

Miguel Reboiro-Jato

List of Publications by Citations

Source: <https://exaly.com/author-pdf/1796411/miguel-reboiro-jato-publications-by-citations.pdf>

Version: 2024-04-29

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.

81

papers

980

citations

16

h-index

28

g-index

90

ext. papers

1,231

ext. citations

4.4

avg, IF

4.14

L-index

#	Paper	IF	Citations
81	ALTER: program-oriented conversion of DNA and protein alignments. <i>Nucleic Acids Research</i> , 2010 , 38, W14-8	20.1	265
80	Mass-Up: an all-in-one open software application for MALDI-TOF mass spectrometry knowledge discovery. <i>BMC Bioinformatics</i> , 2015 , 16, 318	3.6	68
79	Web scraping technologies in an API world. <i>Briefings in Bioinformatics</i> , 2014 , 15, 788-97	13.4	41
78	AlBench: a rapid application development framework for translational research in biomedicine. <i>Computer Methods and Programs in Biomedicine</i> , 2010 , 98, 191-203	6.9	37
77	PanDrugs: a novel method to prioritize anticancer drug treatments according to individual genomic data. <i>Genome Medicine</i> , 2018 , 10, 41	14.4	35
76	LA-iMageS: a software for elemental distribution bioimaging using LA-ICP-MS data. <i>Journal of Cheminformatics</i> , 2016 , 8, 65	8.6	29
75	Fast human serum profiling through chemical depletion coupled to gold-nanoparticle-assisted protein separation. <i>Talanta</i> , 2012 , 100, 239-45	6.2	27
74	Deep Neural Networks approaches for detecting and classifying colorectal polyps. <i>Neurocomputing</i> , 2021 , 423, 721-734	5.4	25
73	BioAnnote: a software platform for annotating biomedical documents with application in medical learning environments. <i>Computer Methods and Programs in Biomedicine</i> , 2013 , 111, 139-47	6.9	23
72	Laser ablation and inductively coupled plasma mass spectrometry focusing on bioimaging from elemental distribution using MatLab software: a practical guide. <i>Journal of Analytical Atomic Spectrometry</i> , 2016 , 31, 832-840	3.7	20
71	Direct matrix assisted laser desorption ionization mass spectrometry-based analysis of wine as a powerful tool for classification purposes. <i>Talanta</i> , 2012 , 91, 72-6	6.2	19
70	Evaluating the effect of unbalanced data in biomedical document classification. <i>Journal of Integrative Bioinformatics</i> , 2011 , 8, 105-117	3.8	19
69	A novel ensemble of classifiers that use biological relevant gene sets for microarray classification. <i>Applied Soft Computing Journal</i> , 2014 , 17, 117-126	7.5	18
68	The <i>Drosophila melanogaster</i> methuselah gene: a novel gene with ancient functions. <i>PLoS ONE</i> , 2013 , 8, e63747	3.7	18
67	Patterns of evolution at the gametophytic self-incompatibility <i>Sorbus aucuparia</i> (Pyrinae) S pollen genes support the non-self recognition by multiple factors model. <i>Journal of Experimental Botany</i> , 2013 , 64, 2423-34	7	16
66	ADOPS--Automatic Detection Of Positively Selected Sites. <i>Journal of Integrative Bioinformatics</i> , 2012 , 9, 200	3.8	16
65	An assessment of the ultrasonic probe-based enhancement of protein cleavage with immobilized trypsin. <i>Proteomics</i> , 2011 , 11, 3866-76	4.8	15

