Tuning the Self-assembly of Short Peptides via Sequence Variations

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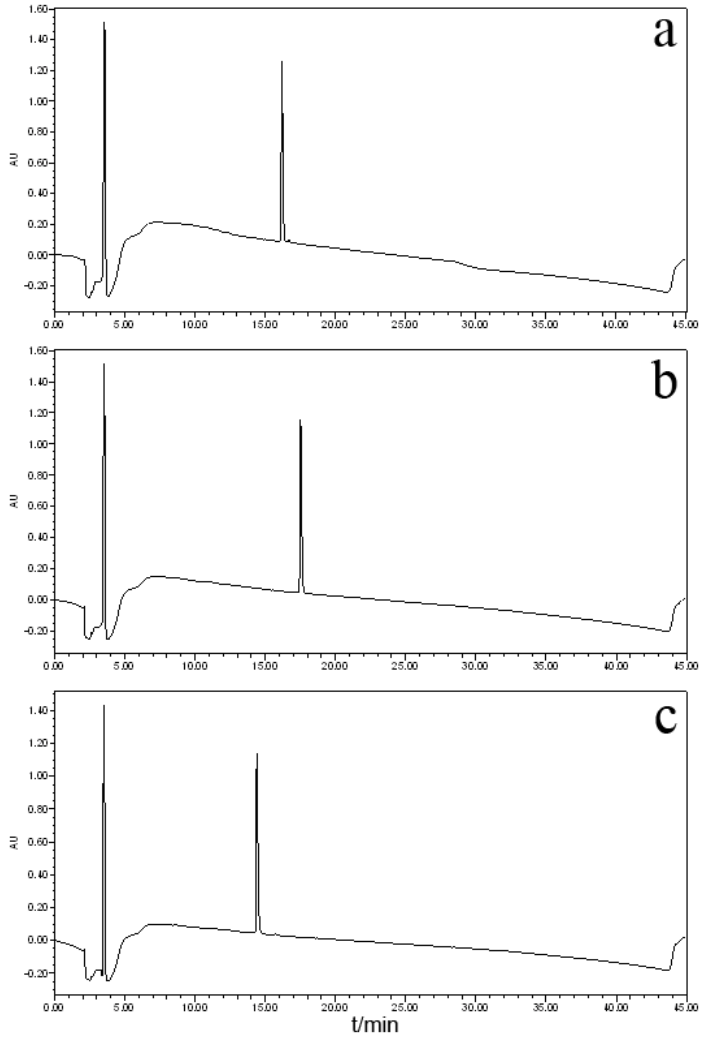

Figure S1. Reversed-phase HPLC profiles of (a) Ac-IIIIKK-$CONH_2$, (b) Ac-IIKKII-$CONH_2$, and (c) Ac-KIIIIK-$CONH_2$. The experimental condition for the HPLC analysis is as follows: eluent A, 0.1% TFA in water, 0→1 min, 95%, 1→40 min, 95%→5%, 40→45 min, 5%→95%; eluent B, 0.1% TFA in acetonitrile, 0→1 min, 5%, 1→40 min, 5%→95%, 40→45 min, 95%→5%. UV, 214 nm; flow rate, 0.6 ml/min; column, RP-C18, 4.6 mm×150 mm. The measurements were performed on Waters 2695 Alliance HPLC system at temperature of 25 ^{o}C. The profiles indicate high purity with the three peptides.

