Supplementary Material

Membrane destabilization is a critical step in antimicrobial peptide effectivity

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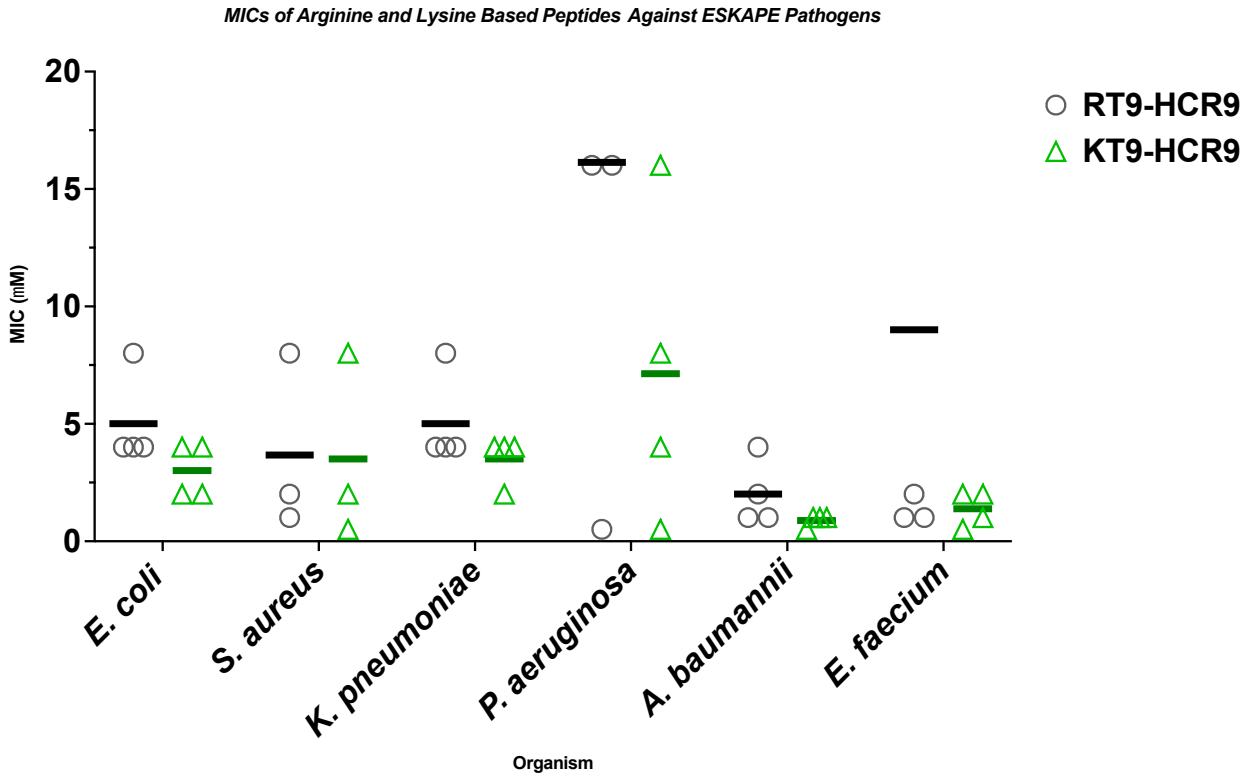

Fig S1 Minimum inhibitory concentrations (MICs) against G(-) bacteria (*E. coli*, *K. pneumoniae*, *P. aeruginosa*, *A. baumannii*) and G(+) bacteria (*S. aureus*, *E. faecium*).

