Supplementary Information:

Lysine is more effective than arginine in two tryptophan-rich antimicrobial peptides

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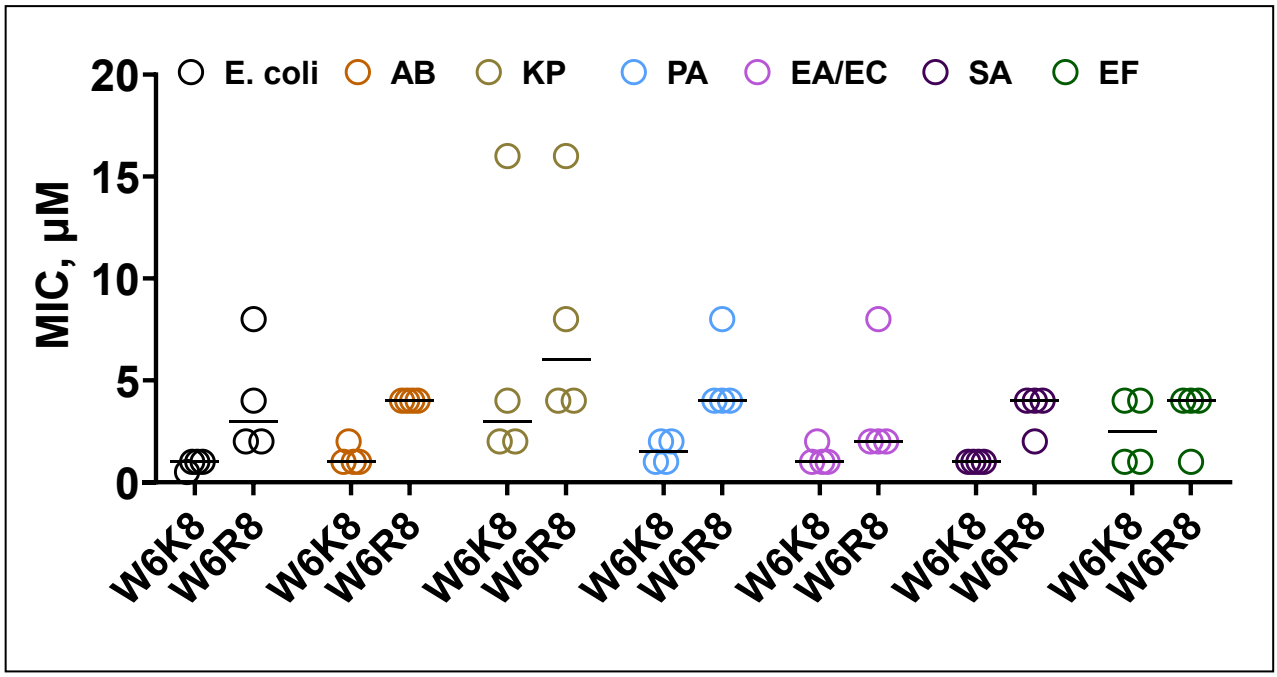


Fig. S1. Minimum inhibitory concentration (MIC) vs. bacterial species. Individual data points are from four different strains of each species. Abbreviations: **E. coli**, *Escherichia coli*; **AB**, *Acinetobacter baumannii*; **KP**, *Klebsiella pneumoniae*; **PA**, *Pseudomonas aeruginosa;* **EA/EC,** *Enterobacteriaceae*; **SA**, *Staphylococcus aureus;* **EF**, *Enterococcus faecalis*.

