

Anlia Maria Garcia Loureno

List of Publications by Year in Descending Order

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Version: 2024-04-26

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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.

99
papers

2,024
citations

19
h-index

44
g-index

108
ext. papers

2,582
ext. citations

5.7
avg, IF

4.93
L-index

#	Paper	IF	Citations
99	Optimism and pessimism analysis using deep learning on COVID-19 related twitter conversations. <i>Information Processing and Management</i> , 2022 , 59, 102918	6.3	2
98	Computational Approach to the Systematic Prediction of Glycolytic Abilities: Looking Into Human Microbiota. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 2302-2313	3	1
97	A Health-Related Study from Food Online Reviews. The Case of Gluten-Free Foods. <i>Advances in Intelligent Systems and Computing</i> , 2021 , 12-22	0.4	
96	The Activity of Bioinformatics Developers and Users in Stack Overflow. <i>Advances in Intelligent Systems and Computing</i> , 2021 , 23-31	0.4	1
95	HaemoKBS: A knowledge-based system for real-time, continuous categorisation of adverse reactions in blood recipients. <i>Neurocomputing</i> , 2021 , 423, 756-767	5.4	
94	Computational resources and strategies to assess single-molecule dynamics of the translation process in <i>S. cerevisiae</i> . <i>Briefings in Bioinformatics</i> , 2021 , 22, 219-231	13.4	1
93	A framework to extract biomedical knowledge from gluten-related tweets: The case of dietary concerns in digital era. <i>Artificial Intelligence in Medicine</i> , 2021 , 118, 102131	7.4	1
92	Computational Resources and Strategies to Construct Single-Molecule Models of FISH. <i>Methods in Molecular Biology</i> , 2021 , 2246, 317-330	1.4	
91	Revisiting the Metabolic Capabilities of susbp. and subsp. from a Glycoside Hydrolase Perspective. <i>Microorganisms</i> , 2020 , 8,	4.9	3
90	In silico and functional analyses of immunomodulatory peptides encrypted in the human gut metaproteome. <i>Journal of Functional Foods</i> , 2020 , 70, 103969	5.1	2
89	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	7.5	3
88	Application of Agent-Based Modelling to Simulate Ribosome Translation. <i>Lecture Notes in Computer Science</i> , 2020 , 200-211	0.9	
87	The extracellular proteins of <i>Lactobacillus acidophilus</i> DSM 20079T display anti-inflammatory effect in both in piglets, healthy human donors and Crohn's Disease patients. <i>Journal of Functional Foods</i> , 2020 , 64, 103660	5.1	2
86	Understanding the social evolution of the Java community in Stack Overflow: A 10-year study of developer interactions. <i>Future Generation Computer Systems</i> , 2020 , 105, 446-454	7.5	3
85	In silico prediction reveals the existence of potential bioactive neuropeptides produced by the human gut microbiota. <i>Food Research International</i> , 2019 , 119, 221-226	7	6
84	DEWE: A novel tool for executing differential expression RNA-Seq workflows in biomedical research. <i>Computers in Biology and Medicine</i> , 2019 , 107, 197-205	7	6
83	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	7	2

