

# Murukarthick Jayakodi

## List of Publications by Year in descending order

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43  
papers

3,047  
citations

361413

20  
h-index

302126

39  
g-index

47  
all docs

47  
docs citations

47  
times ranked

4876  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamic Transcriptome Profiling of Mungbean Genotypes Unveil the Genes Respond to the Infection of Mungbean Yellow Mosaic Virus. <i>Pathogens</i> , 2022, 11, 190.	2.8	6
2	The Barley and Wheat Pan-Genomes. <i>Methods in Molecular Biology</i> , 2022, 2443, 147-159.	0.9	2
3	<i>Aegilops sharonensis</i> genome-assisted identification of stem rust resistance gene Sr62. <i>Nature Communications</i> , 2022, 13, 1607.	12.8	48
4	Advancing Grain Legumes Domestication and Evolution Studies with Genomics. <i>Plant and Cell Physiology</i> , 2022, 63, 1540-1553.	3.1	6
5	High-Resolution Mapping of Barley mild mosaic virus Resistance Gene rym15. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	1
6	Ginseng Genome Structure and Evolution. <i>Compendium of Plant Genomes</i> , 2021, , 85-93.	0.5	0
7	Mining of Miniature Transposable Elements in Brassica Species at BrassicaTED. <i>Methods in Molecular Biology</i> , 2021, 2250, 69-74.	0.9	0
8	The reinvention of potato. <i>Cell Research</i> , 2021, 31, 1144-1145.	12.0	2
9	Building pan-genome infrastructures for crop plants and their use in association genetics. <i>DNA Research</i> , 2021, 28, .	3.4	57
10	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	27.8	314
11	Mitochondrial plastid DNA can cause DNA barcoding paradox in plants. <i>Scientific Reports</i> , 2020, 10, 6112.	3.3	30
12	Comparative transcriptome analysis of heat stress responsiveness between two contrasting ginseng cultivars. <i>Journal of Ginseng Research</i> , 2019, 43, 572-579.	5.7	20
13	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.	3.6	12
14	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.	2.1	12
15	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.	1.9	31
16	Sweet genes in melon and watermelon. <i>Nature Genetics</i> , 2019, 51, 1572-1573.	21.4	7
17	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.	2.1	22
18	Genome and evolution of the shade-requiring medicinal herb <i>Panax ginseng</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1904-1917.	8.3	136

#	ARTICLE	IF	CITATIONS
19	Ginseng Genome Database: an open-access platform for genomics of <i>Panax ginseng</i> . <i>BMC Plant Biology</i> , 2018, 18, 62.	3.6	73
20	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.	4.7	20
21	Rapid and Efficient FISH using Pre-Labeled Oligomer Probes. <i>Scientific Reports</i> , 2018, 8, 8224.	3.3	42
22	Re-exploration of Uâ€™s Triangle Brassica Species Based on Chloroplast Genomes and 45S nrDNA Sequences. <i>Scientific Reports</i> , 2018, 8, 7353.	3.3	36
23	Identification of candidate UDP-glycosyltransferases involved in protopanaxadiol-type ginsenoside biosynthesis in <i>Panax ginseng</i> . <i>Scientific Reports</i> , 2018, 8, 11744.	3.3	41
24	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.	5.7	20
25	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.	3.6	37
26	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.	0.9	3
27	Authentication of Golden-Berry <i>P. ginseng</i> Cultivar â€™Gumpoongâ€™ from a Landrace â€™Hwangsookâ€™ Based on Pooling Method Using Chloroplast-Derived Markers. <i>Plant Breeding and Biotechnology</i> , 2017, 5, 16-24.	0.9	19
28	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.	0.9	17
29	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.	0.9	4
30	The Complete Chloroplast Genome Sequence and Intra-Species Diversity of <i>Rhus chinensis</i> . <i>Plant Breeding and Biotechnology</i> , 2017, 5, 243-251.	0.9	6
31	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.	0.4	12
32	Complete chloroplast and ribosomal sequences for 30 accessions elucidate evolution of <i>Oryza AA</i> genome species. <i>Scientific Reports</i> , 2015, 5, 15655.	3.3	169
33	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.	2.8	73
34	Uncovering the novel characteristics of Asian honey bee, <i>Apis cerana</i> , by whole genome sequencing. <i>BMC Genomics</i> , 2015, 16, 1.	2.8	1,445
35	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.	2.8	34
36	Genome-wide SNP identification and QTL mapping for black rot resistance in cabbage. <i>BMC Plant Biology</i> , 2015, 15, 32.	3.6	63

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37	Comprehensive analysis of Panax ginseng root transcriptomes. BMC Plant Biology, 2015, 15, 138.	3.6	55
38	Genome-Wide Comparative Analysis of 20 Miniature Inverted-Repeat Transposable Element Families in Brassica rapa and B. oleracea. PLoS ONE, 2014, 9, e94499.	2.5	38
39	Transcriptome sequencing of two parental lines of cabbage (Brassica oleracea L. var. capitata L.) and construction of an EST-based genetic map. BMC Genomics, 2014, 15, 149.	2.8	46
40	BrassicaTED - a public database for utilization of miniature transposable elements in Brassica species. BMC Research Notes, 2014, 7, 379.	1.4	18
41	Transcriptome profiling and comparative analysis of Panax ginseng adventitious roots. Journal of Ginseng Research, 2014, 38, 278-288.	5.7	53
42	Paithumbase - Biometrical Traits based Query System for Studying Mungbean [Vigna radiata (L.) Wilczek] Phenomics. International Journal of Applied Information Systems, 2012, 4, 36-39.	0.1	1
43	A web accessible resource for investigating cassava phenomics and genomics information: BIOGEN BASE. Bioinformatics, 2011, 6, 391-392.	0.5	4