

Abhishek Rathore

List of Publications by Year in descending order

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94
papers

4,282
citations

101543

36
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128289

60
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99
all docs

99
docs citations

99
times ranked

3836
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	Whole-genome resequencing of 292 pigeonpea accessions identifies genomic regions associated with domestication and agronomic traits. <i>Nature Genetics</i> , 2017, 49, 1082-1088.	21.4	218
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	Emerging Genomic Tools for Legume Breeding: Current Status and Future Prospects. <i>Frontiers in Plant Science</i> , 2016, 7, 455.	3.6	180
7	Genome-Enabled Prediction Models for Yield Related Traits in Chickpea. <i>Frontiers in Plant Science</i> , 2016, 7, 1666.	3.6	127
8	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
9	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	27.8	106
10	Novel cross linked guar gum-g-poly(acrylate) porous superabsorbent hydrogels: Characterization and swelling behaviour in different environments. <i>Carbohydrate Polymers</i> , 2016, 149, 175-185.	10.2	98
11	The AVRDC “The World Vegetable Center mungbean (<i>Vigna radiata</i>) core and mini core collections. <i>BMC Genomics</i> , 2015, 16, 344.	2.8	95
12	BrAPI—an application programming interface for plant breeding applications. <i>Bioinformatics</i> , 2019, 35, 4147-4155.	4.1	82
13	Plant growth-promoting activities of <i>Streptomyces</i> spp. in sorghum and rice. <i>SpringerPlus</i> , 2013, 2, 574.	1.2	79
14	Mapping Quantitative Trait Loci Controlling High Iron and Zinc Content in Self and Open Pollinated Grains of Pearl Millet [<i>Pennisetum glaucum</i> (L.) R. Br.]. <i>Frontiers in Plant Science</i> , 2016, 7, 1636.	3.6	77
15	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
16	Genetic Variability, Genotype × Environment Interaction, Correlation, and GGE Biplot Analysis for Grain Iron and Zinc Concentration and Other Agronomic Traits in RIL Population of Sorghum (<i>Sorghum bicolor</i> L. Moench). <i>Frontiers in Plant Science</i> , 2017, 8, 712.	3.6	77
17	Molecular Mapping of QTLs for Heat Tolerance in Chickpea. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2166.	4.1	73
18	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

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19	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
20	Genetic structure of wild pea (<i>Pisum sativum</i> subsp. <i>elatius</i>) populations in the northern part of the Fertile Crescent reflects moderate cross-pollination and strong effect of geographic but not environmental distance. <i>PLoS ONE</i> , 2018, 13, e0194056.	2.5	62
21	Mapping Grain Iron and Zinc Content Quantitative Trait Loci in an Inia-di-Derived Immortal Population of Pearl Millet. <i>Genes</i> , 2018, 9, 248.	2.4	61
22	Genomic-enabled prediction models using multi-environment trials to estimate the effect of genotype×environment interaction on prediction accuracy in chickpea. <i>Scientific Reports</i> , 2018, 8, 11701.	3.3	61
23	Genomic diversity and macroecology of the crop wild relatives of domesticated pea. <i>Scientific Reports</i> , 2017, 7, 17384.	3.3	59
24	Genomics-assisted breeding for boosting crop improvement in pigeonpea (<i>Cajanus cajan</i>). <i>Frontiers in Plant Science</i> , 2015, 6, 50.	3.6	57
25	The extent of grain yield and plant growth enhancement by plant growth-promoting broad-spectrum <i>Streptomyces</i> sp. in chickpea. <i>SpringerPlus</i> , 2015, 4, 31.	1.2	55
26	Construction of genotyping-by-sequencing based high-density genetic maps and QTL mapping for fusarium wilt resistance in pigeonpea. <i>Scientific Reports</i> , 2017, 7, 1911.	3.3	55
27	Occurrence of aflatoxins and its management in diverse cropping systems of central Tanzania. <i>Mycotoxin Research</i> , 2017, 33, 323-331.	2.3	55
28	A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. <i>Plant Genome</i> , 2020, 13, e20009.	2.8	54
29	The Ontologies Community of Practice: A CGIAR Initiative for Big Data in Agrifood Systems. <i>Patterns</i> , 2020, 1, 100105.	5.9	53
30	Environmental Influences on Pigeonpea-Fusarium udum Interactions and Stability of Genotypes to Fusarium Wilt. <i>Frontiers in Plant Science</i> , 2016, 7, 253.	3.6	48
31	Genotyping-by-sequencing of three mapping populations for identification of candidate genomic regions for resistance to sterility mosaic disease in pigeonpea. <i>Scientific Reports</i> , 2017, 7, 1813.	3.3	48
32	New sources of resistance to Fusarium wilt and sterility mosaic disease in a mini-core collection of pigeonpea germplasm. <i>European Journal of Plant Pathology</i> , 2012, 133, 707-714.	1.7	47
33	Molecular Evidence for Two Domestication Events in the Pea Crop. <i>Genes</i> , 2018, 9, 535.	2.4	42
34	Towards Defining Heterotic Gene Pools in Pearl Millet [<i>Pennisetum glaucum</i> (L.) R. Br.]. <i>Frontiers in Plant Science</i> , 2017, 8, 1934.	3.6	42
35	Exploring Germplasm Diversity to Understand the Domestication Process in <i>Cicer</i> spp. Using SNP and DArT Markers. <i>PLoS ONE</i> , 2014, 9, e102016.	2.5	42
36	Phenotypic Data from Inbred Parents Can Improve Genomic Prediction in Pearl Millet Hybrids. G3: Genes, Genomes, Genetics, 2018, 8, 2513-2522.	1.8	41

