Supporting Information

Design, Synthesis and Characterization of Non-Hemolytic Antimicrobial Peptides Related to Human Cathelicidin LL-37

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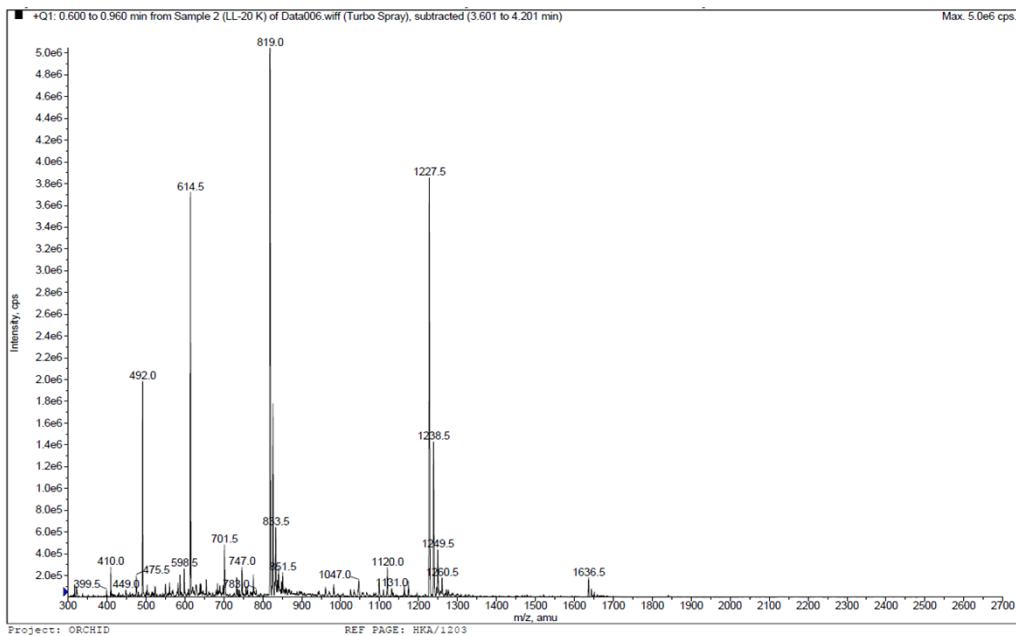Email: krajavenkateshkcmp5@gmail.com / rajavenkateshk2@sethu.ac.in

