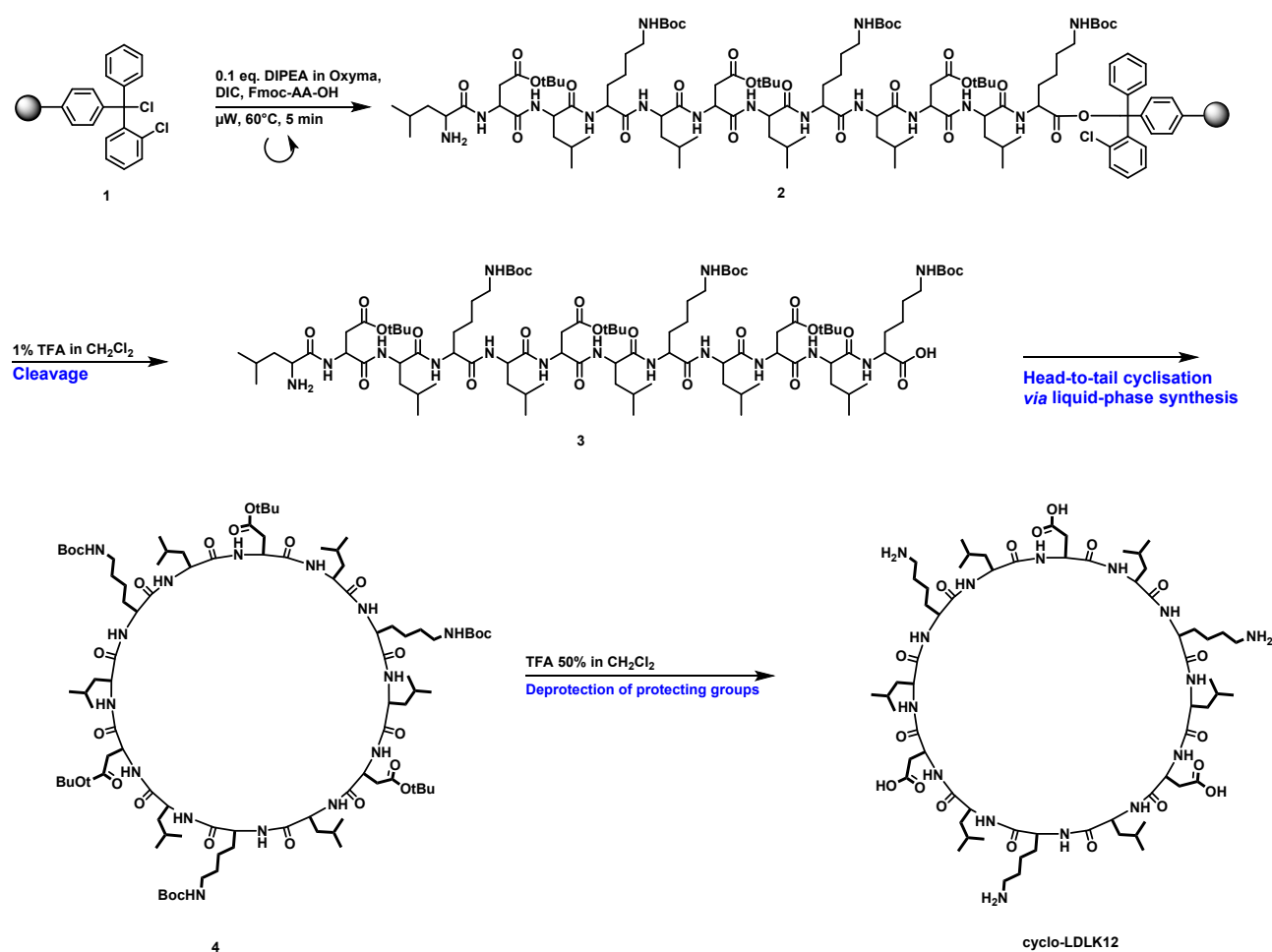


## Electronic Supplementary Information

### Novel self-assembling cyclic peptides with reversible supramolecular nanostructures