64	ADOPS - Automatic Detection Of Positively Selected Sites. <i>Journal of Integrative Bioinformatics</i> , 2012 , 9, 18-32	3.8	14
63	Grindstone4Spam: An optimization toolkit for boosting e-mail classification. <i>Journal of Systems and Software</i> , 2012 , 85, 2909-2920	3.3	13
62	An RNA-seq Based Machine Learning Approach Identifies Latent Tuberculosis Patients With an Active Tuberculosis Profile. <i>Frontiers in Immunology</i> , 2020 , 11, 1470	8.4	11
61	Classifying patients in peritoneal dialysis by mass spectrometry-based profiling. <i>Talanta</i> , 2016 , 152, 364-370	7.0	11
60	Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry-based profiling as a step forward in the characterization of peritoneal dialysis effluent. <i>Analytical Methods</i> , 2015 , 7, 7467-7473	7.2	10
59	Decision peptide-driven: a free software tool for accurate protein quantification using gel electrophoresis and matrix assisted laser desorption ionization time of flight mass spectrometry. <i>Talanta</i> , 2010 , 82, 1412-20	6.2	10
58	Mass spectrometry-based fingerprinting of proteins & peptides in wine quality control: a critical overview. <i>Critical Reviews in Food Science and Nutrition</i> , 2013 , 53, 751-9	11.5	9
57	A JAVA application framework for scientific software development. <i>Software - Practice and Experience</i> , 2012 , 42, 1015-1036	2.5	9
56	A novel (18)O inverse labeling-based workflow for accurate bottom-up mass spectrometry quantification of proteins separated by gel electrophoresis. <i>Electrophoresis</i> , 2010 , 31, 3407-19	3.6	9
55	Bioinformatics Protocols for Quickly Obtaining Large-Scale Data Sets for Phylogenetic Inferences. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019 , 11, 1-9	3.5	9
54	A methodological approach based on gold-nanoparticles followed by matrix assisted laser desorption ionization time of flight mass spectrometry for the analysis of urine profiling of knee osteoarthritis. <i>Talanta</i> , 2016 , 150, 638-45	6.2	8
53	Multiple independent L-gulonolactone oxidase (GULO) gene losses and vitamin C synthesis reacquisition events in non-Deuterostomian animal species. <i>BMC Evolutionary Biology</i> , 2019 , 19, 126	3	8
52	Speeding up the screening of steroids in urine: development of a user-friendly library. <i>Steroids</i> , 2013 , 78, 1226-32	2.8	8
51	Real-time polyp detection model using convolutional neural networks. <i>Neural Computing and Applications</i> , 2021 , 1	4.8	8
50	EvoPPI 1.0: a Web Platform for Within- and Between-Species Multiple Interactome Comparisons and Application to Nine PolyQ Proteins Determining Neurodegenerative Diseases. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019 , 11, 45-56	3.5	7
49	Large Scale Analyses and Visualization of Adaptive Amino Acid Changes Projects. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018 , 10, 24-32	3.5	7
48	Sequential depletion coupled to C18 sequential extraction as a rapid tool for human serum multiple profiling. <i>Talanta</i> , 2014 , 125, 189-95	6.2	7
47	PileLine: a toolbox to handle genome position information in next-generation sequencing studies. <i>BMC Bioinformatics</i> , 2011 , 12, 31	3.6	7

46	BDBM 1.0: A Desktop Application for Efficient Retrieval and Processing of High-Quality Sequence Data and Application to the Identification of the Putative Coffea S-Locus. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019 , 11, 57-67	3.5	6
45	genEnsemble: A new model for the combination of classifiers and integration of biological knowledge applied to genomic data. <i>Expert Systems With Applications</i> , 2013 , 40, 52-63	7.8	6
44	PileLineGUI: a desktop environment for handling genome position files in next-generation sequencing studies. <i>Nucleic Acids Research</i> , 2011 , 39, W562-6	20.1	6
43	A novel ensemble approach for multiclass classification of DNA microarray data using biological relevant gene sets. <i>International Journal of Data Mining and Bioinformatics</i> , 2012 , 6, 602-16	0.5	6
42	geneCommittee: a web-based tool for extensively testing the discriminatory power of biologically relevant gene sets in microarray data classification. <i>BMC Bioinformatics</i> , 2014 , 15, 31	3.6	5
41	Rapid development of proteomic applications with the AIBench framework. <i>Journal of Integrative Bioinformatics</i> , 2011 , 8, 16-30	3.8	5
40	Indirect ultrasonication for protein quantification and peptide mass mapping through mass spectrometry-based techniques. <i>Talanta</i> , 2010 , 82, 587-93	6.2	5
39	Inferring Positive Selection in Large Viral Datasets. <i>Advances in Intelligent Systems and Computing</i> , 2020 , 61-69	0.4	5
38	Compi Hub: A Public Repository for Sharing and Discovering Compi Pipelines. <i>Advances in Intelligent Systems and Computing</i> , 2021 , 51-59	0.4	5
37	GC4S: A bioinformatics-oriented Java software library of reusable graphical user interface components. <i>PLoS ONE</i> , 2018 , 13, e0204474	3.7	5
36	The Artificial Intelligence Workbench: a retrospective review. <i>Advances in Distributed Computing and Artificial Intelligence Journal</i> , 2016 , 5, 73-85	0.4	4
35	SEDA: a Desktop Tool Suite for FASTA Files Processing. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , PP,	3	4
34	Compi: a framework for portable and reproducible pipelines. <i>PeerJ Computer Science</i> , 2021 , 7, e593	2.7	4
33	S2P: A software tool to quickly carry out reproducible biomedical research projects involving 2D-gel and MALDI-TOF MS protein data. <i>Computer Methods and Programs in Biomedicine</i> , 2018 , 155, 1-9	6.9	4
32	PathJam: a new service for integrating biological pathway information. <i>Journal of Integrative Bioinformatics</i> , 2010 , 7,	3.8	4
31	Predicting Specificities Under the Non-self Gametophytic Self-Incompatibility Recognition Model. <i>Frontiers in Plant Science</i> , 2019 , 10, 879	6.2	3
30	A mesofluidic platform integrating on-chip probe ultrasonication for multiple sample pretreatment involving denaturation, reduction, and digestion in protein identification assays by mass spectrometry. <i>Analyst, The</i> , 2014 , 139, 992-5	5	3
29	A comprehensive analysis about the influence of low-level preprocessing techniques on mass spectrometry data for sample classification. <i>International Journal of Data Mining and Bioinformatics</i> , 2014 , 10, 455-73	0.5	3

