

Mahendar Thudi

List of Publications by Year in descending order

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85
papers

6,395
citations

61984

43
h-index

71685

76
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all docs

94
docs citations

94
times ranked

4348
citing authors

#	ARTICLE	IF	CITATIONS
1	Draft genome sequence of chickpea (<i>Cicer arietinum</i>) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013, 31, 240-246.	17.5	1,049
2	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
3	Genetic dissection of drought tolerance in chickpea (<i>Cicer arietinum</i> L.). <i>Theoretical and Applied Genetics</i> , 2014, 127, 445-462.	3.6	304
4	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
5	Genetic Dissection of Drought and Heat Tolerance in Chickpea through Genome-Wide and Candidate Gene-Based Association Mapping Approaches. <i>PLoS ONE</i> , 2014, 9, e96758.	2.5	187
6	Genotyping-by-sequencing based intra-specific genetic map refines a QTL-hotspot region for drought tolerance in chickpea. <i>Molecular Genetics and Genomics</i> , 2015, 290, 559-571.	2.1	180
7	Emerging Genomic Tools for Legume Breeding: Current Status and Future Prospects. <i>Frontiers in Plant Science</i> , 2016, 7, 455.	3.6	180
8	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
9	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
10	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
11	Prioritization of candidate genes in a QTL-hotspot region for drought tolerance in chickpea (<i>Cicer</i>) Tj ETQq1 1.0,784314,rgBT/Ove	3.3	131
12	Multi-parent populations in crops: a toolbox integrating genomics and genetic mapping with breeding. <i>Heredity</i> , 2020, 125, 396-416.	2.6	124
13	Current state-of-art of sequencing technologies for plant genomics research. <i>Briefings in Functional Genomics</i> , 2012, 11, 3-11.	2.7	123
14	Fast-track Introgression of a 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
15	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
16	Molecular mapping of QTLs for resistance to <i>Fusarium</i> wilt (race 1) and <i>Ascochyta</i> blight in chickpea (<i>Cicer arietinum</i> L.). <i>Euphytica</i> , 2013, 193, 121-133.	1.2	111
17	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
18	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	27.8	106

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19	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
20	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
21	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
22	Genomic resources in plant breeding for sustainable agriculture. <i>Journal of Plant Physiology</i> , 2021, 257, 153351.	3.5	90
23	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
24	RNA-Seq analysis revealed genes associated with drought stress response in kabuli chickpea (<i>Cicer</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.5	86
25	Translational Genomics in Agriculture: Some Examples in Grain Legumes. <i>Critical Reviews in Plant Sciences</i> , 2015, 34, 169-194.	5.7	83
26	Integrating genomics for chickpea improvement: achievements and opportunities. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1703-1720.	3.6	82
27	A western Sahara centre of domestication inferred from pearl millet genomes. <i>Nature Ecology and Evolution</i> , 2018, 2, 1377-1380.	7.8	78
28	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
29	Development and evaluation of high-density Axiom [®] Cicer _{SNP} Array for high-resolution genetic mapping and breeding applications in chickpea. <i>Plant Biotechnology Journal</i> , 2018, 16, 890-901.	8.3	76
30	Genomics-assisted breeding for drought tolerance in chickpea. <i>Functional Plant Biology</i> , 2014, 41, 1178.	2.1	75
31	Molecular Mapping of QTLs for Heat Tolerance in Chickpea. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2166.	4.1	73
32	Introgression of QTL hotspot region enhances drought tolerance and grain yield in three elite chickpea cultivars. <i>Plant Genome</i> , 2021, 14, e20076.	2.8	73
33	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
34	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
35	Two key genomic regions harbour QTLs for salinity tolerance in ICCV 2—JG 11 derived chickpea (<i>Cicer</i>) Tj ETQq1 1 0.7843 14	3.6	67
36	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

