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List of Publications by Year in descending order

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Version: 2024-02-01

101
papers

2,923
citations

361296

20
h-index

182361

51
g-index

109
all docs

109
docs citations

109
times ranked

4999
citing authors

#	ARTICLE	IF	CITATIONS
1	Boosting biomedical document classification through the use of domain entity recognizers and semantic ontologies for document representation: The case of gluten bibliome. <i>Neurocomputing</i> , 2022, 484, 223-237.	3.5	2
2	Optimism and pessimism analysis using deep learning on COVID-19 related twitter conversations. <i>Information Processing and Management</i> , 2022, 59, 102918.	5.4	20
3	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
4	HaemoKBS: A knowledge-based system for real-time, continuous categorisation of adverse reactions in blood recipients. <i>Neurocomputing</i> , 2021, 423, 756-767.	3.5	1
5	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.	3.2	3
6	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.	3.8	5
7	Computational Resources and Strategies to Construct Single-Molecule Models of FISH. <i>Methods in Molecular Biology</i> , 2021, 2246, 317-330.	0.4	0
8	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.	0.5	0
9	The Activity of Bioinformatics Developers and Users in Stack Overflow. <i>Advances in Intelligent Systems and Computing</i> , 2021, , 23-31.	0.5	2
10	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.	1.6	6
11	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.	4.9	9
12	Revisiting the Metabolic Capabilities of <i>Bifidobacterium longum</i> subsp. <i>longum</i> and <i>Bifidobacterium longum</i> subsp. <i>infantis</i> from a Glycoside Hydrolase Perspective. <i>Microorganisms</i> , 2020, 8, 723.	1.6	11
13	Computational approach to the systematic prediction of glycolytic abilities: looking into human microbiota. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 18, 1-1.	1.9	3
14	In silico and functional analyses of immunomodulatory peptides encrypted in the human gut metaproteome. <i>Journal of Functional Foods</i> , 2020, 70, 103969.	1.6	3
15	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
16	Application of Agent-Based Modelling to Simulate Ribosome Translation. <i>Lecture Notes in Computer Science</i> , 2020, , 200-211.	1.0	0
17	In silico Approach for Unveiling the Glycoside Hydrolase Activities in <i>Faecalibacterium prausnitzii</i> Through a Systematic and Integrative Large-Scale Analysis. <i>Frontiers in Microbiology</i> , 2019, 10, 517.	1.5	8
18	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

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19	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.	2.9	8
20	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.	3.9	9
21	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
22	Computational prediction of the bioactivity potential of proteomes based on expert knowledge. <i>Journal of Biomedical Informatics</i> , 2019, 91, 103121.	2.5	2
23	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
24	Resources and tools for the high-throughput, multi-omic study of intestinal microbiota. <i>Briefings in Bioinformatics</i> , 2019, 20, 1032-1056.	3.2	10
25	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
26	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
27	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
28	BlasterJS: A novel interactive JavaScript visualisation component for BLAST alignment results. <i>PLoS ONE</i> , 2018, 13, e0205286.	1.1	21
29	The Evolving Role of Information Technology in Haemovigilance Systems. <i>Journal of Healthcare Engineering</i> , 2018, 2018, 1-8.	1.1	3
30	Quorum sensing inhibition in <i>Pseudomonas aeruginosa</i> biofilms: new insights through network mining. <i>Biofouling</i> , 2017, 33, 128-142.	0.8	52
31	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
32	Information Retrieval and Text Mining Technologies for Chemistry. <i>Chemical Reviews</i> , 2017, 117, 7673-7761.	23.0	195
33	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, baw157.	1.4	29
34	P4P: a peptidome-based strain-level genome comparison web tool. <i>Nucleic Acids Research</i> , 2017, 45, W265-W269.	6.5	1
35	Probiotics, gut microbiota, and their influence on host health and disease. <i>Molecular Nutrition and Food Research</i> , 2017, 61, 1600240.	1.5	678
36	Critical review on biofilm methods. <i>Critical Reviews in Microbiology</i> , 2017, 43, 313-351.	2.7	693