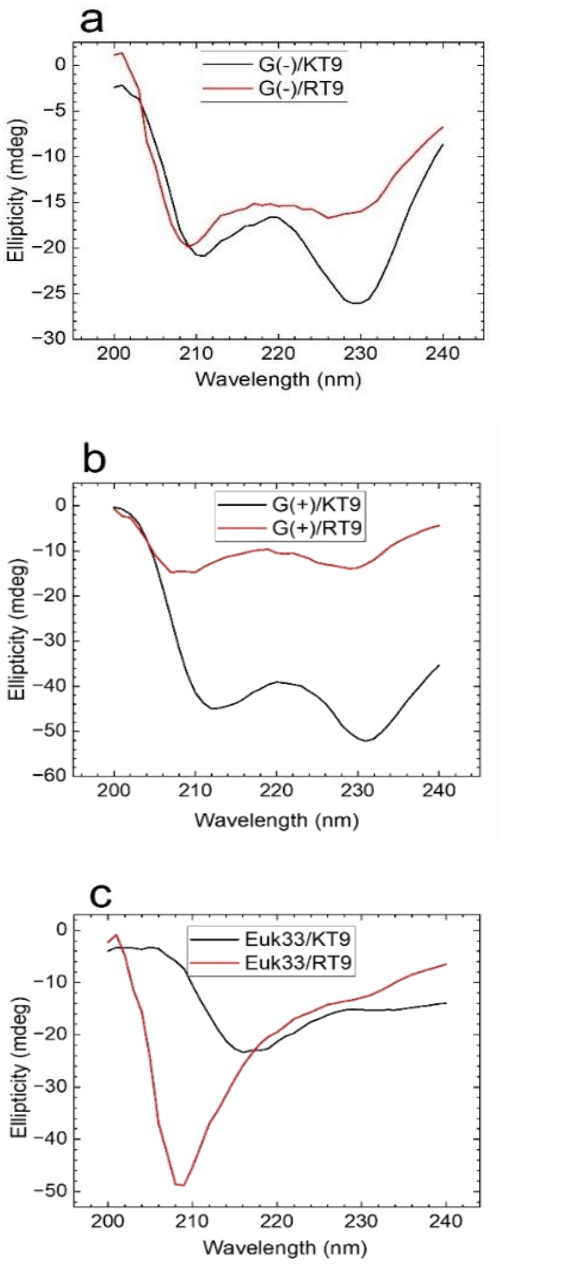

Fig S2 Raw circular dichroism ellipticity data of AMPs at a 50:1 lipid/peptide molar ratio collected at 37 ^{o}C. KT9 (black traces), RT9 (red traces) in **a)** G(-) LMM, **b)** G(+) LMM, **c)** Euk33 LMM.

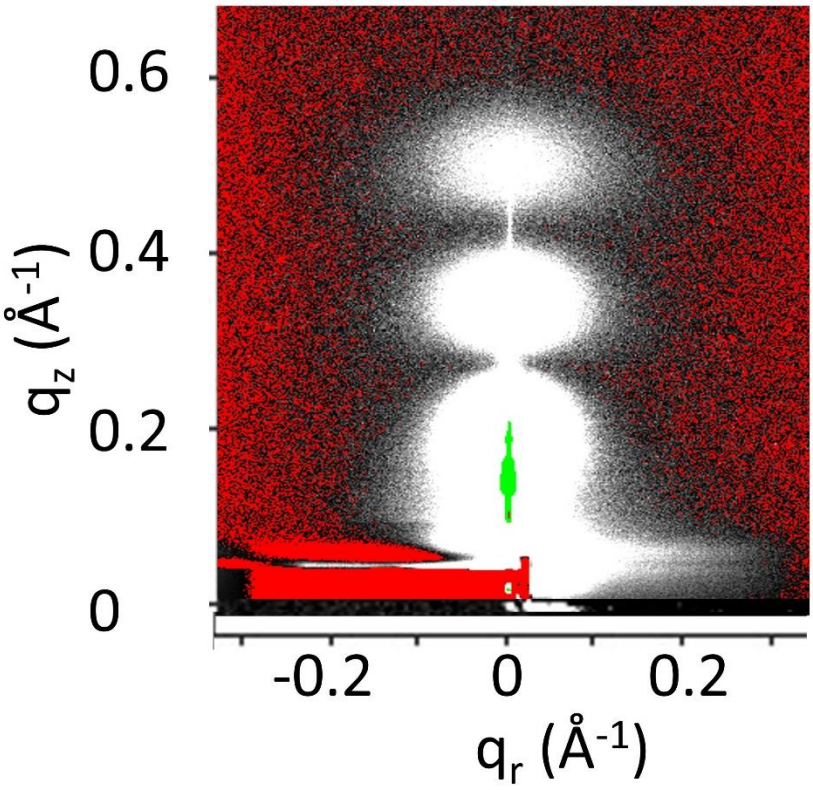

Fig S3 2D low-angle X-ray diffuse scattering image of G(-)/KT9 (100:1) at 37 °C collected at CHESS. The D-spacing is 105 Å. The red/black speckled background indicates zero average intensity produced by using two boxes for background subtraction beneath the diffuse scattering lobes. These data yield K_C using liquid crystal theory and the NFIT computer program.

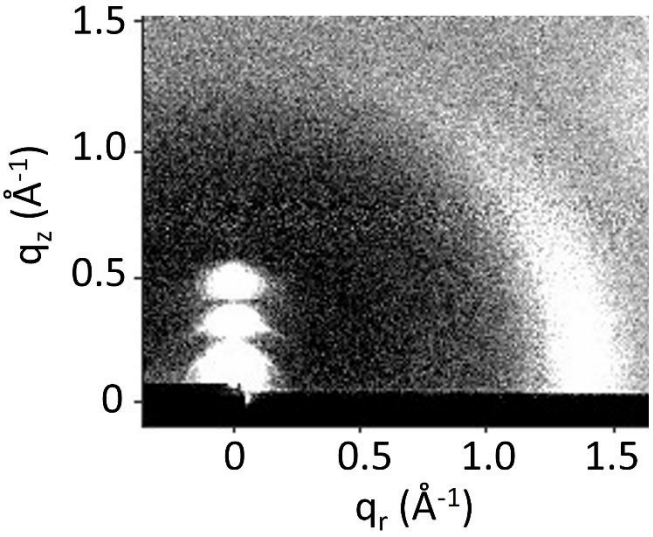

Fig S4 2D wide-angle X-ray diffuse scattering of G(-)/KT9 (100:1) at 37 °C collected at CHESS. The low-angle pattern is near q_r = 0 Å^{-1}, while the wide-angle pattern begins at the equator near q_r = 1.45 Å^{-1}. These data yield S_{xray} using liquid crystal theory and MATLAB.

