

Mohd Firdaus-Raih

List of Publications by Year in descending order

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papers

736
citations

566801

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71
all docs

71
docs citations

71
times ranked

1109
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular basis of specificity and deamidation of eIF4A by Burkholderia Lethal Factor 1. <i>Communications Biology</i> , 2022, 5, 272.	2.0	2
2	GrAfSS: a webserver for substructure similarity searching and comparisons in the structures of proteins and RNA. <i>Nucleic Acids Research</i> , 2022, 50, W375-W383.	6.5	3
3	Regulation of Glycine Cleavage and Detoxification by a Highly Conserved Glycine Riboswitch in <i>Burkholderia</i> spp.. <i>Current Microbiology</i> , 2021, 78, 2943-2955.	1.0	3
4	Calcium ion-selective electrode based on the facile synthesis of CuO over Cu wires. <i>Journal of Materials Science: Materials in Electronics</i> , 2021, 32, 20240-20251.	1.1	5
5	Graph Theoretical Methods and Workflows for Searching and Annotation of RNA Tertiary Base Motifs and Substructures. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8553.	1.8	2
6	Side chain similarity comparisons for integrated drug repositioning and potential toxicity assessments in epidemic response scenarios: The case for COVID-19. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2931-2944.	1.9	4
7	Molecular Characterisation of <i>Eimeria tenella</i> Porin, A Potential Anticoccidial Drug Target. <i>Sains Malaysiana</i> , 2020, 49, 755-764.	0.3	1
8	Computational Design and Experimental Implementation of Synthetic Riboswitches and Riboregulators. , 2019, , 568-573.		0
9	Identifying Functional Relationships Via the Annotation and Comparison of Three-Dimensional Amino Acid Arrangements in Protein Structures. , 2019, , 620-630.		0
10	Predicting RNA-RNA Interactions in Three-Dimensional Structures. , 2019, , 546-553.		1
11	Structural Genomics. , 2019, , 722-728.		0
12	Inference of Horizontal Gene Transfer: Gaining Insights Into Evolution via Lateral Acquisition of Genetic Material. , 2019, , 953-964.		2
13	Engineering of Supramolecular RNA Structures. , 2019, , 535-545.		0
14	Computational Prediction of Nucleic Acid Binding Residues From Sequence. , 2019, , 678-687.		0
15	Applications of Ribosomal RNA Sequence and Structure Analysis for Extracting Evolutionary and Functional Insights. , 2019, , 554-567.		0
16	Predicting and data mining of RNA-ligand pattern interactions against RNA base residue arrangements. <i>AIP Conference Proceedings</i> , 2019, , .	0.3	0
17	Drug ReposER: a web server for predicting similar amino acid arrangements to known drug binding interfaces for potential drug repositioning. <i>Nucleic Acids Research</i> , 2019, 47, W350-W356.	6.5	20
18	Identification of Structural Motifs Using Networks of Hydrogen-Bonded Base Interactions in RNA Crystallographic Structures. <i>Crystals</i> , 2019, 9, 550.	1.0	6

