Supplementary Material

Manuscript Title: Theoretical approach to spot active regions in antimicrobial proteins.

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table S1. Negative resting dataset results.

Protein ID	Predicted	Obseryed
P56508	Ν	Ν
<i>Q05676</i>	Ν	Ν
P40204	Ν	Ν
P41806	Ν	Ν
P22289	Ν	Ν
P37299	Ν	Ν
P07215	Ν	Ν
<i>Q6Q547</i>	Р	Ν
P40422	Ν	Ν
P03094	Р	Ν
P69852	Ν	Ν
<i>Q12287</i>	Ν	Ν
Q3E764	Р	Ν
P04039	Ν	Ν
Q6Q5K6	Р	Ν
P01094	Ν	Ν
P01095	Ν	Ν
P38636	Ν	Ν
<i>Q6Q546</i>	Ν	Ν
P81451	Ν	Ν

Specificity: 80 %

Negative (N) and positive (P) kits for each polypeptide are indicated, as predicted by the theoretical approach (Predicted) and reported from experimental evidence in the literature (Observed).

Protein ID	Predicted	Obseryed
P80032	Р	Р
P81058	Р	Р
P81592	Р	Р
P01376	Р	Р
P60030	Р	Р
Q93X17	Р	Р
Q95NH6	Р	Р
Q07932	Р	Р
P06833	Р	Р
P37363	N	Р
Q7M249	Р	Р
076145	Р	Р
P22749	Р	Р
P32195	Р	Р
Q61V20	Р	Р
B5LURO	Р	Р
Q25054	Ν	Р
<i>Q</i> 29075	Р	Р
P14213	Р	Р
P82358	Р	Р

table S2. Positive testing dataset results.

Sensitivity: 90 %

Negative (N) and positive (P) kits for each polypeptide are indicated, as predicted by the theoretical approach (Predicted) and reported from experimental evidence in the literature (Observed).

Figure S1. Statistical analysis of the results obtained using a 10 amino acid predictive length and different gap inclusion.



FIGURE S2. Statistical analysis of the results obtained using a 12 amino acid predictive length and different gap inclusion.

PREDICTIVE LENGHT 10



PREDICTIVE LENGHT 12

FIGURE S3. Statistical analysis of the results obtained using a 10 amino acid predictive length and different gap inclusion.

PREDICTIVE LENGHT 14

