

Magbubah Essack

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

2,589
citations

257101

24
h-index

214527

47
g-index

69
all docs

69
docs citations

69
times ranked

3800
citing authors

#	ARTICLE	IF	CITATIONS
1	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	9.4	408
2	Leptin and Obesity: Role and Clinical Implication. <i>Frontiers in Endocrinology</i> , 2021, 12, 585887.	1.5	363
3	Rhizosphere microbiome metagenomics of gray mangroves (<i>Avicennia marina</i>) in the Red Sea. <i>Gene</i> , 2016, 576, 626-636.	1.0	116
4	Glutathione Redox Homeostasis and Its Relation to Cardiovascular Disease. <i>Oxidative Medicine and Cellular Longevity</i> , 2019, 2019, 1-14.	1.9	89
5	DASPFIND: new efficient method to predict drug-target interactions. <i>Journal of Cheminformatics</i> , 2016, 8, 15.	2.8	88
6	Conotoxins that Confer Therapeutic Possibilities. <i>Marine Drugs</i> , 2012, 10, 1244-1265.	2.2	86
7	Comparison Study of Computational Prediction Tools for Drug-Target Binding Affinities. <i>Frontiers in Chemistry</i> , 2019, 7, 782.	1.8	85
8	The Genome Sequence of the Wild Tomato <i>Solanum pimpinellifolium</i> Provides Insights Into Salinity Tolerance. <i>Frontiers in Plant Science</i> , 2018, 9, 1402.	1.7	69
9	Bioprospecting desert plant <i>Bacillus</i> endophytic strains for their potential to enhance plant stress tolerance. <i>Scientific Reports</i> , 2019, 9, 18154.	1.6	69
10	Machine learning and deep learning methods that use omics data for metastasis prediction. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5008-5018.	1.9	69
11	Deciphering the transcriptional circuitry of microRNA genes expressed during human monocytic differentiation. <i>BMC Genomics</i> , 2009, 10, 595.	1.2	65
12	TcoF-DB v2: update of the database of human and mouse transcription co-factors and transcription factor interactions. <i>Nucleic Acids Research</i> , 2017, 45, D145-D150.	6.5	63
13	DTiGEMS+: drug-target interaction prediction using graph embedding, graph mining, and similarity-based techniques. <i>Journal of Cheminformatics</i> , 2020, 12, 44.	2.8	62
14	Insights into the Transcriptional Architecture of Behavioral Plasticity in the Honey Bee <i>Apis mellifera</i> . <i>Scientific Reports</i> , 2015, 5, 11136.	1.6	59
15	Recently Confirmed Apoptosis-Inducing Lead Compounds Isolated from Marine Sponge of Potential Relevance in Cancer Treatment. <i>Marine Drugs</i> , 2011, 9, 1580-1606.	2.2	55
16	Atherosclerosis Linked to Aberrant Amino Acid Metabolism and Immunosuppressive Amino Acid Catabolizing Enzymes. <i>Frontiers in Immunology</i> , 2020, 11, 551758.	2.2	44
17	DpubChem: a web tool for QSAR modeling and high-throughput virtual screening. <i>Scientific Reports</i> , 2018, 8, 9110.	1.6	40
18	Database for exploration of functional context of genes implicated in ovarian cancer. <i>Nucleic Acids Research</i> , 2009, 37, D820-D823.	6.5	37

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19	A novel method for improved accuracy of transcription factor binding site prediction. <i>Nucleic Acids Research</i> , 2018, 46, e72-e72.	6.5	35
20	DEOP: a database on osmoprotectants and associated pathways. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	1.4	34
21	Splice2Deep: An ensemble of deep convolutional neural networks for improved splice site prediction in genomic DNA. <i>Gene</i> , 2020, 763, 100035.	2.3	33
22	Bioprospecting Red Sea Coastal Ecosystems for Culturable Microorganisms and Their Antimicrobial Potential. <i>Marine Drugs</i> , 2016, 14, 165.	2.2	30
23	FARNA: knowledgebase of inferred functions of non-coding RNA transcripts. <i>Nucleic Acids Research</i> , 2017, 45, gkw973.	6.5	30
24	Aerobic methanotrophic communities at the Red Sea brine-seawater interface. <i>Frontiers in Microbiology</i> , 2014, 5, 487.	1.5	29
25	DTi2Vec: Drug-target interaction prediction using network embedding and ensemble learning. <i>Journal of Cheminformatics</i> , 2021, 13, 71.	2.8	27
26	Metagenomics as a preliminary screen for antimicrobial bioprospecting. <i>Gene</i> , 2016, 594, 248-258.	1.0	26
27	Distinct profiling of antimicrobial peptide families. <i>Bioinformatics</i> , 2015, 31, 849-856.	1.8	25
28	The X Files: The Mystery of X Chromosome Instability in Alzheimer's Disease. <i>Frontiers in Genetics</i> , 2019, 10, 1368.	1.1	25
29	A low-cost flow cytometric assay for the detection and quantification of apoptosis using an anionic halogenated fluorescein dye. <i>BioTechniques</i> , 2008, 45, 317-320.	0.8	24
30	DDEC: Dragon database of genes implicated in esophageal cancer. <i>BMC Cancer</i> , 2009, 9, 219.	1.1	24
31	Affinity2Vec: drug-target binding affinity prediction through representation learning, graph mining, and machine learning. <i>Scientific Reports</i> , 2022, 12, 4751.	1.6	23
32	Role of C-Reactive Protein in Diabetic Inflammation. <i>Mediators of Inflammation</i> , 2022, 2022, 1-15.	1.4	22
33	Network analysis of microRNAs and their regulation in human ovarian cancer. <i>BMC Systems Biology</i> , 2011, 5, 183.	3.0	21
34	DES-ncRNA: A knowledgebase for exploring information about human micro and long noncoding RNAs based on literature-mining. <i>RNA Biology</i> , 2017, 14, 963-971.	1.5	21
35	Application and evaluation of knowledge graph embeddings in biomedical data. <i>PeerJ Computer Science</i> , 2021, 7, e341.	2.7	21
36	DRABAL: novel method to mine large high-throughput screening assays using Bayesian active learning. <i>Journal of Cheminformatics</i> , 2016, 8, 64.	2.8	20

