Supporting information

N-Terminal Aromatic Tag Induced Self Assembly of Tryptophan-Arginine Rich Ultra Short Sequences and Their Potent Antibacterial Activity

HPLC chromatograms of selected sequences

For sequences **4**, **5**, **6** and **7** RP-HPLC chromatograms (absorbance at 220 nm) are reported. A linear gradient of 10 to 90% buffer 2 was run where, buffer 1 was water (0.1 % TFA) and buffer 2 was acetonitrile (0.1% TFA) over 45 minutes.



Sequence 4







Sequence 6



Sequence 7

ESI-MS data of sequences

The data was acquired on Triple Quadrupole (LC-ESI-MS, Quattro Micro API Waters) using LC-MS method where LC conditions were: column BEH shields RP C_{18} (2.1 X 100mm X 1.7 μ M), flow rate: 0.3 mL/min, Gradient: 10 to 90 buffer 2 (where, buffer 1: MQ (0.1% FA) and buffer 2: acetonitrile (0.1% FA)), run time: 6 min. The MS was run in positive ion mode with capillary voltage: 3.5 kV, cone voltage: 25 V, de-solvation gas: 650 L/h, source temperature: 100 °C and cone gas: 50 L/h.



Sequence 2



Sequence 3



Sequence 4



Sequence 5



Sequence 6

Sequence 7

Size Distribution by Intensity

Fig. S1: Histograms for size distribution of sequences 5-7 using dynamic light scattering

Zeta Potential Distribution

Fig. S2: Histograms for zeta potential distribution of sequences 5-7.

Fig. S3: Critical aggregation concentration determination of sequences 5-7 using light scattering intensity. Normalized fluorescence is plotted against log concentration of sequences. Here, F represents fluorescence intensity at a fixed peptidomimetic concentration and F_0 is fluorescence intensity in buffer.