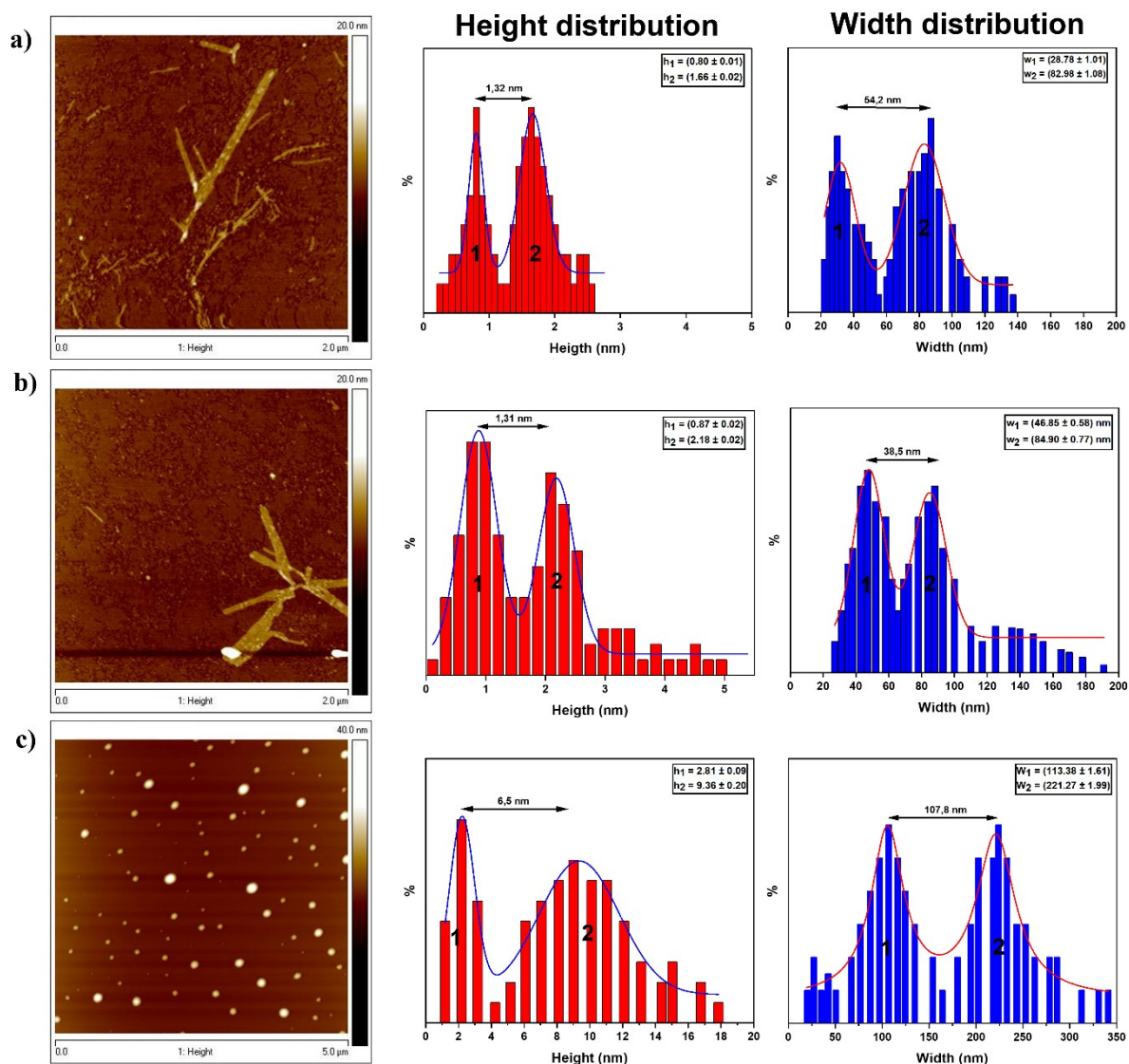
Maria Gessica Ciulla, Federico Fontana, Roberto Lorenzi, Amanda Marchini, Luca Campone, Ehsan Sadeghi, Alberto Paleari, Sara Sattin, and Fabrizio Gelain\*