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37	Sorghum Pan-Genome Explores the Functional Utility for Genomic-Assisted Breeding to Accelerate the Genetic Gain. <i>Frontiers in Plant Science</i> , 2021, 12, 666342.	3.6	41
38	Morphological and molecular characterization of <i>Macrophomina phaseolina</i> isolated from three legume crops and evaluation of mungbean genotypes for resistance to dry root rot. <i>Crop Protection</i> , 2020, 127, 104962.	2.1	39
39	Development and Application of High-Density Axiom <i>Cajanus</i> SNP Array with 56K SNPs to Understand the Genome Architecture of Released Cultivars and Founder Genotypes. <i>Plant Genome</i> , 2018, 11, 180005.	2.8	35
40	Complete genome sequence of sixteen plant growth promoting <i>Streptomyces</i> strains. <i>Scientific Reports</i> , 2020, 10, 10294.	3.3	33
41	Strategies for Effective Use of Genomic Information in Crop Breeding Programs Serving Africa and South Asia. <i>Frontiers in Plant Science</i> , 2020, 11, 353.	3.6	33
42	Exploring the Genetic Cipher of Chickpea (<i>Cicer arietinum</i> L.) Through Identification and Multi-environment Validation of Resistant Sources Against Fusarium Wilt (<i>Fusarium oxysporum</i> f. sp.)	3.8	27
43	Identification of quantitative trait loci for yield and yield related traits in groundnut (<i>Arachis</i>)	1.92	29
44	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
45	Capturing genetic variability and selection of traits for heat tolerance in a chickpea recombinant inbred line (RIL) population under field conditions. <i>Euphytica</i> , 2018, 214, 1.	1.2	28
46	Phenotypic and molecular diversity-based prediction of heterosis in pearl millet (<i>Pennisetum glaucum</i>)	5.2	28
47	Patterns of Molecular Diversity in Current and Previously Developed Hybrid Parents of Pearl Millet [<i>Pennisetum glaucum</i> (L.) R. Br.]. <i>American Journal of Plant Sciences</i> , 2015, 06, 1697-1712.	0.8	23
48	Stability Performance of Inductively Coupled Plasma Mass Spectrometry-Phenotyped Kernel Minerals Concentration and Grain Yield in Maize in Different Agro-Climatic Zones. <i>PLoS ONE</i> , 2015, 10, e0139067.	2.5	22
49	Identification of QTLs and candidate genes for high grain Fe and Zn concentration in sorghum [<i>Sorghum bicolor</i> (L.) Moench]. <i>Journal of Cereal Science</i> , 2019, 90, 102850.	3.7	21
50	Influence of diazotrophic bacteria on nodulation, nitrogen fixation, growth promotion and yield traits in five cultivars of chickpea. <i>Biocatalysis and Agricultural Biotechnology</i> , 2018, 15, 35-42.	3.1	20
51	Fine-Mapping of Sorghum Stay-Green QTL on Chromosome10 Revealed Genes Associated with Delayed Senescence. <i>Genes</i> , 2020, 11, 1026.	2.4	20
52	Genetic variation and relationships of total seed protein content with some agronomic traits in pigeonpea (<i>Cajanus cajan</i> (L.) Millsp.). <i>Australian Journal of Crop Science</i> , 2018, 12, 1859-1865.	0.3	19
53	Genetic diversity and association mapping of Ethiopian and exotic finger millet accessions. <i>Crop and Pasture Science</i> , 2018, 69, 879.	1.5	19
54	Genotyping-by-sequencing and multilocation evaluation of two interspecific backcross populations identify QTLs for yield-related traits in pigeonpea. <i>Theoretical and Applied Genetics</i> , 2020, 133, 737-749.	3.6	18

