

**Table S1. Hydrophobicity score lists derived from the Cowan's scale.**

	<b>Cowan</b>	<b>Cowan-Ser0</b>	<b>Cowan-Gly0</b>
<b>Ile</b>	1.000	1.000	1.000
<b>Leu</b>	0.992	0.988	0.984
<b>Phe</b>	0.965	0.943	0.923
<b>Trp</b>	0.879	0.805	0.738
<b>Val</b>	0.872	0.793	0.721
<b>Met</b>	0.817	0.703	0.601
<b>Pro</b>	0.751	0.598	0.459
<b>Cys</b>	0.731	0.565	0.415
<b>Tyr</b>	0.638	0.415	0.213
<b>Ala</b>	0.628	0.398	0.191
<b>Gly</b>	0.540	0.256	0
<b>Thr</b>	0.472	0.146	0
<b>Ser</b>	0.382	0	0
<b>His</b>	0.377	0	0
<b>Gln</b>	0.307	0	0
<b>Asn</b>	0.291	0	0
<b>Arg</b>	0.163	0	0
<b>Lys</b>	0.153	0	0
<b>Glu</b>	0.050	0	0
<b>Asp</b>	0.000	0	0

**Table S2. Hydrophobicity score lists derived from the Kovacs's scale (a).**

	<b>Kovacs(a)</b>	<b>Kovacs(a)-Glu0</b>	<b>Kovacs(a)-Gln0</b>	<b>Kovacs(a)-Arg0</b>
<b>Trp</b>	1.000	1.000	1.000	1.000
<b>Phe</b>	0.916	0.912	0.906	0.898
<b>Leu</b>	0.760	0.749	0.733	0.709
<b>Ile</b>	0.707	0.694	0.674	0.645
<b>Met</b>	0.551	0.531	0.500	0.457
<b>Tyr</b>	0.514	0.492	0.458	0.411
<b>Val</b>	0.486	0.463	0.427	0.377
<b>Pro</b>	0.355	0.326	0.281	0.219
<b>Cys</b>	0.318	0.287	0.240	0.174
<b>His</b>	0.190	0.153	0.097	0.019
<b>Ala</b>	0.174	0.137	0.080	0
<b>Thr</b>	0.174	0.137	0.080	0
<b>Arg</b>	0.174	0.137	0.080	0
<b>Gln</b>	0.103	0.062	0	0
<b>Ser</b>	0.090	0.049	0	0
<b>Asn</b>	0.084	0.042	0	0
<b>Gly</b>	0.056	0.013	0	0
<b>Glu</b>	0.044	0	0	0
<b>Asp</b>	0.034	0	0	0
<b>Lys</b>	0	0	0	0

**Table S3. Hydrophobicity score lists derived from the Kovacs's scale (b).**

	<b>Kovacs(b)</b>	<b>Kovacs(b)-Ser0</b>	<b>Kovacs(b)-Gln0</b>
<b>Trp</b>	1.000	1.000	1.000
<b>Phe</b>	0.931	0.916	0.915
<b>Leu</b>	0.792	0.749	0.746
<b>Ile</b>	0.740	0.686	0.682
<b>Met</b>	0.590	0.505	0.498
<b>Tyr</b>	0.549	0.456	0.449
<b>Val</b>	0.538	0.443	0.435
<b>Pro</b>	0.422	0.303	0.293
<b>Cys</b>	0.382	0.254	0.244
<b>Arg</b>	0.338	0.202	0.191
<b>Lys</b>	0.266	0.115	0.102
<b>Ala</b>	0.266	0.115	0.102
<b>His</b>	0.266	0.115	0.102
<b>Thr</b>	0.243	0.087	0.074
<b>Gln</b>	0.182	0.014	0
<b>Gly</b>	0.182	0.014	0
<b>Ser</b>	0.171	0	0
<b>Asn</b>	0.165	0	0
<b>Glu</b>	0.012	0	0
<b>Asp</b>	0	0	0

**Table S4. Hydrophobicity score lists derived from the Monera's scale.**

	<b>Monera</b>	<b>Monera-Ser0</b>	<b>Monera-Gly0</b>
<b>Phe</b>	1.000	1.000	1.000
<b>Ile</b>	0.990	0.985	0.984
<b>Trp</b>	0.983	0.975	0.974
<b>Leu</b>	0.983	0.975	0.974
<b>Val</b>	0.843	0.769	0.757
<b>Met</b>	0.833	0.754	0.741
<b>Tyr</b>	0.760	0.645	0.627
<b>Cys</b>	0.670	0.512	0.487
<b>Ala</b>	0.620	0.439	0.409
<b>Thr</b>	0.437	0.168	0.125
<b>His</b>	0.403	0.118	0.073
<b>Gly</b>	0.357	0.050	0
<b>Ser</b>	0.323	0	0
<b>Gln</b>	0.290	0	0
<b>Arg</b>	0.263	0	0
<b>Lys</b>	0.207	0	0
<b>Pro</b>	0.173	0	0
<b>Asn</b>	0.173	0	0
<b>Glu</b>	0.157	0	0
<b>Asp</b>	0	0	0