Figure S1: ESI mass spectrum of P1

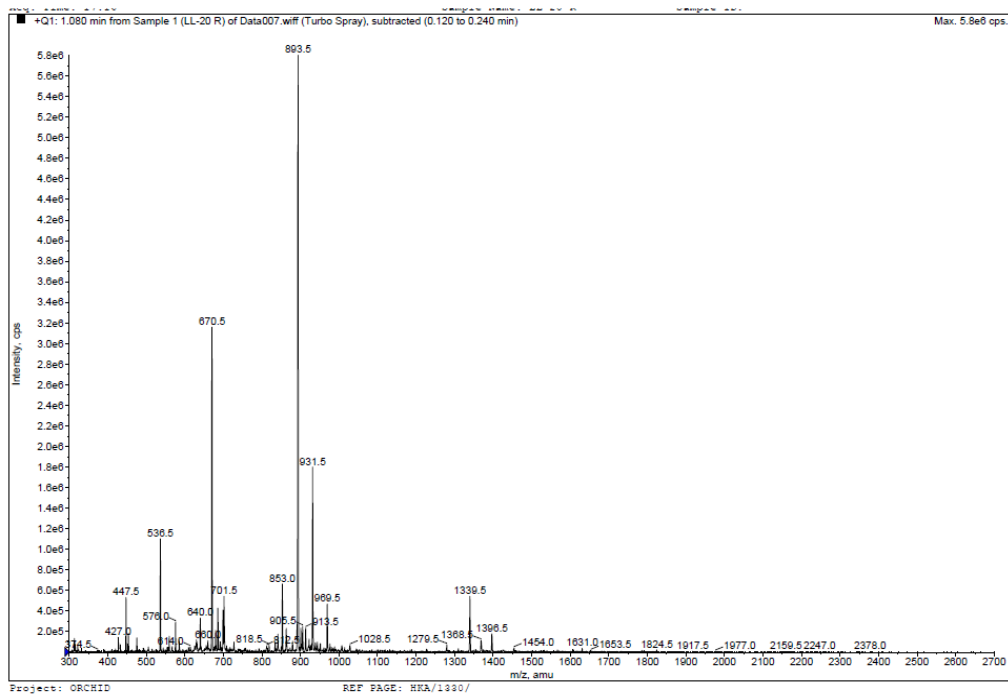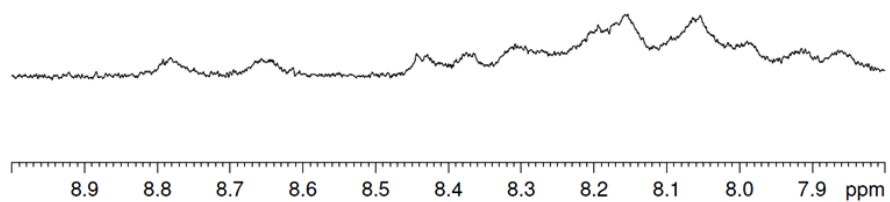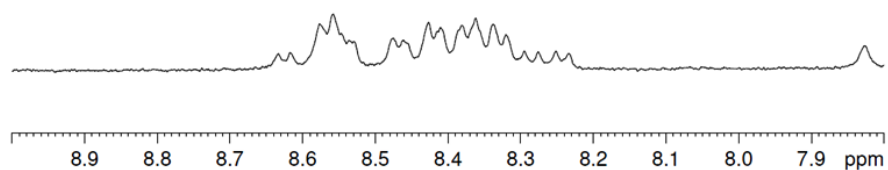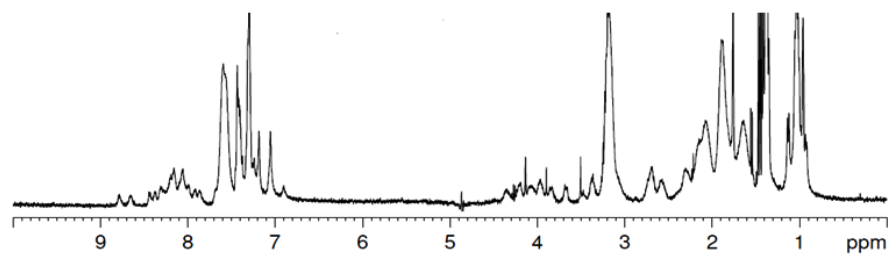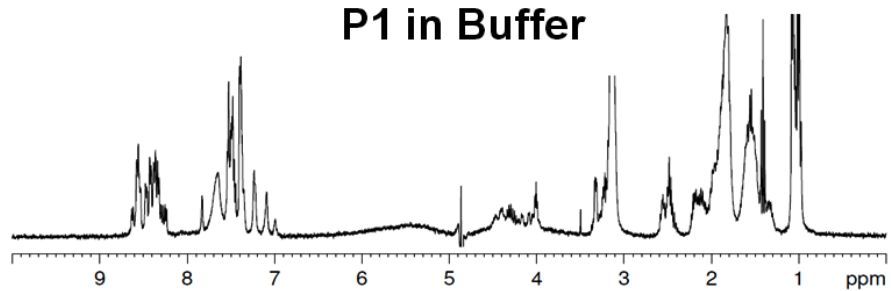**Figure S2:** ESI mass spectrum of P2

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P1 in 80 mM SDS-d25
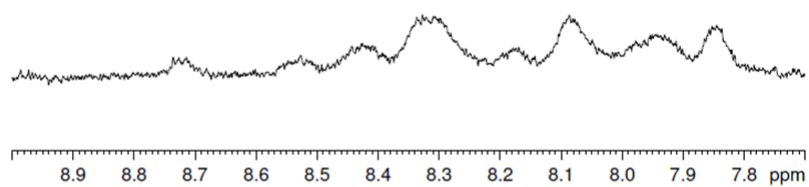