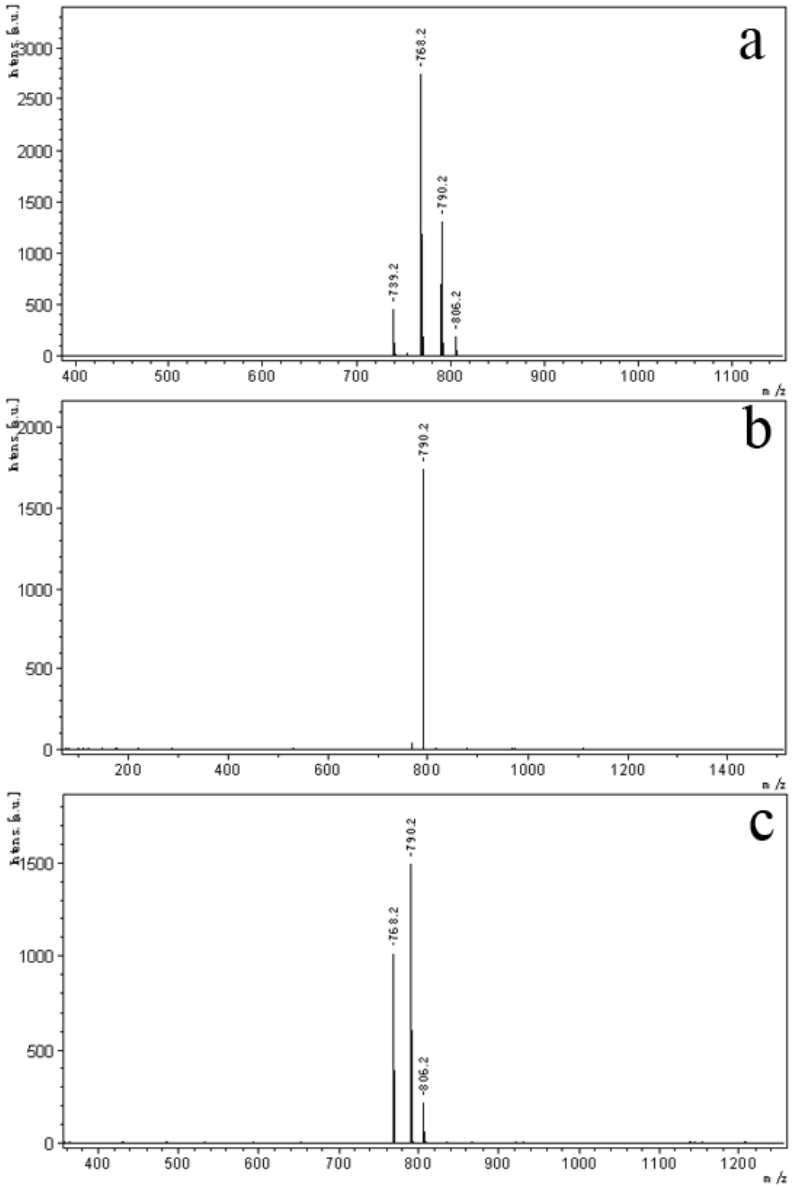

Figure S2. MALDI-TOF mass spectra of the three peptides: (a) Ac-IIIIKK-$CONH_2$, (b) Ac-IIKKII-$CONH_2$, and (c) Ac-KIIIIK-$CONH_2$. The measurements were carried out on a Bruker Biflex III matrix assisted laser desorption/ionization time of flight (MALDI-TOF) mass spectrometer equipped with a 337 nm nitrogen laser and 4-hydroxy-α-cyanocinnamic acid was used as the matrix. The samples were dissolved with the matrix in the mixture of acetonitrile and water (1:1, v/v) which contained 1% trifluoroacetic acid (TFA). About 0.5 µl of the sample solution was placed on a metal sample plate and then allowed to air-dry at ambient temperature. Mass spectra were acquired in positive linear mode and using an acceleration voltage of 19 kV. External mass calibration was performed using a standard peptide mixture. Spectra were obtained

by setting the laser power close to the threshold of ionization and generally 100 pulses were acquired and averaged.

The calculated molecular masses for the three peptides are all well consistent with the observed as follows:

Ac-IIIIKK-$CONH_2$: expected masses $[M+H]^+$=769.06, $[M+Na]^+$=791.06, $[M+K]^+$=807.06; observed masses $[M+H]^+$=768.2, $[M+Na]^+$=790.2, $[M+K]^+$=806.2.

