	B	x,y,z	1_555	26	10	6187	259.1	
8	11	B	24	7	6187	A	x,y-1,z	1_545	20	5	5830	215.9	
9	12	C	14	4	6125	D	x-1,y+1,z	1_465	19	5	5069	146.2	
10	13	[EDO] E:1	4	1	183	A	x,y,z	1_555	23	10	5830	115.3	

The analysis was performed with protein interfaces, surfaces and assemblies service PISA at the European Bioinformatics Institute (http://www.ebi.ac.uk/pdbe/prot_int/pistart.html), authored by E. Krissinel and K. Henrick. (Krissinel & Henrick, 2007).

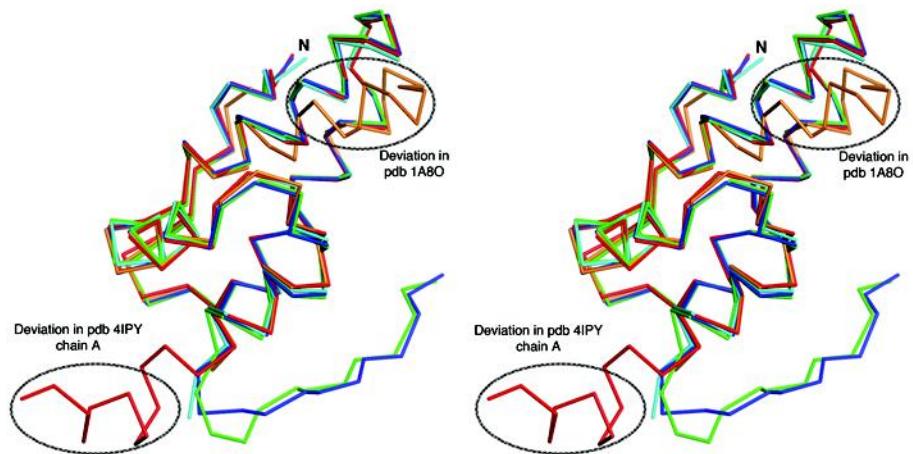
* Interfaces with areas below 100 Å² are not shown.

iNat indicates the number of interfacing atoms in the corresponding structure.

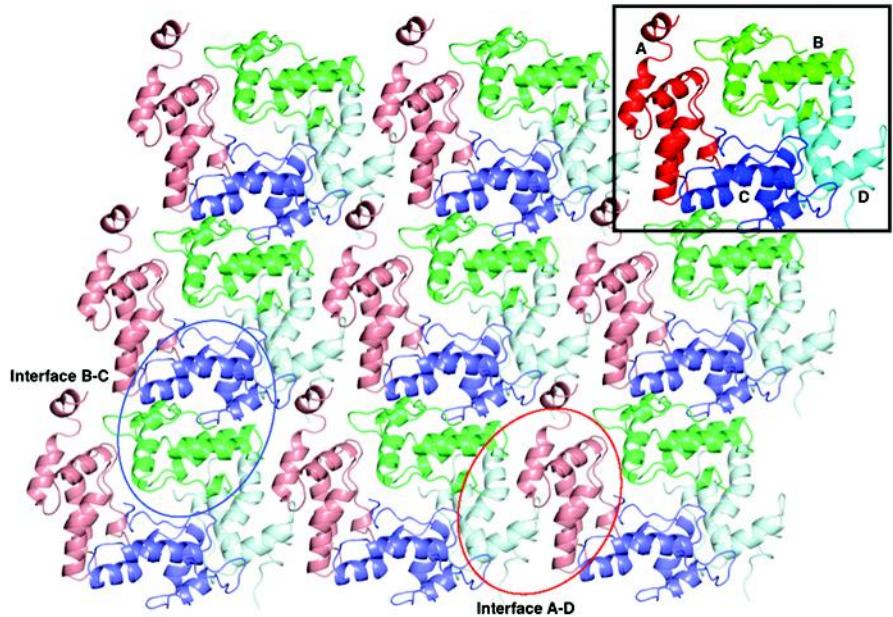
iNres indicates the number of interfacing residues in the corresponding structure.

Symmetry op-n indicates the symmetry operation that should be applied to the 2nd interfacing structure in order to obtain the respective interface.

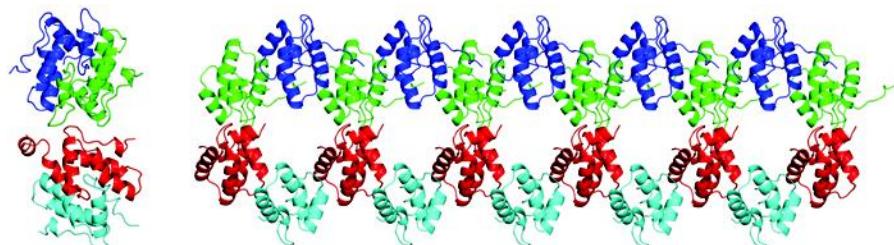
Sym.ID indicates the position of the 2nd interfacing structure in the crystal relative to the position of the 1st interfacing structure.



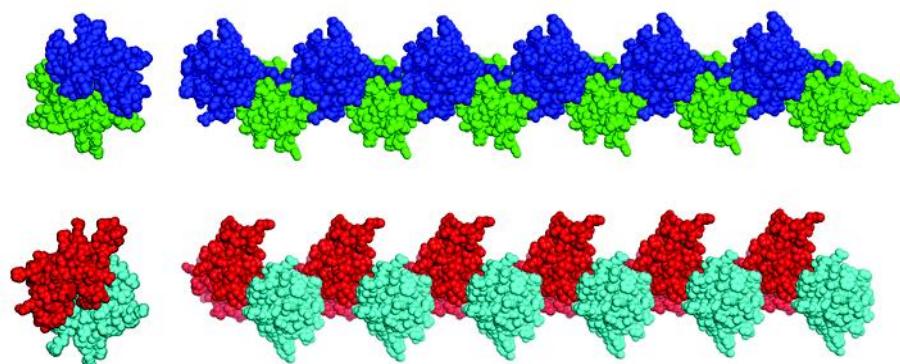
Supplementary Figure S1. Stereo diagram of the superimposed $\text{C}\alpha$ traces of the CA CTD molecules of PDB entry 4IPY (A, red; B, green; C, blue; D, cyan) and 1A8O, orange (Gamble *et al.*, 1996). Upper ellipse: deviation in the conformation of the loop between helices 1 and 2 in PDB 1A8O compared to that in present structure (PDB entry 4IPY). Lower ellipse: location of C-terminal region in molecule A of present structure, compared to the corresponding deviations in molecules B and C (in chain D C-terminal region is not observed on the electron density maps).



(a)



(b)



Supplementary Figure S2. Crystal packing and “fiber” formation in CA CTD. (a) Cartoon representation of the crystal packing. The four molecules in the asymmetric unit are marked in the black rectangle, and are colored and named by molecules. Interfaces responsible for the formation of the infinite fibers are marked in ellipses (blue ellipse marks the interface between molecules B and C; red ellipse marks the interface between molecules A and D). (b) Cartoon representation of the two “filaments” formed by symmetry elements. Left panel, View along the “fibers”. Right panel, “fiber” propagation axis is in the plane of the paper. Infinite “fibers” forms perfect parallel arrays.(c) Figure similar to (b) but rotated

along “fiber” propagation axis by 45° counter-clock-wise. Molecules are represented as water accessible surfaces.