

# Murukarthick Jayakodi

## List of Publications by Year in descending order

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Version: 2024-02-01

43  
papers

3,047  
citations

361045

20  
h-index

301761

39  
g-index

47  
all docs

47  
docs citations

47  
times ranked

4876  
citing authors

#	ARTICLE	IF	CITATIONS
1	Uncovering the novel characteristics of Asian honey bee, <i>Apis cerana</i> , by whole genome sequencing. <i>BMC Genomics</i> , 2015, 16, 1.	1.2	1,445
2	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	13.7	314
3	Complete chloroplast and ribosomal sequences for 30 accessions elucidate evolution of <i>Oryza</i> AA genome species. <i>Scientific Reports</i> , 2015, 5, 15655.	1.6	169
4	Genome and evolution of the shade-requiring medicinal herb <i>Panax ginseng</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1904-1917.	4.1	136
5	Genome-wide characterization of long intergenic non-coding RNAs (lincRNAs) provides new insight into viral diseases in honey bees <i>Apis cerana</i> and <i>Apis mellifera</i> . <i>BMC Genomics</i> , 2015, 16, 680.	1.2	73
6	Ginseng Genome Database: an open-access platform for genomics of <i>Panax ginseng</i> . <i>BMC Plant Biology</i> , 2018, 18, 62.	1.6	73
7	Genome-wide SNP identification and QTL mapping for black rot resistance in cabbage. <i>BMC Plant Biology</i> , 2015, 15, 32.	1.6	63
8	Building pan-genome infrastructures for crop plants and their use in association genetics. <i>DNA Research</i> , 2021, 28, .	1.5	57
9	Comprehensive analysis of <i>Panax ginseng</i> root transcriptomes. <i>BMC Plant Biology</i> , 2015, 15, 138.	1.6	55
10	Transcriptome profiling and comparative analysis of <i>Panax ginseng</i> adventitious roots. <i>Journal of Ginseng Research</i> , 2014, 38, 278-288.	3.0	53
11	<i>Aegilops sharonensis</i> genome-assisted identification of stem rust resistance gene Sr62. <i>Nature Communications</i> , 2022, 13, 1607.	5.8	48
12	Transcriptome sequencing of two parental lines of cabbage ( <i>Brassica oleracea</i> L. var. capitata L.) and construction of an EST-based genetic map. <i>BMC Genomics</i> , 2014, 15, 149.	1.2	46
13	Rapid and Efficient FISH using Pre-Labeled Oligomer Probes. <i>Scientific Reports</i> , 2018, 8, 8224.	1.6	42
14	Identification of candidate UDP-glycosyltransferases involved in protopanaxadiol-type ginsenoside biosynthesis in <i>Panax ginseng</i> . <i>Scientific Reports</i> , 2018, 8, 11744.	1.6	41
15	Genome-Wide Comparative Analysis of 20 Miniature Inverted-Repeat Transposable Element Families in <i>Brassica rapa</i> and <i>B. oleracea</i> . <i>PLoS ONE</i> , 2014, 9, e94499.	1.1	38
16	Integrated Transcriptomic and Metabolomic Analysis of Five <i>Panax ginseng</i> Cultivars Reveals the Dynamics of Ginsenoside Biosynthesis. <i>Frontiers in Plant Science</i> , 2017, 8, 1048.	1.7	37
17	Re-exploration of Uâ€™s Triangle Brassica Species Based on Chloroplast Genomes and 45S nrDNA Sequences. <i>Scientific Reports</i> , 2018, 8, 7353.	1.6	36
18	Transcriptome analysis reveals in vitro cultured <i>Withania somnifera</i> leaf and root tissues as a promising source for targeted withanolide biosynthesis. <i>BMC Genomics</i> , 2015, 16, 14.	1.2	34

