

Figure S1: Calibration curves used with the bacterial strains in this study and their percentage variation. Some curves were used for more than one bacterial strain, as can be seen on this figure's inset. The OD was measured in 270 μ L volume.

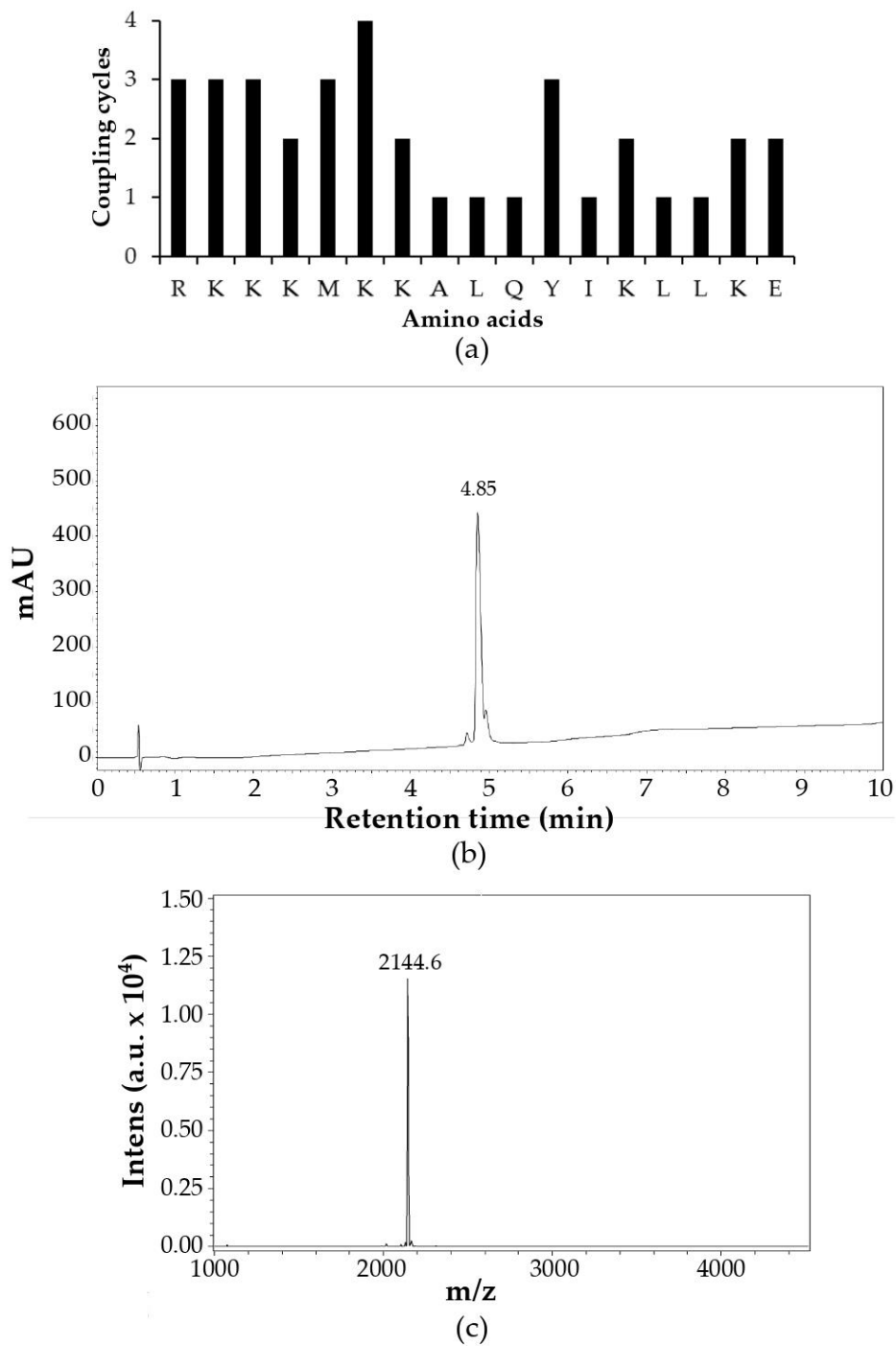


Figure S2: Data regarding the synthesis, purification and characterisation of the most representative peptide from this study (peptide 35409-1). A. Summary of synthesis from the C-terminal extreme to the N-terminal extreme. B. Pure peptide chromatographic profile (HPLC). C. MALDI-TOF mass spectra, the observed signal at 2144.6 corresponds to the $[M + H]^+$ specie.

Table S1. RP-HPLC chromatographic characterisation of 35409 derived-peptides

Peptide	Sequence	Length	Purity ^a (%) RP-HPLC
35409	RYRRKKKMKKALQYIKLLKE	20	96
35409-1	RKKKMKKALQYIKLLKE	17	86-95
35409-2	KKKMKKALQYIKLLKE	16	74
35409-3	KKMKKALQYIKLLKE	15	90
35409-4	KMKKALQYIKLLKE	14	71
35409-5	MKKALQYIKLLKE	13	98
35409-6	ALQYIKLLKE	10	99
35409-7	YIKLLKE	7	98
35409-8	RYRRKKKMKKALQYIKL	17	100
35409-9	RYRRKKKMKKALQY	14	98
35409-10	RYRRKKKMKKA	11	97
35409-11	RYRRKKKMKK	10	97
35409-12	RYRRKKK	7	90
35409-13	KKMKKALQYIKLLK	14	99
35409-14	KKMKKALQYIKL	12	97
35409-15	RKKKMKKALQY	11	98
35409-16	KMKKALQY	8	98

^a Purity according to the percentage of the area below the chromatographic curve regarding the whole chromatogram. Two batches involving different synthesis, purification and characterisation processes were used for 35409-1 peptide, one having 86% chromatographic purity and the other 95%. No change in MIC results was observed between batches of the peptide.