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37	In Silico Screening of the Human Gut Metaproteome Identifies Th17-Promoting Peptides Encrypted in Proteins of Commensal Bacteria. <i>Frontiers in Microbiology</i> , 2017, 8, 1726.	1.5	20
38	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.	1.1	39
39	Collaborative relation annotation and quality analysis in Markyt environment. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	1
40	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.	1.1	36
41	The Complexity of Promoter Regions Based on a Vector Topological Entropy. <i>Current Bioinformatics</i> , 2017, 12, .	0.7	1
42	From amino acid sequence to bioactivity: The biomedical potential of antitumor peptides. <i>Protein Science</i> , 2016, 25, 1084-1095.	3.1	55
43	Single Molecule Simulation of Diffusion and Enzyme Kinetics. <i>Journal of Physical Chemistry B</i> , 2016, 120, 3809-3820.	1.2	6
44	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.	2.6	5
45	FISHji: New ImageJ macros for the quantification of fluorescence in epifluorescence images. <i>Biochemical Engineering Journal</i> , 2016, 112, 61-69.	1.8	16
46	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, ftw036.	0.8	28
47	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, 137-141.	2.1	4
48	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
49	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
50	Tackling probiotic and gut microbiota functionality through proteomics. <i>Journal of Proteomics</i> , 2016, 147, 28-39.	1.2	40
51	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
52	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, baw143.	1.4	10
53	Improving Phylogeny Reconstruction at the Strain Level Using Peptidome Datasets. <i>PLoS Computational Biology</i> , 2016, 12, e1005271.	1.5	4
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.	0.7	6

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55	Extraction of Pharmacokinetic Evidence of Drug-Drug Interactions from the Literature. PLoS ONE, 2015, 10, e0122199.	1.1	32
56	Agent-Based Spatiotemporal Simulation of Biomolecular Systems within the Open Source MASON Framework. BioMed Research International, 2015, 2015, 1-12.	0.9	6
57	Data Quality in Biofilm High-Throughput Routine Analysis: Intralaboratory Protocol Adaptation and Experiment Reproducibility. Journal of AOAC INTERNATIONAL, 2015, 98, 1721-1727.	0.7	4
58	MorphoCol: An ontology-based knowledgebase for the characterisation of clinically significant bacterial colony morphologies. Journal of Biomedical Informatics, 2015, 55, 55-63.	2.5	17
59	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
60	Marky: A tool supporting annotation consistency in multi-user and iterative document annotation projects. Computer Methods and Programs in Biomedicine, 2015, 118, 242-251.	2.6	21
61	Pathogenicity phenomena in three model systems: from network mining to emerging system-level properties. Briefings in Bioinformatics, 2015, 16, 169-182.	3.2	1
62	A Novel Search Engine Supporting Specific Drug Queries and Literature Management. Advances in Intelligent Systems and Computing, 2015, , 99-106.	0.5	0
63	Bringing Named Entity Recognition on Drupal Content Management System. Advances in Intelligent Systems and Computing, 2014, , 261-268.	0.5	2
64	Minimum information about a biofilm experiment (MIABiE): standards for reporting experiments and data on sessile microbial communities living at interfaces. Pathogens and Disease, 2014, 70, 250-256.	0.8	43
65	Web scraping technologies in an API world. Briefings in Bioinformatics, 2014, 15, 788-797.	3.2	84
66	A harmonised vocabulary for communicating and interchanging Biofilms experimental results. Journal of Integrative Bioinformatics, 2014, 11, 32-47.	1.0	2
67	Marky: A Lightweight Web Tracking Tool for Document Annotation. Advances in Intelligent Systems and Computing, 2014, , 269-276.	0.5	2
68	BEW: Bioinformatics Workbench for Analysis of Biofilms Experimental Data. Advances in Intelligent Systems and Computing, 2014, , 49-56.	0.5	2
69	Designing an Ontology Tool for the Unification of Biofilms Data. Advances in Intelligent Systems and Computing, 2014, , 41-48.	0.5	0
70	An harmonised vocabulary for communicating and interchanging biofilms experimental results. Journal of Integrative Bioinformatics, 2014, 11, 249.	1.0	0
71	A new approach to bacterial colony morphotyping by matrix-assisted laser desorption ionization time of flight-based mass spectrometry. Talanta, 2013, 116, 100-107.	2.9	3
72	Evaluating Web Site Structure Based on Navigation Profiles and Site Topology. Advances in Intelligent Systems and Computing, 2013, , 305-311.	0.5	0

