Table S1. Ranking of the Groups by the RobustRankAggreg method on Gram-negative and Gram-positive datasets of Dataset 1.

Gram-negative Dataset				**Gram-positive Dataset**			
Group	**Count**	**Score**	**RobustRankAgg (p-value)**	**Group**	**Count**	**Score**	**RobustRankAgg (p-value)**
Physico-chemical	1000	10	2.36E-25	Physico-chemical	1000	10	1.2E-106
Physicochemical composition	839	8.39	3.17E-13	Physicochemical composition	844	8.44	4.8E-37
Quasi-sequence-order	757	7.57	1.1E-09	Quasi-sequence-order	745	7.45	1.7E-25
Amino acid composition	706	7.06	7.15E-09	Amino acid composition	700	7	2.83E-20
Physicochemical distribution	436	4.36	0.000159	Physicochemical transition	546	5.46	3.21E-11
Pseudo-amino acid composition	472	4.72	0.000159	Pseudo-amino acid composition	505	5.05	3.21E-11
Dipeptide composition	470	4.7	0.000159	Physicochemical distribution	396	3.96	1.1E-09
Physicochemical transition	496	4.96	0.000264	Sequence order coupling number	259	2.59	1.21E-06
Sequence order coupling number	205	2.05	1	Dipeptide Composition	369	3.69	2.54E-05
Moran autocorrelation	53	0.53	1	Normalized Moreau–Broto autocorrelation	99	0.99	1
Geary autocorrelation	43	0.43	1	Moran autocorrelation	25	0.25	1
Normalized Moreau–Broto autocorrelation	23	0.23	1	Geary autocorrelation	12	0.12	1