Table S5 The characteristics of polypeptides in molecular dynamics simulations.

Polypeptide	Sequence	Number of Hydrophobic Residues	Number of Charged Residues	Length
OmpC N-terminal Fragment	AEVYNKDGNKLDLYGKVDGL	8	7	20
OmpA N-terminal Fragment	APKDNTWYTGAKLGFSQYHDT	7	5	21
OmpF N-terminal Fragment	AEIYNKDGNKVDLYGKAVGL	9	6	20
OmpC C-terminal Fragment	FTRDAGINTDNIVALGLVYQF	11	3	21
OmpC Ala Mutant	Ace-AAVYNAAGNALALYGAVAGL-Nhe	15	0	20
OmpC Asn Mutant	Ace-ANVYNNNGNNLNLYGNVNGL-Nhe	8	0	20
OmpA Ala Mutant	Ace-APAANTWYTGAALGFSQYAAT-Nhe	12	0	21
OmpA Asn Mutant	Ace-APNNNTWYTGANLGFSQYNNT-Nhe	7	0	21