**Table S5. Hydrophobicity score lists derived from the scale AVE3.**

	<b>AVE3</b>	<b>AVE3-Gln0</b>	<b>AVE3-Gly0</b>	<b>AVE3-Arg0</b>
<b>Trp</b>	1.000	1.000	1.000	1.000
<b>Phe</b>	0.969	0.960	0.959	0.956
<b>Leu</b>	0.916	0.891	0.888	0.880
<b>Ile</b>	0.882	0.847	0.843	0.832
<b>Met</b>	0.715	0.629	0.621	0.594
<b>Val</b>	0.693	0.601	0.592	0.563
<b>Tyr</b>	0.639	0.531	0.520	0.486
<b>Cys</b>	0.497	0.346	0.331	0.283
<b>Ala</b>	0.430	0.259	0.242	0.188
<b>His</b>	0.357	0.164	0.145	0.084
<b>Pro</b>	0.333	0.133	0.113	0.050
<b>Thr</b>	0.309	0.101	0.081	0.016
<b>Arg</b>	0.298	0.087	0.066	0
<b>Gly</b>	0.248	0.022	0	0
<b>Gln</b>	0.231	0	0	0
<b>Lys</b>	0.225	0	0	0
<b>Ser</b>	0.224	0	0	0
<b>Asn</b>	0.163	0	0	0
<b>Glu</b>	0.093	0	0	0
<b>Asp</b>	0	0	0	0

**Table S6. Values of  $R^2$  values derived from the analysis of the  $(XXYY)_n\text{-NH}_2$  peptide set.**

<b>Scale</b>	<b><i>m</i></b>	<b><i>n</i></b>	<b><math>R^2</math><sup>a</sup></b>	<b><math>R^2</math><sup>b</sup></b>
<b>Kovacs(a)</b>	0.9	0.1	0.846	0.905
<b>Kovacs(a)-Glu0</b>	0.9	0.1	0.846	0.898
<b>Kovacs(a)-Gln0</b>	0.9	0.2	0.832	0.898
<b>Kovacs(a)-Arg0</b>	0.9	0.2	0.815	0.897
<b>Kovacs(b)</b>	0.8	0.2	0.839	0.904
<b>Kovacs(b)-Ser0</b>	0.8	0.3	0.830	0.896
<b>Kovacs(b)-Gln0</b>	0.9	0.1	0.838	0.904
<b>Parker</b>	0.2	0.9	0.865	0.914
<b>Parker-Ser0</b>	0.5	0.7	0.864	0.920
<b>Parker-Gly0</b>	0.5	0.7	0.869	0.919
<b>Parker-Arg0</b>	0.8	0.4	0.840	0.917
<b>Monera</b>	2.8	1.4	0.821	0.906
<b>Monera-Ser0</b>	0.8	0.4	0.837	0.906
<b>Monera-Gly0</b>	0.8	0.4	0.837	0.906
<b>AVE3</b>	0.7	0.4	0.849	0.914
<b>AVE3-Gln0</b>	0.7	0.5	0.844	0.887
<b>AVE3-Gly0</b>	0.7	0.5	0.842	0.906
<b>AVE3-Arg0</b>	0.9	0.2	0.832	0.897

<sup>a</sup>  $R^2$  values calculated using the entire set of nine peptides.

<sup>b</sup>  $R^2$  values calculated omitting peptide  $(LLKK)_2\text{-NH}_2$ .

Table S7. R<sup>2</sup> values derived from the analysis of the (RW)<sub>n</sub>-NH<sub>2</sub> and RV-helices peptide sets.

Scale	Peptide set			
	(RW) <sub>n</sub> -NH <sub>2</sub>		RV-helices	
	<i>E. coli</i>	<i>S. aureus</i>	<i>S. aureus</i>	<i>P. aeruginosa</i>
<b>Kovacs(a)</b>	0.998	0.995	0.940	0.834
<b>Kovacs(a)-Glu0</b>	0.998	0.995	0.940	0.834
<b>Kovacs(a)-Gln0</b>	0.998	0.995	0.940	0.833
<b>Kovacs(a)-Arg0</b>	0.998	0.995	0.939	0.831
<b>Kovacs(b)</b>	0.999	0.996	0.941	0.836
<b>Kovacs(b)-Ser0</b>	0.999	0.997	0.940	0.835
<b>Kovacs(b)-Gln0</b>	0.999	0.996	0.940	0.835
<b>Parker</b>	0.997	0.994	0.940	0.835
<b>Parker-Ser0</b>	0.998	0.995	0.940	0.834
<b>Parker-Gly0</b>	0.998	0.995	0.939	0.832
<b>Parker-Arg0</b>	0.998	0.995	0.939	0.831
<b>Monera</b>	0.997	0.993	0.940	0.834
<b>Monera-Ser0</b>	0.998	0.995	0.939	0.831
<b>Monera-Gln0</b>	0.998	0.995	0.939	0.831
<b>AVE3</b>	0.998	0.994	0.940	0.835
<b>AVE3-Gln0</b>	0.998	0.995	0.939	0.832
<b>AVE3-Gly0</b>	0.998	0.995	0.940	0.832
<b>AVE3-Arg0</b>	0.998	0.995	0.939	0.831

