

# Anlia Maria Garcia Loureno

## List of Publications by Citations

**Source:**

<https://exaly.com/author-pdf/1629647/analia-maria-garcia-loureno-publications-by-citations.pdf>

**Version:** 2024-04-26

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.

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	Critical review on biofilm methods. <i>Critical Reviews in Microbiology</i> , <b>2017</b> , 43, 313-351	7.8	454
98	Probiotics, gut microbiota, and their influence on host health and disease. <i>Molecular Nutrition and Food Research</i> , <b>2017</b> , 61, 1600240	5.9	442
97	Information Retrieval and Text Mining Technologies for Chemistry. <i>Chemical Reviews</i> , <b>2017</b> , 117, 7673-7761	6.1	124
96	Text mining for the biocuration workflow. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2012</b> , 2012, bas020	5	108
95	New trends in peptide-based anti-biofilm strategies: a review of recent achievements and bioinformatic approaches. <i>Biofouling</i> , <b>2012</b> , 28, 1033-61	3.3	101
94	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> , <b>2012</b> , 13, 180	3.6	78
93	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> , <b>2006</b> , 110, 971-8		55
92	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
91	Web scraping technologies in an API world. <i>Briefings in Bioinformatics</i> , <b>2014</b> , 15, 788-97	13.4	41
90	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
89	Tackling probiotic and gut microbiota functionality through proteomics. <i>Journal of Proteomics</i> , <b>2016</b> , 147, 28-39	3.9	33
88	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> , <b>2014</b> , 70, 250-6	4.2	31
87	@Note: a workbench for biomedical text mining. <i>Journal of Biomedical Informatics</i> , <b>2009</b> , 42, 710-20	10.2	28
86	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> , <b>2017</b> , 12, e0170433	3.7	25
85	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> , <b>2017</b> , 2017,	5	24
84	BioOmics: a Web platform for the systematic and standardized collection of high-throughput biofilm data. <i>PLoS ONE</i> , <b>2012</b> , 7, e39960	3.7	24
83	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> , <b>2017</b> , 12, e0174654	3.7	21

82	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
81	Extraction of pharmacokinetic evidence of drug-drug interactions from the literature. <i>PLoS ONE</i> , <b>2015</b> , 10, e0122199	3.7	20
80	Heteroresistance to colistin in <i>Klebsiella pneumoniae</i> is triggered by small colony variants sub-populations within biofilms. <i>Pathogens and Disease</i> , <b>2016</b> , 74,	4.2	18
79	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
78	Catching web crawlers in the act <b>2006</b> ,		16
77	Screening of the Human Gut Metaproteome Identifies Th17-Promoting Peptides Encrypted in Proteins of Commensal Bacteria. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 1726	5.7	14
76	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
75	MorphoCol: An ontology-based knowledgebase for the characterisation of clinically significant bacterial colony morphologies. <i>Journal of Biomedical Informatics</i> , <b>2015</b> , 55, 55-63	10.2	12
74	Lessons Learned: Recommendations for Establishing Critical Periodic Scientific Benchmarking		12
73	FISHji: New ImageJ macros for the quantification of fluorescence in epifluorescence images. <i>Biochemical Engineering Journal</i> , <b>2016</b> , 112, 61-69	4.2	10
72	Stringent response of <i>Escherichia coli</i> : revisiting the bibliome using literature mining. <i>Microbial Informatics and Experimentation</i> , <b>2011</b> , 1, 14		9
71	BioDR: Semantic indexing networks for biomedical document retrieval. <i>Expert Systems With Applications</i> , <b>2010</b> , 37, 3444-3453	7.8	9
70	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
69	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
68	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
67	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
66	Resources and tools for the high-throughput, multi-omic study of intestinal microbiota. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 1032-1056	13.4	8
65	BlasterJS: A novel interactive JavaScript visualisation component for BLAST alignment results. <i>PLoS ONE</i> , <b>2018</b> , 13, e0205286	3.7	8

