

Miguel Reboiro-Jato

List of Publications by Year in descending order

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Version: 2024-02-01

84
papers

1,429
citations

489802

18
h-index

425179

34
g-index

90
all docs

90
docs citations

90
times ranked

2198
citing authors

#	ARTICLE	IF	CITATIONS
1	The pegi3s Bioinformatics Docker Images Project. Lecture Notes in Networks and Systems, 2022, , 31-40.	0.5	4
2	Real-time polyp detection model using convolutional neural networks. Neural Computing and Applications, 2022, 34, 10375-10396.	3.2	29
3	Enhancing sepsis management through machine learning techniques: A review. Medicina Intensiva, 2022, 46, 140-156.	0.4	9
4	Performance of Convolutional Neural Networks for Polyp Localization on Public Colonoscopy Image Datasets. Diagnostics, 2022, 12, 898.	1.3	13
5	Deep Neural Networks approaches for detecting and classifying colorectal polyps. Neurocomputing, 2021, 423, 721-734.	3.5	65
6	DREIMT: a drug repositioning database and prioritization tool for immunomodulation. Bioinformatics, 2021, 37, 578-579.	1.8	9
7	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.	2.2	2
8	Compi: a framework for portable and reproducible pipelines. PeerJ Computer Science, 2021, 7, e593.	2.7	8
9	Inferences on Mycobacterium Leprae Host Immune Response Escape and Antibiotic Resistance Using Genomic Data and GenomeFastScreen. Advances in Intelligent Systems and Computing, 2021, , 42-50.	0.5	3
10	An RNA-seq Based Machine Learning Approach Identifies Latent Tuberculosis Patients With an Active Tuberculosis Profile. Frontiers in Immunology, 2020, 11, 1470.	2.2	25
11	SEDA: a Desktop Tool Suite for FASTA Files Processing. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	1.9	10
12	Inferring Positive Selection in Large Viral Datasets. Advances in Intelligent Systems and Computing, 2020, , 61-69.	0.5	5
13	CHAPTER 5. Statistics, Data Mining and Modeling. New Developments in Mass Spectrometry, 2020, , 120-200.	0.2	0
14	A Bioinformatics Protocol for Quickly Creating Large-Scale Phylogenetic Trees. Advances in Intelligent Systems and Computing, 2019, , 88-96.	0.5	1
15	EvoPPI: A Web Application to Compare Protein-Protein Interactions (PPIs) from Different Databases and Species. Advances in Intelligent Systems and Computing, 2019, , 149-156.	0.5	1
16	Predicting Specificities Under the Non-self Gametophytic Self-Incompatibility Recognition Model. Frontiers in Plant Science, 2019, 10, 879.	1.7	6
17	EvoPPI 1.0: a Web Platform for Within- and Between-Species Multiple Interactome Comparisons and Application to Nine PolyQ Proteins Determining Neurodegenerative Diseases. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 45-56.	2.2	10
18	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. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 57-67.	2.2	13

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19	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.	3.2	13
20	ATXN1 N-terminal region explains the binding differences of wild-type and expanded forms. <i>BMC Medical Genomics</i> , 2019, 12, 145.	0.7	6
21	Bioinformatics Protocols for Quickly Obtaining Large-Scale Data Sets for Phylogenetic Inferences. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 1-9.	2.2	18
22	Large Scale Analyses and Visualization of Adaptive Amino Acid Changes Projects. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018, 10, 24-32.	2.2	14
23	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.	2.6	5
24	GC4S: A bioinformatics-oriented Java software library of reusable graphical user interface components. <i>PLoS ONE</i> , 2018, 13, e0204474.	1.1	5
25	PanDrugs: a novel method to prioritize anticancer drug treatments according to individual genomic data. <i>Genome Medicine</i> , 2018, 10, 41.	3.6	63
26	S2P: A Desktop Application for Fast and Easy Processing of 2D-Gel and MALDI-Based Mass Spectrometry Protein Data. <i>Advances in Intelligent Systems and Computing</i> , 2017, , 1-8.	0.5	1
27	Automated Collection and Sharing of Adaptive Amino Acid Changes Data. <i>Advances in Intelligent Systems and Computing</i> , 2017, , 18-25.	0.5	0
28	Implementing effective machine learning-based workflows for the analysis of mass spectrometry data. <i>Journal of Integrated OMICS</i> , 2016, 6, .	0.5	3
29	LA-iMageS: a software for elemental distribution bioimaging using LA-ICP-MS data. <i>Journal of Cheminformatics</i> , 2016, 8, 65.	2.8	35
30	Classifying patients in peritoneal dialysis by mass spectrometry-based profiling. <i>Talanta</i> , 2016, 152, 364-370.	2.9	12
31	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.	1.6	22
32	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, 638-645.	2.9	10
33	The Artificial Intelligence Workbench: a retrospective review. <i>Advances in Distributed Computing and Artificial Intelligence Journal</i> , 2016, 5, 73-85.	1.1	4
34	Mass-Up: an all-in-one open software application for MALDI-TOF mass spectrometry knowledge discovery. <i>BMC Bioinformatics</i> , 2015, 16, 318.	1.2	86
35	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.	1.3	11
36	Abstract A22: PanDrugsDB: Identifying druggable genetic dependencies for personalized cancer therapy. , 2015, , .		0