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55	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
56	Identification of heterotic groups in South-Asian-bred hybrid parents of pearl millet. <i>Theoretical and Applied Genetics</i> , 2020, 133, 873-888.	3.6	15
57	Development of genomic microsatellite markers in cluster bean using next-generation DNA sequencing and their utility in diversity analysis. <i>Current Plant Biology</i> , 2020, 21, 100134.	4.7	15
58	Genetic Variation for Nitrogen Use Efficiency Traits in Global Diversity Panel and Parents of Mapping Populations in Pearl Millet. <i>Frontiers in Plant Science</i> , 2021, 12, 625915.	3.6	15
59	Structural and Functional Characteristics of miRNAs in Five Strategic Millet Species and Their Utility in Drought Tolerance. <i>Frontiers in Genetics</i> , 2020, 11, 608421.	2.3	14
60	Genome-Wide DARTSeq Genotyping and Phenotypic Based Assessment of Within and Among Accessions Diversity and Effective Sample Size in the Diverse Sorghum, Pearl Millet, and Pigeonpea Landraces. <i>Frontiers in Plant Science</i> , 2020, 11, 587426.	3.6	13
61	Nitrogen Use Efficiency in Sorghum: Exploring Native Variability for Traits Under Variable N-Regimes. <i>Frontiers in Plant Science</i> , 2021, 12, 643192.	3.6	13
62	Translational Pigeonpea Genomics Consortium for Accelerating Genetic Gains in Pigeonpea (<i>Cajanus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	3.8	12
63	Relationship of Parental Genetic Distance with Heterosis and Specific Combining Ability in Sesame (<i>Sesamum indicum</i> L.) Based on Phenotypic and Molecular Marker Analysis. <i>Biochemical Genetics</i> , 2018, 56, 188-209.	1.7	11
64	African and Asian origin pearl millet populations: Genetic diversity pattern and its association with yield heterosis. <i>Crop Science</i> , 2020, 60, 3035-3048.	1.8	11
65	Use of wild <i>Pennisetum</i> species for improving biotic and abiotic stress tolerance in pearl millet. <i>Crop Science</i> , 2021, 61, 289-304.	1.8	11
66	Genome-wide comparative transcriptome analysis of the A4-CMS line ICPA 2043 and its maintainer ICPB 2043 during the floral bud development of pigeonpea. <i>Functional and Integrative Genomics</i> , 2021, 21, 251-263.	3.5	11
67	An Integrated SNP Mining and Utilization (ISMU) Pipeline for Next Generation Sequencing Data. <i>PLoS ONE</i> , 2014, 9, e101754.	2.5	10
68	Identification of microRNAs and their gene targets in cytoplasmic male sterile and fertile maintainer lines of pigeonpea. <i>Planta</i> , 2021, 253, 59.	3.2	10
69	Utilization of Molecular Marker Based Genetic Diversity Patterns in Hybrid Parents to Develop Better Forage Quality Multi-Cut Hybrids in Pearl Millet. <i>Agriculture (Switzerland)</i> , 2019, 9, 97.	3.1	9
70	Evaluation of fodder yield and fodder quality in sorghum and its interaction with grain yield under different water availability regimes. <i>Current Plant Biology</i> , 2021, 25, 100191.	4.7	9
71	Genetic variability, genotype \times environment interaction and correlation analysis for grain iron and zinc contents in recombinant inbred line population of pearl millet [<i>Pennisetum glaucum</i> (L.) R.. <i>Indian Journal of Genetics and Plant Breeding</i> , 2019, 79, .	0.5	9
72	Identification of new sources of resistance to dry root rot caused by <i>Macrophomina phaseolina</i> isolates from India and Myanmar in a mungbean mini-core collection. <i>Crop Protection</i> , 2021, 143, 105569.	2.1	8

