

Thiruvarangan Ramaraj

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5904902/publications.pdf>

Version: 2024-02-01

41
papers

1,842
citations

331670

21
h-index

345221

36
g-index

45
all docs

45
docs citations

45
times ranked

3790
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome, epigenome and RNA sequences of monozygotic twins discordant for multiple sclerosis. <i>Nature</i> , 2010, 464, 1351-1356.	27.8	463
2	Composition Diversity and Abundance of Gut Microbiome in Prediabetes and Type 2 Diabetes. <i>Journal of Diabetes and Obesity</i> , 2015, 2, 108-114.	0.2	159
3	Antigen-antibody interface properties: Composition, residue interactions, and features of 53 non-redundant structures. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 520-532.	2.3	148
4	Genome and secretome analysis of the hemibiotrophic fungal pathogen, <i>Moniliophthora roreri</i> , which causes frosty pod rot disease of cacao: mechanisms of the biotrophic and necrotrophic phases. <i>BMC Genomics</i> , 2014, 15, 164.	2.8	107
5	Genome and evolution of the arbuscular mycorrhizal fungus <i>Diversispora epigaea</i> (formerly <i>Tj ETQq1</i>)	7.3	88
6	Exploring structural variation and gene family architecture with De Novo assemblies of 15 <i>Medicago</i> genomes. <i>BMC Genomics</i> , 2017, 18, 261.	2.8	87
7	De Novo Genome Sequence Assemblies of <i>Gossypium raimondii</i> and <i>Gossypium turneri</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3079-3085.	1.8	72
8	The transcriptome landscape of early maize meiosis. <i>BMC Plant Biology</i> , 2014, 14, 118.	3.6	66
9	Novel Meiotic miRNAs and Indications for a Role of PhasiRNAs in Meiosis. <i>Frontiers in Plant Science</i> , 2016, 7, 762.	3.6	56
10	The complete chloroplast genome sequences for four <i>Amaranthus</i> species (Amaranthaceae). <i>Applications in Plant Sciences</i> , 2016, 4, 1600063.	2.1	54
11	Strategies for optimizing BioNano and Dovetail explored through a second reference quality assembly for the legume model, <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2017, 18, 578.	2.8	54
12	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017, 18, 541.	2.8	51
13	Use of a draft genome of coffee (<i>Coffea arabica</i>) to identify SNPs associated with caffeine content. <i>Plant Biotechnology Journal</i> , 2018, 16, 1756-1766.	8.3	48
14	The Genome Sequence of <i>Gossypoides kirkii</i> Illustrates a Descending Dysploidy in Plants. <i>Frontiers in Plant Science</i> , 2019, 10, 1541.	3.6	41
15	Crude oil impairs immune function and increases susceptibility to pathogenic bacteria in southern flounder. <i>PLoS ONE</i> , 2017, 12, e0176559.	2.5	38
16	Characterization, correction and de novo assembly of an Oxford Nanopore genomic dataset from <i>Agrobacterium tumefaciens</i> . <i>Scientific Reports</i> , 2016, 6, 28625.	3.3	35
17	De novo assembly of a tadpole shrimp (<i>Triops newberryi</i>) transcriptome and preliminary differential gene expression analysis. <i>Molecular Ecology Resources</i> , 2017, 17, 161-171.	4.8	28
18	Salt and oxidative stresses uniquely regulate tomato cytokinin levels and transcriptomic response. <i>Plant Direct</i> , 2018, 2, e00071.	1.9	28