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37	geneCommittee: a web-based tool for extensively testing the discriminatory power of biologically relevant gene sets in microarray data classification. BMC Bioinformatics, 2014, 15, 31.	1.2	7
38	A novel ensemble of classifiers that use biological relevant gene sets for microarray classification. Applied Soft Computing Journal, 2014, 17, 117-126.	4.1	21
39	A mesofluidic platform integrating on-chip probe ultrasonication for multiple sample pretreatment involving denaturation, reduction, and digestion in protein identification assays by mass spectrometry. Analyst, The, 2014, 139, 992-995.	1.7	7
40	A comprehensive analysis about the influence of low-level preprocessing techniques on mass spectrometry data for sample classification. International Journal of Data Mining and Bioinformatics, 2014, 10, 455.	0.1	3
41	Web scraping technologies in an API world. Briefings in Bioinformatics, 2014, 15, 788-797.	3.2	84
42	Sequential depletion coupled to C18 sequential extraction as a rapid tool for human serum multiple profiling. Talanta, 2014, 125, 189-195.	2.9	10
43	Mass Spectrometry-Based Fingerprinting of Proteins & Peptides in Wine Quality Control: A Critical Overview. Critical Reviews in Food Science and Nutrition, 2013, 53, 751-759.	5.4	10
44	A Workflow for the Application of Biclustering to Mass Spectrometry Data. Advances in Intelligent Systems and Computing, 2013, , 145-153.	0.5	2
45	Speeding up the screening of steroids in urine: Development of a user-friendly library. Steroids, 2013, 78, 1226-1232.	0.8	9
46	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
47	genEnsemble: A new model for the combination of classifiers and integration of biological knowledge applied to genomic data. Expert Systems With Applications, 2013, 40, 52-63.	4.4	6
48	BioAnnote: A software platform for annotating biomedical documents with application in medical learning environments. Computer Methods and Programs in Biomedicine, 2013, 111, 139-147.	2.6	26
49	Patterns of evolution at the gametophytic self-incompatibility Sorbus aucuparia (Pyrinae) S pollen genes support the non-self recognition by multiple factors model. Journal of Experimental Botany, 2013, 64, 2423-2434.	2.4	24
50	The Drosophila melanogaster methuselah Gene: A Novel Gene with Ancient Functions. PLoS ONE, 2013, 8, e63747.	1.1	23
51	On the Development of a Pipeline for the Automatic Detection of Positively Selected Sites. Advances in Intelligent and Soft Computing, 2012, , 225-229.	0.2	2
52	ADOPS - Automatic Detection Of Positively Selected Sites. Journal of Integrative Bioinformatics, 2012, 9, 18-32.	1.0	17
53	A novel ensemble approach for multcategory classification of DNA microarray data using biological relevant gene sets. International Journal of Data Mining and Bioinformatics, 2012, 6, 602.	0.1	7
54	Grindstone4Spam: An optimization toolkit for boosting e-mail classification. Journal of Systems and Software, 2012, 85, 2909-2920.	3.3	13