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19	Computational discovery and annotation of conserved small open reading frames in fungal genomes. BMC Bioinformatics, 2019, 19, 551.	1.2	13
20	Unravelling the adaptation strategies employed by Glaciozyma antarctica PI12 on Antarctic sea ice. Marine Environmental Research, 2018, 137, 169-176.	1.1	14
21	Reconstruction of Large-Scale Gene Regulatory Networks Using Regression-based Models. , 2018, , .		0
22	Comparative analysis of nucleus-encoded plastid-targeting proteins in Rafflesia cantleyi against photosynthetic and non-photosynthetic representatives reveals orthologous systems with potentially divergent functions. Scientific Reports, 2018, 8, 17258.	1.6	20
23	Computational mining for hypothetical patterns of amino acid side chains in protein data bank (PDB). AIP Conference Proceedings, 2018, , .	0.3	0
24	The Glaciozyma antarctica genome reveals an array of systems that provide sustained responses towards temperature variations in a persistently cold habitat. PLoS ONE, 2018, 13, e0189947.	1.1	45
25	Analisis dan Penyaringan Data Lewah Interaksi Kelompok Bes Berikatan Hidrogen dalam Struktur RNA 3-Dimensi. Sains Malaysiana, 2018, 47, 1731-1739.	0.3	0
26	Seqping: gene prediction pipeline for plant genomes using self-training gene models and transcriptomic data. BMC Bioinformatics, 2017, 18, 1-7.	1.2	25
27	Evidence-based gene models for structural and functional annotations of the oil palm genome. Biology Direct, 2017, 12, 21.	1.9	24
28	Identification of sRNA mediated responses to nutrient depletion in Burkholderia pseudomallei. Scientific Reports, 2017, 7, 17173.	1.6	11
29	Nematode Peptides with Host-Directed Anti-inflammatory Activity Rescue Caenorhabditis elegans from a Burkholderia pseudomallei Infection. Frontiers in Microbiology, 2016, 7, 1436.	1.5	12
30	An analysis of simple computational strategies to facilitate the design of functional molecular information processors. BMC Bioinformatics, 2016, 17, 438.	1.2	1
31	Self-assembly programming of DNA polyominoes. Journal of Biotechnology, 2016, 236, 141-151.	1.9	2
32	InterRNA: a database of base interactions in RNA structures. Nucleic Acids Research, 2016, 44, D266-D271.	6.5	18
33	Perigone Lobe Transcriptome Analysis Provides Insights into Rafflesia cantleyi Flower Development. PLoS ONE, 2016, 11, e0167958.	1.1	13
34	Pencirian Molekul Glikogen Sintase Kinase-3 daripada Eimeria tenella. Sains Malaysiana, 2016, 45, 1947-1957.	0.3	0
35	Characterization of Burkholderia pseudomallei protein BPSL1375 validates the Putative hemolytic activity of the COG3176 N-Acyltransferase family. BMC Microbiology, 2015, 15, 270.	1.3	6
36	Screening and expression of selected taxonomically conserved and unique hypothetical proteins in Burkholderia pseudomallei K96243. AIP Conference Proceedings, 2015, , .	0.3	0

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37	Comparative differential gene expression analysis of nucleus-encoded proteins for <i>Rafflesia cantleyi</i> against <i>Arabidopsis thaliana</i> . AIP Conference Proceedings, 2015, , .	0.3	0
38	Computational discovery of small open reading frames in <i>Bacillus lehensis</i> . AIP Conference Proceedings, 2015, , .	0.3	0
39	Divergent homologs of the predicted small RNA BpCand697 in <i>Burkholderia</i> spp.. AIP Conference Proceedings, 2015, , .	0.3	0
40	Identification and cloning of four riboswitches from <i>Burkholderia pseudomallei</i> strain K96243. AIP Conference Proceedings, 2015, , .	0.3	0
41	Identification and characterization of secreted proteins in <i>Eimeria tenella</i> . AIP Conference Proceedings, 2015, , .	0.3	0
42	Identification of small open reading frames in the <i>Glaciozyma antarctica</i> genome. AIP Conference Proceedings, 2015, , .	0.3	2
43	Structure prediction of Fe(II) 2-oxoglutarate dioxygenase from a psychrophilic yeast <i>Glaciozyma antarctica</i> PI12. AIP Conference Proceedings, 2015, , .	0.3	1
44	A computational approach for the annotation of hydrogen-bonded base interactions in crystallographic structures of the ribozymes. AIP Conference Proceedings, 2015, , .	0.3	1
45	DNA AMPLIFICATION OPTIMIZATION AND CLONING OF SEVERAL TARGET GENES FROM BURKHOLDERIA PSEUDOMALLEI. Jurnal Teknologi (Sciences and Engineering), 2015, 77, .	0.3	0
46	Reconstructing gene regulatory networks from knock-out data using Gaussian Noise Model and Pearson Correlation Coefficient. Computational Biology and Chemistry, 2015, 59, 3-14.	1.1	54
47	DNA Tetrominoes: The Construction of DNA Nanostructures Using Self-Organised Heterogeneous Deoxyribonucleic Acids Shapes. PLoS ONE, 2015, 10, e0134520.	1.1	3
48	Draft Genome Sequence of <i>Erwinia mallotivora</i> BT-MARDI, Causative Agent of Papaya Dieback Disease. Genome Announcements, 2014, 2, .	0.8	15
49	Identification of the conserved hypothetical protein BPSL0317 in <i>Burkholderia pseudomallei</i> K96243. , 2014, , .		0
50	COGNAC: a web server for searching and annotating hydrogen-bonded base interactions in RNA three-dimensional structures. Nucleic Acids Research, 2014, 42, W382-W388.	6.5	14
51	Crystallization and preliminary crystallographic studies of the hypothetical protein BPSL1038 from <i>Burkholderia pseudomallei</i> . Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1697-1700.	0.4	1
52	The genome of the Tiger Milk mushroom, <i>Lignosus rhinocerotis</i> , provides insights into the genetic basis of its medicinal properties. BMC Genomics, 2014, 15, 635.	1.2	65
53	A comparative genomic analysis of the alkali-tolerant soil bacterium <i>Bacillus lehensis</i> G1. Gene, 2014, 545, 253-261.	1.0	10
54	IMAAAGINE: a webserver for searching hypothetical 3D amino acid side chain arrangements in the Protein Data Bank. Nucleic Acids Research, 2013, 41, W432-W440.	6.5	18