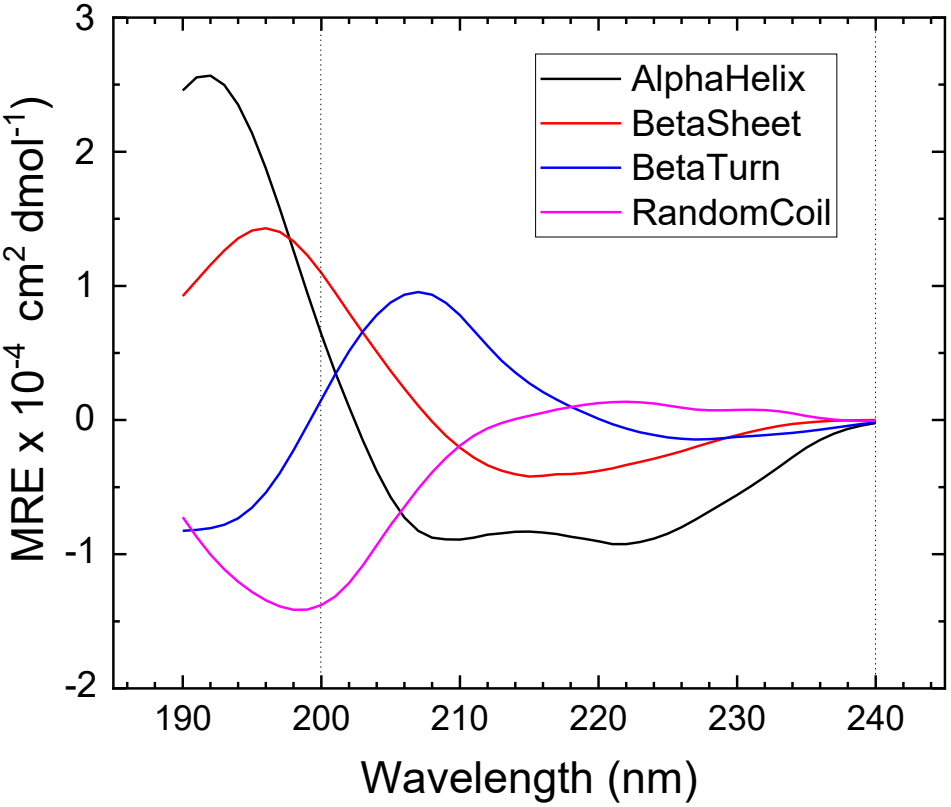


Fig. S2. Four secondary structural motifs used to fit to the CD ellipticity data [1]. Fit is carried out using structural data between 240 and 200 nm.

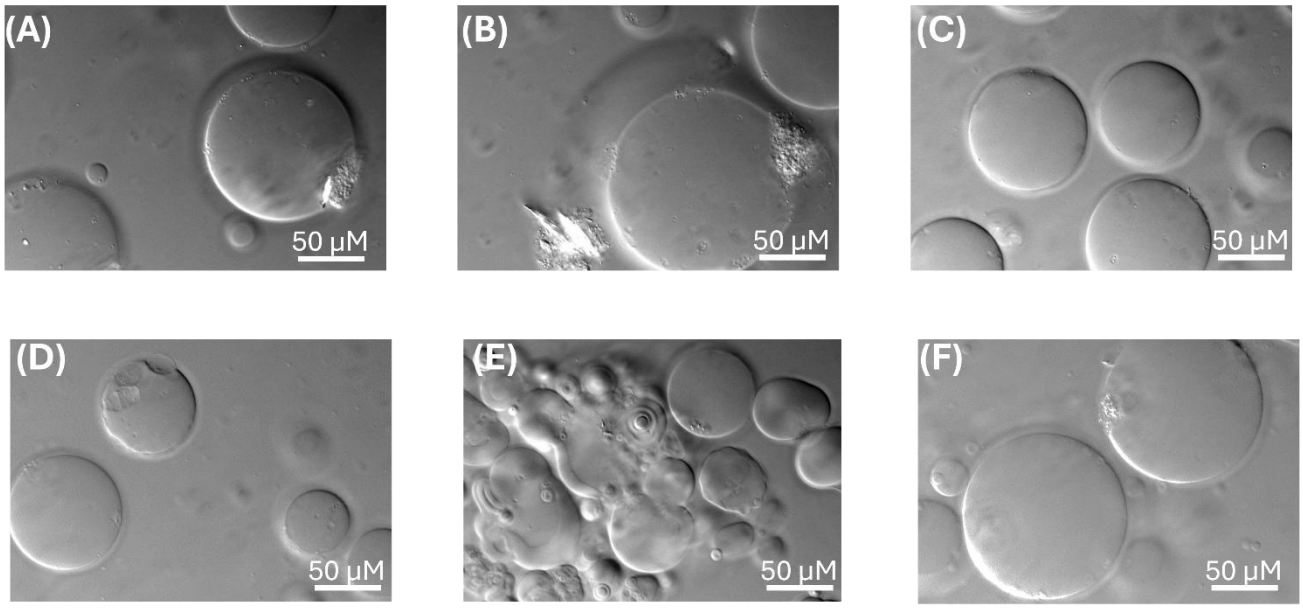


Fig. S3. DIC microscopy of GUVs. **(A)** G(-) LMM control **(B)** G(-) LMM/W6K8 30:1 molar ratio **(C)** G(-) LMM/W6R8 30:1 **(D)** G(+) LMM control **(E)** G(+) LMM/W6K8 30:1 **(F)** G(+) LMM/W6R8 30:1

