

# Gael Prez-Rodriguez

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

22  
papers

192  
citations

8  
h-index

13  
g-index

24  
ext. papers

243  
ext. citations

5.2  
avg, IF

3  
L-index

#	Paper	IF	Citations
22	From amino acid sequence to bioactivity: The biomedical potential of antitumor peptides. <i>Protein Science</i> , <b>2016</b> , 25, 1084-95	6.3	42
21	Quorum sensing inhibition in <i>Pseudomonas aeruginosa</i> biofilms: new insights through network mining. <i>Biofouling</i> , <b>2017</b> , 33, 128-142	3.3	35
20	Using Twitter to Understand the Human Bowel Disease Community: Exploratory Analysis of Key Topics. <i>Journal of Medical Internet Research</i> , <b>2019</b> , 21, e12610	7.6	21
19	A network perspective on antimicrobial peptide combination therapies: the potential of colistin, polymyxin B and nisin. <i>International Journal of Antimicrobial Agents</i> , <b>2017</b> , 49, 668-676	14.3	13
18	Exploring anti-quorum sensing and anti-virulence based strategies to fight <i>Candida albicans</i> infections: an in silico approach. <i>FEMS Yeast Research</i> , <b>2018</b> , 18,	3.1	8
17	Agent-based model of diffusion of N-acyl homoserine lactones in a multicellular environment of <i>Pseudomonas aeruginosa</i> and <i>Candida albicans</i> . <i>Biofouling</i> , <b>2018</b> , 34, 335-345	3.3	8
16	The Markyt visualisation, prediction and benchmark platform for chemical and gene entity recognition at BioCreative/CHEMDNER challenge. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	8
15	Computational resources and strategies to construct single-molecule metabolic models of microbial cells. <i>Briefings in Bioinformatics</i> , <b>2016</b> , 17, 863-76	13.4	8
14	Enabling systematic, harmonised and large-scale biofilms data computation: the Biofilms Experiment Workbench. <i>Computer Methods and Programs in Biomedicine</i> , <b>2015</b> , 118, 309-21	6.9	6
13	Construction of antimicrobial peptide-drug combination networks from scientific literature based on a semi-automated curation workflow. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	6
12	Single Molecule Simulation of Diffusion and Enzyme Kinetics. <i>Journal of Physical Chemistry B</i> , <b>2016</b> , 120, 3809-20	3.4	6
11	Online visibility of software-related web sites: The case of biomedical text mining tools. <i>Information Processing and Management</i> , <b>2019</b> , 56, 565-583	6.3	6
10	Agent-based spatiotemporal simulation of biomolecular systems within the open source MASON framework. <i>BioMed Research International</i> , <b>2015</b> , 2015, 769471	3	5
9	Reconstruction of the Network of Experimentally Validated AMP-Drug Combinations Against <i>Pseudomonas aeruginosa</i> Infections. <i>Current Bioinformatics</i> , <b>2016</b> , 11, 523-530	4.7	5
8	Next generation community assessment of biomedical entity recognition web servers: metrics, performance, interoperability aspects of BeCalm. <i>Journal of Cheminformatics</i> , <b>2019</b> , 11, 42	8.6	4
7	Mining the sociome for Health Informatics: Analysis of therapeutic lifestyle adherence of diabetic patients in Twitter. <i>Future Generation Computer Systems</i> , <b>2020</b> , 110, 214-232	7.5	3
6	Application of agent-based modelling to assess single-molecule transport across the cell envelope of <i>E. coli</i> . <i>Computers in Biology and Medicine</i> , <b>2019</b> , 107, 218-226	7	2

5	High performance computing for three-dimensional agent-based molecular models. <i>Journal of Molecular Graphics and Modelling</i> , <b>2016</b> , 68, 68-77	2.8	2
4	Collaborative relation annotation and quality analysis in Markyt environment. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2017</b> , 2017,	5	1
3	The Complexity of Promoter Regions Based on a Vector Topological Entropy. <i>Current Bioinformatics</i> , <b>2017</b> , 12,	4.7	1
2	BEW: Bioinformatics Workbench for Analysis of Biofilms Experimental Data. <i>Advances in Intelligent Systems and Computing</i> , <b>2014</b> , 49-56	0.4	1
1	Application of Agent-Based Modelling to Simulate Ribosome Translation. <i>Lecture Notes in Computer Science</i> , <b>2020</b> , 200-211	0.9	