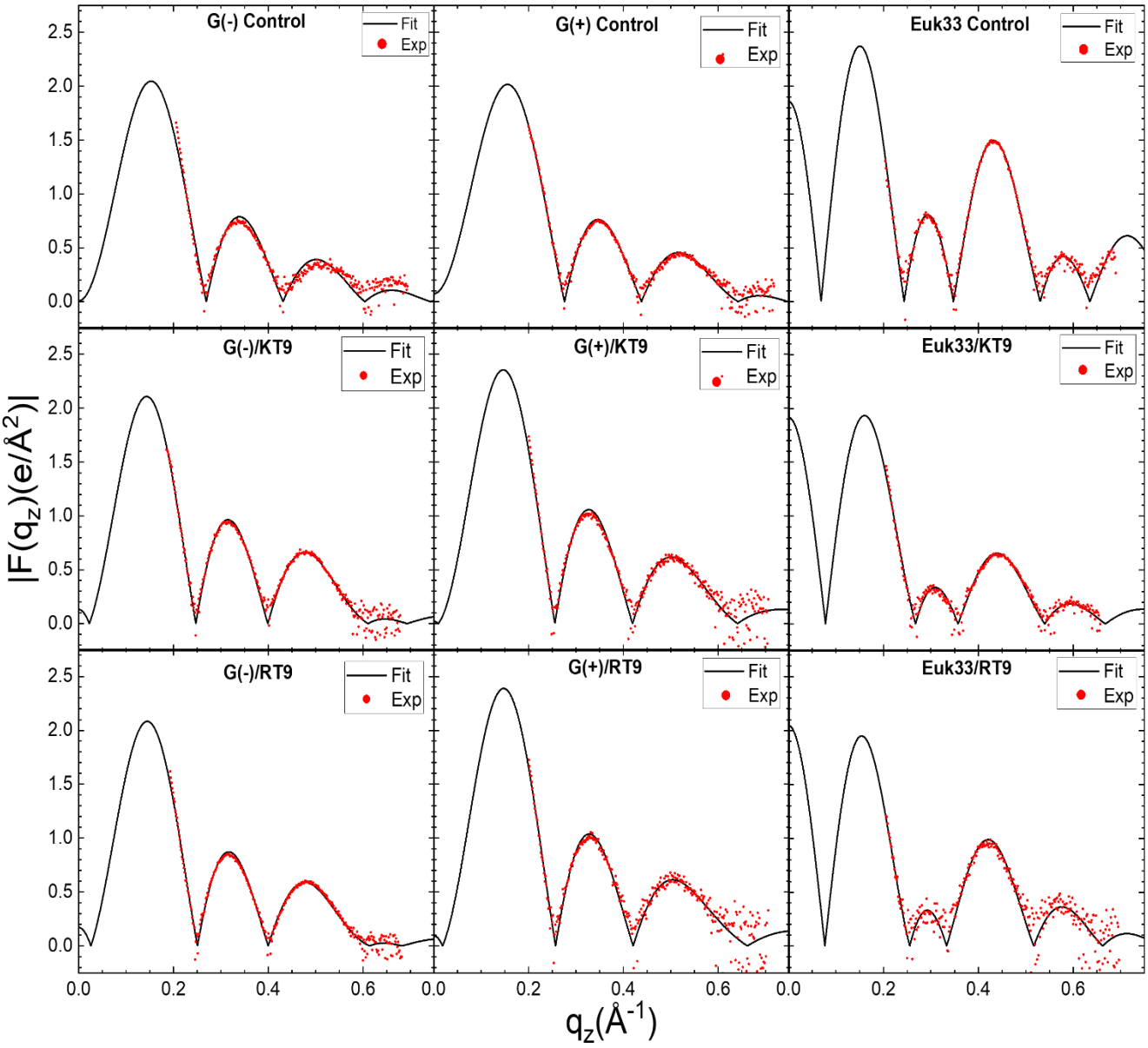

Fig S5 X-ray form factors obtained using the intensity data from the final fit of the X-ray diffuse data to the NFIT liquid crystal analysis computer program. These form factors were used in the Scattering Density Program (SDP) to produce the electron density profiles.