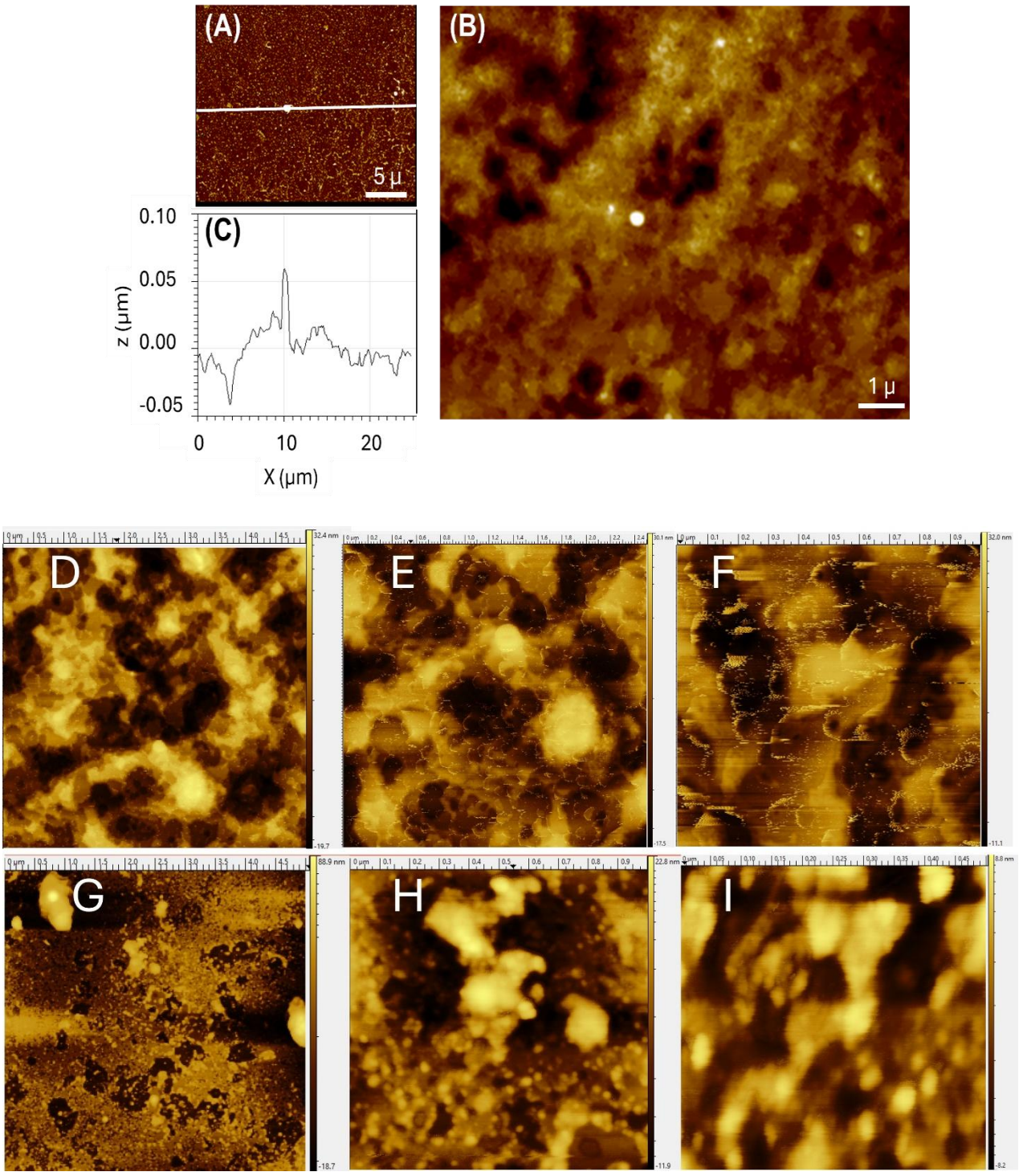


Fig. S4. AFM images of dried films G(-) LMM/peptide at 15:1 molar ratio on silicon wafers. G(-)/W6R8 15:1 lipid:peptide molar ratio: **(A)** 25 µm x 25 µm scan **(B)** 10 µm x 10µm scan **(C)** Height profile along white line in **(A)**. **(D-F)** G(-)/W6K8 15:1 **(G-H)** G(-)/W6R8 15:1. Lateral scale on top of each image has units of micrometers, and height color bar to the right of each image has units of nanometers.

