

# Joel P Arrais

## List of Publications by Year in descending order

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Version: 2024-02-01

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	From the salivary proteome to the OralOme: Comprehensive molecular oral biology. Archives of Oral Biology, 2012, 57, 853-864.	0.8	53
2	Diversity oriented Deep Reinforcement Learning for targeted molecule generation. Journal of Cheminformatics, 2021, 13, 21.	2.8	36
3	Computational prediction of the human-microbial oral interactome. BMC Systems Biology, 2014, 8, 24.	3.0	33
4	Concept-based query expansion for retrieving gene related publications from MEDLINE. BMC Bioinformatics, 2010, 11, 212.	1.2	32
5	Computational Discovery of Putative Leads for Drug Repositioning through Drug-Target Interaction Prediction. PLoS Computational Biology, 2016, 12, e1005219.	1.5	32
6	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
7	OralCard: A bioinformatic tool for the study of oral proteome. Archives of Oral Biology, 2013, 58, 762-772.	0.8	23
8	From Protein-Protein Interactions to Rational Drug Design: Are Computational Methods Up to the Challenge? Current Topics in Medicinal Chemistry, 2013, 13, 602-618.	1.0	23
9	New Targets for Zika Virus Determined by Human-Viral Interactomic: A Bioinformatics Approach. BioMed Research International, 2017, 2017, 1-15.	0.9	16
10	The Road to Personalized Medicine in Alzheimer's Disease: The Use of Artificial Intelligence. Biomedicine, 2022, 10, 315.	1.4	15
11	Reconstructing the temporal progression of HIV-1 immune response pathways. Bioinformatics, 2016, 32, i253-i261.	1.8	14
12	Optimizing blood-brain barrier permeation through deep reinforcement learning for de novo drug design. Bioinformatics, 2021, 37, i84-i92.	1.8	13
13	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
14	CanisOme – The protein signatures of Canis lupus familiaris diseases. Journal of Proteomics, 2016, 136, 193-201.	1.2	12
15	DTITR: End-to-end drug-target binding affinity prediction with transformers. Computers in Biology and Medicine, 2022, 147, 105772.	3.9	12
16	The Landscape of Protein Biomarkers Proposed for Periodontal Disease: Markers with Functional Meaning. BioMed Research International, 2014, 2014, 1-15.	0.9	11
17	Enchytraeus albidus Microarray: Enrichment, Design, Annotation and Database (EnchyBASE). PLoS ONE, 2012, 7, e34266.	1.1	10
18	Interactive and coordinated visualization approaches for biological data analysis. Briefings in Bioinformatics, 2019, 20, 1513-1523.	3.2	10

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19	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
20	Deep generative model for therapeutic targets using transcriptomic disease-associated data—USP7 case study. Briefings in Bioinformatics, 2022, 23, .	3.2	7
21	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
22	Exploring a Siamese Neural Network Architecture for One-Shot Drug Discovery. , 2020, , .		6
23	GeneBrowser 2: an application to explore and identify common biological traits in a set of genes. BMC Bioinformatics, 2010, 11, 389.	1.2	5
24	Ensemble-Based Methodology for the Prediction of Drug-Target Interactions. , 2016, , .		5
25	Handling Noise in Protein Interaction Networks. BioMed Research International, 2019, 2019, 1-13.	0.9	5
26	An Online Platform For Real-Time Air Quality Monitoring. , 2019, , .		4
27	A Hybrid Application for Real-Time Air Quality Monitoring. , 2019, , .		4
28	A Microarray Information Database. , 2008, , .		3
29	SalivaPRINT Toolkit — Protein profile evaluation and phenotype stratification. Journal of Proteomics, 2018, 171, 81-86.	1.2	3
30	CroPa—Coordinated Panel visualization for biological networks analysis. Bioinformatics, 2020, 36, 1298-1299.	1.8	3
31	Optimizing Recurrent Neural Network Architectures for De Novo Drug Design. , 2021, , .		3
32	Improving Literature Searches in Gene Expression Studies. Advances in Soft Computing, 2009, , 74-82.	0.4	3
33	NanoSen-AQM: From Sensors to Users. International Journal of Online and Biomedical Engineering, 2020, 16, 51.	0.9	3
34	On the exploitation of cloud computing in bioinformatics. , 2010, , .		2
35	Interactive Network Visualization of Gene Expression Time-Series Data. , 2018, , .		2
36	Decay Momentum for Improving Federated Learning. , 2021, , .		2

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37	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
38	Deep Neural Network Architecture for Drug-Target Interaction Prediction. Lecture Notes in Computer Science, 2019, , 804-809.	1.0	2
39	Gene-disease prioritization through biomedical networks. , 2010, , .		1
40	RecRWR: A Recursive Random Walk Method for Improved Identification of Diseases. BioMed Research International, 2015, 2015, 1-7.	0.9	1
41	On the role of aesthetics in genetic algorithms applied to graph drawing. , 2017, , .		1
42	Analysing Games for Health through Users' Opinion Mining. , 2021, , .		1
43	Data Integration Solution for Organ-Specific Studies: An Application for Oral Biology. Communications in Computer and Information Science, 2013, , 401-412.	0.4	1
44	Challenges Storing and Representing Biomedical Data. Lecture Notes in Computer Science, 2011, , 53-62.	1.0	1
45	Metagenomic Analysis of the Saliva Microbiome with Merlin. Advances in Intelligent Systems and Computing, 2014, , 191-199.	0.5	1
46	Using a Novel Unbiased Dataset and Deep Learning Architectures to Predict Protein-Protein Interactions. , 2020, , .		1
47	Force-Directed Timelines: Visualizing & Exploring Temporal Patterns. Big Data Research, 2022, 27, 100291.	2.6	1
48	Uncovering microbial duality within human microbiomes: A novel algorithm for the analysis of host-pathogen interactions. , 2015, 2015, 3254-7.		0
49	Mixed-Integer Programming Model for Profiling Disease Biomarkers from Gene Expression Studies. Lecture Notes in Computer Science, 2017, , 50-61.	1.0	0
50	Multiobjective Reinforcement Learning in Optimized Drug Design. , 2021, , .		0
51	Improvement on Generative Adversarial Network for Targeted Drug Design. , 2021, , .		0
52	Expanding Gene-Based PubMed Queries. Advances in Intelligent and Soft Computing, 2010, , 61-68.	0.2	0
53	Quantitative Characterization of Protein Networks of the Oral Cavity. Advances in Intelligent Systems and Computing, 2013, , 61-68.	0.5	0
54	A Cytoscape-Based Web Tool for Representing Protein Networks. IFMBE Proceedings, 2014, , 311-314.	0.2	0

#	ARTICLE	IF	CITATIONS
55	Prediction of Cancer using Network Topological Features. , 2016, , .		0
56	Fighting Fire with Fire: Computational Prediction of Microbial Targets for Bacteriocins. Lecture Notes in Computer Science, 2018, , 221-234.	1.0	0
57	Exploring Time-Series Through Force-Directed Timelines. , 2020, , .		0