

Marouen Ben Guebila

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

1,005
citations

1307594

7
h-index

996975

15
g-index

22
all docs

22
docs citations

22
times ranked

1799
citing authors

#	ARTICLE	IF	CITATIONS
1	GRAND: a database of gene regulatory network models across human conditions. <i>Nucleic Acids Research</i> , 2022, 50, D610-D621.	14.5	31
2	Correction for Rando et al., "Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure". <i>MSystems</i> , 2022, , e0144721.	3.8	2
3	gpuZoo: Cost-effective estimation of gene regulatory networks using the Graphics Processing Unit. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac002.	3.2	1
4	Predicting genotype-specific gene regulatory networks. <i>Genome Research</i> , 2022, 32, 524-533.	5.5	9
5	An online notebook resource for reproducible inference, analysis and publication of gene regulatory networks. <i>Nature Methods</i> , 2022, 19, 511-513.	19.0	7
6	Gene Targeting in Disease Networks. <i>Frontiers in Genetics</i> , 2021, 12, 649942.	2.3	11
7	Dynamic flux balance analysis of whole-body metabolism for type 1 diabetes. <i>Nature Computational Science</i> , 2021, 1, 348-361.	8.0	11
8	Regulatory Network of PD1 Signaling Is Associated with Prognosis in Glioblastoma Multiforme. <i>Cancer Research</i> , 2021, 81, 5401-5412.	0.9	15
9	Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure. <i>MSystems</i> , 2021, 6, e0009521.	3.8	26
10	Identification and Development of Therapeutics for COVID-19. <i>MSystems</i> , 2021, 6, e0023321.	3.8	20
11	Gene regulatory network inference as relaxed graph matching. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2021, 35, 10263-10272.	4.9	3
12	VFFVA: dynamic load balancing enables large-scale flux variability analysis. <i>BMC Bioinformatics</i> , 2020, 21, 424.	2.6	6
13	Predicting gastrointestinal drug effects using contextualized metabolic models. <i>PLoS Computational Biology</i> , 2019, 15, e1007100.	3.2	16
14	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. <i>Nature Protocols</i> , 2019, 14, 639-702.	12.0	833
15	ACHR.cu: GPU-accelerated sampling of metabolic networks. <i>Journal of Open Source Software</i> , 2019, 4, 1363.	4.6	0