

Mahendar Thudi

List of Publications by Year in descending order

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85
papers

6,395
citations

61984

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71685

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all docs

94
docs citations

94
times ranked

4348
citing authors

#	ARTICLE	IF	CITATIONS
1	BSA-seq and genetic mapping reveals AhRt2 as a candidate gene responsible for red testa of peanut. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1529-1540.	3.6	19
2	Raffinose Family Oligosaccharides: Friend or Foe for Human and Plant Health?. <i>Frontiers in Plant Science</i> , 2022, 13, 829118.	3.6	62
3	High-Density Genetic Variation Map Reveals Key Candidate Loci and Genes Associated With Important Agronomic Traits in Peanut. <i>Frontiers in Genetics</i> , 2022, 13, 845602.	2.3	3
4	Genomic resources in plant breeding for sustainable agriculture. <i>Journal of Plant Physiology</i> , 2021, 257, 153351.	3.5	90
5	Novel Genes and Genetic Loci Associated With Root Morphological Traits, Phosphorus-Acquisition Efficiency and Phosphorus-Use Efficiency in Chickpea. <i>Frontiers in Plant Science</i> , 2021, 12, 636973.	3.6	15
6	Molecular mapping of dry root rot resistance genes in chickpea (<i>Cicer arietinum</i> L.). <i>Euphytica</i> , 2021, 217, 1.	1.2	8
7	MAGIC lines in chickpea: development and exploitation of genetic diversity. <i>Euphytica</i> , 2021, 217, 1.	1.2	6
8	Molecular Genetic Diversity and Population Structure in Ethiopian Chickpea Germplasm Accessions. <i>Diversity</i> , 2021, 13, 247.	1.7	7
9	MutMap Approach Enables Rapid Identification of Candidate Genes and Development of Markers Associated With Early Flowering and Enhanced Seed Size in Chickpea (<i>Cicer arietinum</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 688694.	3.6	7
10	Major QTLs and Potential Candidate Genes for Heat Stress Tolerance Identified in Chickpea (<i>Cicer</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	3.6	38
11	Identification of stable heat tolerance QTLs using inter-specific recombinant inbred line population derived from GPF 2 and ILWC 292. <i>PLoS ONE</i> , 2021, 16, e0254957.	2.5	16
12	Transcriptome analysis reveals key genes associated with root-lesion nematode <i>Pratylenchus thornei</i> resistance in chickpea. <i>Scientific Reports</i> , 2021, 11, 17491.	3.3	13
13	Identification of novel sources for resistance against ascochyta blight and botrytis grey mould of chickpea. <i>Agricultural Research Journal</i> , 2021, 58, 581-585.	0.2	1
14	Introgression of a QTL hotspot region enhances drought tolerance and grain yield in three elite chickpea cultivars. <i>Plant Genome</i> , 2021, 14, e20076.	2.8	73
15	Translational Chickpea Genomics Consortium to Accelerate Genetic Gains in Chickpea (<i>Cicer arietinum</i>) Tj ETQq1 1,0,784314,rgBT/Over	3.5	2
16	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	27.8	106
17	Screening and Validation of Drought Tolerance and Fusarium Wilt Resistance in Advance Breeding Lines of Chickpea (<i>Cicer arietinum</i> L.). <i>Legume Research</i> , 2021, , .	0.1	0
18	Genome-Wide SNP Discovery and Mapping QTLs for Seed Iron and Zinc Concentrations in Chickpea (<i>Cicer arietinum</i> L.). <i>Frontiers in Nutrition</i> , 2020, 7, 559120.	3.7	29

