## Mohamed Helmy

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6970537/publications.pdf

Version: 2024-02-01

1039880 996849 1,146 15 9 citations h-index papers

g-index 20 20 20 1956 docs citations times ranked citing authors all docs

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#	Article	IF	CITATIONS
1	Identifying toggle genes from transcriptome-wide scatter: A new perspective for biological regulation. Genomics, 2022, 114, 215-228.	1.3	6
2	The transformation of our food system using cellular agriculture: What lies ahead and who will lead it?. Trends in Food Science and Technology, 2022, 127, 368-376.	7.8	12
3	OpenPIP: An Open-source Platform for Hosting, Visualizing and Analyzing Protein Interaction Data. Journal of Molecular Biology, 2022, 434, 167603.	2.0	3
4	A high rate of COVID-19 vaccine hesitancy in a large-scale survey on Arabs. ELife, 2021, 10, .	2.8	87
5	GeneCloudOmics: A Data Analytic Cloud Platform for High-Throughput Gene Expression Analysis. Frontiers in Bioinformatics, 2021, $1$ , .	1.0	4
6	Systems Biology to Understand and Regulate Human Retroviral Proinflammatory Response. Frontiers in Immunology, 2021, 12, 736349.	2.2	5
7	Systems biology approaches integrated with artificial intelligence for optimized metabolic engineering. Metabolic Engineering Communications, 2020, 11, e00149.	1.9	46
8	A reference map of the human binary protein interactome. Nature, 2020, 580, 402-408.	13.7	724
9	Identification of effective DNA barcodes for Triticum plants through chloroplast genome-wide analysis. Computational Biology and Chemistry, 2017, 71, 20-31.	1.1	28
10	Omics and System Biology Approaches in Plant Stress Research. SpringerBriefs in Systems Biology, 2017, , 21-34.	0.1	35
11	Limited resources of genome sequencing in developing countries: Challenges and solutions. Applied & Translational Genomics, 2016, 9, 15-19.	2.1	91
12	Ten Simple Rules for Developing Public Biological Databases. PLoS Computational Biology, 2016, 12, e1005128.	1.5	27
13	FN-Identify: Novel Restriction Enzymes-Based Method for Bacterial Identification in Absence of Genome Sequencing. Advances in Bioinformatics, 2015, 2015, 1-14.	5.7	5
14	Predicting Novel Features of Toll-Like Receptor 3 Signaling in Macrophages. PLoS ONE, 2009, 4, e4661.	1.1	25
15	Signaling Flux Redistribution at Toll-Like Receptor Pathway Junctions. PLoS ONE, 2008, 3, e3430.	1.1	43