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Electronic Supplementary Information on

Stability and growth mechanism of self-assembling putative anti-freeze cyclic peptides

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Straightforward MD and nanotube sequences

This Supplementary Information details some of the settings and outcome of the straightforward MD simulation discussed in the Main Text. Table 1 reports the literature values for the dihedral angles for beta strands¹. Table 2 gives the composition of the system for each of the MD simulations. Table 3 and 4 summarize the outcome of the MD simulations of the original and altered CPNT systems, respectively. Fig. 1 plots the radial distribution function of water around the hydroxyl oxygen of THR of AFCP. Table 5 and 6 list the sequence and the orientation of the original and altered CPNT systems, respectively. Finally, Table 7 and 8 report the measured average and standard deviation of backbone ϕ and ψ angles for each aminoacid of the different size nanotubes of the original and altered CP sequence, respectively.

Amino acid	Φ_{aver}	σ_{Φ}	Ψ_{aver}	σ_{Ψ}
L-ALA	-130.2	21.4	143.8	14.6
L-LEU	-115.2	15.8	131.8	13.5
L-LYS	-118.9	17.5	134.2	15.3
L-THR	-123.9	14.0	138.1	14.3
D-ALA	130.2	-	-143.8	-

Table 1 Average values for the dihedral angles Φ, Ψ and their estimated standard deviations $\sigma_{\phi, \psi}$ for anti-parallel β -strands¹.

Original CP sequence					
System	#CP	#AA	#H ₂ O	#atoms	V (nm ³)
CPNT2	2	16	4093	12519	127.48
CPNT3	3	24	4519	13917	139.09
CPNT4	4	32	4847	15021	151.47
CPNT5	5	40	5549	17247	174.34
CPNT6	6	48	6280	19560	197.25
AFCP sequence					
System	#CP	#AA	#H ₂ O	#atoms	V (nm ³)
CPNT2	2	16	4035	12325	122.57
CPNT3	3	24	4100	12630	131.07
CPNT4	4	32	4662	14426	144.55
CPNT5	5	40	5417	16801	169.58
CPNT6	6	48	6267	19317	195.47

Table 2 Original CP sequence: Composition of systems containing CPNTs of sequence cyclo-[(L-LYS-D-ALA-L-LEU- D-ALA)₂]. AFCP sequence: Composition of systems containing nanotubes of AFCP sequence cyclo-[(L-LYS-D-ALA)₂-(L-THR-D-ALA)₂].

System	Run 1	Run 2	Run 3	Run 4	Run 5
CPNT2	B	B	B	B	B
CPNT3	B	B	B	B	B
CPNT4	B	B	B	B	B
CPNT5	B	B	B	B	B
CPNT6	B	B	B	B	B → I

Table 3 Original sequence: Visiting states of different size CPNTs in the course of a 100 ns NPT simulations. *B* denotes the bound state and *I* the area of phase space which does not belong neither to *B* nor *U*.

System	Run 1	Run 2	Run 3	Run 4	Run 5
CPNT2	B → I → U → I → U → I	B	B → I → U → I	B	B → I → B
CPNT3	B	B	B	B	B
CPNT4	B	B	B	B	B
CPNT5	B	B	B	B	B
CPNT6	B	B	B	B	B

Table 4 AFCP sequence: Visiting states of different size CPNTs in the course of a 100 ns NPT simulations. *B* denotes the bound state and *U* the unbound state. *I* denotes the area of phase space which does not belong neither to *B* nor *U*.

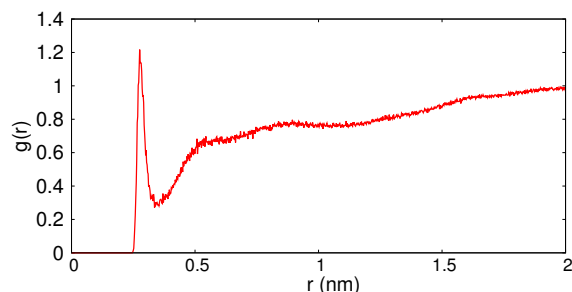


Figure 1 Radial distribution function of the water oxygen around the side chain oxygen of the THR residue in the AFCP sequence hexamer.