**Table S8. Values of the exponents  $m$  and  $n$  derived from the analysis of the RANDOM19 set.**

Scale	<i>P. aeruginosa</i> H103						<i>P. aeruginosa</i> Brazil 9						<i>P. aeruginosa</i> LES400					
	$m$	$n$	$fH^a$	$a^b$	$b^b$	$R^2$	$m$	$n$	$fH^a$	$a^b$	$b^b$	$R^2$	$m$	$n$	$fH^a$	$a^b$	$b^b$	$R^2$
<b>Kovacs(a)</b>	0.50	1.10	0.69	1.52	4.18	0.907	1.10	2.00	0.65	3.16	1.60	0.880	0.60	1.40	0.70	2.04	3.20	0.852
<b>Kovacs(a)-Glu0</b>	0.50	1.00	0.67	1.52	4.34	0.906	0.90	1.60	0.64	3.00	2.25	0.878	0.50	1.20	0.71	1.95	3.51	0.851
<b>Kovacs(a)-Gln0</b>	0.40	0.80	0.67	1.42	4.78	0.903	0.70	1.20	0.63	2.77	3.04	0.874	0.40	1.00	0.71	1.86	3.77	0.847
<b>Kovacs(a)-Arg0</b>	0.30	0.60	0.67	1.29	5.25	0.895	0.50	0.90	0.64	2.57	3.62	0.866	0.30	0.70	0.70	1.65	4.59	0.838
<b>Kovacs(b)</b>	0.30	1.30	0.81	1.31	4.58	0.904	0.60	2.00	0.77	2.63	2.90	0.875	0.30	1.50	0.83	1.63	3.93	0.849
<b>Kovacs(b)-Ser0</b>	0.30	0.90	0.75	1.33	4.77	0.902	0.60	1.50	0.71	2.81	2.70	0.873	0.30	1.10	0.79	1.73	3.89	0.847
<b>Kovacs(b)-Gln0</b>	0.30	0.90	0.75	1.36	4.67	0.902	0.60	1.40	0.70	2.76	2.89	0.873	0.30	1.10	0.79	1.76	3.78	0.847
<b>Parker</b>	1.00	2.20	0.69	1.64	4.25	0.851	3.10	6.10	0.66	4.07	-0.19	0.849	1.30	3.00	0.70	2.30	2.96	0.801
<b>Parker-Ser0</b>	0.90	1.50	0.63	1.62	4.44	0.856	3.00	4.40	0.59	4.22	-0.25	0.852	1.20	2.10	0.64	2.33	3.07	0.804
<b>Parker-Gly0</b>	1.00	1.50	0.60	1.74	4.12	0.859	2.50	3.40	0.58	4.03	0.38	0.853	1.20	1.90	0.61	2.33	3.12	0.805
<b>Parker-Arg0</b>	0.70	1.00	0.59	1.47	5.11	0.860	1.60	2.10	0.57	3.69	1.88	0.848	0.80	1.20	0.60	1.94	4.42	0.802
<b>Monera</b>	4.60	8.10	0.64	2.37	1.40	0.793	6.30	10.60	0.63	3.70	0.00	0.806	4.90	8.90	0.64	2.86	0.98	0.748
<b>Monera-Ser0</b>	2.10	2.40	0.53	1.84	4.13	0.811	5.00	5.50	0.52	4.29	0.27	0.819	3.30	3.90	0.54	2.91	2.15	0.755
<b>Monera-Gly0</b>	1.90	2.20	0.54	1.79	4.30	0.812	1.60	1.60	0.50	1.98	0.52	0.760	3.10	3.70	0.54	2.91	2.19	0.756
<b>AVE3</b>	0.90	2.10	0.70	1.54	4.49	0.876	2.70	5.90	0.69	3.93	0.03	0.865	1.20	3.00	0.71	2.24	3.02	0.823
<b>AVE3-Gln0</b>	0.90	1.40	0.61	1.65	4.29	0.882	2.30	3.20	0.58	3.95	0.57	0.867	1.20	1.90	0.61	2.34	3.05	0.825
<b>AVE3-Gly0</b>	0.80	1.20	0.60	1.53	4.76	0.882	2.30	3.20	0.58	4.06	0.44	0.866	1.00	1.60	0.62	2.15	3.61	0.825
<b>AVE3-Arg0</b>	0.70	1.00	0.59	1.47	5.09	0.880	1.50	2.00	0.57	3.52	2.08	0.860	0.90	1.40	0.61	2.15	3.78	0.820

<sup>a</sup>  $fH$ , the ratio  $n/(n+m)$ , is the fraction of hydrophobic residues in the highest scoring peptides.