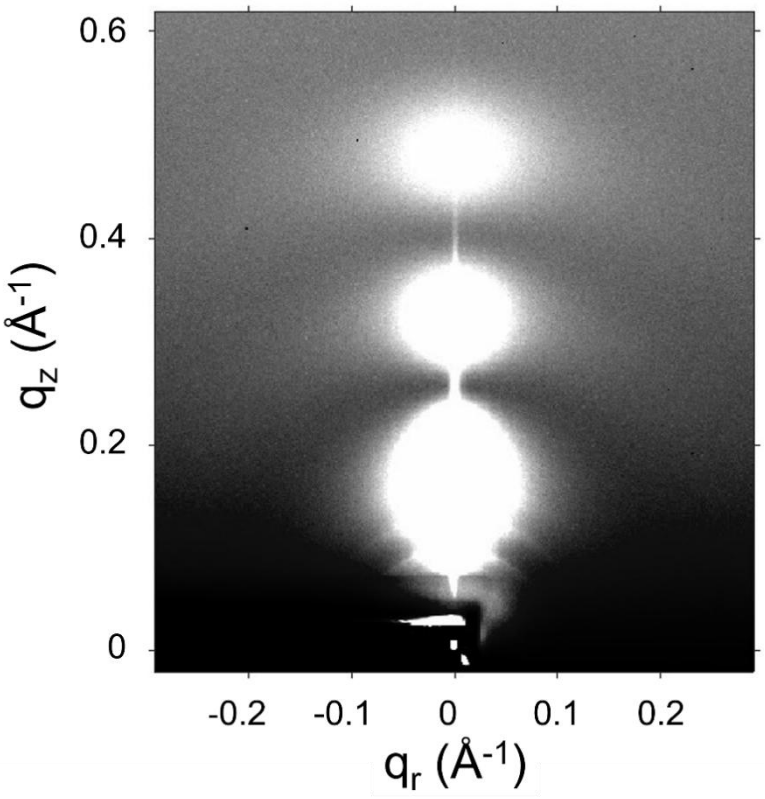


Fig. S5. Example of low-angle x-ray scattering (LAXS, XDS) collected at CHESS at 37 °C. Sample is 500:1 G(-)/W6K8 molar ratio, D-spacing = 180 Å. Negative angle background was subtracted.

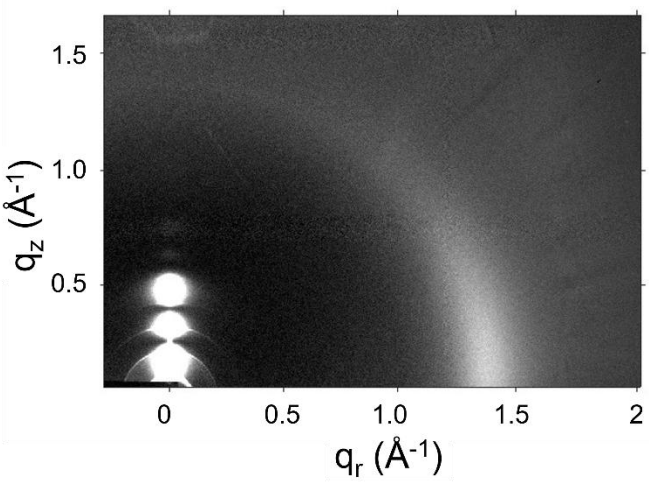


Fig. S6. Example of wide-angle x-ray scattering (WAXS, XDS) collected at CHESS at 37 °C. Sample is the same as in Fig. S5. Negative angle background scan and black line were subtracted.

