

Zeti-Azura Mohamed-Hussein

List of Publications by Year in descending order

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64
papers

626
citations

777949

13
h-index

799663

21
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all docs

65
docs citations

65
times ranked

784
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of Potential Genes Encoding Protein Transporters in <i>Arabidopsis thaliana</i> Glucosinolate (GSL) Metabolism. <i>Life</i> , 2022, 12, 326.	1.1	2
2	Protein-Protein Interaction (PPI) Network of Zebrafish Oestrogen Receptors: A Bioinformatics Workflow. <i>Life</i> , 2022, 12, 650.	1.1	1
3	TCGA-My: A Systematic Repository for Systems Biology of Malaysian Colorectal Cancer. <i>Life</i> , 2022, 12, 772.	1.1	0
4	ADAP is a possible negative regulator of glucosinolate biosynthesis in <i>Arabidopsis thaliana</i> based on clustering and gene expression analyses. <i>Journal of Plant Research</i> , 2021, 134, 327-339.	1.2	9
5	Molecular characterization and enzyme inhibition studies of NADP ⁺ - farnesol dehydrogenase from diamondback moth, <i>Plutella xylostella</i> (Lepidoptera: Plutellidae). <i>Bioscience, Biotechnology and Biochemistry</i> , 2021, 85, 1628-1638.	0.6	10
6	Dietary polyphenols suppress chronic inflammation by modulation of multiple inflammation-associated cell signaling pathways. <i>Journal of Nutritional Biochemistry</i> , 2021, 93, 108634.	1.9	65
7	Potential <i>Arabidopsis thaliana</i> glucosinolate genes identified from the co-expression modules using graph clustering approach. <i>PeerJ</i> , 2021, 9, e11876.	0.9	7
8	Comparative genome-wide analysis of WRKY, MADS-box and MYB transcription factor families in <i>Arabidopsis</i> and rice. <i>Scientific Reports</i> , 2021, 11, 19678.	1.6	38
9	Construction of Protein Expression Network. <i>Methods in Molecular Biology</i> , 2021, 2189, 119-132.	0.4	1
10	Graph cluster approach in identifying novel proteins and significant pathways involved in polycystic ovary syndrome. <i>Reproductive BioMedicine Online</i> , 2020, 40, 319-330.	1.1	9
11	A Comprehensive Gene Inventory for Glucosinolate Biosynthetic Pathway in <i>Arabidopsis thaliana</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 7281-7297.	2.4	67
12	Data on genome resequencing of pigmented and non-pigmented Malaysian rice varieties. <i>Data in Brief</i> , 2020, 31, 105806.	0.5	1
13	Computational Systems Analysis on Polycystic Ovarian Syndrome (PCOS). , 2020, , .		2
14	RNA-seq data from whole rice grains of pigmented and non-pigmented Malaysian rice varieties. <i>Data in Brief</i> , 2020, 30, 105432.	0.5	6
15	In silico analysis on the functional and structural impact of Rad50 mutations involved in DNA strand break repair. <i>PeerJ</i> , 2020, 8, e9197.	0.9	8
16	Investigating Metabolic Pathways and Networks. , 2019, , 489-503.		4
17	Discovery of Functional SNPs via Genome-Wide Exploration of Malaysian Pigmented Rice Varieties. <i>International Journal of Genomics</i> , 2019, 2019, 1-12.	0.8	4
18	Protein-Protein Interaction Network Analysis Reveals Several Diseases Highly Associated with Polycystic Ovarian Syndrome. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2959.	1.8	31

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19	Transcriptomic View of <i>Jatropha curcas</i> L. Inflorescence. , 2019, , 111-130.		0
20	SuCComBase: a manually curated repository of plant sulfur-containing compounds. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	10
21	Evaluation of potential molecular interaction between quorum sensing receptor, LuxP and grouper fatty acids: in-silico screening and simulation. PeerJ, 2019, 7, e6568.	0.9	8
22	Structural and kinetic studies of a novel nerol dehydrogenase from <i>Persicaria minor</i> , a nerol-specific enzyme for citral biosynthesis. Plant Physiology and Biochemistry, 2018, 123, 359-368.	2.8	15
23	Citral dehydrogenase involved in geraniol oxidation pathway: purification, characterization and kinetic studies from <i>Persicaria minor</i> (<i>Polygonum minus</i> Huds.). Journal of Plant Biochemistry and Biotechnology, 2018, 27, 1-12.	0.9	2
24	RNA-seq data of the <i>Jatropha curcas</i> L. shoot system. Data in Brief, 2018, 21, 71-74.	0.5	1
25	An integration of phenotypic and transcriptomic data analysis reveals yield-related hub genes in <i>Jatropha curcas</i> inflorescence. PLoS ONE, 2018, 13, e0203441.	1.1	4
26	Somatic embryogenesis-related gene expression and functional genomics in mangosteen. Plant Gene, 2018, 15, 51-66.	1.4	4
27	A gene co-expression network model identifies yield-related vicinity networks in <i>Jatropha curcas</i> shoot system. Scientific Reports, 2018, 8, 9211.	1.6	5
28	Reconstruction of <i>Curcuma aeruginosa</i> Secondary Metabolite Biosynthetic Pathway using Omics Data. Sains Malaysiana, 2018, 47, 2985-2992.	0.3	1
29	Reconstruction of the Transcriptional Regulatory Network in <i>Arabidopsis thaliana</i> Aliphatic Glucosinolate Biosynthetic Pathway. Sains Malaysiana, 2018, 47, 2993-3002.	0.3	8
30	Crystal structure and functional analysis of human C1ORF123. PeerJ, 2018, 6, e5377.	0.9	7
31	Transcriptome analysis of reproductive tissue differentiation in <i>Jatropha curcas</i> Linn.. Genomics Data, 2017, 13, 11-14.	1.3	4
32	PCOSBase: a manually curated database of polycystic ovarian syndrome. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	10
33	Transcriptome analysis of <i>Polygonum minus</i> reveals candidate genes involved in important secondary metabolic pathways of phenylpropanoids and flavonoids. PeerJ, 2017, 5, e2938.	0.9	37
34	Cloning, expression, purification, crystallization and X-ray crystallographic analysis of recombinant human C1ORF123 protein. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 207-213.	0.4	1
35	RNA-seq analysis for secondary metabolite pathway gene discovery in <i>Polygonum minus</i> . Genomics Data, 2016, 7, 12-13.	1.3	20
36	Novel NAD ⁺ -Farnesal Dehydrogenase from <i>Polygonum minus</i> Leaves. Purification and Characterization of Enzyme in Juvenile Hormone III Biosynthetic Pathway in Plant. PLoS ONE, 2016, 11, e0161707.	1.1	4

