

Supporting Information

Unique behavior of α -helix in bending deformation

Dong-in Kim, Seong-jae Han and Yong-beom Lim*

Department of Materials Science and Engineering, Yonsei University, Seoul 03722, Republic of Korea

E-mail: yblim@yonsei.ac.kr

Table of Contents

1. Materials and methods.....	2
2. Figure S1. Sequences of peptides.....	5
3. Figure S2. MALDI-TOF MS spectra.....	7
4. Figure S3. Mechanism of intein-mediated peptide cyclization.....	9
5. Figure S4. Intein-mediated ligation of large peptides.....	10
6. Figure S5. Additional CD spectra.....	11
7. Figure S6. CD data.....	12
8. Figure S7. Additional CD spectra.....	13
9. Table S1. Quantitative description of Thermal behaviour.....	14
10. Figure S8. Size exclusion chromatography data.....	15

Materials and Methods

Materials. gBlock gene fragments for the cloning of target genes were obtained from Integrated DNA Technologies (USA). The pTWIN2 vector was purchased from New England Biolabs (USA). *E. coli* strains for cloning and protein expression were obtained from New England Biolabs (USA) and Novagen (USA). 2-Cholorotrityl chloride resin and Fmoc-amino acids were purchased from Novabiochem (Germany) and AAPPTec (USA), respectively. All other general chemicals for solid-phase peptide synthesis (SPPS) were obtained from Thermo Fisher Scientific (USA) and Samchun (Korea).

Intein-mediated cyclization of bacterially expressed peptides. Target genes for **C64** and **C118** were cloned into the Sap I sites of the pTWIN2 vector for intein-mediated cyclization. The precursors of **C64** and **C118** were expressed in *E. coli* strains lysY and Rosetta(DE3), respectively. For **C64**, transformed lysY cells were grown in Luria-Bertani (LB) medium containing ampicillin (100 µg/mL) at 37 °C. When the OD₆₀₀ reached 0.5, 0.5 mM isopropyl β-D-1-thiogalactopyranoside (IPTG) was added to the cells to induce the protein expression for 8 h at 25 °C. For **C118**, transformed Rosetta(DE3) cells were grown in LB medium containing ampicillin (100 µg/mL) at 37 °C. When the OD₆₀₀ reached 0.4, 0.5 mM IPTG was added to the cells for 5 h at 37 °C. After harvesting, the cells were resuspended in lysis buffer (20 mM Na-HEPES, pH 8.5, 500 mM NaCl, 1 mM EDTA), and the lysate was centrifuged at 10,000 ×g for 1 h. Then, the clarified cell extract in supernatant was applied to a chitin column at a flow rate of 1 mL/min. Unbound proteins were washed off from the column using 100 mL of lysis buffer. On-column cleavage of intein1 was induced by equilibrating the chitin beads in a buffer containing 20 mM Na-HEPES, pH 6.5, 500 mM NaCl, and 1 mM EDTA. The column was incubated overnight at room

temperature to allow the cleavage reaction to proceed. After washing the column to remove impurities, both on-column cleavage of intein2 and the peptide cyclization were induced by equilibrating the chitin beads in a buffer containing 20 mM HEPES, pH 8.5, 500 mM NaCl, 50 mM 2-mercaptoethanesulfonic acid, and 1 mM EDTA. The column was incubated overnight at 4 °C. Then, the cyclic and linear peptides were eluted from the chitin column. The peptides were purified by reverse-phase high-performance liquid chromatography (RP-HPLC) using a water/acetonitrile gradient containing 0.1% trifluoroacetic acid (TFA). The molecular weight was characterized by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS; LRF20, Bruker Daltonics, Germany).

SPPS and cyclization. Peptides were elongated on 2-chlorotrityl chloride (CTC) resin by following a standard Fmoc SPPS protocol. To attach the first amino acid to the CTC resin, the resin was treated with 5 equiv. of the first amino acid and 10 equiv. of diisopropylethylamine (DIPEA) dissolved in 2 mL of methylene chloride (MC) in a glass vial, and the mixture was shaken for 3 h. Further elongation was performed in a solid-phase extraction tube using 1-[bis(dimethylamino)methylene]-1H-1,2,3-triazolo[4,5-b] pyridinium 3-oxide hexafluorophosphate (HATU) as a coupling reagent. Cyclic peptides were synthesized by the head-to-tail cyclization of protected linear peptide fragments. One syringe was filled with the protected linear peptide fragment (20 μmol, 1 equiv.) and DIPEA (16 equiv.) in 20 mL of dimethylformamide (DMF), while the other syringe was filled with HATU (20 μmol, 1 equiv.) in 20 mL of DMF. The two solutions were simultaneously added at a rate of 0.05 mL/min to a stirred solution of 20 mL of DMF in a round-bottom flask using a syringe pump. Final deprotection was performed in a cleavage cocktail (TFA: triisopropylsilane: water = 95: 2.5: 2.5), and the peptide was triturated with *tert*-

butyl methyl ether (3×). The peptides were purified by RP-HPLC using a water/acetonitrile gradient containing 0.1% TFA. The molecular weight was determined by MALDI-TOF MS.

