

Hugo Lopez-Fernandez

List of Publications by Year in Descending Order

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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.

57
papers

451
citations

10
h-index

18
g-index

60
ext. papers

608
ext. citations

3.9
avg, IF

3.79
L-index

#	Paper	IF	Citations
57	On the Reproducibility of MiRNA-Seq Differential Expression Analyses in Neuropsychiatric Diseases. <i>Lecture Notes in Networks and Systems</i> , 2022 , 41-51	0.5	1
56	The pegi3s Bioinformatics Docker Images Project. <i>Lecture Notes in Networks and Systems</i> , 2022 , 31-40	0.5	1
55	Performance of Convolutional Neural Networks for Polyp Localization on Public Colonoscopy Image Datasets.. <i>Diagnostics</i> , 2022 , 12,	3.8	3
54	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}	0.4	3
53	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
52	On the Identification of Clinically Relevant Bacterial Amino Acid Changes at the Whole Genome Level Using Auto-PSS-Genome. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2021 , 13, 334-343	3.5	0
51	Compi: a framework for portable and reproducible pipelines. <i>PeerJ Computer Science</i> , 2021 , 7, e593	2.7	4
50	Deep Neural Networks approaches for detecting and classifying colorectal polyps. <i>Neurocomputing</i> , 2021 , 423, 721-734	5.4	25
49	DREIMT: a drug repositioning database and prioritization tool for immunomodulation. <i>Bioinformatics</i> , 2021 , 37, 578-579	7.2	2
48	Application of miRNA-seq in neuropsychiatry: A methodological perspective. <i>Computers in Biology and Medicine</i> , 2021 , 135, 104603	7	2
47	Real-time polyp detection model using convolutional neural networks. <i>Neural Computing and Applications</i> , 2021 , 1	4.8	8
46	Metatax: Metataxonomics with a Compi-Based Pipeline for Precision Medicine. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2020 , 12, 252-257	3.5	2
45	Inferring Positive Selection in Large Viral Datasets. <i>Advances in Intelligent Systems and Computing</i> , 2020 , 61-69	0.4	5
44	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
43	SEDA: a Desktop Tool Suite for FASTA Files Processing. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , PP,	3	4
42	Ultrasonic-assisted extraction and digestion of proteins from solid biopsies followed by peptide sequential extraction hyphenated to MALDI-based profiling holds the promise of distinguishing renal oncocytoma from chromophobe renal cell carcinoma. <i>Talanta</i> , 2020 , 206, 120180	6.2	3
41	Deep Learning Techniques for Real Time Computer-Aided Diagnosis in Colorectal Cancer. <i>Advances in Intelligent Systems and Computing</i> , 2020 , 209-212	0.4	1

40	Proposal of a New Bioinformatics Pipeline for Metataxonomics in Precision Medicine. <i>Advances in Intelligent Systems and Computing</i> , 2020 , 8-15	0.4	3
39	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
38	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
37	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
36	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
35	A Bioinformatics Protocol for Quickly Creating Large-Scale Phylogenetic Trees. <i>Advances in Intelligent Systems and Computing</i> , 2019 , 88-96	0.4	1
34	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
33	Predicting Specificities Under the Non-self Gametophytic Self-Incompatibility Recognition Model. <i>Frontiers in Plant Science</i> , 2019 , 10, 879	6.2	3
32	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
31	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
30	Modulating the protein content of complex proteomes using acetonitrile. <i>Talanta</i> , 2018 , 182, 333-339	6.2	2
29	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
28	Perceptions of the use of intelligent information access systems in university level active learning activities among teachers of biomedical subjects. <i>International Journal of Medical Informatics</i> , 2018 , 112, 21-33	5.3	17
27	Bicycle: a bioinformatics pipeline to analyze bisulfite sequencing data. <i>Bioinformatics</i> , 2018 , 34, 1414-1415	15.2	13
26	Ultrasonic-based membrane aided sample preparation of urine proteomes. <i>Talanta</i> , 2018 , 178, 864-869	6.2	9
25	Dithiothreitol-based protein equalization technology to unravel biomarkers for bladder cancer. <i>Talanta</i> , 2018 , 180, 36-46	6.2	3
24	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
23	GC4S: A bioinformatics-oriented Java software library of reusable graphical user interface components. <i>PLoS ONE</i> , 2018 , 13, e0204474	3.7	5

22	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	0.4	
21	RUBioSeq+: A multiplatform application that executes parallelized pipelines to analyse next-generation sequencing data. <i>Computer Methods and Programs in Biomedicine</i> , 2017 , 138, 73-81	6.9	7
20	Automated Collection and Sharing of Adaptive Amino Acid Changes Data. <i>Advances in Intelligent Systems and Computing</i> , 2017 , 18-25	0.4	
19	RUBioSeq+: An Application that Executes Parallelized Pipelines to Analyse Next-Generation Sequencing Data. <i>Advances in Intelligent Systems and Computing</i> , 2016 , 141-149	0.4	
18	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
17	The Artificial Intelligence Workbench: a retrospective review. <i>Advances in Distributed Computing and Artificial Intelligence Journal</i> , 2016 , 5, 73-85	0.4	4
16	Implementing effective machine learning-based workflows for the analysis of mass spectrometry data. <i>Journal of Integrated OMICS</i> , 2016 , 6,	0.5	1
15	LA-iMageS: a software for elemental distribution bioimaging using LA-ICP-MS data. <i>Journal of Cheminformatics</i> , 2016 , 8, 65	8.6	29
14	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
13	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
12	Web scraping technologies in an API world. <i>Briefings in Bioinformatics</i> , 2014 , 15, 788-97	13.4	41
11	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
10	Speeding up the screening of steroids in urine: development of a user-friendly library. <i>Steroids</i> , 2013 , 78, 1226-32	2.8	8
9	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
8	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
7	Fast human serum profiling through chemical depletion coupled to gold-nanoparticle-assisted protein separation. <i>Talanta</i> , 2012 , 100, 239-45	6.2	27
6	A JAVA application framework for scientific software development. <i>Software - Practice and Experience</i> , 2012 , 42, 1015-1036	2.5	9
5	Applying AIBench Framework to Develop Rich User Interfaces in NGS Studies. <i>Advances in Intelligent and Soft Computing</i> , 2012 , 189-196		

4	Using CBR as Design Methodology for Developing Adaptable Decision Support Systems 2011 ,		2
3	Rapid development of proteomic applications with the AlBench framework. <i>Journal of Integrative Bioinformatics</i> , 2011 , 8, 16-30	3.8	5
2	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
1	DREIMT: a drug repositioning database and prioritization tool for immunomodulation		1