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37	MetaCancer: A deep learning-based pan-cancer metastasis prediction model developed using multi-omics data. Computational and Structural Biotechnology Journal, 2021, 19, 4404-4411.	1.9	19
38	Hybrid model for efficient prediction of poly(A) signals in human genomic DNA. Methods, 2019, 166, 31-39.	1.9	18
39	In silico exploration of Red Sea Bacillus genomes for natural product biosynthetic gene clusters. BMC Genomics, 2018, 19, 382.	1.2	17
40	Redox control of vascular biology. BioFactors, 2020, 46, 246-262.	2.6	15
41	Mining Chemical Activity Status from High-Throughput Screening Assays. PLoS ONE, 2015, 10, e0144426.	1.1	15
42	Information Exploration System for Sickle Cell Disease and Repurposing of Hydroxyfasudil. PLoS ONE, 2013, 8, e65190.	1.1	14
43	DES-Mutation: System for Exploring Links of Mutations and Diseases. Scientific Reports, 2018, 8, 13359.	1.6	13
44	DESM: portal for microbial knowledge exploration systems. Nucleic Acids Research, 2016, 44, D624-D633.	6.5	12
45	In silico screening for candidate chassis strains of free fatty acid-producing cyanobacteria. BMC Genomics, 2017, 18, 33.	1.2	11
46	Chemical Compounds Toxic to Invertebrates Isolated from Marine Cyanobacteria of Potential Relevance to the Agricultural Industry. Toxins, 2014, 6, 3058-3076.	1.5	10
47	Building a bio-based industry in the Middle East through harnessing the potential of the Red Sea biodiversity. Applied Microbiology and Biotechnology, 2017, 101, 4837-4851.	1.7	10
48	Predicting Bone Metastasis Using Gene Expression-Based Machine Learning Models. Frontiers in Genetics, 2021, 12, 771092.	1.1	10
49	Levothyroxine Treatment and the Risk of Cardiac Arrhythmias – Focus on the Patient Submitted to Thyroid Surgery. Frontiers in Endocrinology, 2021, 12, 758043.	1.5	9
50	DES-TOMATO: A Knowledge Exploration System Focused On Tomato Species. Scientific Reports, 2017, 7, 5968.	1.6	8
51	Literature-Based Enrichment Insights into Redox Control of Vascular Biology. Oxidative Medicine and Cellular Longevity, 2019, 2019, 1-16.	1.9	8
52	Mining biosynthetic gene clusters in Virgibacillus genomes. BMC Genomics, 2019, 20, 696.	1.2	7
53	PATH ⁸ : A Tool That Facilitates the Searching for Heterologous Biosynthetic Routes. ACS Synthetic Biology, 2020, 9, 3217-3227.	1.9	7
54	Comparative genomics study reveals Red Sea Bacillus with characteristics associated with potential microbial cell factories (MCFs). Scientific Reports, 2019, 9, 19254.	1.6	6

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55	Automated Counting of Colony Forming Units Using Deep Transfer Learning From a Model for Congested Scenes Analysis. IEEE Access, 2020, 8, 164340-164346.	2.6	6
56	Metastatic State of Colorectal Cancer can be Accurately Predicted with Methylome. , 2019, , .		6
57	Combining biomedical knowledge graphs and text to improve predictions for drug-target interactions and drug-indications. PeerJ, 2022, 10, e13061.	0.9	6
58	HbA1C as a marker of retrograde glycaemic control in diabetes patient with coâ€existed betaâ€thalassaemia: A case report and a literature review. Journal of Clinical Pharmacy and Therapeutics, 2020, 45, 379-383.	0.7	5
59	BioPS: System for screening and assessment of biofuel-production potential of cyanobacteria. PLoS ONE, 2018, 13, e0202002.	1.1	4
60	DES-ROD: Exploring Literature to Develop New Links between RNA Oxidation and Human Diseases. Oxidative Medicine and Cellular Longevity, 2020, 2020, 1-13.	1.9	3
61	Computational Drug-target Interaction Prediction based on Graph Embedding and Graph Mining. , 2020, , .		3
62	Identification of estrogen responsive genes using esophageal squamous cell carcinoma (ESCC) as a model. BMC Systems Biology, 2012, 6, 135.	3.0	2
63	Genes and comorbidities of thyroid cancer. Informatics in Medicine Unlocked, 2021, 25, 100680.	1.9	2
64	Draft Genome Sequences of Four <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Enteritidis Strains Implicated in Infections of Avian and Human Hosts. Genome Announcements, 2018, 6, .	0.8	1
65	Antioxidant enzymes expression in lymphocytes of patients undergoing carotid endarterectomy. Medical Hypotheses, 2020, 134, 109419.	0.8	1
66	DES-Tcell is a knowledgebase for exploring immunology-related literature. Scientific Reports, 2021, 11, 14344.	1.6	1