P1 in Buffer
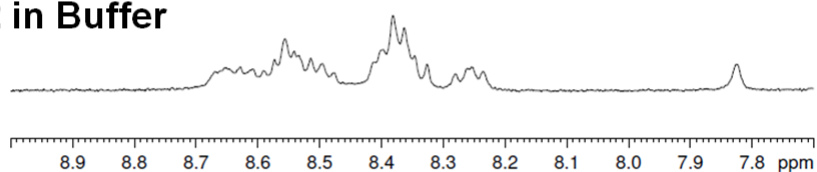

P1 in 80 mM SDS-d25

P1 in Buffer

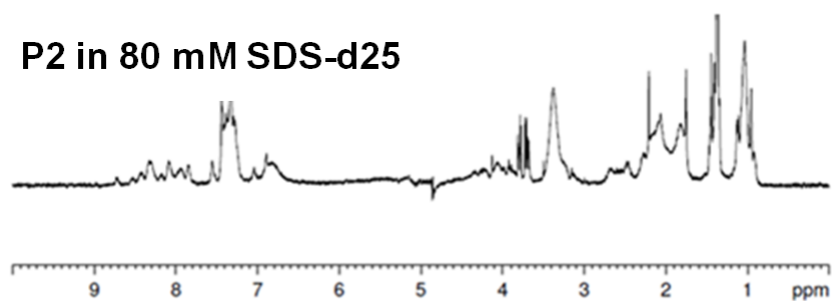**Figure S3:** An overlay of ^{1}H NMR Spectraof P1 in Buffer and SDS-d$_{25}$.
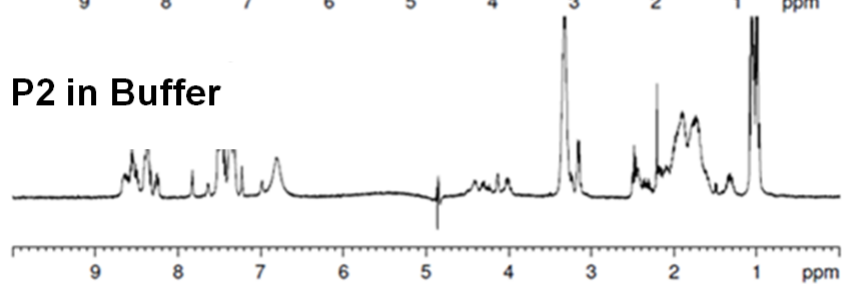
P2 in 80 mM SDS-d25
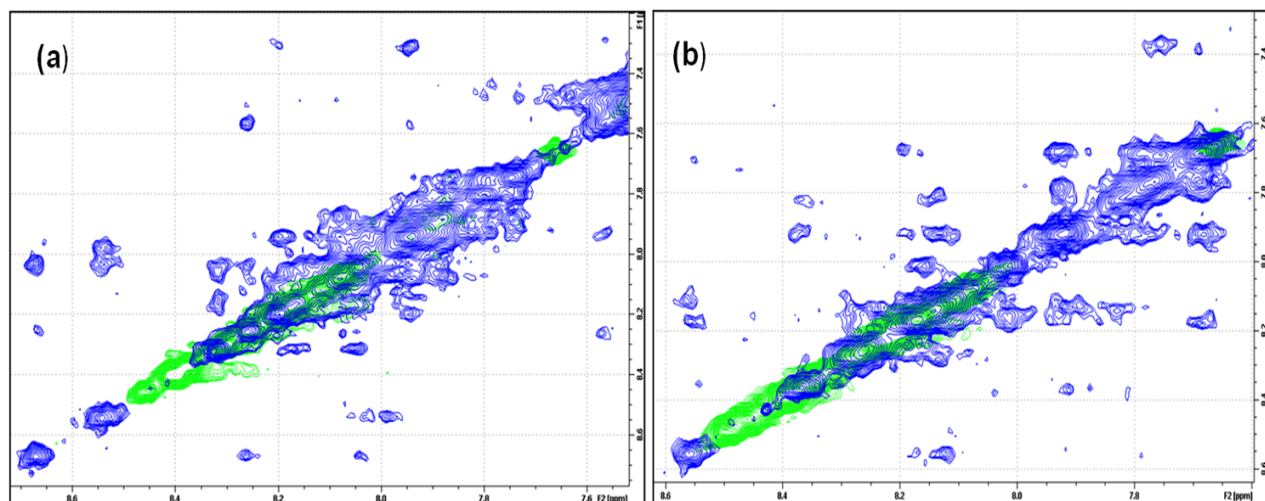

