

# Martn Prez-Prez

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/7826950/martin-perez-perez-publications-by-citations.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	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
23	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
22	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
21	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
20	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
19	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
18	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
17	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
16	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
15	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
14	Single Molecule Simulation of Diffusion and Enzyme Kinetics. <i>Journal of Physical Chemistry B</i> , <b>2016</b> , 120, 3809-20	3.4	6
13	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
12	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
11	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
10	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
9	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
8	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

7	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
6	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
5	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
4	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
3	The Complexity of Promoter Regions Based on a Vector Topological Entropy. <i>Current Bioinformatics</i> , <b>2017</b> , 12,	4.7	1
2	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
1	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	