#	ARTICLE	IF	CITATIONS
19	Comparative Genomics of an Unusual Biogeographic Disjunction in the Cotton Tribe (Gossypieae) Yields Insights into Genome Downsizing. <i>Genome Biology and Evolution</i> , 2017, 9, 3328-3344.	2.5	26
20	Sequencing-based large-scale genomics approaches with small numbers of isolated maize meiocytes. <i>Frontiers in Plant Science</i> , 2014, 5, 57.	3.6	25
21	Histone Citrullination Represses MicroRNA Expression, Resulting in Increased Oncogene mRNAs in Somatolactotrope Cells. <i>Molecular and Cellular Biology</i> , 2018, 38, .	2.3	22
22	Gene Evolutionary Trajectories and GC Patterns Driven by Recombination in <i>Zea mays</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1433.	3.6	16
23	Genome Sequence of <i>Janthinobacterium</i> sp. CG23_2, a Viocaine-Producing Isolate from an Antarctic Supraglacial Stream. <i>Genome Announcements</i> , 2016, 4, .	0.8	16
24	Zinc-Dependent Transcriptional Regulation in <i>Paracoccus denitrificans</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 569.	3.5	15
25	Repertoire of virus-derived small RNAs produced by mosquito and mammalian cells in response to dengue virus infection. <i>Virology</i> , 2015, 476, 54-60.	2.4	13
26	Augmenting Chinese hamster genome assembly by identifying regions of high confidence. <i>Biotechnology Journal</i> , 2016, 11, 1151-1157.	3.5	11
27	Molecular and Biological Characterization of a New Isolate of Guinea Pig Cytomegalovirus. <i>Viruses</i> , 2014, 6, 448-475.	3.3	10
28	Pangenome-Wide Association Studies with Frequented Regions. , 2019, , .		10
29	Complete Genome Sequence of <i>Streptomyces venezuelae</i> ATCC 15439, Producer of the Methymycin/Pikromycin Family of Macrolide Antibiotics, Using PacBio Technology. <i>Genome Announcements</i> , 2016, 4, .	0.8	9
30	Exploring Frequented Regions in Pan-Genomic Graphs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1424-1435.	3.0	9
31	<i>Janthinobacterium</i> CG23_2: Comparative Genome Analysis Reveals Enhanced Environmental Sensing and Transcriptional Regulation for Adaptation to Life in an Antarctic Supraglacial Stream. <i>Microorganisms</i> , 2019, 7, 454.	3.6	7
32	High-Quality Draft Genome Sequence of <i>Actinobacterium Kibdelosporangium</i> sp. MJ126-NF4, Producer of Type II Polyketide Azicemicins, Using Illumina and PacBio Technologies. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
33	Draft Genome Sequence of a Metabolically Diverse Antarctic Supraglacial Stream Organism, <i>Polaromonas</i> sp. Strain CG9_12, Determined Using Pacific Biosciences Single-Molecule Real-Time Sequencing Technology. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
34	Genome Sequence of a Novel, Newly Identified Isolate of Guinea Pig Cytomegalovirus, the CIDMTR Strain. <i>Genome Announcements</i> , 2013, 1, .	0.8	3
35	Draft Genome Sequences of Vancomycin-Susceptible <i>Staphylococcus aureus</i> Related to Heterogeneous Vancomycin-Intermediate <i>S. aureus</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	3
36	Draft Genomes of Heterogeneous Vancomycin-Intermediate <i>Staphylococcus aureus</i> Strain MM66 and MM66 Derivatives with Altered Vancomycin Resistance Levels. <i>Genome Announcements</i> , 2014, 2, .	0.8	3

#	ARTICLE	IF	CITATIONS
37	Exploring Frequented Regions in Pan-Genomic Graphs. , 2017, , .		3
38	Cranberry-derived proanthocyanidins induce a differential transcriptomic response within <i>Candida albicans</i> urinary biofilms. PLoS ONE, 2018, 13, e0201969.	2.5	3
39	Poster: Pangenome-Wide Association Studies with Frequented Regions. , 2019, , .		1
40	Improved Hybrid Genome Assemblies of Two Strains of <i>Bacteroides xylanisolvens</i> , SD_CC_1b and SD_CC_2a, Obtained Using Illumina and 454 Sequencing Technologies. Genome Announcements, 2014, 2, .	0.8	0
41	Organelle Genomics: The Chloroplast Genome of Amaranth. Compendium of Plant Genomes, 2021, , 17-26.	0.5	0