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73	Text mining for the biocuration workflow. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas020-bas020.	1.4	132
74	Computational approaches to standard-compliant biofilm data for reliable analysis and integration. Journal of Integrative Bioinformatics, 2012, 9, 57-68.	1.0	3
75	A Rational Framework for Production Decision Making in Blood Establishments. Journal of Integrative Bioinformatics, 2012, 9, 69-79.	1.0	2
76	New trends in peptide-based anti-biofilm strategies: a review of recent achievements and bioinformatic approaches. Biofouling, 2012, 28, 1033-1061.	0.8	128
77	MorphoCol: A Powerful Tool for the Clinical Profiling of Pathogenic Bacteria. Advances in Intelligent and Soft Computing, 2012, , 181-188.	0.2	2
78	BiofOmics: A Web Platform for the Systematic and Standardized Collection of High-Throughput Biofilm Data. PLoS ONE, 2012, 7, e39960.	1.1	35
79	A Systematic Approach to the Interrogation and Sharing of Standardised Biofilm Signatures. Advances in Intelligent and Soft Computing, 2012, , 113-120.	0.2	0
80	Computational approaches to standard-compliant biofilm data for reliable analysis and integration. Journal of Integrative Bioinformatics, 2012, 9, 203.	1.0	2
81	A rational framework for production decision making in blood establishments. Journal of Integrative Bioinformatics, 2012, 9, 204.	1.0	1
82	A Study of the Short and Long-term Regulation of E. coli Metabolic Pathways. Journal of Integrative Bioinformatics, 2011, 8, 195-209.	1.0	7
83	Stringent response of Escherichia coli: revisiting the bibliome using literature mining. Microbial Informatics and Experimentation, 2011, 1, 14.	7.6	9
84	Semantic annotation of biological concepts interplaying microbial cellular responses. BMC Bioinformatics, 2011, 12, 460.	1.2	5
85	A linear classifier based on entity recognition tools and a statistical approach to method extraction in the protein-protein interaction literature. BMC Bioinformatics, 2011, 12, S12.	1.2	10
86	Challenges in integrating Escherichia coli molecular biology data. Briefings in Bioinformatics, 2011, 12, 91-103.	3.2	4
87	Interpreting the Regulatory Interplay in E. coli Metabolic Pathways. Advances in Intelligent and Soft Computing, 2011, , 303-312.	0.2	0
88	A study of the short and long-term regulation of E. coli metabolic pathways. Journal of Integrative Bioinformatics, 2011, 8, 183.	1.0	2
89	BioDR: Semantic indexing networks for biomedical document retrieval. Expert Systems With Applications, 2010, 37, 3444-3453.	4.4	14
90	Bringing Text Miners and Biologists Closer Together. Nature Precedings, 2009, , .	0.1	0

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91	@Note: A workbench for Biomedical Text Mining. Journal of Biomedical Informatics, 2009, 42, 710-720.	2.5	34
92	Data Integration Issues in the Reconstruction of the Genome-Scale Metabolic Model of Zymomonas Mobillis. Advances in Soft Computing, 2009, , 92-101.	0.4	2
93	Biomedical Text Mining Applied to Document Retrieval and Semantic Indexing. Lecture Notes in Computer Science, 2009, , 954-963.	1.0	1
94	A framework for the integrated analysis of metabolic and regulatory networks. , 2008, , .		0
95	A framework for the development of Biomedical Text Mining software tools. , 2008, , .		1
96	Applying Clickstream Data Mining to Real-Time Web Crawler Detection and Containment Using ClickTips Platform. Studies in Classification, Data Analysis, and Knowledge Organization, 2007, , 351-358.	0.1	2
97	Catching web crawlers in the act. , 2006, , .		21
98	Application of classification-tree models to characterize the mycobiota of grapes on the basis of origin. Revista Iberoamericana De Micologia, 2006, 23, 171-175.	0.4	1
99	Influence of the region of origin on the mycobiota of grapes with emphasis on Aspergillus and Penicillium species. Mycological Research, 2006, 110, 971-978.	2.5	70
100	Agent-based knowledge extraction services inside enterprise data warehousing systems environments. , 0, , .		4
101	Mortality risk classification for decision support in neonatal critical care. , 0, , .		0