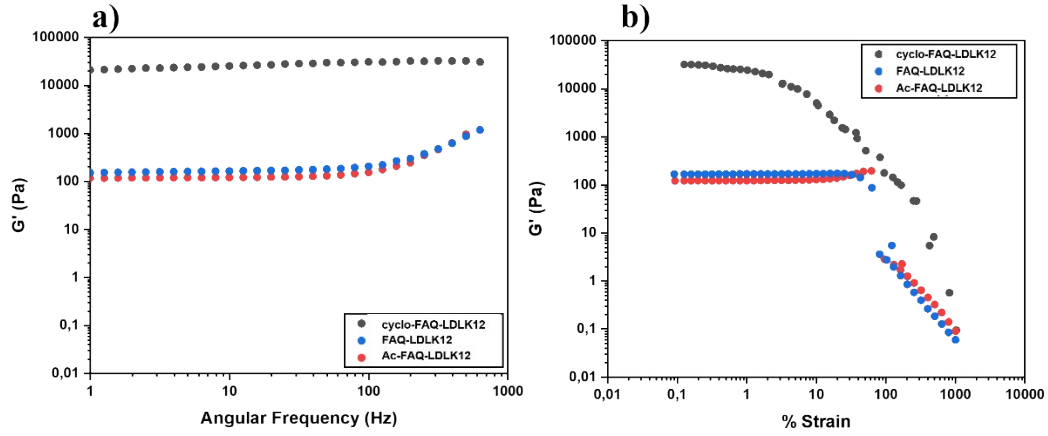
**Scheme S1.** Total synthesis of cyclo-LDLK12. The general procedure includes a Fmoc-based SPPS strategy, followed by a solution phase cyclization. Overall yield was 56%.

Entry	Peptide	Solvent	Activator	Conditions	Yield %
1	4	DMF, DCM	HBTU, DIPEA	RT, 1h	35
2	4	DMF, DCM	0.002 M HATU, DIPEA	RT, 4h	18
3	4	NMP	DIPEA, HOBt, PyBOP	RT, 2h	58
4	4	NMP	DIPEA, HOBt, PyBOP	RT, 6h	75

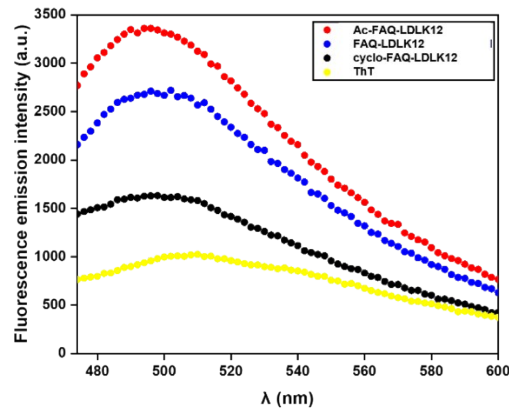
**Table S1.** Optimization of the solution phase cyclization. Yields are isolated yields for the purified final compounds.