64	A Study of the Short and Long-term Regulation of E. coli Metabolic Pathways. <i>Journal of Integrative Bioinformatics</i> , <b>2011</b> , 8, 195-209	3.8	7
63	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> , <b>2011</b> , 12 Suppl 8, S12	3.6	7
62	In silico prediction reveals the existence of potential bioactive neuropeptides produced by the human gut microbiota. <i>Food Research International</i> , <b>2019</b> , 119, 221-226	7	6
61	DEWE: A novel tool for executing differential expression RNA-Seq workflows in biomedical research. <i>Computers in Biology and Medicine</i> , <b>2019</b> , 107, 197-205	7	6
60	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
59	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
58	Single Molecule Simulation of Diffusion and Enzyme Kinetics. <i>Journal of Physical Chemistry B</i> , <b>2016</b> , 120, 3809-20	3.4	6
57	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
56	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
55	Semantic annotation of biological concepts interplaying microbial cellular responses. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 460	3.6	5
54	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
53	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
52	Challenges in integrating Escherichia coli molecular biology data. <i>Briefings in Bioinformatics</i> , <b>2011</b> , 12, 91-103	13.4	4
51	Revisiting the Metabolic Capabilities of subsp. and subsp. from a Glycoside Hydrolase Perspective. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	3
50	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
49	A peptidome-based phylogeny pipeline reveals differential peptides at the strain level within <i>Bifidobacterium animalis</i> subsp. lactis. <i>Food Microbiology</i> , <b>2016</b> , 60, 137-41	6	3
48	Approach for Unveiling the Glycoside Hydrolase Activities in Through a Systematic and Integrative Large-Scale Analysis. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 517	5.7	3
47	A new approach to bacterial colony morphotyping by matrix-assisted laser desorption ionization time of flight-based mass spectrometry. <i>Talanta</i> , <b>2013</b> , 116, 100-7	6.2	3

46	Computational approaches to standard-compliant biofilm data for reliable analysis and integration. <i>Journal of Integrative Bioinformatics</i> , <b>2012</b> , 9, 57-68	3.8	3
45	Improving Phylogeny Reconstruction at the Strain Level Using Peptidome Datasets. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1005271	5	3
44	Understanding the social evolution of the Java community in Stack Overflow: A 10-year study of developer interactions. <i>Future Generation Computer Systems</i> , <b>2020</b> , 105, 446-454	7.5	3
43	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
42	In silico and functional analyses of immunomodulatory peptides encrypted in the human gut metaproteome. <i>Journal of Functional Foods</i> , <b>2020</b> , 70, 103969	5.1	2
41	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
40	A harmonised vocabulary for communicating and interchanging Biofilms experimental results. <i>Journal of Integrative Bioinformatics</i> , <b>2014</b> , 11, 32-47	3.8	2
39	Data Quality in Biofilm High-Throughput Routine Analysis: Intralaboratory Protocol Adaptation and Experiment Reproducibility. <i>Journal of AOAC INTERNATIONAL</i> , <b>2015</b> , 98, 1721-7	1.7	2
38	A Rational Framework for Production Decision Making in Blood Establishments. <i>Journal of Integrative Bioinformatics</i> , <b>2012</b> , 9, 69-79	3.8	2
37	Agent-based knowledge extraction services inside enterprise data warehousing systems environments		2
36	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> , <b>2007</b> , 351-358	0.2	2
35	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
34	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> , <b>2020</b> , 64, 103660	5.1	2
33	BIOMedical Search Engine Framework: Lightweight and customized implementation of domain-specific biomedical search engines. <i>Computer Methods and Programs in Biomedicine</i> , <b>2016</b> , 131, 63-77	6.9	2
32	The Evolving Role of Information Technology in Haemovigilance Systems. <i>Journal of Healthcare Engineering</i> , <b>2018</b> , 2018, 6183468	3.7	2
31	Optimism and pessimism analysis using deep learning on COVID-19 related twitter conversations. <i>Information Processing and Management</i> , <b>2022</b> , 59, 102918	6.3	2
30	Computational prediction of the bioactivity potential of proteomes based on expert knowledge. <i>Journal of Biomedical Informatics</i> , <b>2019</b> , 91, 103121	10.2	1
29	Computational Approach to the Systematic Prediction of Glycolytic Abilities: Looking Into Human Microbiota. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2021</b> , 18, 2302-2313	3	1