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55	Reconstructing Gene Regulatory Networks from Homozygous and Heterozygous Deletion Data Using Gaussian Noise Model. , 2013, , .		0
56	Comparative Sequence and Structure Analysis Reveals the Conservation and Diversity of Nucleotide Positions and Their Associated Tertiary Interactions in the Riboswitches. PLoS ONE, 2013, 8, e73984.	1.1	16
57	Proteins of Unknown Function in the Protein Data Bank (PDB): An Inventory of True Uncharacterized Proteins and Computational Tools for Their Analysis. International Journal of Molecular Sciences, 2012, 13, 12761-12772.	1.8	41
58	SPRITE and ASSAM: web servers for side chain 3D-motif searching in protein structures. Nucleic Acids Research, 2012, 40, W380-W386.	6.5	45
59	Comparative Genome Sequence Analysis Reveals the Extent of Diversity and Conservation for Glycan-Associated Proteins in <i>Burkholderia</i> spp.. Comparative and Functional Genomics, 2012, 2012, 1-15.	2.0	2
60	NASSAM: a server to search for and annotate tertiary interactions and motifs in three-dimensional structures of complex RNA molecules. Nucleic Acids Research, 2012, 40, W35-W41.	6.5	18
61	Computational discovery and RT-PCR validation of novel <i>Burkholderia</i> conserved and <i>Burkholderia pseudomallei</i> unique sRNAs. BMC Genomics, 2012, 13, S13.	1.2	31
62	A <i>Burkholderia pseudomallei</i> Toxin Inhibits Helicase Activity of Translation Factor eIF4A. Science, 2011, 334, 821-824.	6.0	107
63	Novel base triples in RNA structures revealed by graph theoretical searching methods. BMC Bioinformatics, 2011, 12, S2.	1.2	19
64	Solvent accessibility in native and isolated domain environments: general features and implications to interface predictability. Biophysical Chemistry, 2005, 114, 63-69.	1.5	14
65	ProLysED. Applied Bioinformatics, 2005, 4, 147-150.	1.7	2
66	A nationwide biotechnology outreach and awareness program for Malaysian high schools. Electronic Journal of Biotechnology, 2005, 8, .	1.2	4
67	A predicted structure of the cytochrome c oxidase from <i>Burkholderia pseudomallei</i> . Electronic Journal of Biotechnology, 2003, 6, .	1.2	0
68	NBBnet - The National Biotechnology and Bioinformatics Network: A Malaysian initiative towards a national infrastructure for bioinformatics. Electronic Journal of Biotechnology, 2003, 6, .	1.2	0