28	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
27	Inferences on Mycobacterium Leprae Host Immune Response Escape and Antibiotic Resistance Using Genomic Data and GenomeFastScreen. <i>Advances in Intelligent Systems and Computing</i> , 2021 , 42-50 ^{0.4}		3
26	ATXN1 N-terminal region explains the binding differences of wild-type and expanded forms. <i>BMC Medical Genomics</i> , 2019 , 12, 145	3.7	3
25	Performance of Convolutional Neural Networks for Polyp Localization on Public Colonoscopy Image Datasets.. <i>Diagnostics</i> , 2022 , 12,	3.8	3
24	Evaluating the effect of unbalanced data in biomedical document classification. <i>Journal of Integrative Bioinformatics</i> , 2011 , 8, 177	3.8	3
23	A Workflow for the Application of Biclustering to Mass Spectrometry Data. <i>Advances in Intelligent Systems and Computing</i> , 2013 , 145-153	0.4	2
22	Using CBR as Design Methodology for Developing Adaptable Decision Support Systems 2011 ,		2
21	On the Development of a Pipeline for the Automatic Detection of Positively Selected Sites. <i>Advances in Intelligent and Soft Computing</i> , 2012 , 225-229		2
20	Building Proteomics Applications with the AIBench Application Framework. <i>Advances in Intelligent and Soft Computing</i> , 2011 , 99-107		2
19	Assessing the Suitability of MeSH Ontology for Classifying Medline Documents. <i>Advances in Intelligent and Soft Computing</i> , 2011 , 337-344		2
18	Assessing the Impact of Class-Imbalanced Data for Classifying Relevant/Irrelevant Medline Documents. <i>Advances in Intelligent and Soft Computing</i> , 2011 , 345-353		2
17	Enhancing sepsis management through machine learning techniques: A review. <i>Medicina Intensiva</i> , 2020 , 46, 140-140	1.2	2
16	DREIMT: a drug repositioning database and prioritization tool for immunomodulation. <i>Bioinformatics</i> , 2021 , 37, 578-579	7.2	2
15	A Bioinformatics Protocol for Quickly Creating Large-Scale Phylogenetic Trees. <i>Advances in Intelligent Systems and Computing</i> , 2019 , 88-96	0.4	1
14	EvoPPI: A Web Application to Compare Protein-Protein Interactions (PPIs) from Different Databases and Species. <i>Advances in Intelligent Systems and Computing</i> , 2019 , 149-156	0.4	1
13	Incorporating biological knowledge to microarray data classification through genomic data fusion 2010 ,		1
12	DREIMT: a drug repositioning database and prioritization tool for immunomodulation		1
11	Implementing effective machine learning-based workflows for the analysis of mass spectrometry data. <i>Journal of Integrated OMICS</i> , 2016 , 6,	0.5	1

- 10 The pegi3s Bioinformatics Docker Images Project. *Lecture Notes in Networks and Systems*, **2022**, 31-40 0.5 1
- 9 On the Identification of Clinically Relevant Bacterial Amino Acid Changes at the Whole Genome Level Using Auto-PSS-Genome. *Interdisciplinary Sciences, Computational Life Sciences*, **2021**, 13, 334-343 3.5 0
- 8 S2P: A Desktop Application for Fast and Easy Processing of 2D-Gel and MALDI-Based Mass Spectrometry Protein Data. *Advances in Intelligent Systems and Computing*, **2017**, 1-8 0.4
- 7 Automated Collection and Sharing of Adaptive Amino Acid Changes Data. *Advances in Intelligent Systems and Computing*, **2017**, 18-25 0.4
- 6 An Experimental Evaluation of a Novel Stochastic Method for Iterative Class Discovery on Real Microarray Datasets. *Advances in Intelligent and Soft Computing*, **2010**, 9-16
- 5 PathAgent: Multi-agent System for Updated Pathway Information Integration. *Advances in Intelligent and Soft Computing*, **2010**, 77-85
- 4 Multi-agent System for Mass Spectrometry Analysis. *Advances in Intelligent and Soft Computing*, **2010**, 87-95
- 3 A Comparative Study of Microarray Data Classification Methods Based on Ensemble Biological Relevant Gene Sets. *Advances in Intelligent and Soft Computing*, **2010**, 25-32
- 2 An Intuitive Workflow to Retrieve Somatic Mutations in Next Generation Sequencing Studies. *Advances in Intelligent and Soft Computing*, **2011**, 83-86
- 1 Applying AIBench Framework to Develop Rich User Interfaces in NGS Studies. *Advances in Intelligent and Soft Computing*, **2012**, 189-196