

# Rozaimi Razali

## List of Publications by Year in descending order

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Version: 2024-02-01

23  
papers

763  
citations

567144

15  
h-index

610775

24  
g-index

25  
all docs

25  
docs citations

25  
times ranked

1524  
citing authors

#	ARTICLE	IF	CITATIONS
1	Qatar genome: Insights on genomics from the Middle East. <i>Human Mutation</i> , 2022, 43, 499-510.	1.1	29
2	Thousands of Qatari genomes inform human migration history and improve imputation of Arab haplotypes. <i>Nature Communications</i> , 2021, 12, 5929.	5.8	18
3	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
4	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
5	DES-Mutation: System for Exploring Links of Mutations and Diseases. <i>Scientific Reports</i> , 2018, 8, 13359.	1.6	13
6	Comparative genomic analysis of ten clinical <i>Streptococcus pneumoniae</i> collected from a Malaysian hospital reveal 31 new unique drug-resistant SNPs using whole genome sequencing. <i>Journal of Biomedical Science</i> , 2018, 25, 15.	2.6	3
7	In silico exploration of Red Sea <i>Bacillus</i> genomes for natural product biosynthetic gene clusters. <i>BMC Genomics</i> , 2018, 19, 382.	1.2	17
8	bTSSfinder: a novel tool for the prediction of promoters in cyanobacteria and <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2017, 33, 334-340.	1.8	80
9	DES-TOMATO: A Knowledge Exploration System Focused On Tomato Species. <i>Scientific Reports</i> , 2017, 7, 5968.	1.6	8
10	Identification of Putative Transmembrane Proteins Involved in Salinity Tolerance in <i>Chenopodium quinoa</i> by Integrating Physiological Data, RNAseq, and SNP Analyses. <i>Frontiers in Plant Science</i> , 2017, 8, 1023.	1.7	47
11	Genome wide profiling in oral squamous cell carcinoma identifies a four genetic marker signature of prognostic significance. <i>PLoS ONE</i> , 2017, 12, e0174865.	1.1	26
12	Next generation sequencing reveals the antibiotic resistant variants in the genome of <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2017, 12, e0182524.	1.1	34
13	Semantic prioritization of novel causative genomic variants. <i>PLoS Computational Biology</i> , 2017, 13, e1005500.	1.5	28
14	Transcriptome analysis of <i>Streptococcus pneumoniae</i> treated with the designed antimicrobial peptides, DM3. <i>Scientific Reports</i> , 2016, 6, 26828.	1.6	34
15	Metagenomics as a preliminary screen for antimicrobial bioprospecting. <i>Gene</i> , 2016, 594, 248-258.	1.0	26
16	Immortalization of epithelial cells in oral carcinogenesis as revealed by genome-wide array comparative genomic hybridization: A meta-analysis. <i>Head and Neck</i> , 2016, 38, E783-97.	0.9	6
17	Deciphering the Draft Genome of <i>Toxoplasma gondii</i> RH Strain. <i>PLoS ONE</i> , 2016, 11, e0157901.	1.1	28
18	Draft genome of <i>Brugia pahangi</i> : high similarity between <i>B. pahangi</i> and <i>B. malayi</i> . <i>Parasites and Vectors</i> , 2015, 8, 451.	1.0	19

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19	Autoantibody profile of patients infected with knowlesi malaria. <i>Clinica Chimica Acta</i> , 2015, 448, 33-38.	0.5	8
20	Draft genome of neurotropic nematode parasite <i>Angiostrongylus cantonensis</i> , causative agent of human eosinophilic meningitis. <i>Acta Tropica</i> , 2015, 148, 51-57.	0.9	16
21	A whole genome analyses of genetic variants in two Kelantan Malay individuals. <i>The HUGO Journal</i> , 2014, 8, 4.	4.1	3
22	Genome-Wide Analysis of Copy Number Variation Identifies Candidate Gene Loci Associated with the Progression of Non-Alcoholic Fatty Liver Disease. <i>PLoS ONE</i> , 2014, 9, e95604.	1.1	30
23	Protein-protein interaction sites are hot spots for disease-associated nonsynonymous SNPs. <i>Human Mutation</i> , 2012, 33, 359-363.	1.1	149