

SUPPORTING INFORMATION

Impedimetric Detection of Pathogenic Gram-Positive Bacteria using An Antimicrobial Peptide from Class IIa Bacteriocins

Hashem Etayash^{a,b}, Keren Jiang^b, Thomas Thundat^b and Kamaljit Kaur^{a,*}

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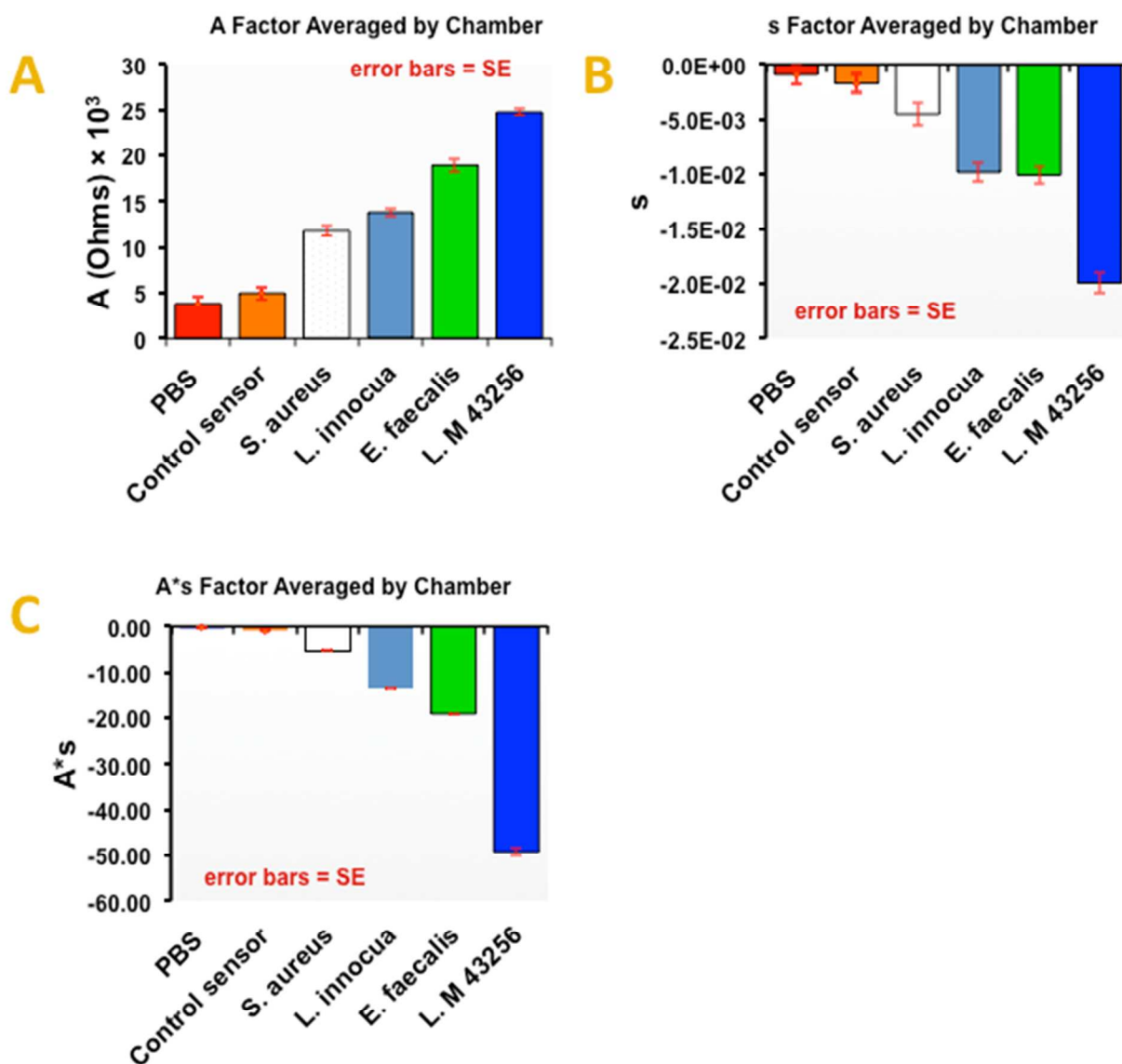


Figure S1. Binding curve parameters of normalized impedance signal responses to peptide sensor interactions to bacterial species. (A) Amplitude A (B) time constant (s value) and (C) $A \times s$ value, the initial binding rate. The studies were performed with contaminated buffer samples with different bacterial species at concentrations of 10^3 cfu mL⁻¹. Bars represent an average of five replications.