Ac-IIKKII-$CONH_2$: expected masses $[M+H]^+$=769.06, $[M+Na]^+$=791.06, $[M+K]^+$=807.06; observed masses $[M+ Na]^+$=790.2.

Ac-KIIIIK-$CONH_2$: expected masses $[M+H]^+$=769.06, $[M+Na]^+$=791.06, $[M+K]^+$=807.06; observed masses $[M+H]^+$=768.2, $[M+Na]^+$=790.2, $[M+K]^+$=806.2.

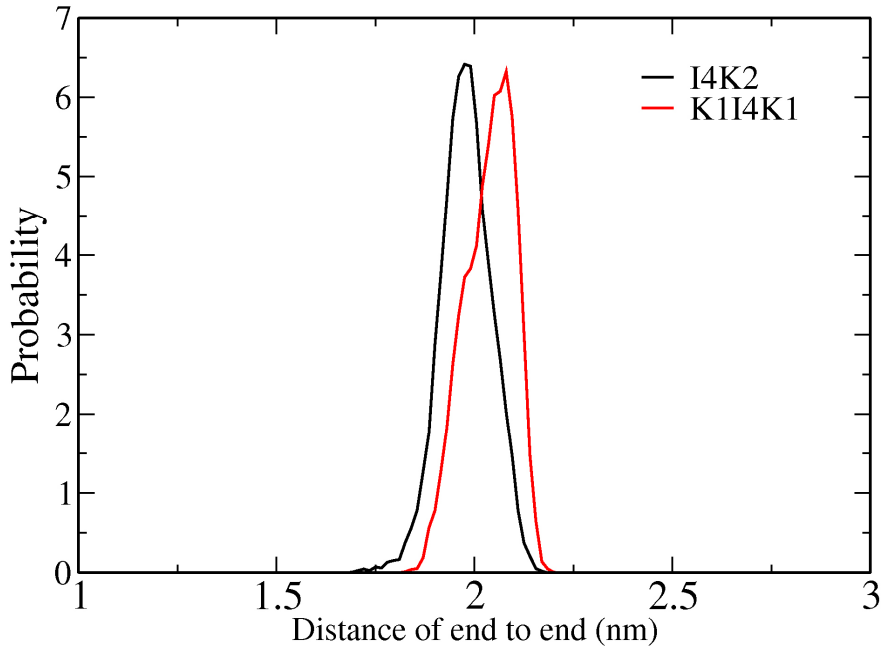

Figure S3. End-to-end distance of KI_4K and I_4K_2 molecules constrained in a β-sheet conformation.