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37	Raffinose Family Oligosaccharides: Friend or Foe for Human and Plant Health?. <i>Frontiers in Plant Science</i> , 2022, 13, 829118.	3.6	62
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	Genomic tools and germplasm diversity for chickpea improvement. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 45-58.	0.8	58
40	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
41	Marker-trait association study for protein content in chickpea (<i>Cicer arietinum</i> L.). <i>Journal of Genetics</i> , 2015, 94, 279-286.	0.7	50
42	Integrated physical, genetic and genome map of chickpea (<i>Cicer arietinum</i> L.). <i>Functional and Integrative Genomics</i> , 2014, 14, 59-73.	3.5	49
43	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
44	Allele diversity for abiotic stress responsive candidate genes in chickpea reference set using gene based SNP markers. <i>Frontiers in Plant Science</i> , 2014, 5, 248.	3.6	46
45	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.). <i>BMC Genomics</i> , 2014, 15, 454.	2.8	40
46	Identification of QTLs for resistance to <i>Fusarium</i> wilt and <i>Ascochyta</i> blight in a recombinant inbred population of chickpea (<i>Cicer arietinum</i> L.). <i>Euphytica</i> , 2018, 214, 1.	1.2	40
47	Major QTLs and Potential Candidate Genes for Heat Stress Tolerance Identified in Chickpea (<i>Cicer</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 101	3.6	38
48	NGS-QCbox and Raspberry for Parallel, Automated and Rapid Quality Control Analysis of Large-Scale Next Generation Sequencing (Illumina) Data. <i>PLoS ONE</i> , 2015, 10, e0139868.	2.5	37
49	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
50	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. <i>Field Crops Research</i> , 2015, 174, 1-11.	5.1	32
51	Surveying the genome and constructing a high-density genetic map of napiergrass (<i>Cenchrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 101	3.3	32
52	Resistance to Plant-Parasitic Nematodes in Chickpea: Current Status and Future Perspectives. <i>Frontiers in Plant Science</i> , 2019, 10, 966.	3.6	32
53	Vernalization response in chickpea is controlled by a major QTL. <i>Euphytica</i> , 2016, 207, 453-461.	1.2	31
54	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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55	Genomics, genetics and breeding of tropical legumes for better livelihoods of smallholder farmers. <i>Plant Breeding</i> , 2019, 138, 487-499.	1.9	28
56	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
57	CicArVarDB: SNP and InDel database for advancing genetics research and breeding applications in chickpea. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav078.	3.0	22
58	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
59	Analysis of Genetic Diversity in Pongamia [<i>Pongamia pinnata</i> (L) Pierre] using AFLP Markers. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2010, 19, 209-216.	1.7	18
60	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.). <i>Euphytica</i> , 2015, 205, 381-394.	1.2	18
61	Advances in Chickpea Genomics. , 2014, , 73-94.		16
62	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
63	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
64	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
65	A comparative assessment of the utility of PCR-based marker systems in pearl millet. <i>Euphytica</i> , 2010, 174, 253-260.	1.2	13
66	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
67	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
68	Molecular mapping of dry root rot resistance genes in chickpea (<i>Cicer arietinum</i> L.). <i>Euphytica</i> , 2021, 217, 1.	1.2	8
69	Molecular Genetic Diversity and Population Structure in Ethiopian Chickpea Germplasm Accessions. <i>Diversity</i> , 2021, 13, 247.	1.7	7
70	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
71	The Chickpea Genome: An Introduction. <i>Compendium of Plant Genomes</i> , 2017, , 1-4.	0.5	6
72	MAGIC lines in chickpea: development and exploitation of genetic diversity. <i>Euphytica</i> , 2021, 217, 1.	1.2	6

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73	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
74	Impact of Genomics on Chickpea Breeding. Compendium of Plant Genomes, 2017, , 125-134.	0.5	3
75	Advances in Chickpea Genomic Resources for Accelerating the Crop Improvement. Compendium of Plant Genomes, 2017, , 53-67.	0.5	3
76	Genomics, trait mapping and molecular breeding in pigeonpea and chickpea. Indian Journal of Genetics and Plant Breeding, 2016, 76, 504.	0.5	3
77	High-Density Genetic Variation Map Reveals Key Candidate Loci and Genes Associated With Important Agronomic Traits in Peanut. Frontiers in Genetics, 2022, 13, 845602.	2.3	3
78	Translational Chickpea Genomics Consortium to Accelerate Genetic Gains in Chickpea (<i>Cicer arietinum</i>) Tj ETQq0 0,0,rgBT /Oyerlock 10	3.5	2
79	Future Prospects for Chickpea Research. Compendium of Plant Genomes, 2017, , 135-142.	0.5	1
80	Identification of novel sources for resistance against ascochyta blight and botrytis grey mould of chickpea. Agricultural Research Journal, 2021, 58, 581-585.	0.2	1
81	Transcription Factors Evaluation in a Transcriptome Analysis on Chickpea (<i>Cicer arietinum</i> L.) Under Drought Stress. Journal of Crop Breeding, 2019, 11, 133-141.	0.1	1
82	Sequencing the Chickpea Genome. Compendium of Plant Genomes, 2017, , 117-123.	0.5	0
83	Requirement of Whole-Genome Sequencing and Background History of the National and International Genome Initiatives. Compendium of Plant Genomes, 2017, , 107-115.	0.5	0
84	Crop crop/cropping Breeding breeding/breed, see also animal breeding for Sustainable Agriculture breeding/breed, see also animal breeding for sustainable agriculture , Genomics Interventions in. , 2013, , 501-513.		0
85	Screening and Validation of Drought Tolerance and Fusarium Wilt Resistance in Advance Breeding Lines of Chickpea (<i>Cicer arietinum</i> L.). Legume Research, 2021, , .	0.1	0