P2 in Buffer

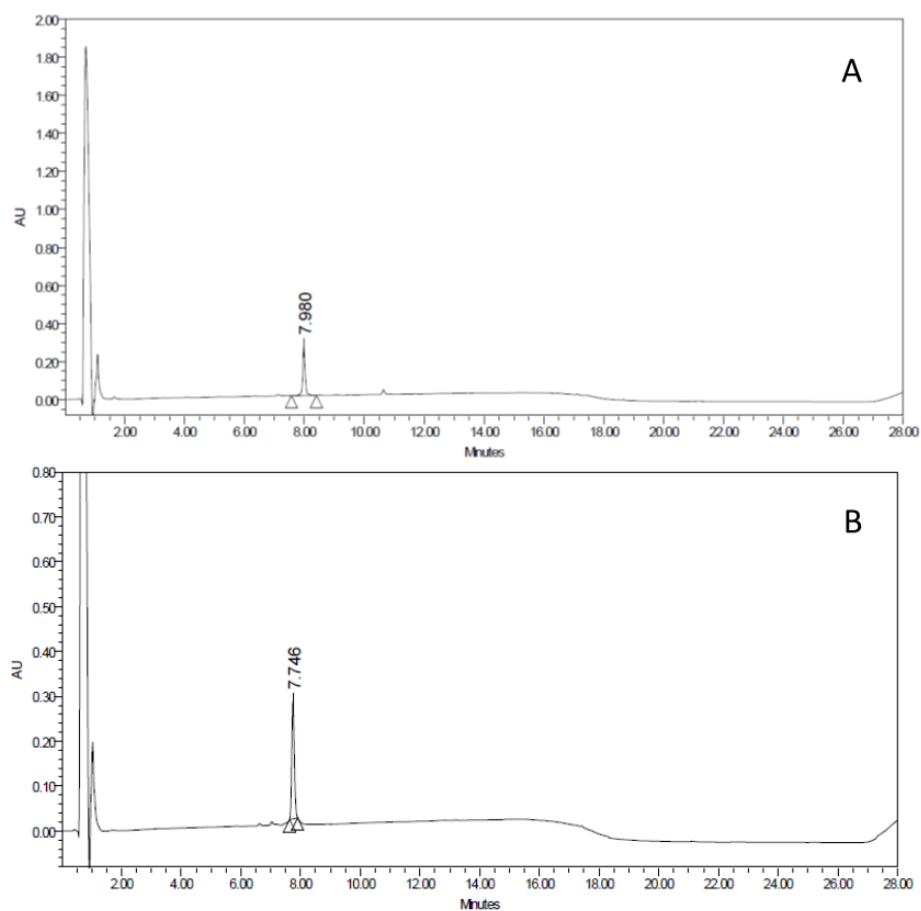**P2 in 80 mM SDS-d25**

P2 in Buffer

Figure S4: An overlay of ^{1}H NMR Spectra of P2 in Buffer and SDS-d$_{25}$.

Figure S5: NH-NH Region of NOESY Spectra of (a) P1 and (b) P2 in buffer (green), and SDS-d_{25}(blue)

Figure S6: Optimization of elution conditions and column suitable for HPLC based binding assay: B) Detection of unbound peptides isolated from Peptide-MLVs mixtures.

Table S1: Antimicrobial activity of synthesized peptides

Microorganism	Zone of Inhibition(mm)			MIC (µg/mL)		
	LL-37 (5-24)	P1	P2	LL-37 (5-24)	P1	P2
Staphylococcus aureus	19.54±0.84	21.66±0.41	15.66±0.95	10	25.00	35.00
Bacillus subtilis	21.22±0.65	15.00±0.38	17.00±0.33	0.6	35.00	30.00
Escherichia coli	22.89±0.25	23.33±0.20	13.66±0.35	0.8	20.00	35.00
Pseudomonas aeruginosa	20.22±0.83	14.00±0.84	17.00±0.28	25	35. 00	30.00