Circular dichroism (CD) spectroscopy. CD spectra were recorded using a Chirascan CD spectrometer equipped with a Peltier temperature controller (Applied Photophysics, UK). The spectra were obtained from 190 nm to 260 nm using a 2-mm pathlength cuvette. In the temperature ramping experiment, the temperature was varied from 10 °C to 80 °C, and the measurements were repeated more than twice. The peptide concentration was typically 30 μM. Most CD studies were performed in distilled water.

Atomic force microscopy (AFM). Two microlitres of the sample at a concentration of 0.5 μM was loaded on a disc-shaped mica surface. Immediately after loading, the mica was mounted on a spin coater (ACE-200, Dong-Ah Trade Corp, Korea). The spin speed was ramped to 3000 rpm over 5 s, and the speed was maintained for 30 s. The mica was dried at room temperature for approximately 10 min. AFM scans were conducted in tapping mode with a Park NX10 instrument (Park Systems, Korea). The scanning was performed at a scan rate of 0.3 Hz and a Z-gain of 1. The images were processed using XEN software.

Fourier transform infrared (FTIR). Ten microlitres of the peptide sample (10 μM) was cast from the solution onto a ZnSe window and dried at room temperature. The solution casting processes were repeated five times. The FT-IR spectra were recorded using a Vertex 70 spectrometer (Bruker, Germany). The typical scanning range was 1800 cm⁻¹ to 1500 cm⁻¹. The spectra were deconvoluted using Origin software.

A

Name	Sequence
L20	EAAAKEAAARETFSDLWKLL
L25	EAAAREAAAKEAAARETFSDLWKLL
L26	KEAAAREAAAKEAAARETFSDLWKLL
L27	AKEAAAREAAAKEAAARETFSDLWKLL
L28	AAKEAAAREAAAKEAAARETFSDLWKLL
L29	AAAKEAAAREAAAKEAAARETFSDLWKLL
L30	EAAAKEAAAREAAAKEAAARETFSDLWKLL
L31	REAAAKEAAAREAAAKEAAARETFSDLWKLL
L32	AREAAAKEAAAREAAAKEAAARETFSDLWKLL
L33	AAREAAAKEAAAREAAAKEAAARETFSDLWKLL
L34	AAAREAAAKEAAAREAAAKEAAARETFSDLWKLL
L35	EAAAREAAAKEAAAREAAAKEAAARETFSDLWKLL
L40	EAAAKEAAAREAAAKEAAAREAAAKEAAARETFSDLWKLL
L64	CRAAEAAAKEAAAREAAAKEAAARETFSDLWKLLEAAAKEAAAREAAAKEAAAREAAAKAAMRM
L118	CRAAEAAAKEAAAREAAAKEAAARETFSDLWKLLEAAAKEAAAREATAKEAAAREAAAKDARAKEAAA REAAAKEAAAREAAAKARADEASAKEAAAREAAAKEAAAREAAAKAAMRM