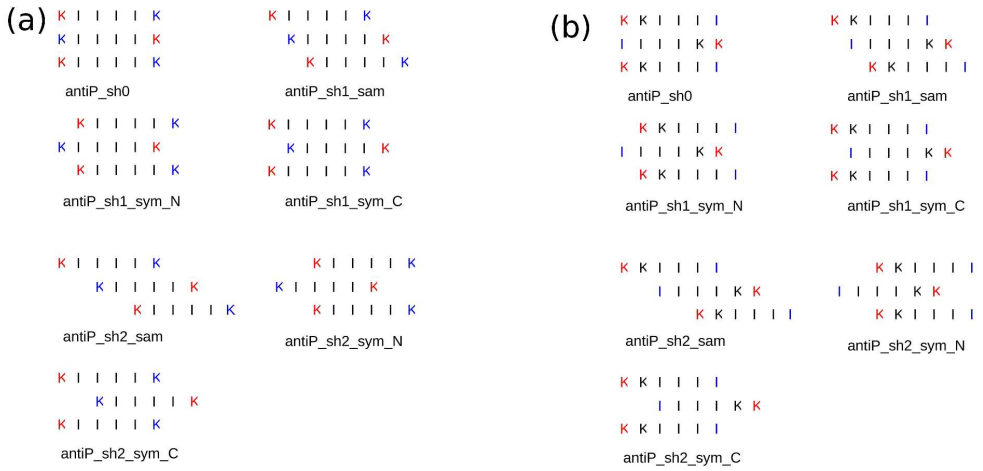

Figure S4. Different arrangements of trimers with anti-parallel β-sheet conformations and their designated names: (a) KI_4K and (b) I_4K_2. The C-terminal of the peptide is marked in red and the N-terminal is in blue. "AntiP" means anti-parallel, "sh_*n*" means shifted alignment of two neighboring monomers with *n* residues, "sam" means the two neighboring monomers shift in the same direction, "sym" means the top and bottom monomers are symmetric with respect to the middle one, and "N" ("C") means the N-terminal (C-terminal) of the monomer in the middle is exposed.

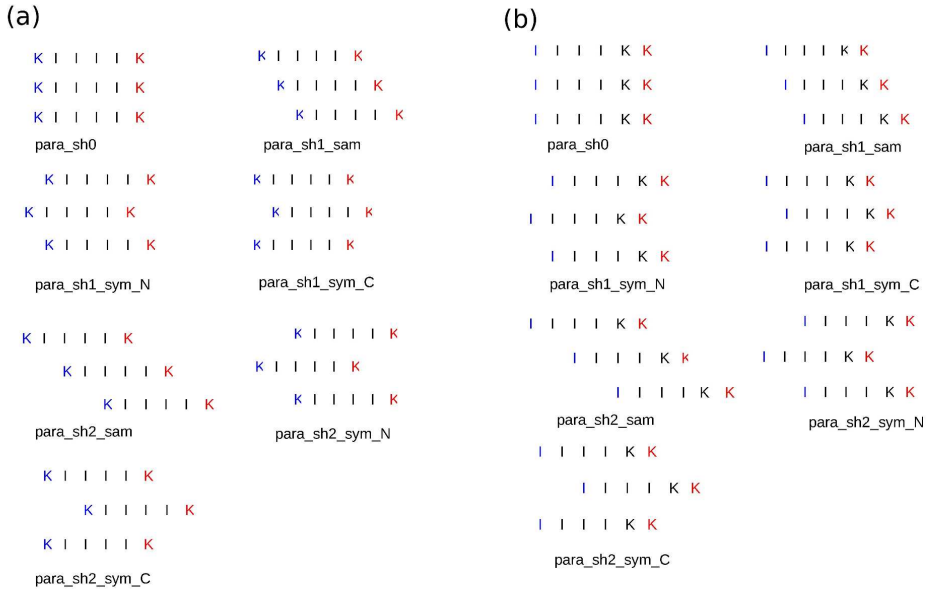

Figure S5. Different arrangements of trimers with parallel *β*-sheet conformations and their designated names: (a) KI_4K and (b) I_4K_2. The C-terminal of the peptide is marked in red and the N-terminal is in blue. "para" means parallel, "sh_*n*" means shifted alignment of two neighboring monomers with *n* residues, "sam" means the two neighboring monomers shift in the same direction, "sym" means the top and bottom monomers are symmetric with respect to the middle one, and "N" ("C") means the N-terminal (C-terminal) of the monomer in the middle is exposed.