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19	Multi-parent populations in crops: a toolbox integrating genomics and genetic mapping with breeding. <i>Heredity</i> , 2020, 125, 396-416.	2.6	124
20	Integrating genomics for chickpea improvement: achievements and opportunities. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1703-1720.	3.6	82
21	Allelic Diversity, Structural Analysis, and Genome-Wide Association Study (GWAS) for Yield and Related Traits Using Unexplored Common Bean (<i>Phaseolus vulgaris</i> L.) Germplasm From Western Himalayas. <i>Frontiers in Genetics</i> , 2020, 11, 609603.	2.3	25
22	Fine mapping and gene cloning in the post-NGS era: advances and prospects. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1791-1810.	3.6	94
23	Genomics, genetics and breeding of tropical legumes for better livelihoods of smallholder farmers. <i>Plant Breeding</i> , 2019, 138, 487-499.	1.9	28
24	Resistance to Plant-Parasitic Nematodes in Chickpea: Current Status and Future Perspectives. <i>Frontiers in Plant Science</i> , 2019, 10, 966.	3.6	32
25	Resequencing of 429 chickpea accessions from 45 countries provides insights into genome diversity, domestication and agronomic traits. <i>Nature Genetics</i> , 2019, 51, 857-864.	21.4	219
26	Integrated breeding approaches for improving drought and heat adaptation in chickpea (<i>Cicer</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.9	68
27	Toward the sequence-based breeding in legumes in the post-genome sequencing era. <i>Theoretical and Applied Genetics</i> , 2019, 132, 797-816.	3.6	147
28	Super Annigeri 1 and improved JG 74: two Fusarium wilt-resistant introgression lines developed using marker-assisted backcrossing approach in chickpea (<i>Cicer arietinum</i> L.). <i>Molecular Breeding</i> , 2019, 39, 2.	2.1	62
29	Transcription Factors Evaluation in a Transcriptome Analysis on Chickpea (<i>Cicer arietinum</i> L.) Under Drought Stress. <i>Journal of Crop Breeding</i> , 2019, 11, 133-141.	0.1	1
30	Identification of QTLs for resistance to Fusarium wilt and Ascochyta blight in a recombinant inbred population of chickpea (<i>Cicer arietinum</i> L.). <i>Euphytica</i> , 2018, 214, 1.	1.2	40
31	Accelerating genetic gains in legumes for the development of prosperous smallholder agriculture: integrating genomics, phenotyping, systems modelling and agronomy. <i>Journal of Experimental Botany</i> , 2018, 69, 3293-3312.	4.8	87
32	Development and evaluation of high-density Axiom [®] <i>Cicer</i> SNP Array for high-resolution genetic mapping and breeding applications in chickpea. <i>Plant Biotechnology Journal</i> , 2018, 16, 890-901.	8.3	76
33	Surveying the genome and constructing a high-density genetic map of napiergrass (<i>Cenchrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	3.3	32
34	Genetic Diversity Patterns and Heterosis Prediction Based on SSRs and SNPs in Hybrid Parents of Pearl Millet. <i>Crop Science</i> , 2018, 58, 2379-2390.	1.8	15
35	RNA-Seq analysis revealed genes associated with drought stress response in kabuli chickpea (<i>Cicer</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	2.5	86
36	Molecular Mapping of QTLs for Heat Tolerance in Chickpea. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2166.	4.1	73