28	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
27	Bringing Named Entity Recognition on Drupal Content Management System. <i>Advances in Intelligent Systems and Computing</i> , <b>2014</b> , 261-268	0.4	1
26	Application of classification-tree models to characterize the mycobiota of grapes on the basis of origin. <i>Revista Iberoamericana De Micologia</i> , <b>2006</b> , 23, 171-5	1.6	1
25	The Activity of Bioinformatics Developers and Users in Stack Overflow. <i>Advances in Intelligent Systems and Computing</i> , <b>2021</b> , 23-31	0.4	1
24	The Complexity of Promoter Regions Based on a Vector Topological Entropy. <i>Current Bioinformatics</i> , <b>2017</b> , 12,	4.7	1
23	Networking the Way towards Antimicrobial Combination Therapies. <i>Advances in Intelligent Systems and Computing</i> , <b>2014</b> , 201-206	0.4	1
22	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
21	Data Integration Issues in the Reconstruction of the Genome-Scale Metabolic Model of <i>Zymomonas Mobilis</i> . <i>Advances in Soft Computing</i> , <b>2009</b> , 92-101		1
20	MorphoCol: A Powerful Tool for the Clinical Profiling of Pathogenic Bacteria. <i>Advances in Intelligent and Soft Computing</i> , <b>2012</b> , 181-188		1
19	Computational resources and strategies to assess single-molecule dynamics of the translation process in <i>S. cerevisiae</i> . <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22, 219-231	13.4	1
18	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
17	A study of the short and long-term regulation of <i>E. coli</i> metabolic pathways. <i>Journal of Integrative Bioinformatics</i> , <b>2011</b> , 8, 183	3.8	1
16	Computational approaches to standard-compliant biofilm data for reliable analysis and integration. <i>Journal of Integrative Bioinformatics</i> , <b>2012</b> , 9, 203	3.8	1
15	A rational framework for production decision making in blood establishments. <i>Journal of Integrative Bioinformatics</i> , <b>2012</b> , 9, 204	3.8	1
14	Pathogenicity phenomena in three model systems: from network mining to emerging system-level properties. <i>Briefings in Bioinformatics</i> , <b>2015</b> , 16, 169-82	13.4	0
13	P4P: a peptidome-based strain-level genome comparison web tool. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, W265-W269		
12	Application of Agent-Based Modelling to Simulate Ribosome Translation. <i>Lecture Notes in Computer Science</i> , <b>2020</b> , 200-211	0.9	
11	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	

- 10 A Novel Search Engine Supporting Specific Drug Queries and Literature Management. *Advances in Intelligent Systems and Computing*, **2015**, 99-106 0.4
- 9 Biomedical Text Mining Applied to Document Retrieval and Semantic Indexing. *Lecture Notes in Computer Science*, **2009**, 954-963 0.9
- 8 Interpreting the Regulatory Interplay in E. coli Metabolic Pathways. *Advances in Intelligent and Soft Computing*, **2011**, 303-312
- 7 SAD\_BaSe: A Blood Bank Data Analysis Software. *Advances in Intelligent and Soft Computing*, **2012**, 165-171
- 6 A Systematic Approach to the Interrogation and Sharing of Standardised Biofilm Signatures. *Advances in Intelligent and Soft Computing*, **2012**, 113-120
- 5 Evaluating Web Site Structure Based on Navigation Profiles and Site Topology. *Advances in Intelligent Systems and Computing*, **2013**, 305-311 0.4
- 4 Designing an Ontology Tool for the Unification of Biofilms Data. *Advances in Intelligent Systems and Computing*, **2014**, 41-48 0.4
- 3 HaemoKBS: A knowledge-based system for real-time, continuous categorisation of adverse reactions in blood recipients. *Neurocomputing*, **2021**, 423, 756-767 5.4
- 2 Computational Resources and Strategies to Construct Single-Molecule Models of FISH. *Methods in Molecular Biology*, **2021**, 2246, 317-330 1.4
- 1 An harmonised vocabulary for communicating and interchanging biofilms experimental results. *Journal of Integrative Bioinformatics*, **2014**, 11, 249 3.8