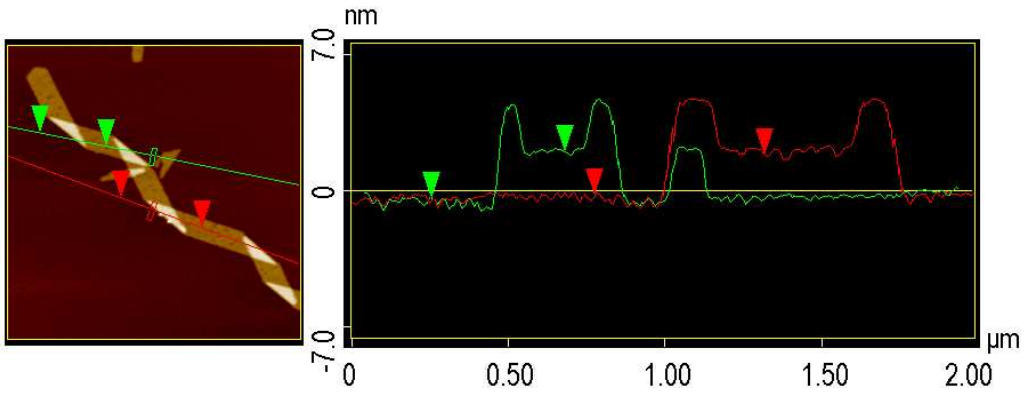

Figure S6. Thickness measurements of a representative KI_4K helical ribbon, which was formed in the mixture of acetonitrile and water (1:4, v/v) after 12 days of incubation

Table S1. Key Physicochemical Parameters of Designed Peptides

Peptide	Sequence	Net charge pH 3.0	Molecular weight, Da		RP-HPLC retention time[2], min
			calculated	Observed[1]	
I_4K_2	Ac-IIIIKK-CO NH_2	+2	768.06	767.2	16.3
$I_2K_2I_2$	Ac-IIKKII-CO NH_2	+2	768.06	767.2	17.7
KI_4K	Ac-KIIIIK-CO NH_2	+2	768.06	767.2	14.5

1) From MALDI-ToF mass spectra and 2) from RP-HPLC profiles. See Figures S1 and S2 in the Support Information for details.

Table S2. The best fitted parameters for the SANS curves shown in Figure 3.

PeptideParameter	I_4K_2	KI_4K
Fitting Model	LamellarModel+ Flexible Cylinder Ellipsoidal Model	LamellarModel+ HollowCylinderModel
p1_background	0.017	0.02
p1_radius	63 Å	450 Å
p1_core_radius	–––	431 Å
p1_length	>1000 Å	>1000 Å
p1_axis_ratio	0.95	–––
p1_scale	0.0045	0.00015
p1_sldCyl	3.701e-06	3.8e-06
p1_sldSlov	6.35e-06	6.35e-06
p2_background	0.017	0.02
p2_bi_thick	16.95 Å	19 Å
p2_scale	0.029	0.033
p2_sld_bi	3.73e-06	3.8e-06
p2_sld_sol	6.35e-06	6.35e-06
Scale_factor	0.443	0.4609

Table S3. Structural Arrangements and Non-bonded Potential Energies of Peptide Trimers with Parallel Conformations and Monomers

	Molecular arrangement	Non-bonded energies (KJ/mol)		Number of hydrogen bonds	
		Average	Standard deviation	Average	Standard deviation
KI_4K trimer	para_sh0	1430.78	32.32	11.09	0.85
	para_sh1_sam	1441.39	34.09	10.3	0.87
	para_sh1_sym_N	1467.43	31.85	9.98	0.89
	para_sh1_sym_C	1444.98	29.86	10.17	0.81
	para_sh2_sam	1538.74	37.71	7.56	0.82
	para_sh2_sym_N	1526.97	48.87	7.37	1.05
	para_sh2_sym_C	1531.34	43.94	8.3	1.08
KI_4K monomer		604.98	18.10	0	0
I_4K_2 trimer	para_sh0	1465.67	40.92	10.35	1.06
	para_sh1_sam	1477.46	43.23	9.69	1.09
	para_sh1_sym_N	1465.33	35.18	9.72	0.73
	para_sh1_sym_C	1487.45	34.67	9.63	1.04
	para_sh2_sam	1560.59	37.51	8.3	1.28
	para_sh2_sym_N	1579.52	37.31	7.92	0.91
	para_sh2_sym_C	1568.17	31.99	7.48	1.01
I_4K_2 monomer		651.65	17.22	0	0

"para" means parallel, "sh_*n*" means shifted alignment of two neighboring monomers with *n* residues, "sam" means the two neighboring monomers shift in the same direction, "sym" means the top and bottom monomers are symmetric with respect to the middle one, and "N" ("C") means the N-terminal (C-terminal) of the monomer in the middle is exposed (see Figure S5 in the Support Information for detailed conformations).