Joel P Arrais

List of Publications by Year
in descending order

57 papers	474 citations	840119 11 h-index	752256 20 g-index
62 all docs	62 docs citations	62 times ranked	626 citing authors

#	Article	IF	Citations
1	Force-Directed Timelines: Visualizing & Exploring Temporal Patterns. Big Data Research, 2022, 27, 100291.	2.6	1
2	The Road to Personalized Medicine in Alzheimerâ€™s Disease: The Use of Artificial Intelligence. Biomedicines, 2022, 10, 315.	1.4	15
3	DTITR: End-to-end drugâ€"target binding affinity prediction with transformers. Computers in Biology and Medicine, 2022, 147, 105772.	3.9	12
4	Deep generative model for therapeutic targets using transcriptomic disease-associated dataâ€"USP7 case study. Briefings in Bioinformatics, 2022, 23, .	3.2	7
5	Drug-Target Interaction Prediction: End-to-End Deep Learning Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2364-2374.	1.9	30
6	Diversity oriented Deep Reinforcement Learning for targeted molecule generation. Journal of Cheminformatics, 2021, 13, 21.	2.8	36
7	Analysing Games for Health through Users' Opinion Mining. , 2021, , .		1
8	Optimizing Recurrent Neural Network Architectures for De Novo Drug Design. , 2021, , .		3
9	Optimizing bloodâ€"brain barrier permeation through deep reinforcement learning for <i>de novo</i> drug design. Bioinformatics, 2021, 37, i84-i92.	1.8	13
10	Multiobjective Reinforcement Learning in Optimized Drug Design. , 2021, , .		0
11	Decay Momentum for Improving Federated Learning. , 2021, , .		2
12	Improvement on Generative Adversarial Network for Targeted Drug Design. , 2021, , .		0
13	CroPâ€"Coordinated Panel visualization for biological networks analysis. Bioinformatics, 2020, 36, 1298-1299.	1.8	3
14	NanoSen-AQM: From Sensors to Users. International Journal of Online and Biomedical Engineering, 2020, 16, 51.	0.9	3
15	Using a Novel Unbiased Dataset and Deep Learning Architectures to Predict Protein-Protein Interactions. , 2020, , .		1
16	Exploring Time-Series Through Force-Directed Timelines. , 2020, , .		0
17	Exploring a Siamese Neural Network Architecture for One-Shot Drug Discovery. , 2020, , .		6
18	An Online Platform For Real-Time Air Quality Monitoring. , 2019, , .		4

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19	A Hybrid Application for Real-Time Air Quality Monitoring. , 2019, , .		4
20	Handling Noise in Protein Interaction Networks. BioMed Research International, 2019, 2019, 1-13.	0.9	5
21	Interactive and coordinated visualization approaches for biological data analysis. Briefings in Bioinformatics, 2019, 20, 1513-1523.	3.2	10
22	Deep Neural Network Architecture for Drug-Target Interaction Prediction. Lecture Notes in Computer Science, 2019, , 804-809.	1.0	2
23	SalivaPRINT Toolkit â€" Protein profile evaluation and phenotype stratification. Journal of Proteomics, 2018, 171, 81-86.	1.2	3
24	Interactive Network Visualization of Gene Expression Time-Series Data. , 2018, , .		2
25	Fighting Fire with Fire: Computational Prediction of Microbial Targets for Bacteriocins. Lecture Notes in Computer Science, 2018, , 221-234.	1.0	0
26	Mixed-Integer Programming Model for Profiling Disease Biomarkers from Gene Expression Studies. Lecture Notes in Computer Science, 2017, , 50-61.	1.0	0
27	On the role of aesthetics in genetic algorithms applied to graph drawing. , 2017, , .		1
28	New Targets for *Zika* Virus Determined by Human-Viral Interactomic: A Bioinformatics Approach. BioMed Research International, 2017, 2017, 1-15.	0.9	16
29	Deep learning in digital marketing: brand detection and emotion recognition. International Journal of Machine Intelligence and Sensory Signal Processing, 2017, 2, 32.	0.2	6
30	Deep learning in digital marketing: brand detection and emotion recognition. International Journal of Machine Intelligence and Sensory Signal Processing, 2017, 2, 32.	0.2	2
31	Ensemble-Based Methodology for the Prediction of Drug-Target Interactions. , 2016, , .		5
32	Reconstructing the temporal progression of HIV-1 immune response pathways. Bioinformatics, 2016, 32, i253-i261.	1.8	14
33	CanisOme â€" The protein signatures of Canis lupus familiaris diseases. Journal of Proteomics, 2016, 136, 193-201.	1.2	12
34	Computational Discovery of Putative Leads for Drug Repositioning through Drug-Target Interaction Prediction. PLoS Computational Biology, 2016, 12, e1005219.	1.5	32
35	Prediction of Cancer using Network Topological Features. , 2016, , .		0
36	RecRWR: A Recursive Random Walk Method for Improved Identification of Diseases. BioMed Research International, 2015, 2015, 1-7.	0.9	1