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19	Detection of QTLs associated with mungbean yellow mosaic virus (MYMV) resistance using the interspecific cross of <i>Vigna radiata</i> × <i>Vigna umbellata</i> . <i>Journal of Applied Genetics</i> , 2019, 60, 255-268.	1.0	31
20	Mitochondrial plastid DNA can cause DNA barcoding paradox in plants. <i>Scientific Reports</i> , 2020, 10, 6112.	1.6	30
21	Transcriptomes of Indian barnyard millet and barnyardgrass reveal putative genes involved in drought adaptation and micronutrient accumulation. <i>Acta Physiologiae Plantarum</i> , 2019, 41, 1.	1.0	22
22	Comparative analysis of the transcriptomes and primary metabolite profiles of adventitious roots of five <i>Panax ginseng</i> cultivars. <i>Journal of Ginseng Research</i> , 2017, 41, 60-68.	3.0	20
23	Genetic diversity in the barnyard millet ( <i>Echinochloa frumentacea</i> ) germplasms revealed by morphological traits and simple sequence repeat markers. <i>Current Plant Biology</i> , 2018, 14, 71-78.	2.3	20
24	Comparative transcriptome analysis of heat stress responsiveness between two contrasting ginseng cultivars. <i>Journal of Ginseng Research</i> , 2019, 43, 572-579.	3.0	20
25	Authentication of Golden-Berry <i>P. ginseng</i> Cultivar "Gumpoong"™ from a Landrace "Hwangsook"™ Based on Pooling Method Using Chloroplast-Derived Markers. <i>Plant Breeding and Biotechnology</i> , 2017, 5, 16-24.	0.3	19
26	BrassicaTED - a public database for utilization of miniature transposable elements in Brassica species. <i>BMC Research Notes</i> , 2014, 7, 379.	0.6	18
27	A Glimpse of <i>Panax ginseng</i> Genome Structure Revealed from Ten BAC Clone Sequences Obtained by SMRT Sequencing Platform. <i>Plant Breeding and Biotechnology</i> , 2017, 5, 25-35.	0.3	17
28	The complete chloroplast genome sequence of Indian barnyard millet, <i>Echinochloa frumentacea</i> (Poaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 79-80.	0.2	12
29	Identification of consistent QTL with large effect on anther extrusion in doubled haploid populations developed from spring wheat accessions in German Federal ex situ Genebank. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3035-3045.	1.8	12
30	QTL mapping in <i>Vigna radiata</i> × <i>Vigna umbellata</i> population uncovers major genomic regions associated with bruchid resistance. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	12
31	Sweet genes in melon and watermelon. <i>Nature Genetics</i> , 2019, 51, 1572-1573.	9.4	7
32	The Complete Chloroplast Genome Sequence and Intra-Species Diversity of <i>Rhus chinensis</i> . <i>Plant Breeding and Biotechnology</i> , 2017, 5, 243-251.	0.3	6
33	Dynamic Transcriptome Profiling of Mungbean Genotypes Unveil the Genes Respond to the Infection of Mungbean Yellow Mosaic Virus. <i>Pathogens</i> , 2022, 11, 190.	1.2	6
34	Advancing Grain Legumes Domestication and Evolution Studies with Genomics. <i>Plant and Cell Physiology</i> , 2022, 63, 1540-1553.	1.5	6
35	Discrimination and Authentication of <i>Eclipta prostrata</i> and <i>E. alba</i> Based on the Complete Chloroplast Genomes. <i>Plant Breeding and Biotechnology</i> , 2017, 5, 334-343.	0.3	4
36	A web accessible resource for investigating cassava phenomics and genomics information: BIOGEN BASE. <i>Bioinformatics</i> , 2011, 6, 391-392.	0.2	4

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37	A Glimpse of Panax ginseng Genome Structure Revealed from Ten BAC Clone Sequences Obtained by SMRT Sequencing Platform. <i>Plant Breeding and Biotechnology</i> , 2017, 5, 25-35.	0.3	3
38	The reinvention of potato. <i>Cell Research</i> , 2021, 31, 1144-1145.	5.7	2
39	The Barley and Wheat Pan-Genomes. <i>Methods in Molecular Biology</i> , 2022, 2443, 147-159.	0.4	2
40	Paithumbase - Biometrical Traits based Query System for Studying Mungbean [ <i>Vigna radiata</i> (L.) Wilczek] Phenomics. <i>International Journal of Applied Information Systems</i> , 2012, 4, 36-39.	0.1	1
41	High-Resolution Mapping of Barley mild mosaic virus Resistance Gene rym15. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	1
42	Ginseng Genome Structure and Evolution. <i>Compendium of Plant Genomes</i> , 2021, , 85-93.	0.3	0
43	Mining of Miniature Transposable Elements in Brassica Species at BrassicaTED. <i>Methods in Molecular Biology</i> , 2021, 2250, 69-74.	0.4	0