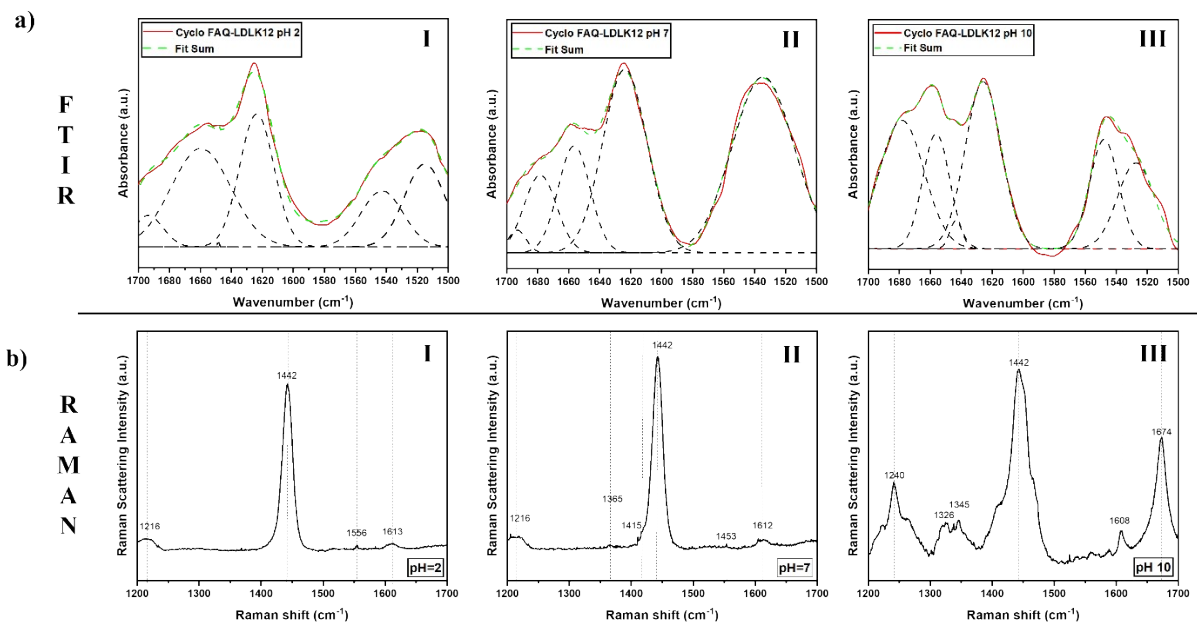
**Figure S1.** AFM profiles of cyclo-LDLK12 detected on mica by tapping mode. a) pH~2; b) pH~7; c) pH~10. All measurements were obtained with an image size  $1 \times 1 \mu\text{m}^2$ .



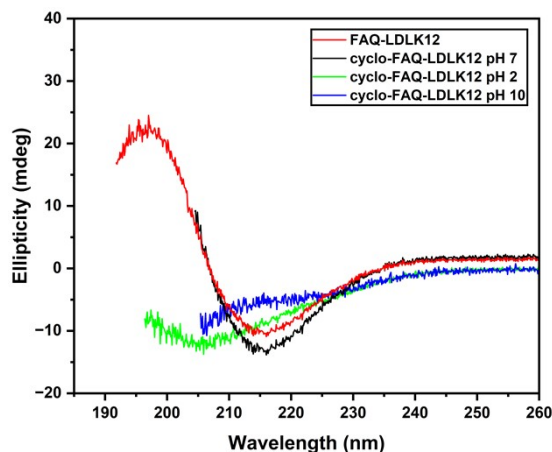
**Figure S2.** Characterization of cyclo-FAQ-LDLK12 by rheological experiments: a) frequency-sweep test performed to evaluate the stiffness of cyclo-FAQ-LDLK12, and b) strain-sweep experiment to evaluate the rheological stability of cyclo-FAQ-LDLK12.



**Figure S3.** ThT-binding assay to study the  $\beta$ -sheet content of cyclo-FAQ-LDLK12 in comparison with the corresponding linear SAPs FAQ-LDLK12 and Ac-FAQ-LDLK12.