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37	Uncovering microbial duality within human microbiomes: A novel algorithm for the analysis of host-pathogen interactions. , 2015, 2015, 3254-7.		0
38	Computational methodology for predicting the landscape of the human–microbial interactome region level influence. Journal of Bioinformatics and Computational Biology, 2015, 13, 1550023.	0.3	12
39	The Landscape of Protein Biomarkers Proposed for Periodontal Disease: Markers with Functional Meaning. BioMed Research International, 2014, 2014, 1-15.	0.9	11
40	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
41	Computational prediction of the human-microbial oral interactome. BMC Systems Biology, 2014, 8, 24.	3.0	33
42	Metagenomic Analysis of the Saliva Microbiome with Merlin. Advances in Intelligent Systems and Computing, 2014, , 191-199.	0.5	1
43	A Cytoscape-Based Web Tool for Representing Protein Networks. IFMBE Proceedings, 2014, , 311-314.	0.2	0
44	OralCard: A bioinformatic tool for the study of oral proteome. Archives of Oral Biology, 2013, 58, 762-772.	0.8	23
45	From Protein-Protein Interactions to Rational Drug Design: Are Computational Methods Up to the Challenge&#63;. Current Topics in Medicinal Chemistry, 2013, 13, 602-618.	1.0	23
46	Data Integration Solution for Organ-Specific Studies: An Application for Oral Biology. Communications in Computer and Information Science, 2013, , 401-412.	0.4	1
47	Quantitative Characterization of Protein Networks of the Oral Cavity. Advances in Intelligent Systems and Computing, 2013, , 61-68.	0.5	0
48	From the salivary proteome to the OralOme: Comprehensive molecular oral biology. Archives of Oral Biology, 2012, 57, 853-864.	0.8	53
49	Enchytraeus albidus Microarray: Enrichment, Design, Annotation and Database (EnchyBASE). PLoS ONE, 2012, 7, e34266.	1.1	10
50	Challenges Storing and Representing Biomedical Data. Lecture Notes in Computer Science, 2011, , 53-62.	1.0	1
51	Concept-based query expansion for retrieving gene related publications from MEDLINE. BMC Bioinformatics, 2010, 11, 212.	1.2	32
52	GeneBrowser 2: an application to explore and identify common biological traits in a set of genes. BMC Bioinformatics, 2010, 11, 389.	1.2	5
53	Gene-disease prioritization through biomedical networks. , 2010, , .		1
54	On the exploitation of cloud computing in bioinformatics. , 2010, , .		2

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55	Expanding Gene-Based PubMed Queries. Advances in Intelligent and Soft Computing, 2010, , 61-68.	0.2	0
56	Improving Literature Searches in Gene Expression Studies. Advances in Soft Computing, 2009, , 74-82.	0.4	3
57	A Microarray Information Database. , 2008, , .		3