

# Martn Prez-Prez

## List of Publications by Year in Descending Order

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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.

24  
papers

204  
citations

8  
h-index

13  
g-index

26  
ext. papers

257  
ext. citations

5.5  
avg, IF

3.1  
L-index

#	Paper	IF	Citations
24	A deep learning relation extraction approach to support a biomedical semi-automatic curation task: The case of the gluten bibliome. <i>Expert Systems With Applications</i> , <b>2022</b> , 195, 116616	7.8	1
23	A Health-Related Study from Food Online Reviews. The Case of Gluten-Free Foods. <i>Advances in Intelligent Systems and Computing</i> , <b>2021</b> , 12-22	0.4	
22	A framework to extract biomedical knowledge from gluten-related tweets: The case of dietary concerns in digital era. <i>Artificial Intelligence in Medicine</i> , <b>2021</b> , 118, 102131	7.4	1
21	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
20	Application of agent-based modelling to assess single-molecule transport across the cell envelope of E. coli. <i>Computers in Biology and Medicine</i> , <b>2019</b> , 107, 218-226	7	2
19	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
18	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
17	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
16	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
15	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
14	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
13	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
12	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
11	The Complexity of Promoter Regions Based on a Vector Topological Entropy. <i>Current Bioinformatics</i> , <b>2017</b> , 12,	4.7	1
10	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
9	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
8	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

7	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
6	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
5	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
4	Single Molecule Simulation of Diffusion and Enzyme Kinetics. <i>Journal of Physical Chemistry B</i> , <b>2016</b> , 120, 3809-20	3.4	6
3	Marky: a tool supporting annotation consistency in multi-user and iterative document annotation projects. <i>Computer Methods and Programs in Biomedicine</i> , <b>2015</b> , 118, 242-51	6.9	16
2	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
1	Marky: A Lightweight Web Tracking Tool for Document Annotation. <i>Advances in Intelligent Systems and Computing</i> , <b>2014</b> , 269-276	0.4	2