<sup>b</sup>  $a$  and  $b$  are the slope and the intercept of the least squares line.

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Scale	<i>P. aeruginosa</i> H1030						<i>P. aeruginosa</i> H1027						<i>P. maltophilia</i> ATCC13637					
	<i>m</i>	<i>n</i>	<i>fH<sup>a</sup></i>	<i>a<sup>b</sup></i>	<i>b<sup>b</sup></i>	<i>R<sup>2</sup></i>	<i>m</i>	<i>n</i>	<i>fH<sup>a</sup></i>	<i>a<sup>b</sup></i>	<i>b<sup>b</sup></i>	<i>R<sup>2</sup></i>	<i>m</i>	<i>n</i>	<i>fH<sup>a</sup></i>	<i>a<sup>b</sup></i>	<i>b<sup>b</sup></i>	<i>R<sup>2</sup></i>
<b>Kovacs(a)</b>	0.5	1.4	0.74	2.028	3.268	0.7145	0.50	0.90	0.64	1.10	4.91	0.815	0.40	0.70	0.64	1.180	3.920	0.828
<b>Kovacs(a)-Glu0</b>	0.40	1.20	0.75	1.93	3.53	0.717	0.40	0.70	0.64	0.97	5.51	0.818	0.40	0.60	0.60	0.839	5.820	0.876
<b>Kovacs(a)-Gln0</b>	0.30	0.90	0.75	1.76	4.21	0.717	0.40	0.60	0.60	0.96	5.74	0.818	0.30	0.50	0.63	0.800	6.000	0.886
<b>Kovacs(a)-Arg0</b>	0.20	0.70	0.78	1.63	4.46	0.713	0.30	0.50	0.63	0.94	5.81	0.820	0.30	0.40	0.57	0.762	6.300	0.881
<b>Kovacs(b)</b>	0.20	1.50	0.88	1.57	3.73	0.722	0.30	1.00	0.77	0.91	5.56	0.807	0.30	0.90	0.75	0.819	5.750	0.859
<b>Kovacs(b)-Ser0</b>	0.20	1.10	0.85	1.67	3.74	0.719	0.30	0.70	0.70	0.93	5.66	0.809	0.30	0.60	0.67	0.803	5.960	0.868
<b>Kovacs(b)-Gln0</b>	0.20	1.10	0.85	1.70	3.63	0.719	0.30	0.70	0.70	0.95	5.57	0.811	0.30	0.60	0.67	0.820	5.880	0.869
<b>Parker</b>	1.10	2.90	0.73	2.33	3.16	0.698	0.80	1.60	0.67	1.06	5.35	0.742	0.60	1.20	0.67	0.823	5.960	0.799
<b>Parker-Ser0</b>	1.00	2.00	0.67	2.34	3.34	0.696	0.80	1.20	0.60	1.12	5.21	0.751	0.60	0.90	0.60	0.873	5.840	0.816
<b>Parker-Gly0</b>	1.00	1.80	0.64	2.33	3.42	0.695	0.80	1.10	0.58	1.13	5.19	0.757	0.60	0.80	0.57	0.855	5.900	0.821
<b>Parker-Arg0</b>	0.70	1.20	0.63	2.03	4.47	0.698	0.60	0.80	0.57	1.01	5.79	0.764	0.50	0.60	0.55	0.782	6.390	0.829
<b>Monera</b>	3.60	7.20	0.67	2.75	2.02	0.613	2.80	4.80	0.63	1.46	3.46	0.653	1.50	2.60	0.63	0.971	5.250	0.742
<b>Monera-Ser0</b>	2.50	3.30	0.57	2.67	3.01	0.624	1.60	1.70	0.52	1.13	5.30	0.686	1.20	1.30	0.52	0.920	5.800	0.788
<b>Monera-Gly0</b>	2.20	2.90	0.57	2.54	3.36	0.627	1.40	1.50	0.52	1.06	5.55	0.688	1.10	1.20	0.52	0.892	5.900	0.790
<b>AVE3</b>	1	2.90	0.74	2.25	3.24	0.701	0.80	1.70	0.68	1.09	5.23	0.765	0.60	1.30	0.68	0.861	5.790	0.836
<b>AVE3-Gln0</b>	0.90	1.70	0.65	2.22	3.57	0.697	0.80	1.10	0.58	1.14	5.14	0.778	0.60	0.80	0.57	0.869	5.850	0.854
<b>AVE3-Gly0</b>	0.90	1.70	0.65	2.28	3.45	0.698	0.70	0.90	0.56	1.00	5.68	0.780	0.60	0.80	0.57	0.897	5.800	0.858
<b>AVE3-Arg0</b>	0.70	1.30	0.65	2.10	4.13	0.698	0.60	0.80	0.57	1.01	5.77	0.784	0.50	0.60	0.55	0.784	6.360	0.862