82	Computational prediction of the bioactivity potential of proteomes based on expert knowledge. <i>Journal of Biomedical Informatics</i> , 2019 , 91, 103121	10.2	1
81	Approach for Unveiling the Glycoside Hydrolase Activities in Through a Systematic and Integrative Large-Scale Analysis. <i>Frontiers in Microbiology</i> , 2019 , 10, 517	5.7	3
80	Next generation community assessment of biomedical entity recognition web servers: metrics, performance, interoperability aspects of BeCalm. <i>Journal of Cheminformatics</i> , 2019 , 11, 42	8.6	4
79	Using Twitter to Understand the Human Bowel Disease Community: Exploratory Analysis of Key Topics. <i>Journal of Medical Internet Research</i> , 2019 , 21, e12610	7.6	21
78	Online visibility of software-related web sites: The case of biomedical text mining tools. <i>Information Processing and Management</i> , 2019 , 56, 565-583	6.3	6
77	Resources and tools for the high-throughput, multi-omic study of intestinal microbiota. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1032-1056	13.4	8
76	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,	3.1	8
75	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	3.3	8
74	BlasterJS: A novel interactive JavaScript visualisation component for BLAST alignment results. <i>PLoS ONE</i> , 2018 , 13, e0205286	3.7	8
73	The Evolving Role of Information Technology in Haemovigilance Systems. <i>Journal of Healthcare Engineering</i> , 2018 , 2018, 6183468	3.7	2
72	Quorum sensing inhibition in <i>Pseudomonas aeruginosa</i> biofilms: new insights through network mining. <i>Biofouling</i> , 2017 , 33, 128-142	3.3	35
71	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	14.3	13
70	Information Retrieval and Text Mining Technologies for Chemistry. <i>Chemical Reviews</i> , 2017 , 117, 7673-7761	66.1	124
69	Searching for new strategies against biofilm infections: Colistin-AMP combinations against <i>Pseudomonas aeruginosa</i> and <i>Staphylococcus aureus</i> single- and double-species biofilms. <i>PLoS ONE</i> , 2017 , 12, e0174654	3.7	21
68	Collaborative relation annotation and quality analysis in Markyt environment. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	1
67	MAHMI database: a comprehensive MetaHit-based resource for the study of the mechanism of action of the human microbiota. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	24
66	P4P: a peptidome-based strain-level genome comparison web tool. <i>Nucleic Acids Research</i> , 2017 , 45, W265-W269	65.1	69
65	Probiotics, gut microbiota, and their influence on host health and disease. <i>Molecular Nutrition and Food Research</i> , 2017 , 61, 1600240	5.9	442

64	Critical review on biofilm methods. <i>Critical Reviews in Microbiology</i> , 2017 , 43, 313-351	7.8	454
63	Screening of the Human Gut Metaproteome Identifies Th17-Promoting Peptides Encrypted in Proteins of Commensal Bacteria. <i>Frontiers in Microbiology</i> , 2017 , 8, 1726	5.7	14
62	Polymicrobial Ventilator-Associated Pneumonia: Fighting In Vitro <i>Candida albicans</i> - <i>Pseudomonas aeruginosa</i> Biofilms with Antifungal-Antibacterial Combination Therapy. <i>PLoS ONE</i> , 2017 , 12, e0170433	3.7	25
61	The Complexity of Promoter Regions Based on a Vector Topological Entropy. <i>Current Bioinformatics</i> , 2017 , 12,	4.7	1
60	A peptidome-based phylogeny pipeline reveals differential peptides at the strain level within <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> . <i>Food Microbiology</i> , 2016 , 60, 137-41	6	3
59	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,	5	8
58	High performance computing for three-dimensional agent-based molecular models. <i>Journal of Molecular Graphics and Modelling</i> , 2016 , 68, 68-77	2.8	2
57	Tackling probiotic and gut microbiota functionality through proteomics. <i>Journal of Proteomics</i> , 2016 , 147, 28-39	3.9	33
56	Computational resources and strategies to construct single-molecule metabolic models of microbial cells. <i>Briefings in Bioinformatics</i> , 2016 , 17, 863-76	13.4	8
55	Improving Phylogeny Reconstruction at the Strain Level Using Peptidome Datasets. <i>PLoS Computational Biology</i> , 2016 , 12, e1005271	5	3
54	Reconstruction of the Network of Experimentally Validated AMP-Drug Combinations Against <i>Pseudomonas aeruginosa</i> Infections. <i>Current Bioinformatics</i> , 2016 , 11, 523-530	4.7	5
53	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> , 2016 , 2016,	5	6
52	From amino acid sequence to bioactivity: The biomedical potential of antitumor peptides. <i>Protein Science</i> , 2016 , 25, 1084-95	6.3	42
51	Single Molecule Simulation of Diffusion and Enzyme Kinetics. <i>Journal of Physical Chemistry B</i> , 2016 , 120, 3809-20	3.4	6
50	BIOMedical Search Engine Framework: Lightweight and customized implementation of domain-specific biomedical search engines. <i>Computer Methods and Programs in Biomedicine</i> , 2016 , 131, 63-77	6.9	2
49	FISHji: New ImageJ macros for the quantification of fluorescence in epifluorescence images. <i>Biochemical Engineering Journal</i> , 2016 , 112, 61-69	4.2	10
48	Heteroresistance to colistin in <i>Klebsiella pneumoniae</i> is triggered by small colony variants sub-populations within biofilms. <i>Pathogens and Disease</i> , 2016 , 74,	4.2	18
47	MorphoCol: An ontology-based knowledgebase for the characterisation of clinically significant bacterial colony morphologies. <i>Journal of Biomedical Informatics</i> , 2015 , 55, 55-63	10.2	12

