

Gael PÃ©rez-RodrÃ©guez

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

280
citations

1162889

8
h-index

940416

16
g-index

24
all docs

24
docs citations

24
times ranked

516
citing authors

#	ARTICLE	IF	CITATIONS
1	Use Social Media Knowledge for Exploring the Portuguese Wine Industry: Following Talks and Perceptions?. <i>Scientific Programming</i> , 2022, 2022, 1-17.	0.5	1
2	Mining the sociome for Health Informatics: Analysis of therapeutic lifestyle adherence of diabetic patients in Twitter. <i>Future Generation Computer Systems</i> , 2020, 110, 214-232.	4.9	9
3	Application of Agent-Based Modelling to Simulate Ribosome Translation. <i>Lecture Notes in Computer Science</i> , 2020, , 200-211.	1.0	0
4	Next generation community assessment of biomedical entity recognition web servers: metrics, performance, interoperability aspects of BeCalm. <i>Journal of Cheminformatics</i> , 2019, 11, 42.	2.8	4
5	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> , 2019, 107, 218-226.	3.9	3
6	Online visibility of software-related web sites: The case of biomedical text mining tools. <i>Information Processing and Management</i> , 2019, 56, 565-583.	5.4	7
7	Using Twitter to Understand the Human Bowel Disease Community: Exploratory Analysis of Key Topics. <i>Journal of Medical Internet Research</i> , 2019, 21, e12610.	2.1	47
8	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> , 2018, 18, .	1.1	12
9	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> , 2018, 34, 335-345.	0.8	9
10	Quorum sensing inhibition in <i>Pseudomonas aeruginosa</i> biofilms: new insights through network mining. <i>Biofouling</i> , 2017, 33, 128-142.	0.8	52
11	A network perspective on antimicrobial peptide combination therapies: the potential of colistin, polymyxin B and nisin. <i>International Journal of Antimicrobial Agents</i> , 2017, 49, 668-676.	1.1	19
12	Collaborative relation annotation and quality analysis in Markyt environment. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	1
13	The Complexity of Promoter Regions Based on a Vector Topological Entropy. <i>Current Bioinformatics</i> , 2017, 12, .	0.7	1
14	From amino acid sequence to bioactivity: The biomedical potential of antitumor peptides. <i>Protein Science</i> , 2016, 25, 1084-1095.	3.1	55
15	Single Molecule Simulation of Diffusion and Enzyme Kinetics. <i>Journal of Physical Chemistry B</i> , 2016, 120, 3809-3820.	1.2	6
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> , 2016, 2016, baw120.	1.4	10
17	High performance computing for three-dimensional agent-based molecular models. <i>Journal of Molecular Graphics and Modelling</i> , 2016, 68, 68-77.	1.3	2
18	Computational resources and strategies to construct single-molecule metabolic models of microbial cells. <i>Briefings in Bioinformatics</i> , 2016, 17, 863-876.	3.2	11

#	ARTICLE	IF	CITATIONS
19	Construction of antimicrobial peptide-drug combination networks from scientific literature based on a semi-automated curation workflow. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw143.	1.4	10
20	Reconstruction of the Network of Experimentally Validated AMP-Drug Combinations Against Pseudomonas aeruginosa Infections. Current Bioinformatics, 2016, 11, 523-530.	0.7	6
21	Agent-Based Spatiotemporal Simulation of Biomolecular Systems within the Open Source MASON Framework. BioMed Research International, 2015, 2015, 1-12.	0.9	6
22	Enabling systematic, harmonised and large-scale biofilms data computation: The Biofilms Experiment Workbench. Computer Methods and Programs in Biomedicine, 2015, 118, 309-321.	2.6	7
23	BEW: Bioinformatics Workbench for Analysis of Biofilms Experimental Data. Advances in Intelligent Systems and Computing, 2014, , 49-56.	0.5	2