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Scale	<i>E. coli</i> 63103						<i>E. coli</i> 64771						<i>K. pneumoniae</i> 63575					
	<i>m</i>	<i>n</i>	<i>fH<sup>a</sup></i>	<i>a<sup>b</sup></i>	<i>b<sup>b</sup></i>	<i>R<sup>2</sup></i>	<i>m</i>	<i>n</i>	<i>fH<sup>a</sup></i>	<i>a<sup>b</sup></i>	<i>b<sup>b</sup></i>	<i>R<sup>2</sup></i>	<i>m</i>	<i>n</i>	<i>fH<sup>a</sup></i>	<i>a<sup>b</sup></i>	<i>b<sup>b</sup></i>	<i>R<sup>2</sup></i>
<b>Kovacs(a)</b>	0.40	0.80	0.67	1.25	5.31	0.747	0.50	0.80	0.62	1.22	5.18	0.813	0.90	3.80	0.81	1.96	0.01	0.769
<b>Kovacs(a)-Glu0</b>	0.40	0.70	0.64	1.21	5.59	0.743	0.50	0.70	0.58	1.18	5.40	0.824	0.90	3.90	0.81	1.85	-0.13	0.771
<b>Kovacs(a)-Gln0</b>	0.30	0.60	0.67	1.17	5.70	0.738	0.40	0.60	0.60	1.16	5.57	0.834	0.90	4.20	0.82	1.57	-0.31	0.771
<b>Kovacs(a)-Arg0</b>	0.30	0.50	0.63	1.14	5.92	0.719	0.40	0.50	0.56	1.17	5.74	0.840	0.50	3.50	0.88	1.29	0.23	0.767
<b>Kovacs(b)</b>	0.30	1.00	0.77	1.14	5.63	0.739	0.40	1.10	0.73	1.22	5.19	0.824	0.50	6.00	0.92	1.07	-0.12	0.776
<b>Kovacs(b)-Ser0</b>	0.30	0.70	0.70	1.16	5.73	0.737	0.40	0.70	0.64	1.15	5.59	0.828	0.50	4.60	0.90	1.18	-0.20	0.773
<b>Kovacs(b)-Gln0</b>	0.30	0.70	0.70	1.18	5.65	0.737	0.40	0.70	0.64	1.18	5.50	0.829	0.50	4.50	0.90	1.19	-0.20	0.773
<b>Parker</b>	0.70	1.50	0.68	1.30	5.51	0.7225	0.90	1.60	0.64	1.27	5.17	0.7419	1.80	5.20	0.74	2.82	1.12	0.718
<b>Parker-Ser0</b>	0.70	1.10	0.61	1.34	5.49	0.721	0.90	1.20	0.57	1.34	5.02	0.751	1.80	4.00	0.69	2.96	0.90	0.716
<b>Parker-Gly0</b>	0.70	1.00	0.59	1.34	5.51	0.722	0.90	1.10	0.55	1.35	5.00	0.754	1.70	3.50	0.67	2.95	1.04	0.715
<b>Parker-Arg0</b>	0.50	0.70	0.58	1.14	6.16	0.712	0.70	0.80	0.53	1.23	5.67	0.775	1.50	3.10	0.67	3.00	0.94	0.716
<b>Monera</b>	1.70	3.00	0.64	1.41	5.07	0.651	2.10	3.40	0.62	1.35	4.59	0.605	4.30	8.80	0.67	2.73	1.63	0.599
<b>Monera-Ser0</b>	1.30	1.50	0.54	1.33	5.70	0.658	1.60	1.60	0.50	1.30	5.23	0.652	3.30	4.50	0.58	2.87	2.18	0.604
<b>Monera-Gly0</b>	1.20	1.40	0.54	1.30	5.77	0.660	1.50	1.50	0.50	1.24	5.43	0.653	3.10	4.30	0.58	2.86	2.16	0.608
<b>AVE3</b>	0.70	1.60	0.70	1.31	5.39	0.729	0.80	1.60	0.67	1.25	5.27	0.765	1.80	5.90	0.77	2.62	0.72	0.729
<b>AVE3-Gln0</b>	0.60	0.90	0.60	1.23	5.75	0.728	0.80	1.00	0.56	1.26	5.27	0.773	1.80	3.90	0.68	2.87	0.63	0.722
<b>AVE3-Gly0</b>	0.60	0.90	0.60	1.26	5.67	0.726	0.80	1.00	0.56	1.31	5.20	0.778	1.80	3.90	0.68	2.88	0.53	0.723
<b>AVE3-Arg0</b>	0.50	0.70	0.58	1.13	6.16	0.716	0.70	0.80	0.53	1.23	5.65	0.792	1.60	2.80	0.64	3.03	1.52	0.712