B

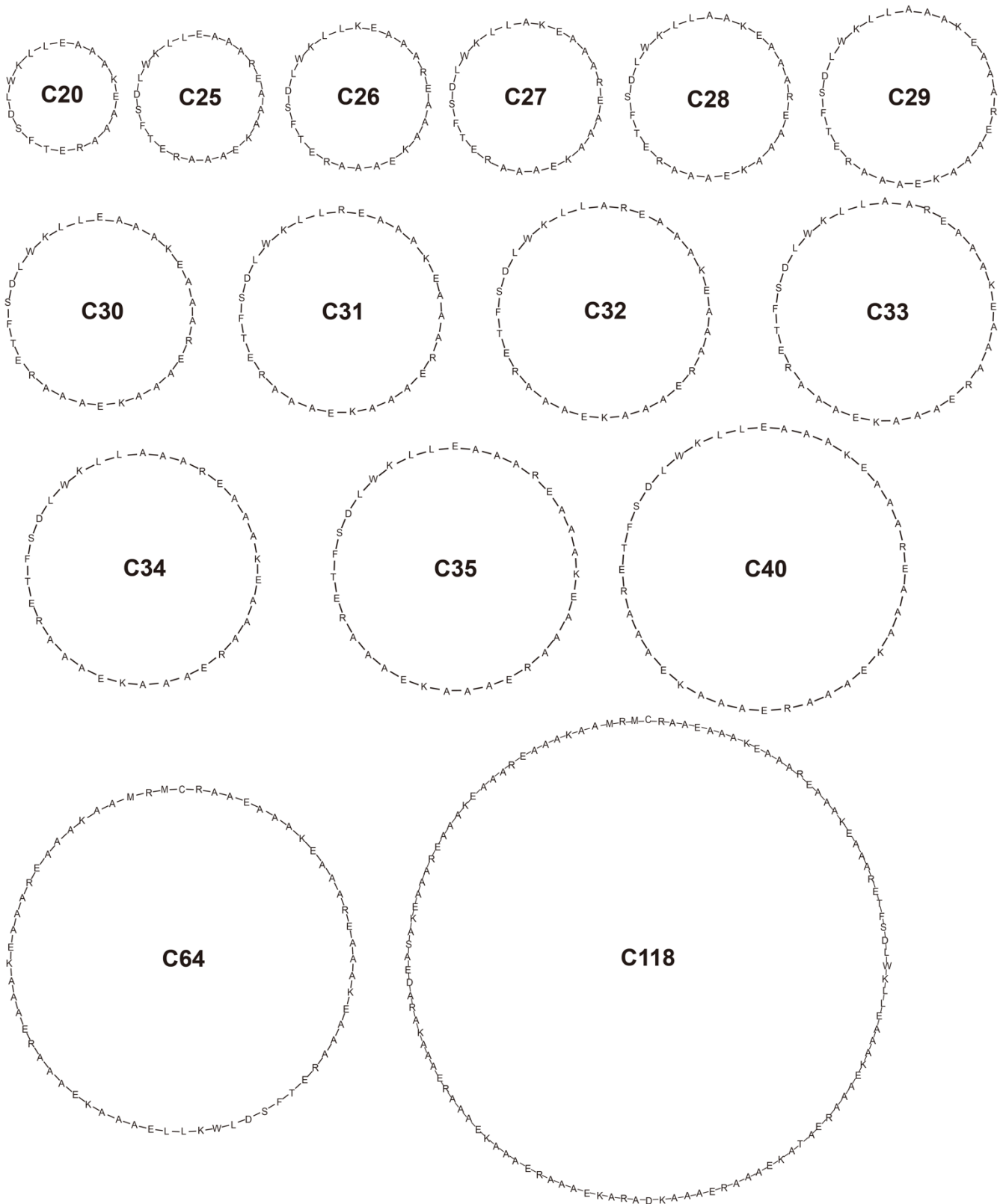
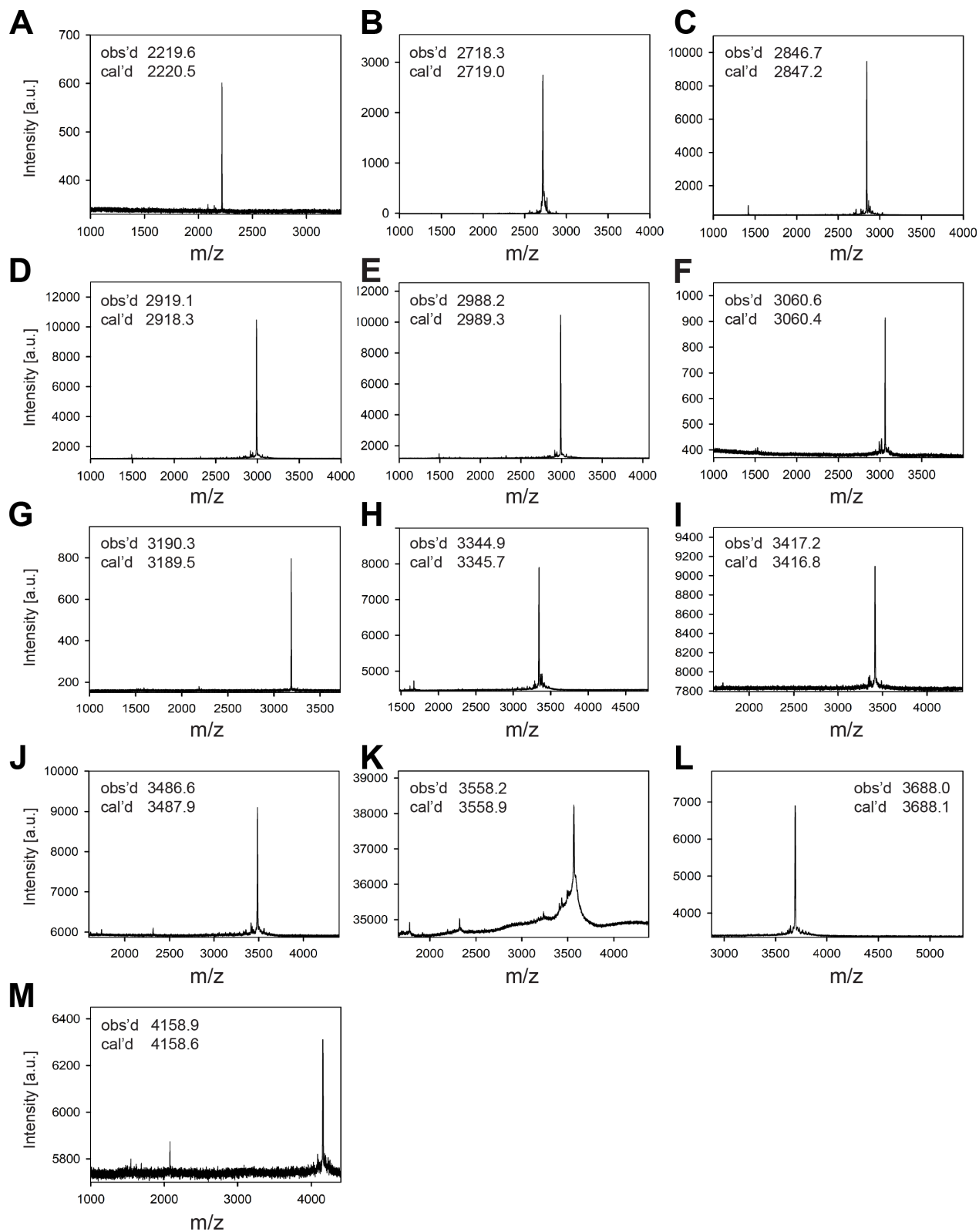


Figure S1. Sequences (A) linear peptides. (B) cyclic peptides.