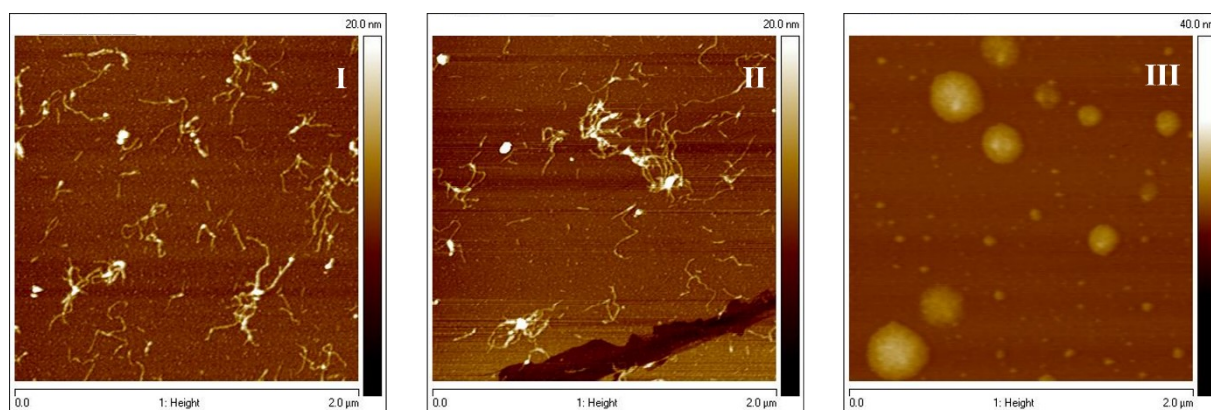
**Figure S4.** a) FT-IR absorption spectra and b) Raman spectra of cyclo-FAQ-LDLK12 at respectively I) pH 2, II) pH 7, III) pH 10; e) AFM images of cyclo-FAQ-LDLK12 at different pH conditions, showing liner nanostructures at I) pH 2 and II) pH 7, and round-shaped aggregates at III) pH 10.



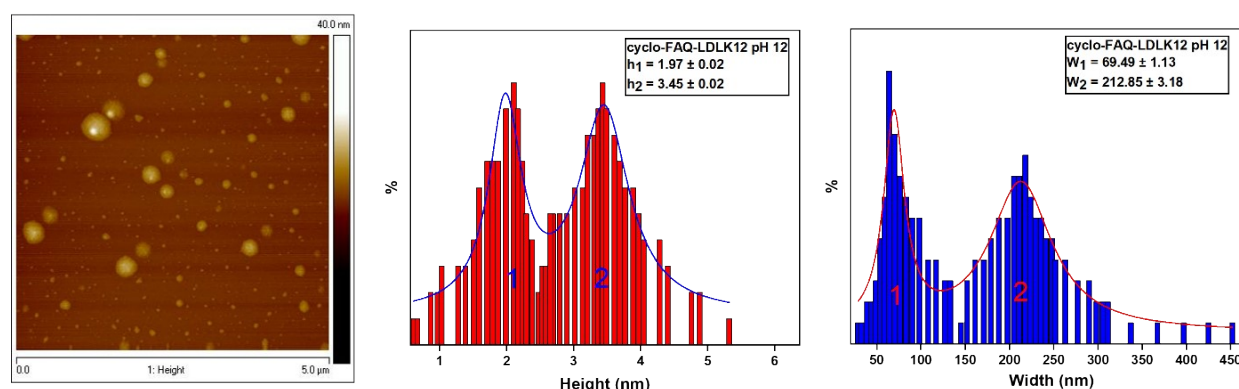
**Figure S5.** Far-UV spectra analysis by circular dichroism for cyclo-FAQ-LDLK12 at different pH.

pH	% $\beta$ -pleated sheets		% turns	% helix	% random coil
	parallel	antiparallel			
2	3	37	11	16	33
7	2	52	23	11	12
10	6	24	17	25	28