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Scale	<i>S. aureus</i> C623						<i>S. aureus</i> ATCC25923						<i>E. faecalis</i> ATCC29212					
	<i>m</i>	<i>n</i>	<i>fH<sup>a</sup></i>	<i>a<sup>b</sup></i>	<i>b<sup>b</sup></i>	<i>R<sup>2</sup></i>	<i>m</i>	<i>n</i>	<i>fH<sup>a</sup></i>	<i>a<sup>b</sup></i>	<i>b<sup>b</sup></i>	<i>R<sup>2</sup></i>	<i>m</i>	<i>n</i>	<i>fH<sup>a</sup></i>	<i>a<sup>b</sup></i>	<i>b<sup>b</sup></i>	<i>R<sup>2</sup></i>
<b>Kovacs(a)</b>	0.60	0.90	0.60	1.31	4.72	0.912	0.60	0.80	0.57	1.16	5.13	0.901	0.10	0.60	0.86	1.24	5.27	0.827
<b>Kovacs(a)-Glu0</b>	0.50	0.70	0.58	1.16	5.36	0.914	0.50	0.70	0.58	1.12	5.40	0.904	0.10	0.50	0.83	1.17	5.71	0.819
<b>Kovacs(a)-Gln0</b>	0.40	0.60	0.60	1.12	5.55	0.914	0.50	0.60	0.55	1.10	5.58	0.905	0.00	0.50	1.00	1.29	5.95	0.809
<b>Kovacs(a)-Arg0</b>	0.40	0.50	0.56	1.12	5.75	0.901	0.40	0.50	0.56	1.09	5.77	0.901	0.00	0.40	1.00	1.06	5.07	0.794
<b>Kovacs(b)</b>	0.40	1.10	0.73	1.19	5.16	0.911	0.40	1.00	0.71	1.07	5.53	0.902	0.00	0.80	1.00	1.04	4.68	0.821
<b>Kovacs(b)-Ser0</b>	0.40	0.80	0.67	1.24	5.10	0.912	0.40	0.70	0.64	1.09	5.59	0.906	0.00	0.50	1.00	1.02	5.19	0.818
<b>Kovacs(b)-Gln0</b>	0.40	0.70	0.64	1.15	5.48	0.913	0.40	0.70	0.64	1.11	5.51	0.906	0.00	0.50	1.00	1.03	5.13	0.819
<b>Parker</b>	0.90	1.80	0.67	1.33	4.90	0.853	1.00	1.70	0.63	1.27	4.93	0.831	0.30	1.20	0.80	1.42	5.34	0.8196
<b>Parker-Ser0</b>	0.90	1.20	0.57	1.33	4.94	0.862	1.00	1.30	0.57	1.36	4.72	0.837	0.30	0.80	0.73	1.37	5.73	0.816
<b>Parker-Gly0</b>	0.90	1.10	0.55	1.34	4.93	0.864	0.90	1.10	0.55	1.28	4.99	0.840	0.30	0.70	0.70	1.34	5.91	0.816
<b>Parker-Arg0</b>	0.70	0.80	0.53	1.21	5.63	0.862	0.80	0.90	0.53	1.28	5.30	0.845	0.20	0.60	0.75	1.31	5.75	0.804
<b>Monera</b>	2.10	3.40	0.62	1.40	4.40	0.757	2.20	3.50	0.61	1.35	4.37	0.720	1.00	2.20	0.69	1.58	5.46	0.781
<b>Monera-Ser0</b>	1.70	1.70	0.50	1.34	5.03	0.779	1.70	1.70	0.50	1.28	5.10	0.752	0.80	1.20	0.60	1.54	5.72	0.786
<b>Monera-Gly0</b>	1.60	1.60	0.50	1.33	5.09	0.783	1.60	1.60	0.50	1.27	5.16	0.757	0.70	1.00	0.59	1.38	6.16	0.788
<b>AVE3</b>	0.90	1.70	0.65	1.30	4.99	0.877	0.90	1.70	0.65	1.25	5.04	0.857	0.30	1.20	0.80	1.36	5.47	0.825
<b>AVE3-Gln0</b>	0.90	1.10	0.55	1.35	4.88	0.881	0.90	1.10	0.55	1.30	4.93	0.862	0.30	0.70	0.70	1.33	5.88	0.820
<b>AVE3-Gly0</b>	0.80	1.00	0.56	1.29	5.14	0.882	0.90	1.00	0.53	1.25	5.15	0.865	0.30	0.70	0.70	1.35	5.82	0.818
<b>AVE3-Arg0</b>	0.70	0.80	0.53	1.20	5.61	0.879	0.70	0.80	0.53	1.16	5.65	0.865	0.20	0.60	0.75	1.29	5.76	0.807