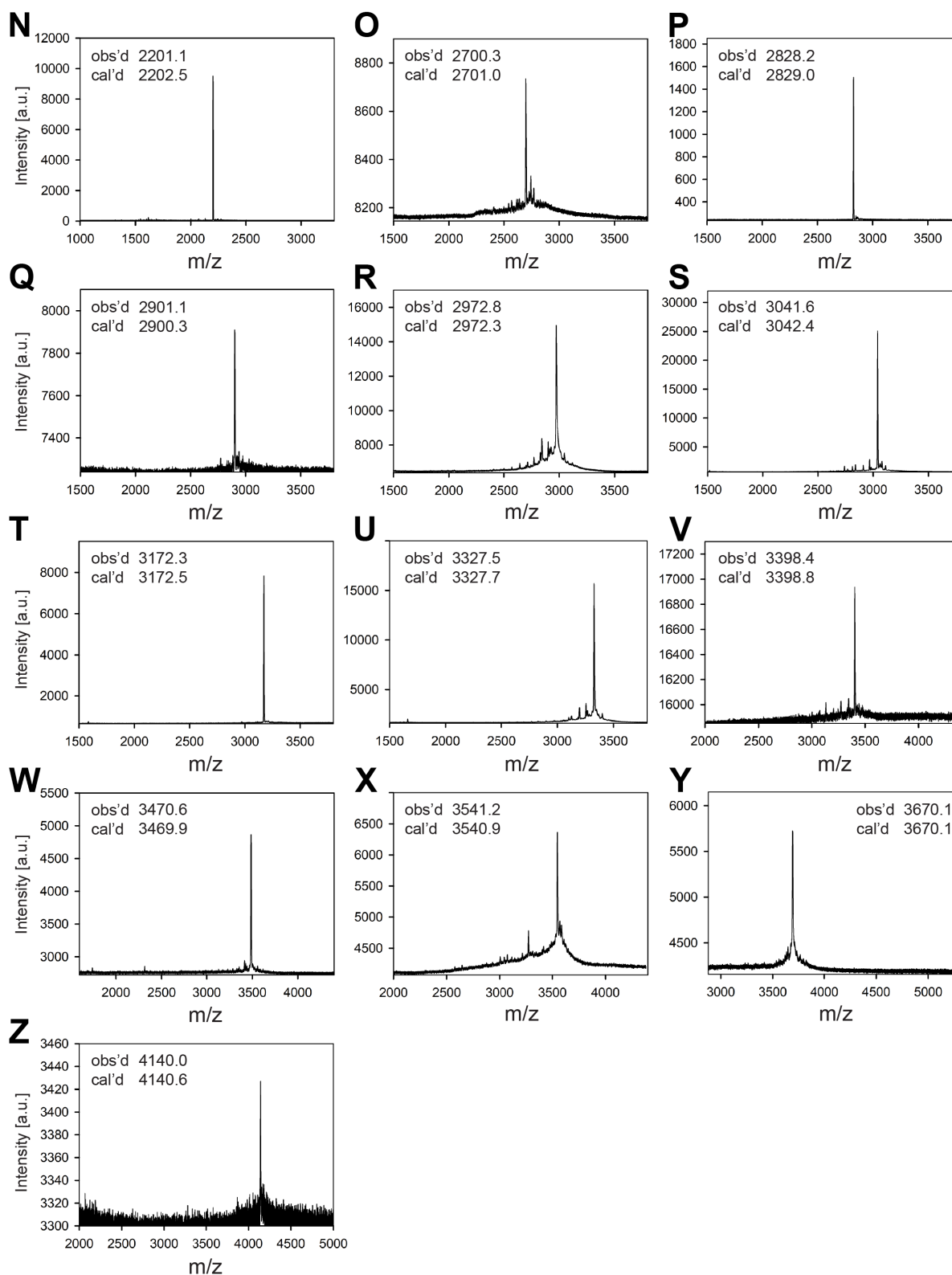


Figure S2. MALDI-TOF MS spectra. (A) L20. (B) L25. (C) L26. (D) L27. (E) L28. (F) L29. (G) L30. (H) L31. (I) L32. (J) L33. (K) L34. (L) L35. (M) L40. (N) C20. (O) C25. (P) C26. (Q) C27. (R) C28. (S) C29. (T) C30. (U) C31. (V) C32. (W) C33. (X) C34. (Y) C35. (Z) C40.

