A computationally designed peptide derived from *Escherichia coli* as a potential drug template for antibacterial and antibiofilm therapies

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Table S1

Figure S1

Table S1. Minimal inhibitory concentration (MIC) and minimal bactericidal concentration (MBC) for ampicillin, cefaclor, chloramphenicol, ciprofloxacin and imipinem against the resistant strains and clinical isolates used in the present study.

	MIC (MBC) μg.mL^{-1}				
Bacterial strains	Ampicillin	Cefaclor	Chloramphenicol	Ciprofloxacin	Imipinem
A. baumannii (clinical isolate 003326263)	nd (nd)[a]	nd (nd)	2 (4)	nd (nd)	nd (nd)
E. cloacae (clinical isolate 1383251)	nd (nd)	nd (nd)	2 (16)	2 (2)	nd (nd)
E. coli (KpC+ 001812446)	nd (nd)	16 (32)	8 (64)	2 (2)	nd (nd)
K. pneumoniae (KpC+ 001825971)	nd (nd)	nd (nd)	8 (16)	2 (2)	nd (nd)
MRSA (clinical isolate 713623)	nd (nd)	nd (nd)	2 (16)	16 (32)	nd (nd)

nd: not determined at the highest concentration tested (64 μg.mL^{-1}). Three replicates for each condition were performed.

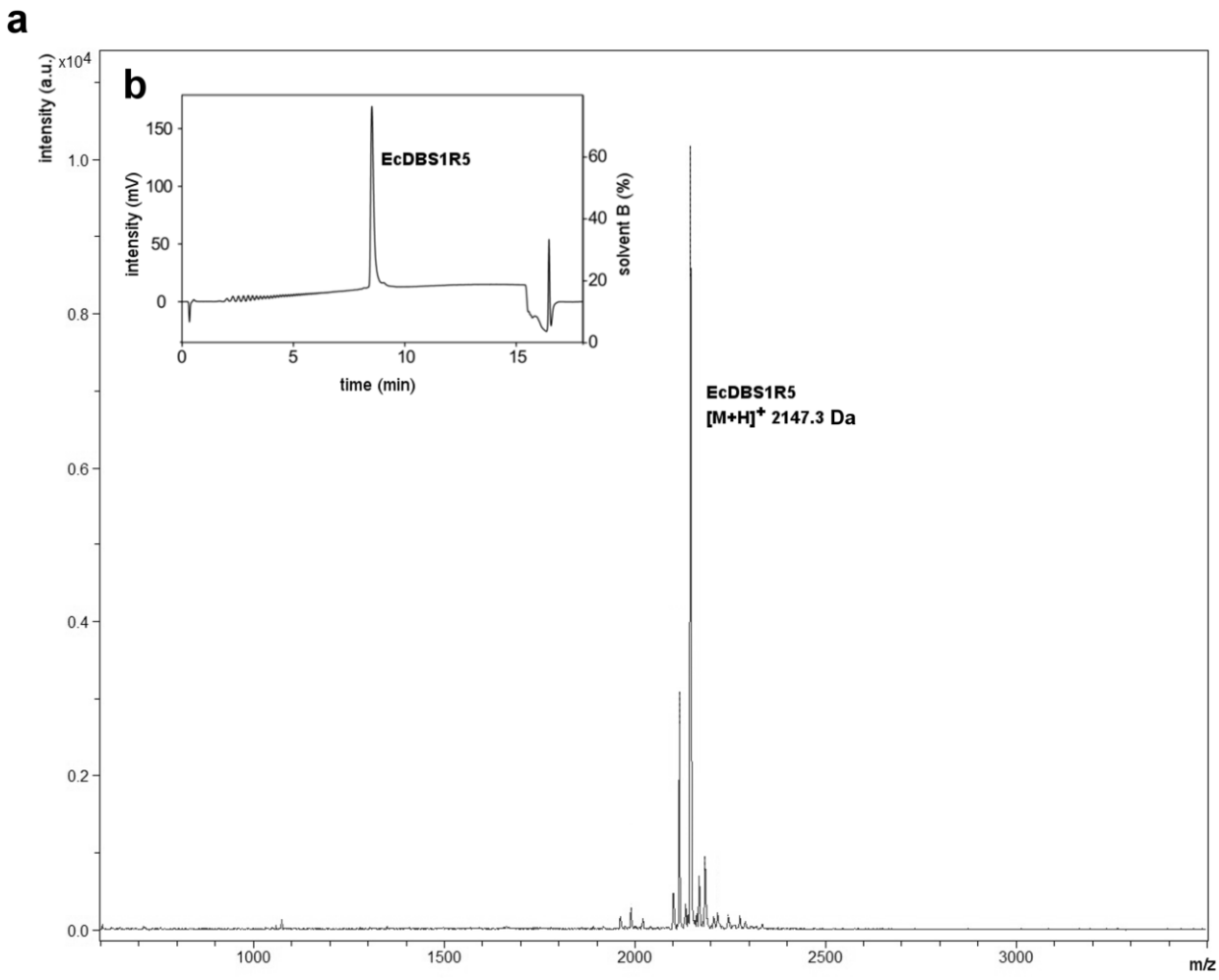

Figure S1. UHPLC and MALDI-TOF analyzes of EcDBS1R5. The molecular mass of EcDBS1R5 was confirmed by MALDI-TOF, revealing a monoisotopic mass of 2147.3 Da (a). The purity (>95%) of EcDBS1R5 after F-moc synthesis was confirmed by UHPLC (b) with a volumetric flow rate of 0.4 $mL.min^{-1}$ on a 0.8 $mL.min^{-1}$ Agilent column using a 4% gradient of 0-60% solvent B (90% MeCN in 0.045% aq. TFA).