46	Enabling systematic, harmonised and large-scale biofilms data computation: the Biofilms Experiment Workbench. <i>Computer Methods and Programs in Biomedicine</i> , 2015 , 118, 309-21	6.9	6
45	Marky: a tool supporting annotation consistency in multi-user and iterative document annotation projects. <i>Computer Methods and Programs in Biomedicine</i> , 2015 , 118, 242-51	6.9	16
44	Pathogenicity phenomena in three model systems: from network mining to emerging system-level properties. <i>Briefings in Bioinformatics</i> , 2015 , 16, 169-82	13.4	0
43	Extraction of pharmacokinetic evidence of drug-drug interactions from the literature. <i>PLoS ONE</i> , 2015 , 10, e0122199	3.7	20
42	Agent-based spatiotemporal simulation of biomolecular systems within the open source MASON framework. <i>BioMed Research International</i> , 2015 , 2015, 769471	3	5
41	Data Quality in Biofilm High-Throughput Routine Analysis: Intralaboratory Protocol Adaptation and Experiment Reproducibility. <i>Journal of AOAC INTERNATIONAL</i> , 2015 , 98, 1721-7	1.7	2
40	A Novel Search Engine Supporting Specific Drug Queries and Literature Management. <i>Advances in Intelligent Systems and Computing</i> , 2015 , 99-106	0.4	
39	Minimum information about a biofilm experiment (MIABiE): standards for reporting experiments and data on sessile microbial communities living at interfaces. <i>Pathogens and Disease</i> , 2014 , 70, 250-6	4.2	31
38	Web scraping technologies in an API world. <i>Briefings in Bioinformatics</i> , 2014 , 15, 788-97	13.4	41
37	A harmonised vocabulary for communicating and interchanging Biofilms experimental results. <i>Journal of Integrative Bioinformatics</i> , 2014 , 11, 32-47	3.8	2
36	Bringing Named Entity Recognition on Drupal Content Management System. <i>Advances in Intelligent Systems and Computing</i> , 2014 , 261-268	0.4	1
35	Networking the Way towards Antimicrobial Combination Therapies. <i>Advances in Intelligent Systems and Computing</i> , 2014 , 201-206	0.4	1
34	Marky: A Lightweight Web Tracking Tool for Document Annotation. <i>Advances in Intelligent Systems and Computing</i> , 2014 , 269-276	0.4	2
33	BEW: Bioinformatics Workbench for Analysis of Biofilms Experimental Data. <i>Advances in Intelligent Systems and Computing</i> , 2014 , 49-56	0.4	1
32	Designing an Ontology Tool for the Unification of Biofilms Data. <i>Advances in Intelligent Systems and Computing</i> , 2014 , 41-48	0.4	
31	An harmonised vocabulary for communicating and interchanging biofilms experimental results. <i>Journal of Integrative Bioinformatics</i> , 2014 , 11, 249	3.8	
30	A new approach to bacterial colony morphotyping by matrix-assisted laser desorption ionization time of flight-based mass spectrometry. <i>Talanta</i> , 2013 , 116, 100-7	6.2	3
29	Evaluating Web Site Structure Based on Navigation Profiles and Site Topology. <i>Advances in Intelligent Systems and Computing</i> , 2013 , 305-311	0.4	