Orientation	Sequence								Name
N → C	L-LYS-1	D-ALA-2	L-LEU-3	D-ALA-4	L-LYS-5	D-ALA-6	L-LEU-7	D-ALA-8	CP1
C ← N	L-LYS-9	D-ALA-10	L-LEU-11	D-ALA-12	L-LYS-13	D-ALA-14	L-LEU-15	D-ALA-16	CP2
N → C	L-LYS-17	D-ALA-18	L-LEU-19	D-ALA-20	L-LYS-21	D-ALA-22	L-LEU-23	D-ALA-24	CP3
C ← N	L-LYS-25	D-ALA-26	L-LEU-27	D-ALA-28	L-LYS-29	D-ALA-30	L-LEU-31	D-ALA-32	CP4
N → C	L-LYS-33	D-ALA-34	L-LEU-35	D-ALA-36	L-LYS-37	D-ALA-38	L-LEU-39	D-ALA-40	CP5
C ← N	L-LYS-41	D-ALA-42	L-LEU-43	D-ALA-44	L-LYS-45	D-ALA-46	L-LEU-47	D-ALA-48	CP6

Table 5 Original CP sequence: schematic representation of the arrangement and chirality of the amino acids in the CP chains of sequence cyclo-[(L-LYS-D-ALA-L-LEU-D-ALA)₂] within various CPNTs. The sequential chains are named as CP1 to CP6. The terminals are assumed to be bonded in order to form the cyclic structure.

Orientation	Sequence								Name
N → C	L-LYS-1	D-ALA-2	L-THR-3	D-ALA-4	L-THR-5	D-ALA-6	L-LYS-7	D-ALA-8	CP1
C ← N	L-LYS-9	D-ALA-10	L-THR-11	D-ALA-12	L-THR-13	D-ALA-14	L-LYS-15	D-ALA-16	CP2
N → C	L-LYS-17	D-ALA-18	L-THR-19	D-ALA-20	L-THR-21	D-ALA-22	L-LYS-23	D-ALA-24	CP3
C ← N	L-LYS-25	D-ALA-26	L-THR-27	D-ALA-28	L-THR-29	D-ALA-30	L-LYS-31	D-ALA-32	CP4
N → C	L-LYS-33	D-ALA-34	L-THR-35	D-ALA-36	L-THR-37	D-ALA-38	L-LYS-39	D-ALA-40	CP5
C ← N	L-LYS-41	D-ALA-42	L-THR-43	D-ALA-44	L-THR-45	D-ALA-46	L-LYS-47	D-ALA-48	CP6

Table 6 AFCP sequence: schematic representation of the arrangement and chirality of the amino acids in the CP Chains of sequence cyclo-[(L-LYS-D-ALA)₂-(L-THR-D-ALA)₂] within various CPNTs. The sequential chains are named as CP1 to CP6. The terminals are assumed to be bonded in order to form the cyclic structure

angles	CPNT2			CPNT3			CPNT4			CPNT5			CPNT6		
	LYS	LEU	ALA	LYS	LEU	ALA	LYS	LEU	ALA	LYS	LEU	ALA	LYS	LEU	ALA
Φ	-116 ₂₇	-102 ₁₈	130 ₂₁	-119 ₂₄	-116 ₁₉	135 ₁₇	-116 ₂₇	-113 ₁₉	136 ₁₇	-119 ₂₆	-119 ₁₈	137 ₁₅	118 ₂₇	-116 ₁₉	138 ₁₅
Ψ	138 ₂₃	130 ₁₁	-129 ₄₇	137 ₁₆	129 ₁₄	-127 ₄₅	138 ₁₇	128 ₁₃	-123 ₄₇	138 ₁₆	127 ₁₃	-117 ₅₇	138 ₁₆	127 ₁₂	-116 ₅₆

Table 7 Average and standard deviation of backbone φ and ψ angles for each aminoacid of the different size nanotubes of the original CP sequence.

angles	CPNT2			CPNT3			CPNT4			CPNT5			CPNT6		
	LYS	THR	ALA	LYS	THR	ALA	LYS	THR	ALA	LYS	THR	ALA	LYS	THR	ALA
Φ	-92 ₅₀	-111 ₂₉	114 ₂₉	-126 ₁₇	-124 ₁₈	134 ₁₈	-130 ₁₃	-128 ₁₄	136 ₁₅	-128 ₁₄	-127 ₁₅	137 ₁₄	-132 ₁₄	-129 ₁₄	138 ₁₄
Ψ	131 ₄₄	116 ₆₀	-110 ₆₉	137 ₁₈	137 ₁₄	-125 ₅₃	137 ₁₄	136 ₁₃	-127 ₄₇	137 ₁₃	134 ₁₃	-122 ₅₄	136 ₁₄	134 ₁₅	-130 ₃₉

Table 8 Average and standard deviation of backbone φ and ψ angles for each aminoacid of the different size nanotubes of the AFCP sequence.

References

- [1] S. Hovmo, *Acta. Crystallogr. D.*, 2002, **58**, 768.