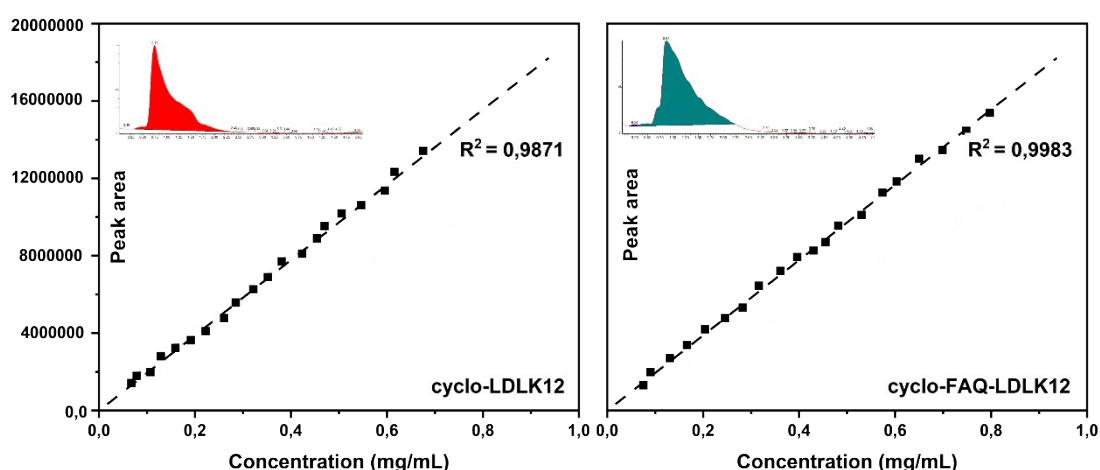
**Table S2.** Deconvolution results of cyclo-FAQ-LDLK12 CD spectra performed by Spectra deconvolution version 2.1.



**Figure S6.** AFM images of cyclo-FAQ-LDLK12 at different pH conditions, showing liner nanostructures at I) pH 2 and II) pH 7, and round-shaped aggregates at III) pH 10.



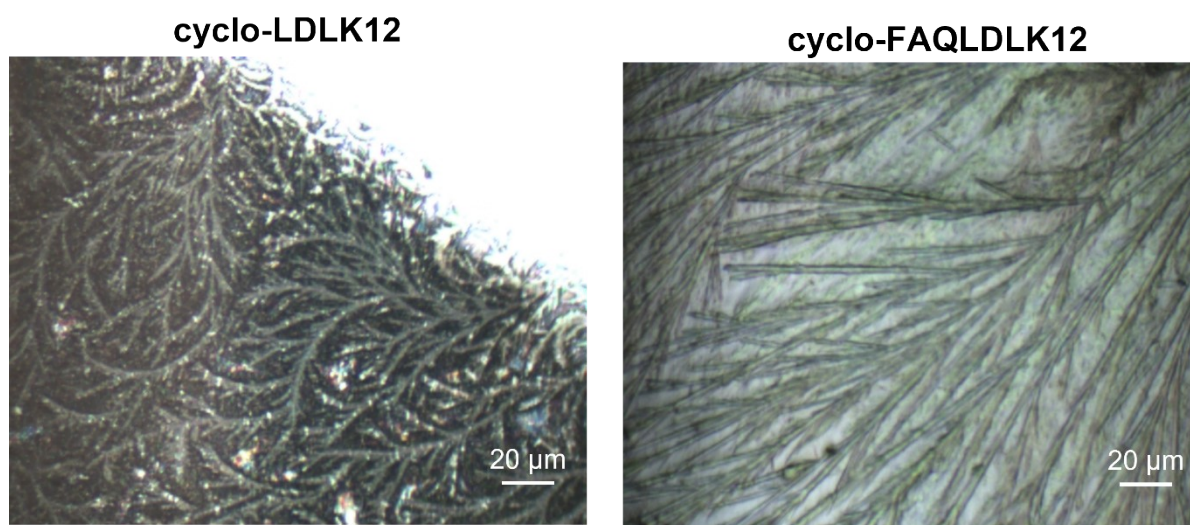
**Figure S7.** AFM image of cyclo-FAQ-LDLK12 at pH~10 with corresponding height and width profiles. All measurements were conducted with an image size of 1x1  $\mu\text{m}^2$ .