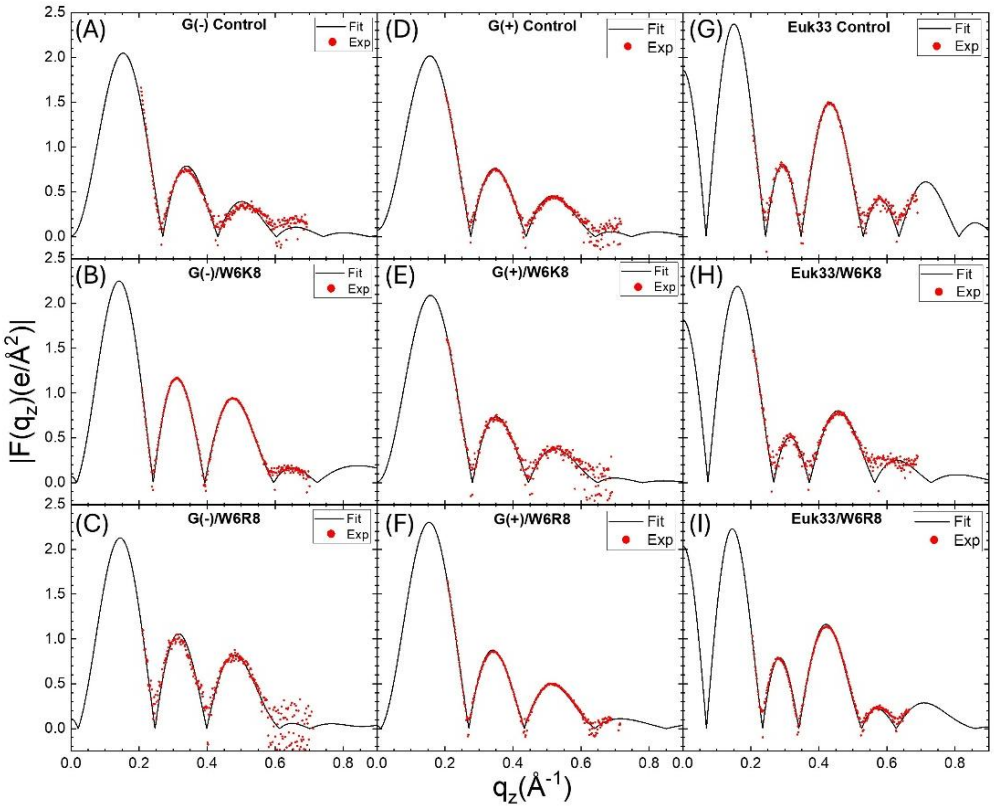


Fig. S7. Form factors corresponding to electron density profiles shown in Fig. 5 in the main paper: G(-) **(A,B,C) G(-)**, **(D,E,F)** G(+), **(G,H,I)** Euk33. Experimental data points (solid red circles), SDP fit to data (black lines).