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Scale	<i>E. faecalis</i> f43559						<i>E. faecium</i> mic80						<i>E. faecium</i> t62764					
	<i>m</i>	<i>n</i>	fH <sup>a</sup>	<i>a</i> <sup>b</sup>	<i>b</i> <sup>b</sup>	R <sup>2</sup>	<i>m</i>	<i>n</i>	fH <sup>a</sup>	<i>a</i> <sup>b</sup>	<i>b</i> <sup>b</sup>	R <sup>2</sup>	<i>m</i>	<i>n</i>	fH <sup>a</sup>	<i>a</i> <sup>b</sup>	<i>b</i> <sup>b</sup>	R <sup>2</sup>
<b>Kovacs(a)</b>	0.00	0.60	1.00	1.60	4.49	0.729	0.30	0.70	0.70	1.18	5.37	0.815	0.30	0.60	0.67	0.96	5.68	0.811
<b>Kovacs(a)-Glu0</b>	0.00	0.60	1.00	1.62	4.37	0.713	0.30	0.70	0.70	1.24	5.18	0.814	0.30	0.60	0.67	1.00	5.53	0.800
<b>Kovacs(a)-Gln0</b>	0.00	0.50	1.00	1.54	4.73	0.689	0.20	0.60	0.75	1.18	5.16	0.811	0.20	0.50	0.71	0.94	5.65	0.782
<b>Kovacs(a)-Arg0</b>	0.00	0.40	1.00	1.44	5.13	0.653	0.20	0.40	0.67	0.99	6.17	0.796	0.20	0.40	0.67	0.88	6.04	0.755
<b>Kovacs(b)</b>	0.00	0.80	1.00	1.43	4.73	0.698	0.20	0.90	0.82	1.07	5.48	0.807	0.20	0.80	0.80	0.89	5.72	0.785
<b>Kovacs(b)-Ser0</b>	0.00	0.50	1.00	1.40	5.24	0.686	0.20	0.70	0.78	1.17	5.23	0.808	0.20	0.60	0.75	0.94	5.61	0.787
<b>Kovacs(b)-Gln0</b>	0.00	0.50	1.00	1.41	5.18	0.686	0.20	0.60	0.75	1.07	5.68	0.807	0.20	0.50	0.71	0.85	6.11	0.788
<b>Parker</b>	0.10	1.50	0.94	2.05	3.26	0.771	0.60	1.50	0.71	1.32	5.13	0.766	0.50	1.10	0.69	0.97	5.87	0.791
<b>Parker-Ser0</b>	0.00	1.00	1.00	1.87	3.14	0.756	0.50	1.00	0.67	1.28	5.32	0.766	0.50	0.80	0.62	0.99	5.88	0.790
<b>Parker-Gly0</b>	0.00	0.90	1.00	1.89	3.24	0.754	0.50	0.90	0.64	1.27	5.38	0.768	0.50	0.70	0.58	0.96	6.01	0.790
<b>Parker-Arg0</b>	0.00	0.70	1.00	1.77	3.80	0.729	0.40	0.70	0.64	1.18	5.77	0.762	0.40	0.60	0.60	0.94	6.08	0.758
<b>Monera</b>	1.70	6.40	0.79	3.70	0.35	0.745	1.40	2.70	0.66	1.38	5.08	0.700	1.20	2.10	0.64	1.04	5.58	0.729
<b>Monera-Ser0</b>	0.80	2.20	0.73	3.26	2.45	0.711	1.10	1.40	0.56	1.32	5.53	0.712	1.00	1.20	0.55	1.06	5.81	0.711
<b>Monera-Gly0</b>	0.60	1.60	0.73	2.85	3.62	0.714	1.00	1.20	0.55	1.20	5.92	0.714	0.90	1.00	0.53	0.93	6.18	0.716
<b>AVE3</b>	0.10	1.50	0.94	1.96	3.41	0.762	0.50	1.40	0.74	1.22	5.36	0.785	0.50	1.20	0.71	0.99	5.70	0.792
<b>AVE3-Gln0</b>	0.00	0.90	1.00	1.85	3.23	0.746	0.50	0.90	0.64	1.27	5.34	0.787	0.50	0.70	0.58	0.96	6.00	0.793
<b>AVE3-Gly0</b>	0.00	0.90	1.00	1.85	3.17	0.740	0.50	0.80	0.62	1.19	5.69	0.786	0.50	0.70	0.58	0.98	5.95	0.786
<b>AVE3-Arg0</b>	0.00	0.70	1.00	1.73	3.82	0.721	0.40	0.70	0.64	1.17	5.75	0.780	0.40	0.60	0.60	0.93	6.08	0.761