**Figure S8.** Twenty points calibration curves for LC-MS analysis were built (by using a peptide reference standard) in order to estimate the amount of nonhydrolyzed peptide after microwave-assisted acid hydrolysis. The correlation coefficient ( $R^2$ ) was obtained for each linear regression curve.

Peptide	% nonhydrolyzed	Linear Counterpart	% nonhydrolyzed
Cyclo-LDLK12	43	LDLK12	12
Cyclo-FAQ-LDLK12	57	FAQ-LDLK12	18

**Table S3.** Comparison of experimental values between cyclic and linear peptides after partial hydrolysis *via* microwave-assisted acid hydrolysis.



**Figure S9.** Micrographs of cyclo-LDLK12 and cyclo-FAQLDLK12 samples acquired with a 10x magnification right before Raman spectroscopy measurements at pH 7.

Mapping (force-field)	Multiplicity	Duration (ns)	Number of replicas
Gromos53a6	1	500	4
Gromos53a6	8	500	4
MARTINI	40	500	4
MARTINI	4 x 10-mer (nanotubes)	500	1
MARTINI	4 x 10-mer (aggregates)	500	1
MARTINI	100	2000	1

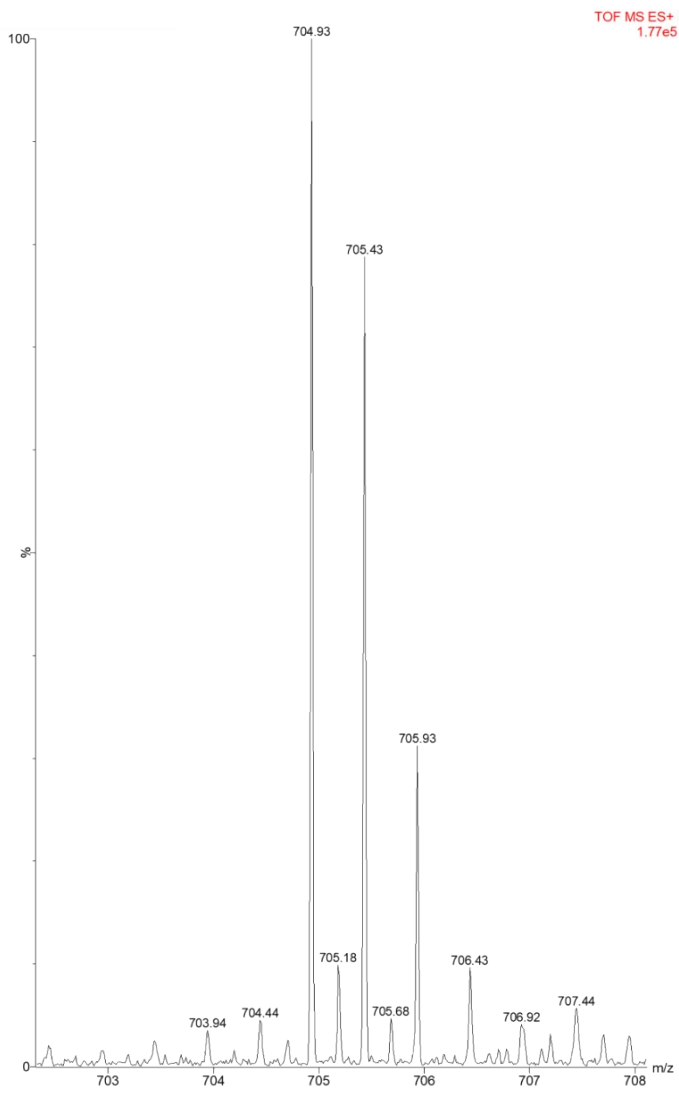
**Table S4.** Molecular Dynamics simulation details. Cyclo-LDLK12 self-assembling propensity was evaluated through united-atom molecular dynamics (UA-MD) simulations. Each system was represented according to Gromos53a6 force-field mapping. The peptide conformations, obtained from monomer simulations, have been used to prepare the starting configuration of 8-mer systems. Cyclo-LDLK12 SAPs aggregation propensity was evaluated through CG-MD simulations. Secondary structure (SS) parameters have been assigned according to experimental evidence. The 40-mers (fibril nuclei) and 100-mers (proto-fibril) were modeled adopting the standard MARTINI approach. Legend: mapping, force-field used for running MDs; Multiplicity, number of peptides in the simulation box; duration, length of the simulation; number of replicas, for statistical purposes.