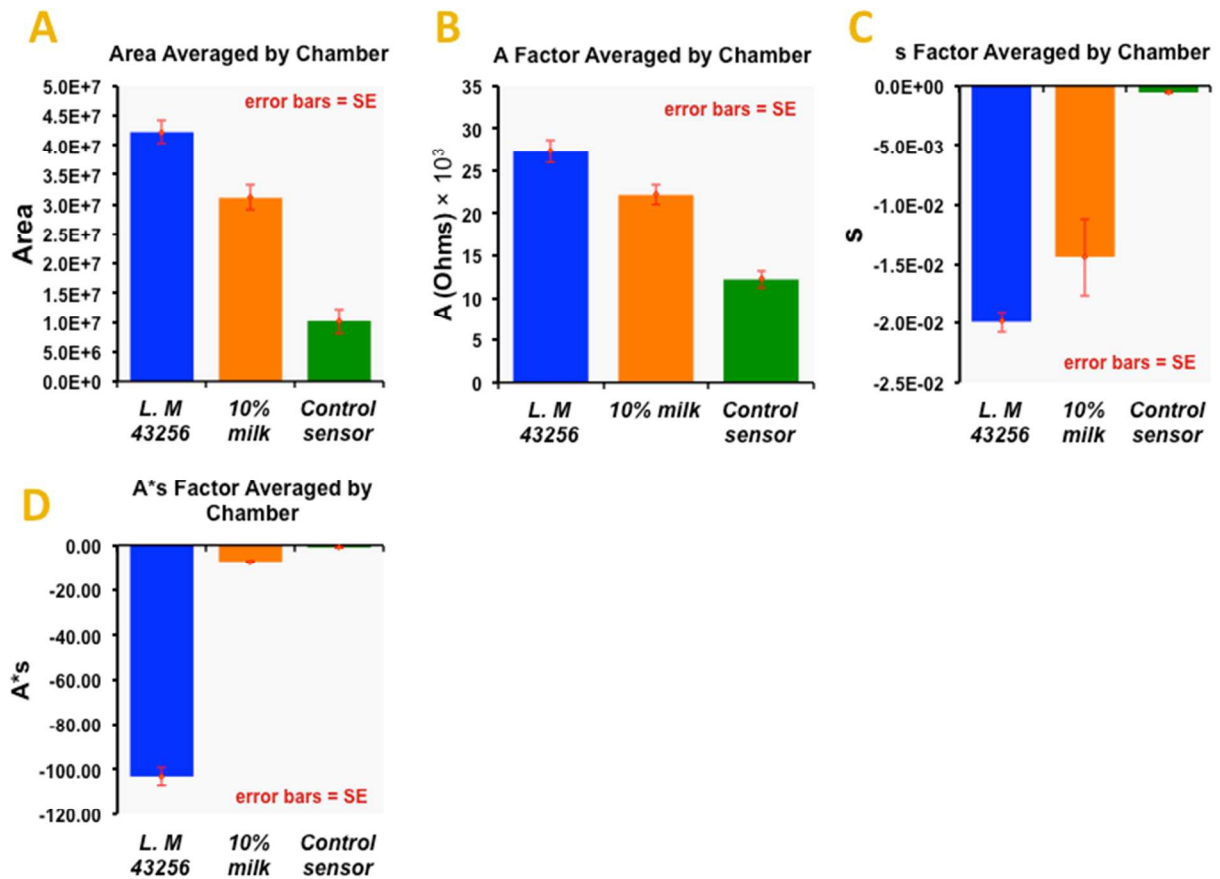


Figure S2. Binding kinetic parameters of normalized impedance signals to peptide sensor responses to 10% milk contaminated with *L. monocytogenes* (*L. M*) at 10^3 cfu mL⁻¹; (A) area under the binding curve, (B) Amplitude A, (C) s value, and (D) A × s. Bars represent an average of five replications.

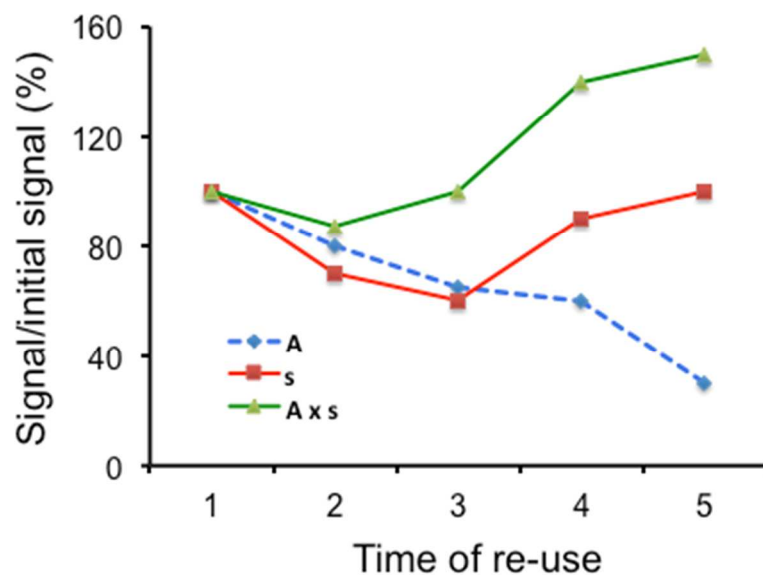


Figure S3. Changes of the binding curve parameters as a result of the peptide sensor array regeneration (x-axis). The array performance after regeneration was evaluated against *Listeria monocytogenes* at a concentration of 10^3 cfu mL⁻¹ in 1X PBS solution at a fixed frequency. The values were calculated as percentage of the initial measurements obtained during the first time use. The blue dashed line shows amplitude A, red line is for time constant and green line is for $A \times s$.