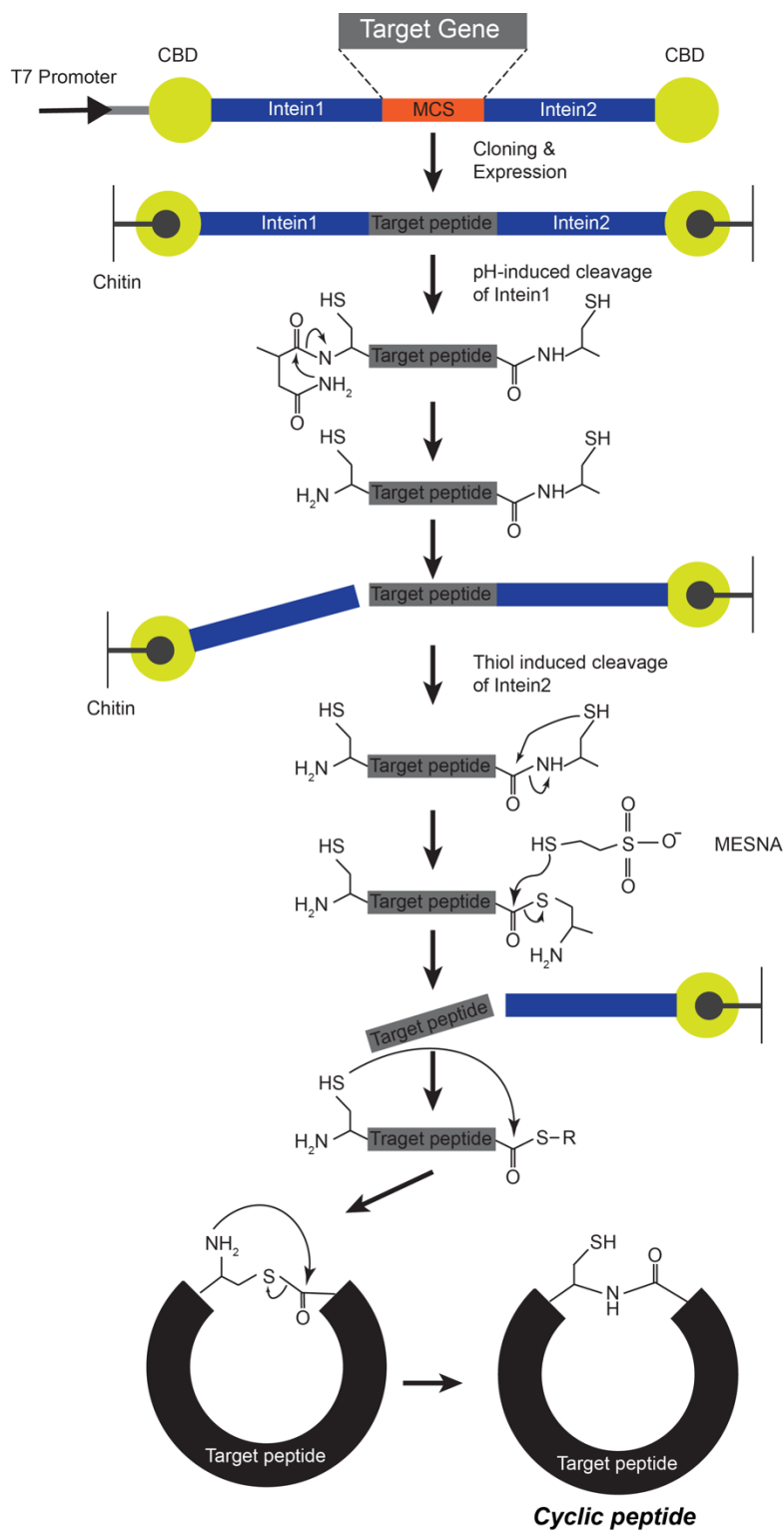


Figure S3. Mechanism of intein-mediated peptide cyclization. Extremely large cyclic peptides (C64 and C118) were prepared using this method.