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55	Fast human serum profiling through chemical depletion coupled to gold-nanoparticle-assisted protein separation. <i>Talanta</i> , 2012, 100, 239-245.	2.9	28
56	Direct matrix assisted laser desorption ionization mass spectrometry-based analysis of wine as a powerful tool for classification purposes. <i>Talanta</i> , 2012, 91, 72-76.	2.9	21
57	A JAVA application framework for scientific software development. <i>Software - Practice and Experience</i> , 2012, 42, 1015-1036.	2.5	10
58	ADOPS--Automatic Detection Of Positively Selected Sites. <i>Journal of Integrative Bioinformatics</i> , 2012, 9, 200.	1.0	25
59	Applying AIBench Framework to Develop Rich User Interfaces in NGS Studies. <i>Advances in Intelligent and Soft Computing</i> , 2012, , 189-196.	0.2	0
60	A simulated annealing-based algorithm for iterative class discovery using fuzzy logic for informative gene selection. <i>Journal of Integrated OMICS</i> , 2011, 1, .	0.5	0
61	Rapid development of proteomic applications with the AIBench framework. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 16-30.	1.0	5
62	Evaluating the effect of unbalanced data in biomedical document classification. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 105-117.	1.0	32
63	PileLine: a toolbox to handle genome position information in next-generation sequencing studies. <i>BMC Bioinformatics</i> , 2011, 12, 31.	1.2	10
64	An assessment of the ultrasonic probeâ€based enhancement of protein cleavage with immobilized trypsin. <i>Proteomics</i> , 2011, 11, 3866-3876.	1.3	16
65	Using inductive learning to assess compound feed production in cooperative poultry farms. <i>Expert Systems With Applications</i> , 2011, , .	4.4	1
66	PileLineGUI: a desktop environment for handling genome position files in next-generation sequencing studies. <i>Nucleic Acids Research</i> , 2011, 39, W562-W566.	6.5	6
67	Building Proteomics Applications with the AIBench Application Framework. <i>Advances in Intelligent and Soft Computing</i> , 2011, , 99-107.	0.2	2
68	Rapid development of Proteomic applications with the AIBench framework. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 171.	1.0	4
69	Evaluating the effect of unbalanced data in biomedical document classification. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 177.	1.0	10
70	ALTER: program-oriented conversion of DNA and protein alignments. <i>Nucleic Acids Research</i> , 2010, 38, W14-W18.	6.5	367
71	AIBench: A rapid application development framework for translational research in biomedicine. <i>Computer Methods and Programs in Biomedicine</i> , 2010, 98, 191-203.	2.6	41
72	A novel ¹⁸O inverse labelingâ€based workflow for accurate bottomâ€up mass spectrometry quantification of proteins separated by gel electrophoresis. <i>Electrophoresis</i> , 2010, 31, 3407-3419.	1.3	9

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73	PathJam: a new service for integrating biological pathway information. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	3
74	Incorporating biological knowledge to microarray data classification through genomic data fusion. , 2010, , .		2
75	Indirect ultrasonication for protein quantification and peptide mass mapping through mass spectrometry-based techniques. Talanta, 2010, 82, 587-593.	2.9	5
76	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. Talanta, 2010, 82, 1412-1420.	2.9	12
77	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.	0.2	0
78	PathAgent: Multi-agent System for Updated Pathway Information Integration. Advances in Intelligent and Soft Computing, 2010, , 77-85.	0.2	0
79	A Comparative Study of Microarray Data Classification Methods Based on Ensemble Biological Relevant Gene Sets. Advances in Intelligent and Soft Computing, 2010, , 25-32.	0.2	1
80	A robust algorithm for forming note complexes. Inteligencia Artificial, 2010, 14, .	0.5	0
81	PathJam: a new service for integrating biological pathway information. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	4
82	Using CBR as Design Methodology for Developing Adaptable Decision Support Systems. , 0, , .		5
83	Desarrollo inicial de un Sistema de DiagnÃ³stico Asistido por Computadora (CAD) que facilite el diagnÃ³stico Ã³ptico de pÃ³lipos colorrectales Ã. , 0, , .		0
84	Desarrollo de un sistema de Inteligencia Artificial para la detecciÃ³n de polÃ­pos en tiempo real. , 0, , .		0