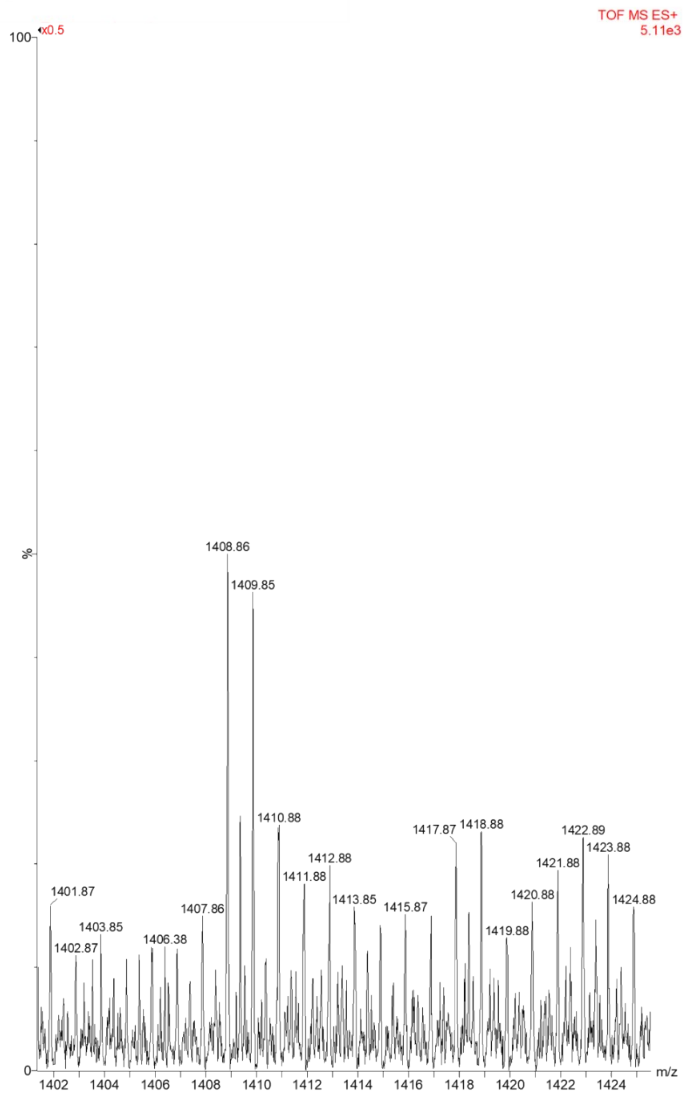
## Quadrupole time-of-flight (Qtof) Mass Spectra

### cyclo-LDLK12

Calculated:  $m/z$  1407,87; found:  $M + 1 = 1408,86$ ;  $M/2 + 1 = 704,93$







**cyclo-FAQ-LDLK12**

Calculated:  $m/z$  2377,36; found:  $M/3 + 1 = 793,18$