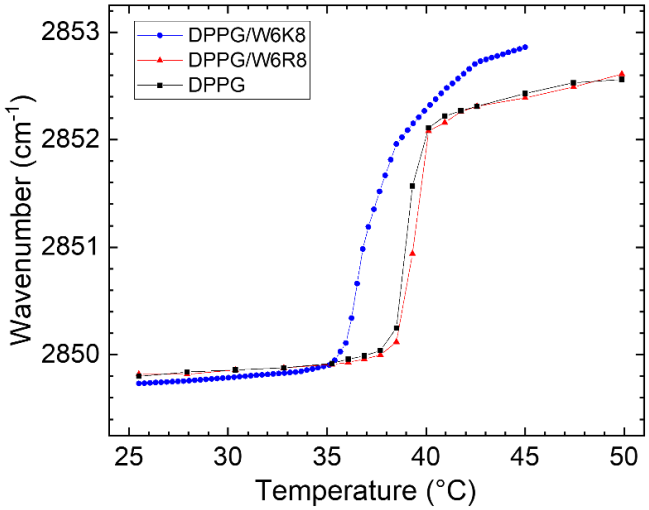
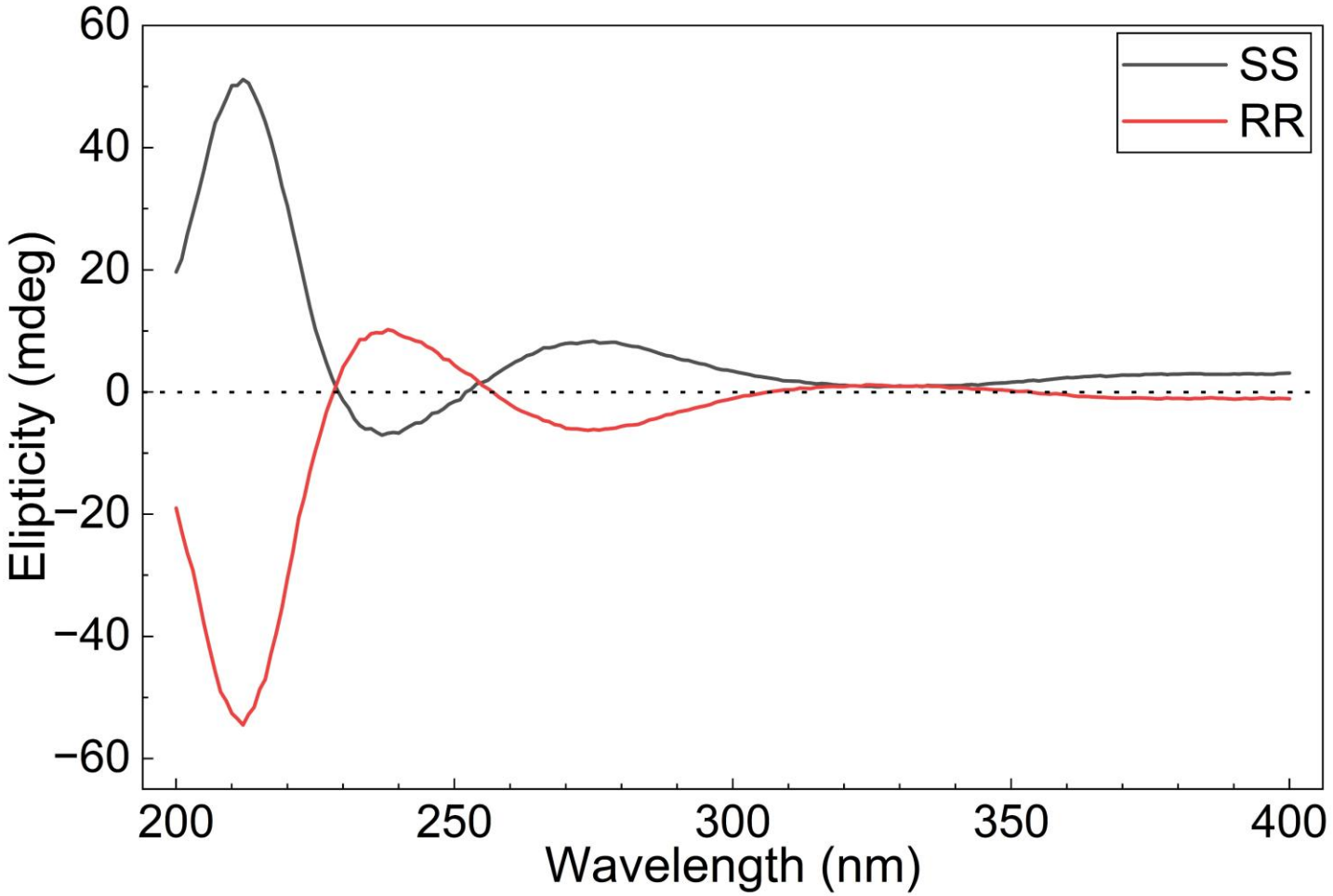


Fig. S8. FTIR spectroscopy results of DPPG control (black), DPPG/W6K8 (blue) and DPPG/W6R8 (red) at a lipid:peptide molar ratio of 20:1.

Supplementary References

[1] S. Brahms, J. Brahms, Determination of protein secondary structure in solution by vacuum ultraviolet circular dichroism, Journal of molecular biology, 138 (1980) 149-178.

Calibration of the JASCO 810 used in this study. Calibrant is both enantiomers of Na[Co(EDDS)] H2O (EDDS = *N,N*-ethylenediaminedisuccinic acid)
Damianoglou et al., Chirality 20:1029-1038 (2008).
Scan speed, 20 nm/min, response time = 4 msec, bandwidth = 1nm, T = 37 degC, 2 accumulations



Scan speed, 20 nm/min, response time = 4 msec, bandwidth = 1nm, T = 37 degC, 2 accumulations, data are smoothed, 10 pts adjacent averaging.