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37	A western Sahara centre of domestication inferred from pearl millet genomes. <i>Nature Ecology and Evolution</i> , 2018, 2, 1377-1380.	7.8	78
38	Plant vigour QTLs co-map with an earlier reported QTL hotspot for drought tolerance while water saving QTLs map in other regions of the chickpea genome. <i>BMC Plant Biology</i> , 2018, 18, 29.	3.6	59
39	Gene/QTL discovery for Anthracnose in common bean (<i>Phaseolus vulgaris</i> L.) from North-western Himalayas. <i>PLoS ONE</i> , 2018, 13, e0191700.	2.5	34
40	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	17.5	356
41	The Chickpea Genome: An Introduction. <i>Compendium of Plant Genomes</i> , 2017, , 1-4.	0.5	6
42	Sequencing the Chickpea Genome. <i>Compendium of Plant Genomes</i> , 2017, , 117-123.	0.5	0
43	Impact of Genomics on Chickpea Breeding. <i>Compendium of Plant Genomes</i> , 2017, , 125-134.	0.5	3
44	Future Prospects for Chickpea Research. <i>Compendium of Plant Genomes</i> , 2017, , 135-142.	0.5	1
45	Advances in Chickpea Genomic Resources for Accelerating the Crop Improvement. <i>Compendium of Plant Genomes</i> , 2017, , 53-67.	0.5	3
46	Requirement of Whole-Genome Sequencing and Background History of the National and International Genome Initiatives. <i>Compendium of Plant Genomes</i> , 2017, , 107-115.	0.5	0
47	Molecular Mapping of Flowering Time Major Genes and QTLs in Chickpea (<i>Cicer arietinum</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1140.	3.6	48
48	Emerging Genomic Tools for Legume Breeding: Current Status and Future Prospects. <i>Frontiers in Plant Science</i> , 2016, 7, 455.	3.6	180
49	QTL-seq for rapid identification of candidate genes for 100-seed weight and root/total plant dry weight ratio under rainfed conditions in chickpea. <i>Plant Biotechnology Journal</i> , 2016, 14, 2110-2119.	8.3	177
50	Recent breeding programs enhanced genetic diversity in both desi and kabuli varieties of chickpea (<i>Cicer arietinum</i> L.). <i>Scientific Reports</i> , 2016, 6, 38636.	3.3	77
51	Genome-wide dissection of AP2/ERF and HSP90 gene families in five legumes and expression profiles in chickpea and pigeonpea. <i>Plant Biotechnology Journal</i> , 2016, 14, 1563-1577.	8.3	109
52	Whole genome re-sequencing reveals genome-wide variations among parental lines of 16 mapping populations in chickpea (<i>Cicer arietinum</i> L.). <i>BMC Plant Biology</i> , 2016, 16, 10.	3.6	101
53	Vernalization response in chickpea is controlled by a major QTL. <i>Euphytica</i> , 2016, 207, 453-461.	1.2	31
54	Genomics, trait mapping and molecular breeding in pigeonpea and chickpea. <i>Indian Journal of Genetics and Plant Breeding</i> , 2016, 76, 504.	0.5	3

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55	Prioritization of candidate genes in a QTL-hotspot region for drought tolerance in chickpea (<i>Cicer</i> Tj ETQq1 1,0,784314 rgBT /Ome	3.3	131
56	CicArVarDB: SNP and InDel database for advancing genetics research and breeding applications in chickpea. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav078.	3.0	22
57	Two key genomic regions harbour QTLs for salinity tolerance in ICCV 2011 derived chickpea (<i>Cicer</i> Tj ETQq1 1,0,784314 rgBT /Ome	3.6	67
58	Association of mid-reproductive stage canopy temperature depression with the molecular markers and grain yields of chickpea (<i>Cicer arietinum</i> L.) germplasm under terminal drought. Field Crops Research, 2015, 174, 1-11.	5.1	32
59	Translational Genomics in Agriculture: Some Examples in Grain Legumes. Critical Reviews in Plant Sciences, 2015, 34, 169-194.	5.7	83
60	Genotyping-by-sequencing based intra-specific genetic map refines a QTL-hotspot region for drought tolerance in chickpea. Molecular Genetics and Genomics, 2015, 290, 559-571.	2.1	180
61	Marker-trait association study for protein content in chickpea (<i>Cicer arietinum</i> L.). Journal of Genetics, 2015, 94, 279-286.	0.7	50
62	Identification of a non-redundant set of 202 in silico SSR markers and applicability of a select set in chickpea (<i>Cicer arietinum</i> L.). Euphytica, 2015, 205, 381-394.	1.2	18
63	NGS-QCbox and Raspberry for Parallel, Automated and Rapid Quality Control Analysis of Large-Scale Next Generation Sequencing (Illumina) Data. PLoS ONE, 2015, 10, e0139868.	2.5	37
64	Allele diversity for abiotic stress responsive candidate genes in chickpea reference set using gene based SNP markers. Frontiers in Plant Science, 2014, 5, 248.	3.6	46
65	Advances in Chickpea Genomics. , 2014, , 73-94.		16
66	A SSR kit to study genetic diversity in chickpea (<i>Cicer arietinum</i> L.). Plant Genetic Resources: Characterisation and Utilisation, 2014, 12, S118-S120.	0.8	5
67	Genetic dissection of drought tolerance in chickpea (<i>Cicer arietinum</i> L.). Theoretical and Applied Genetics, 2014, 127, 445-462.	3.6	304
68	Development of DArT markers and assessment of diversity in <i>Fusarium oxysporum</i> f. sp. <i>ciceris</i> , wilt pathogen of chickpea (<i>Cicer arietinum</i> L.). BMC Genomics, 2014, 15, 454.	2.8	40
69	Integrated physical, genetic and genome map of chickpea (<i>Cicer arietinum</i> L.). Functional and Integrative Genomics, 2014, 14, 59-73.	3.5	49
70	Genomics-assisted breeding for drought tolerance in chickpea. Functional Plant Biology, 2014, 41, 1178.	2.1	75
71	Genetic Dissection of Drought and Heat Tolerance in Chickpea through Genome-Wide and Candidate Gene-Based Association Mapping Approaches. PLoS ONE, 2014, 9, e96758.	2.5	187
72	Draft genome sequence of chickpea (<i>Cicer arietinum</i>) provides a resource for trait improvement. Nature Biotechnology, 2013, 31, 240-246.	17.5	1,049