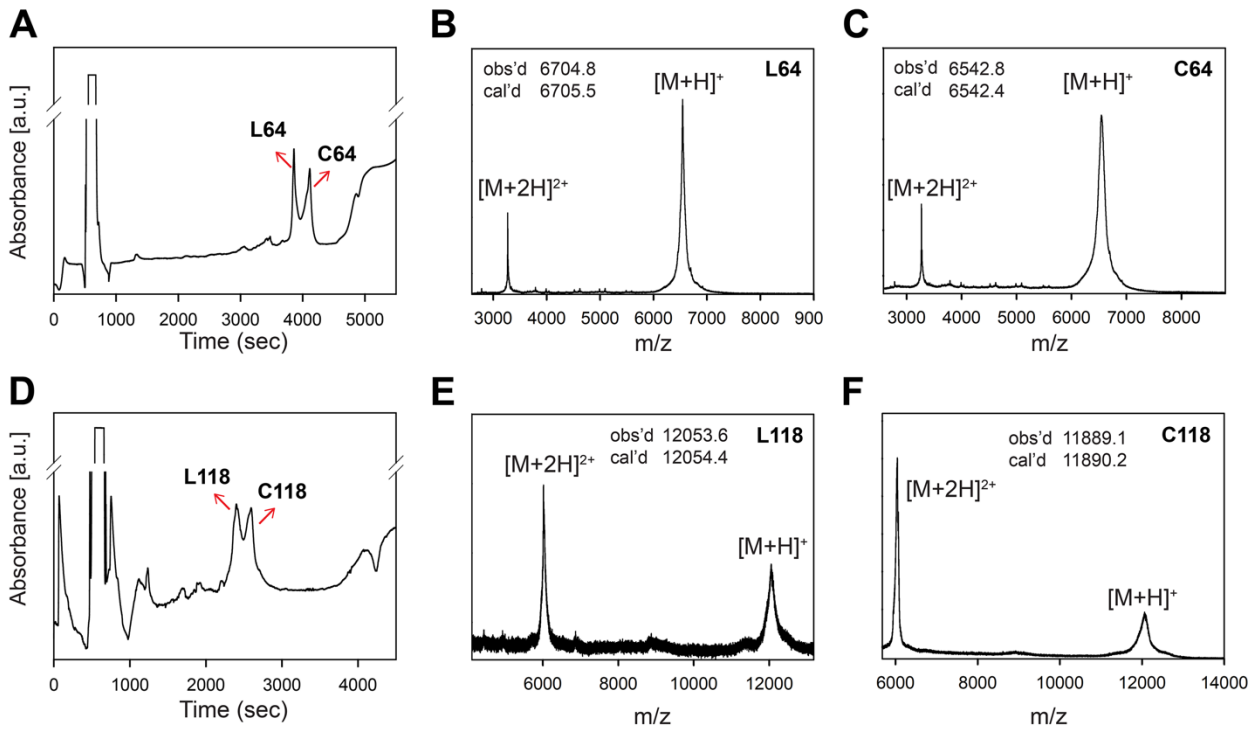


Figure S4. Purification and characterization of linear and cyclic peptides by intein-mediated ligation of bacterially expressed peptides. (A) HPLC chromatogram. MALDI-TOF MS spectra of (B) L64 and (C) C64. (D) HPLC chromatogram. MALDI-TOF MS spectra of (E) L118 and (F) C118.

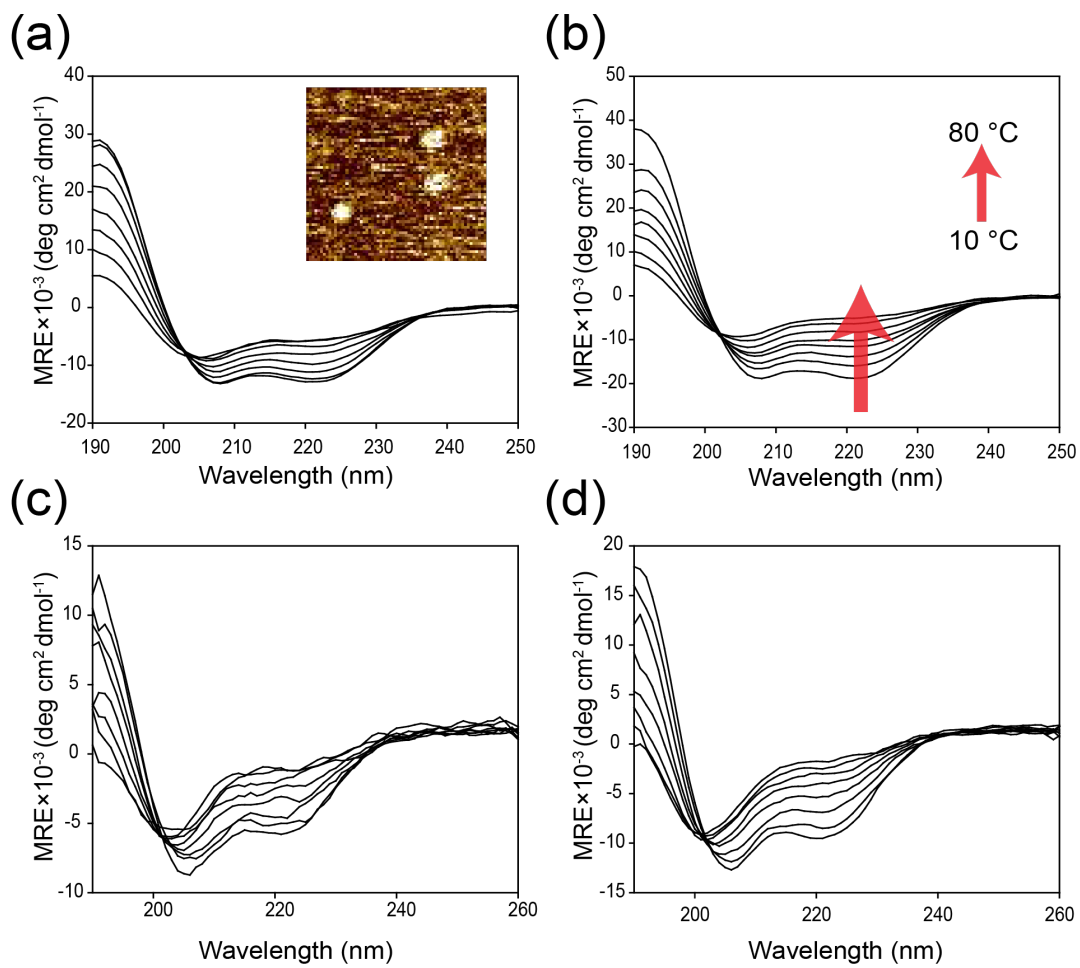


Figure S5. CD spectra of (A) C64, (b) L64, (c) C40, and (d) L40. An inset in (A): An AFM image of C64.