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73	Identification of Candidate Genes Regulating Drought Tolerance in Pearl Millet. International Journal of Molecular Sciences, 2022, 23, 6907.	4.1	8
74	Multiple Genome Wide Association Mapping Models Identify Quantitative Trait Nucleotides for Brown Planthopper (<i>Nilaparvata lugens</i>) Resistance in MAGIC Indica Population of Rice. Vaccines, 2020, 8, 608.	4.4	7
75	Genome-Wide Association Studies (GWAS) for Traits Related to Fodder Quality and Biofuel in Sorghum: Progress and Prospects. Protein and Peptide Letters, 2021, 28, 843-854.	0.9	7
76	Survey of Fungal Foliar and Panicle Diseases of Sorghum in Important Agroecological Zones of Tanzania and Uganda. Plant Health Progress, 2018, 19, 265-271.	1.4	6
77	Identification of quantitative trait loci associated with iron deficiency chlorosis resistance in groundnut (<i>Arachis hypogaea</i>). Plant Breeding, 2020, 139, 790-803.	1.9	6
78	Characterization of heterosis and genomic prediction-based establishment of heterotic patterns for developing better hybrids in pigeonpea. Plant Genome, 2021, 14, e20125.	2.8	6
79	Availability of soil iron determines the distribution strategy and seed iron content in mungbean (<i>Vigna radiata</i>) plants. Plant and Soil, 2020, 446, 413-423.	3.7	5
80	Combining ability and gene action controlling rust resistance in groundnut (<i>Arachis hypogaea</i> L.). Scientific Reports, 2021, 11, 16513.	3.3	5
81	Genetic Dissection and Quantitative Trait Loci Mapping of Agronomic and Fodder Quality Traits in Sorghum Under Different Water Regimes. Frontiers in Plant Science, 2022, 13, 810632.	3.6	5
82	Combining ability of some sorghum lines for dry lands and sub-humid environments of East Africa. African Journal of Agricultural Research Vol Pp, 2015, 10, 2048-2060.	0.5	4
83	Current Status and Future Prospects of Next-Generation Data Management and Analytical Decision Support Tools for Enhancing Genetic Gains in Crops. Advances in Biochemical Engineering/Biotechnology, 2018, 164, 277-292.	1.1	4
84	Identification of Ideal Locations and Stable High Biomass Sorghum Genotypes in semiarid Tropics. Sugar Tech, 2018, 20, 323-335.	1.8	4
85	Survey sequencing and in-silico development and validation of genomic SSR markers in Indian dill seed. Journal of King Saud University - Science, 2020, 32, 862-866.	3.5	4
86	Genome-Wide Association Study for Major Biofuel Traits in Sorghum Using Minicore Collection. Protein and Peptide Letters, 2021, 28, 909-928.	0.9	4
87	The Ontologies Community of Practice: An Initiative by the CGIAR Platform for Big Data in Agriculture. SSRN Electronic Journal, 0, , .	0.4	4
88	Field-Relevant New Sources of Resistance to Anthracnose Caused by <i>Colletotrichum truncatum</i> in a Mungbean Mini-Core Collection. Plant Disease, 2021, 105, 2001-2010.	1.4	3
89	Understanding Heterosis, Genetic Effects, and Genome Wide Associations for Forage Quantity and Quality Traits in Multi-Cut Pearl Millet. Frontiers in Plant Science, 2021, 12, 687859.	3.6	3
90	Heterotic pools in African and Asian origin populations of pearl millet [<i>Pennisetum glaucum</i> (L.) R. Br.]. Scientific Reports, 2021, 11, 12197.	3.3	2

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91	Translational Chickpea Genomics Consortium to Accelerate Genetic Gains in Chickpea (<i>Cicer arietinum</i>) Tj ETQq1 1,0,784314,rgBT /O	3.5	2
92	Bayesian analysis for genotype x environment interactions and the GGE-biplot assessment: Evaluation of balanced classifications with missing values. <i>International Journal of Applied Sciences and Biotechnology</i> , 2015, 3, 210-217.	0.8	1
93	Forecasting fish yield using statistical nonlinear growth models – A reparameterization concept. <i>Indian Journal of Extension Education</i> , 2020, 56, 9-14.	0.0	0
94	Construction of Practical Haplotype Graph (PHG) with the Whole-Genome Sequence Data. <i>Methods in Molecular Biology</i> , 2022, 2443, 273-284.	0.9	0