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73	Molecular mapping of QTLs for resistance to Fusarium wilt (race 1) and Ascochyta blight in chickpea (<i>Cicer arietinum</i> L.). <i>Euphytica</i> , 2013, 193, 121-133.	1.2	111
74	Integrated Consensus Map of Cultivated Peanut and Wild Relatives Reveals Structures of the A and B Genomes of <i>Arachis</i> and Divergence of the Legume Genomes. <i>DNA Research</i> , 2013, 20, 173-184.	3.4	113
75	FastTrack Introgression of QTL hotspot for Root Traits and Other Drought Tolerance Traits in JG 11, an Elite and Leading Variety of Chickpea. <i>Plant Genome</i> , 2013, 6, plantgenome2013.07.0022.	2.8	118
76	Single Nucleotide Polymorphism Genotyping for Breeding and Genetics Applications in Chickpea and Pigeonpea using the BeadXpress Platform. <i>Plant Genome</i> , 2013, 6, plantgenome2013.05.0017.	2.8	55
77	Crop crop/cropping Breeding breeding/breed, see also animal breeding for Sustainable Agriculture breeding/breed, see also animal breeding for sustainable agriculture , <i>Genomics Interventions in</i> , 2013, , 501-513.		0
78	Current state-of-art of sequencing technologies for plant genomics research. <i>Briefings in Functional Genomics</i> , 2012, 11, 3-11.	2.7	123
79	Advances in genetics and molecular breeding of three legume crops of semi-arid tropics using next-generation sequencing and high-throughput genotyping technologies. <i>Journal of Biosciences</i> , 2012, 37, 811-820.	1.1	68
80	Assessment of ICCV 2—JG 62 chickpea progenies shows sensitivity of reproduction to salt stress and reveals QTL for seed yield and yield components. <i>Molecular Breeding</i> , 2012, 30, 9-21.	2.1	90
81	Identification of unique alleles and assessment of genetic diversity of rabi sorghum accessions using simple sequence repeat markers. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2011, 20, 74-83.	1.7	11
82	Genomic tools and germplasm diversity for chickpea improvement. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 45-58.	0.8	58
83	Novel SSR Markers from BAC-End Sequences, DArT Arrays and a Comprehensive Genetic Map with 1,291 Marker Loci for Chickpea (<i>Cicer arietinum</i> L.). <i>PLoS ONE</i> , 2011, 6, e27275.	2.5	160
84	A comparative assessment of the utility of PCR-based marker systems in pearl millet. <i>Euphytica</i> , 2010, 174, 253-260.	1.2	13
85	Analysis of Genetic Diversity in <i>Pongamia</i> [<i>Pongamia pinnata</i> (L) Pierre] using AFLP Markers. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2010, 19, 209-216.	1.7	18