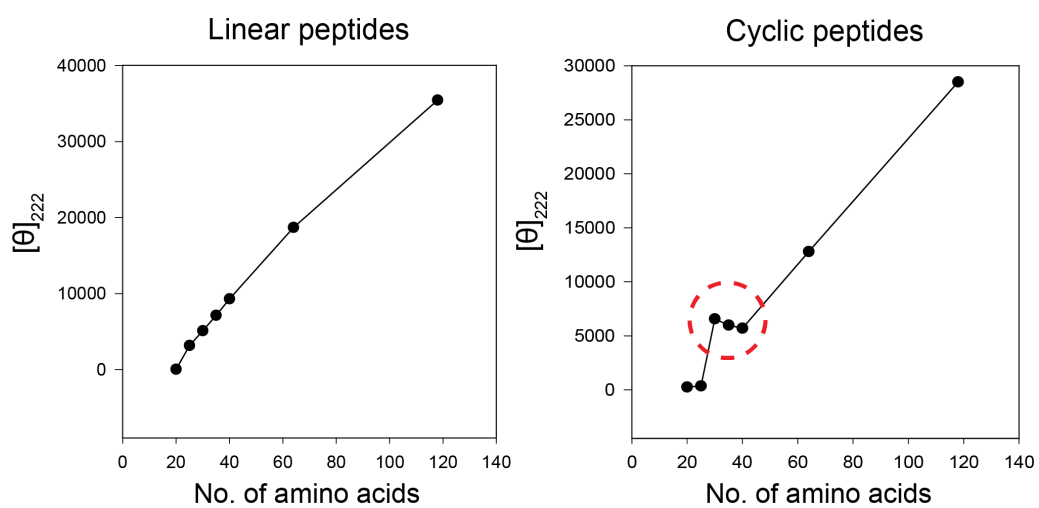


Figure S6. A break in continuity for cyclic peptides. A plot of $[\theta]_{222}$ as a function of peptide size.