28	Correction: A linear classifier based on entity recognition tools and a statistical approach to method extraction in the protein-protein interaction literature. <i>BMC Bioinformatics</i> , 2012 , 13, 180	3.6	78
27	New trends in peptide-based anti-biofilm strategies: a review of recent achievements and bioinformatic approaches. <i>Biofouling</i> , 2012 , 28, 1033-61	3.3	101
26	Text mining for the biocuration workflow. <i>Database: the Journal of Biological Databases and Curation</i> , 2012 , 2012, bas020	5	108
25	Computational approaches to standard-compliant biofilm data for reliable analysis and integration. <i>Journal of Integrative Bioinformatics</i> , 2012 , 9, 57-68	3.8	3
24	A Rational Framework for Production Decision Making in Blood Establishments. <i>Journal of Integrative Bioinformatics</i> , 2012 , 9, 69-79	3.8	2
23	BioOmics: a Web platform for the systematic and standardized collection of high-throughput biofilm data. <i>PLoS ONE</i> , 2012 , 7, e39960	3.7	24
22	MorphoCol: A Powerful Tool for the Clinical Profiling of Pathogenic Bacteria. <i>Advances in Intelligent and Soft Computing</i> , 2012 , 181-188		1
21	SAD_BaSe: A Blood Bank Data Analysis Software. <i>Advances in Intelligent and Soft Computing</i> , 2012 , 165-171		
20	A Systematic Approach to the Interrogation and Sharing of Standardised Biofilm Signatures. <i>Advances in Intelligent and Soft Computing</i> , 2012 , 113-120		
19	Computational approaches to standard-compliant biofilm data for reliable analysis and integration. <i>Journal of Integrative Bioinformatics</i> , 2012 , 9, 203	3.8	1
18	A rational framework for production decision making in blood establishments. <i>Journal of Integrative Bioinformatics</i> , 2012 , 9, 204	3.8	1
17	A Study of the Short and Long-term Regulation of E. coli Metabolic Pathways. <i>Journal of Integrative Bioinformatics</i> , 2011 , 8, 195-209	3.8	7
16	Stringent response of Escherichia coli: revisiting the bibliome using literature mining. <i>Microbial Informatics and Experimentation</i> , 2011 , 1, 14		9
15	Semantic annotation of biological concepts interplaying microbial cellular responses. <i>BMC Bioinformatics</i> , 2011 , 12, 460	3.6	5
14	A linear classifier based on entity recognition tools and a statistical approach to method extraction in the protein-protein interaction literature. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 8, S12	3.6	7
13	Challenges in integrating Escherichia coli molecular biology data. <i>Briefings in Bioinformatics</i> , 2011 , 12, 91-103	13.4	4
12	Interpreting the Regulatory Interplay in E. coli Metabolic Pathways. <i>Advances in Intelligent and Soft Computing</i> , 2011 , 303-312		
11	A study of the short and long-term regulation of E. coli metabolic pathways. <i>Journal of Integrative Bioinformatics</i> , 2011 , 8, 183	3.8	1

10	BioDR: Semantic indexing networks for biomedical document retrieval. <i>Expert Systems With Applications</i> , 2010 , 37, 3444-3453	7.8	9
9	@Note: a workbench for biomedical text mining. <i>Journal of Biomedical Informatics</i> , 2009 , 42, 710-20	10.2	28
8	Data Integration Issues in the Reconstruction of the Genome-Scale Metabolic Model of <i>Zymomonas Mobilis</i> . <i>Advances in Soft Computing</i> , 2009 , 92-101		1
7	Biomedical Text Mining Applied to Document Retrieval and Semantic Indexing. <i>Lecture Notes in Computer Science</i> , 2009 , 954-963	0.9	
6	Applying Clickstream Data Mining to Real-Time Web Crawler Detection and Containment Using ClickTips Platform. <i>Studies in Classification, Data Analysis, and Knowledge Organization</i> , 2007 , 351-358	0.2	2
5	Application of classification-tree models to characterize the mycobiota of grapes on the basis of origin. <i>Revista Iberoamericana De Micologia</i> , 2006 , 23, 171-5	1.6	1
4	Influence of the region of origin on the mycobiota of grapes with emphasis on <i>Aspergillus</i> and <i>Penicillium</i> species. <i>Mycological Research</i> , 2006 , 110, 971-8		55
3	Catching web crawlers in the act 2006 ,		16
2	Agent-based knowledge extraction services inside enterprise data warehousing systems environments		2
1	Lessons Learned: Recommendations for Establishing Critical Periodic Scientific Benchmarking		12