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37	Purification and Characterization of a Novel NAD(P) ⁺ -Farnesol Dehydrogenase from <i>Polygonum minus</i> Leaves. <i>PLoS ONE</i> , 2015, 10, e0143310.	1.1	13
38	An Improved Particle Swarm Optimization via Velocity-Based Reinitialization for Feature Selection. <i>Communications in Computer and Information Science</i> , 2015, , 3-12.	0.4	2
39	Functional Characterization of Sesquiterpene Synthase from <i>Polygonum minus</i> . <i>Scientific World Journal</i> , The, 2014, 2014, 1-11.	0.8	15
40	Transcriptome profiling of genes induced by salicylic acid and methyl jasmonate in <i>Polygonum minus</i> . <i>Molecular Biology Reports</i> , 2013, 40, 2231-2241.	1.0	24
41	Optimizing Big Data in Bioinformatics with Swarm Algorithms. , 2013, , .		8
42	Draft Genome Sequences of Four Nosocomial Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) Strains (PPUKM-261-2009, PPUKM-332-2009, PPUKM-377-2009, and PPUKM-775-2009) Representative of Dominant MRSA Pulsotypes Circulating in a Malaysian University Teaching Hospital. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
43	Improving Molecular Dynamics Simulation Performance on Low-Cost Systems. <i>Computing in Science and Engineering</i> , 2013, 15, 64-70.	1.2	0
44	Feature Selection on Pectin Lyase-Like Enzyme Using Computational Methods. <i>Advanced Science Letters</i> , 2013, 19, 3374-3380.	0.2	0
45	Flavonoid Biosynthesis Genes Putatively Identified in the Aromatic Plant <i>Polygonum minus</i> via Expressed Sequences Tag (EST) Analysis. <i>International Journal of Molecular Sciences</i> , 2012, 13, 2692-2706.	1.8	17
46	An intelligent data pre-processing of complex datasets. <i>Intelligent Data Analysis</i> , 2012, 16, 305-325.	0.4	14
47	In vitro conservation of Malaysian biodiversityâ€™ achievements, challenges and future directions. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2011, 47, 26-36.	0.9	19
48	Identification of cDNAs for jasmonic acid-responsive genes in <i>Polygonum minus</i> roots by suppression subtractive hybridization. <i>Acta Physiologiae Plantarum</i> , 2011, 33, 283-294.	1.0	18
49	Velocity-based reinitialisation approach in Particle Swarm Optimisation for feature selection. , 2011, , .		3
50	A protein short motif search tool using amino acid sequence and their secondary structure assignment. <i>Bioinformation</i> , 2011, 7, 304-306.	0.2	3
51	EuDBase: An online resource for automated EST analysis pipeline (ESTFrontier) and database for red seaweed <i>Eucheuma denticulatum</i> . <i>Bioinformation</i> , 2011, 7, 157-162.	0.2	1
52	Simulation of a Petri net-based Model of the Terpenoid Biosynthesis Pathway. <i>BMC Bioinformatics</i> , 2010, 11, 83.	1.2	7
53	Multivariate filter and PSO in protein function classification. , 2010, , .		1
54	Integrating Rough Set Theory and Particle Swarm Optimisation in feature selection. , 2010, , .		2

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55	Bioinformatics in Malaysia: Hope, Initiative, Effort, Reality, and Challenges. PLoS Computational Biology, 2009, 5, e1000457.	1.5	13
56	Construction of a polycystic ovarian syndrome (PCOS) pathway based on the interactions of PCOS-related proteins retrieved from bibliomic data. Theoretical Biology and Medical Modelling, 2009, 6, 18.	2.1	28
57	The Phylogenetic Tree of RNA Polymerase Constructed Using MOM Method. , 2009, , .		0
58	Experimental Study of Different FSAs in Classifying Protein Function. , 2009, , .		3
59	Filter-wrapper approach to feature selection using RST-DPSO for mining protein function. , 2009, , .		4
60	Feature selection and classification of protein subfamilies using Rough Sets. , 2009, , .		7
61	Data mining framework for protein function prediction. , 2008, , .		3
62	Predicting Dynamic Behavior of a Biological System Using ANNs. AIP Conference Proceedings, 2008, , .	0.3	0
63	Mosquito Repellent Activity of the Methanol Extracts of Some Ascidian Species. Pharmaceutical Biology, 2002, 40, 358-361.	1.3	6
64	Insecticidal Activity of the Methanol Extracts of Some Tunicate Species against Aedes aegypti and Anopheles maculatus. Pharmaceutical Biology, 2001, 39, 213-216.	1.3	5