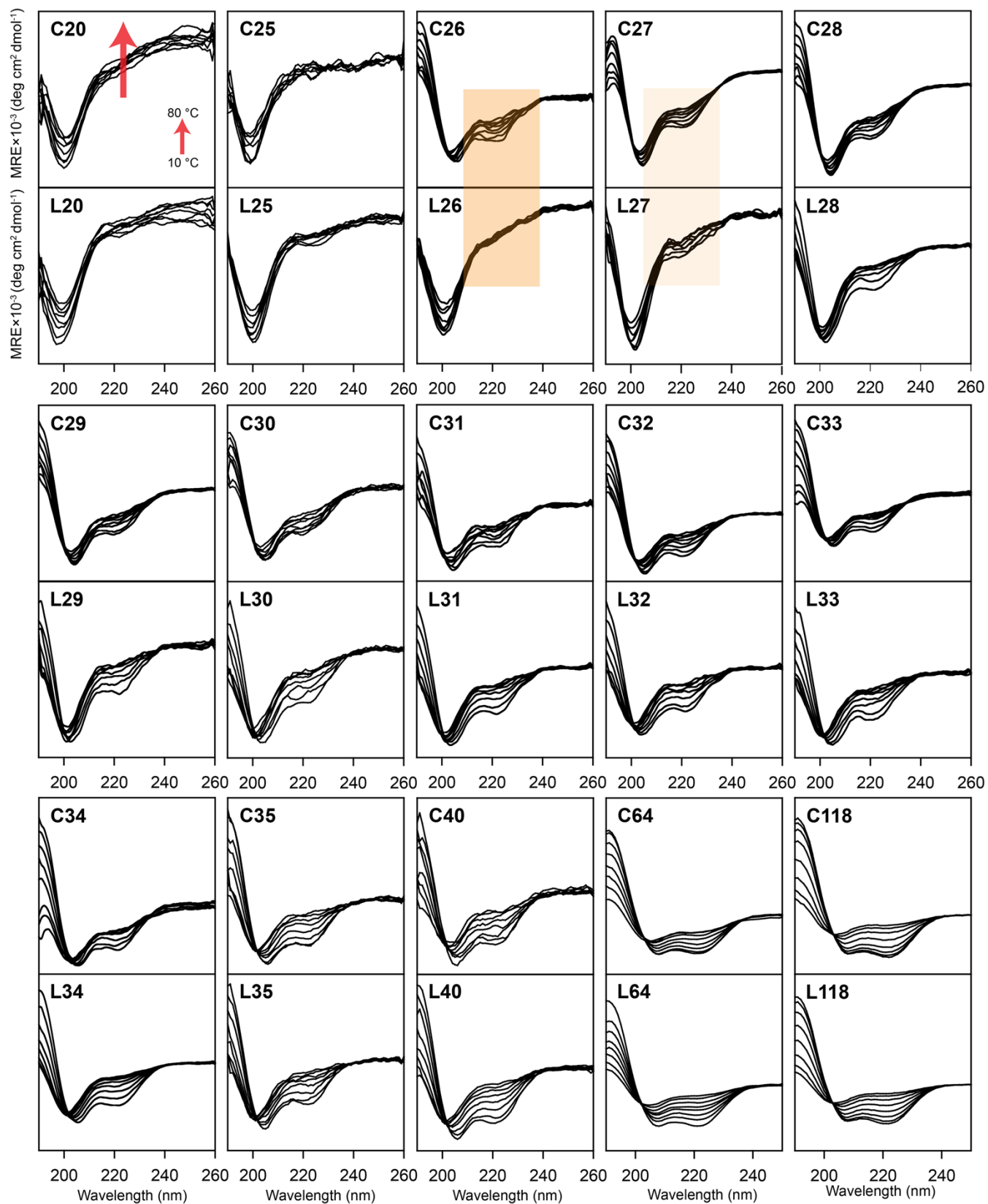


Figure S7. CD spectra of cyclic and linear peptides.

Table S1. Quantitative description of thermal behaviours as determined from the CD data

[θ] _{222/208}	Cyclic			Linear		
	10 °C	80 °C	$\Delta[\theta]_{222/208}$ ^a	10 °C	80 °C	$\Delta[\theta]_{222/208}$
25-mer	<i>n.d.</i> ^b	<i>n.d.</i>	<i>n.d.</i>	<i>n.d.</i>	<i>n.d.</i>	<i>n.d.</i>
26-mer	0.7366	0.4663	0.2703	<i>n.d.</i>	<i>n.d.</i>	<i>n.d.</i>
27-mer	0.6796	0.5989	0.0807	0.4323	0.3258	0.1065
28-mer	0.6888	0.5836	0.1052	0.6146	0.4471	0.1675
29-mer	0.7084	0.551	0.1574	0.6439	0.3593	0.2846
30-mer	0.6307	0.4364	0.1943	0.6049	0.2404	0.3645
31-mer	0.7342	0.5285	0.2057	0.7003	0.4137	0.2866
32-mer	0.7642	0.4877	0.2765	0.7291	0.4451	0.284
33-mer	0.7888	0.5386	0.2502	0.7198	0.4665	0.2533
34-mer	0.7969	0.5782	0.2187	0.7789	0.4517	0.3272
35-mer	0.761	0.3439	0.4171	0.7487	0.3402	0.4085
40-mer	0.7187	0.3231	0.3956	0.7919	0.3144	0.4775
64-mer	0.9749	0.7058	0.2691	0.9945	0.599	0.3955
118-mer	1.091	0.6035	0.4875	1.0706	0.5885	0.4821

^a $\Delta[\theta]_{222/208} = [\theta]_{222/208}$ at 10 °C – $[\theta]_{222/208}$ at 80 °C

^b *n.d.* = not determined (because the helicity of the peptides was too small to give meaningful interpretation)

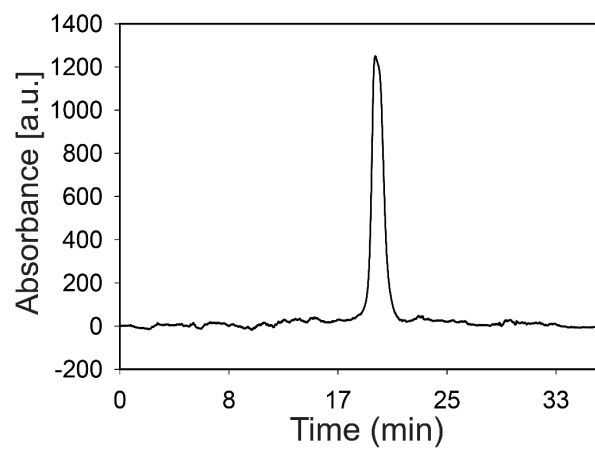
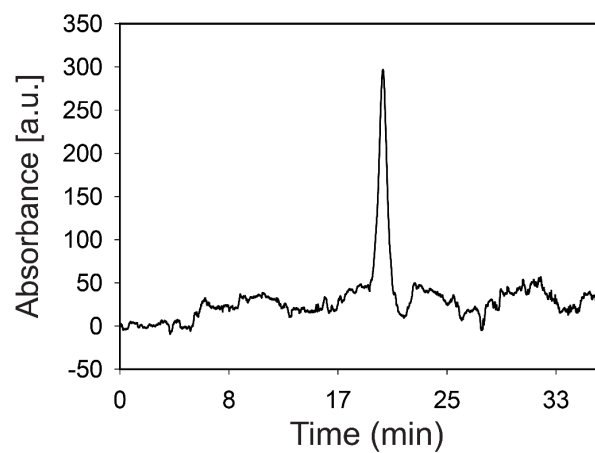


Figure S8. Size exclusion chromatography data for **C26** (top) and **L26** (bottom).