**Table S9. Window analysis of CAMP-RPs described in literature.**

Protein (UniProt ID)	reference	length	experimental CAMPs	Local maxima (score) <sup>a</sup>	Highest scoring peptides (score) <sup>a</sup>	Identification strategy/Analyzed peptides
Human thimic stromal lymphopoietin (Q969D9)	[1]	131	91-110 96-115 96-129	90-110 (6.6) 95-116 (6.6)	96-129 (14)*	Overlapping 20mer peptides: 1-20, 4-23, 16-35, 32-51, 52-71, 63-82, 80-99, 91-110, 96-115, 112-131 34mer peptide: 96-129
Human Cathepsin G (P08311)	[2]	235	61-80 117-136 198-223	61-85 (4.7) 116-134 (5.8) 199-228 (8.3)	89-111 (9.5) 207-228 (8.9)	non-overlapping peptides: 1-20, 21-40, 41-60, 61-80, 77-96, 97-116, 117-136, 137-156, 157-176, 177-197, 198-223
Heparin-cofactor 2 (P05546)	[3]	480	101-125  173-200	101-123 (10.9)  173-200 (10.7)	97-123 (12) 94-123 (13) 176-202 (11)	3D-structure-based peptides ( $\alpha$ -helices): 101-125, 150-172, 173-200, 235-252
Fragment C3a of human Complement C3 (P01024)	[4]	77	4-24 19-44 45-71 57-77	4-23 (4.7) 19-45 (6.1) 41-69 (5.9) 56-77 (4.6)	32-54 (8.3) 38-65 (7.2) 48-77 (6.9)	Partially overlapping peptides: 4-24, 19-44, 45-71, 57-77
Human tissue factor pathway inhibitor (P10646)	[5]	276	250-276 252-268 255-276	249-276 (10.8)  256-276 (8)	235-274 (16.7)*	N- and C-termini: 1-25, 250-276, 252-268, 255-276
Human tissue factor pathway inhibitor 2 (P48307)	[6]	213	180-213	179-213 (14.8)	182-213 (16.1)*	C-terminus: 180-213
Human platelet factor 4 (P02776)	[7]	70	58-70	55-68 (7.7)	41-68 (12.2) 45-68 (11.2)	C-terminal $\alpha$ -helix: 58-70
Human mucin-7 (Q8TAX7)	[8]	357	1-51 32-51	31-54 (11.2) 335-351 (9) <b>new</b>	10-49 (12.2) 25-64 (13.3)	N-terminus: 1-51, 3-17, 32-51
Chicken Leukocyte ribonuclease A-2 (Q27J90)	[9]	115	68-76 88-104	66-82 (6.9) 66-89 (7.8) 88-110 (6.6)	66-103 (11.7)*	by sequence comparison to non-antimicrobial chicken RNase A-1: 68-76, 88-104

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Protein (UniProt ID)	reference	length	experimental CAMPs	Local maxima (score) <sup>a</sup>	Highest scoring peptides (score) <sup>a</sup>	Identification strategy/Analyzed peptides
Human laminin subunit $\beta$ -1 (P07942)	[10]	1765	202-218	202-219 (9.8)	202-222 (10.2)	Heparin binding motif: 202-218
Human laminin subunit $\alpha$ -1 (P25391)	[10]	3058	2079-2094 2079-2107 2334-2348 2714-2728	2078-2103 (7.3)  2334-2349 (4.6) 2715-2730 (5.1) 2707-2736 (7.3)	197-217 (9.3) <b>new</b> 2363-2387 (8.7) <b>new</b> 2417-2444 (9.5) <b>new</b>  3004-3030 (10) <b>new</b>	Heparin binding motifs: 2079-2094, 2079-2107, 2334-2348, 2714-2728
Human laminin subunit $\alpha$ -5 (P25391)	[10]	3660	2981-3005  3373-3397 3376-3397 3387-3397		215-244 (10.9) <b>new</b> 2979-3008 (9.3) 3042-3071 (11.2) <b>new</b> 3322-3351 (114) <b>new</b> 3376-3405 (11.8)  3445-3472 (9.3) <b>new</b>	Heparin binding motifs: 2981-3005, 3373-3397, 3376-3397, 3387-3397
Human Protein C inhibitor (P05154)	[10]	387	264-283		266-289 (13) 354-383 (9.6) <b>new</b> 357-386 (9.8) <b>new</b>	Heparin binding motif: 264-283
Human fibronectin (P02751)	[10]	2355	1893-1910		607-624 (8.8) <b>new</b> 982-1009 (8.8) <b>new</b> 1888-1914 (7.0) 1892-1921 (7.0)	Heparin binding motif: 1893-1910
Human vitronectin (P02751)	[10]	459	347-361	340-361 (7.4)	334-361 (10.3)	Heparin binding motif: 347-361

<sup>a</sup> Peptides not included in the experimental set of peptides are followed by the word “**new**” to underline that they can be considered new predictions..

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