

# Abhishek Rathore

## List of Publications by Year in descending order

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94  
papers

4,282  
citations

101543

36  
h-index

128289

60  
g-index

99  
all docs

99  
docs citations

99  
times ranked

3836  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Genetic Dissection and Quantitative Trait Loci Mapping of Agronomic and Fodder Quality Traits in Sorghum Under Different Water Regimes. <i>Frontiers in Plant Science</i> , 2022, 13, 810632.	3.6	5
3	Identification of Candidate Genes Regulating Drought Tolerance in Pearl Millet. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6907.	4.1	8
4	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
5	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
6	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
7	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
8	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
9	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
10	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
11	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
12	Heterotic pools in African and Asian origin populations of pearl millet [ <i>Pennisetum glaucum</i> (L.) R. Br.]. <i>Scientific Reports</i> , 2021, 11, 12197.	3.3	2
13	Field-Relevant New Sources of Resistance to Anthracnose Caused by <i>Colletotrichum truncatum</i> in a Mungbean Mini-Core Collection. <i>Plant Disease</i> , 2021, 105, 2001-2010.	1.4	3
14	Combining ability and gene action controlling rust resistance in groundnut ( <i>Arachis hypogaea</i> L.). <i>Scientific Reports</i> , 2021, 11, 16513.	3.3	5
15	Characterization of heterosis and genomic prediction-based establishment of heterotic patterns for developing better hybrids in pigeonpea. <i>Plant Genome</i> , 2021, 14, e20125.	2.8	6
16	Genome-Wide Association Studies (GWAS) for Traits Related to Fodder Quality and Biofuel in Sorghum: Progress and Prospects. <i>Protein and Peptide Letters</i> , 2021, 28, 843-854.	0.9	7
17	Genome-Wide Association Study for Major Biofuel Traits in Sorghum Using Minicore Collection. <i>Protein and Peptide Letters</i> , 2021, 28, 909-928.	0.9	4
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	Translational Chickpea Genomics Consortium to Accelerate Genetic Gains in Chickpea ( <i>Cicer arietinum</i> ) Tj ETQq1 1,0,784314,rgBT /Ove	3.5	2
20	Understanding Heterosis, Genetic Effects, and Genome Wide Associations for Forage Quantity and Quality Traits in Multi-Cut Pearl Millet. <i>Frontiers in Plant Science</i> , 2021, 12, 687859.	3.6	3
21	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	27.8	106
22	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
23	Survey sequencing and in-silico development and validation of genomic SSR markers in Indian dill seed. <i>Journal of King Saud University - Science</i> , 2020, 32, 862-866.	3.5	4
24	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
25	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
26	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
27	Availability of soil iron determines the distribution strategy and seed iron content in mungbean ( <i>Vigna radiata</i> ) plants. <i>Plant and Soil</i> , 2020, 446, 413-423.	3.7	5
28	The Ontologies Community of Practice: A CGIAR Initiative for Big Data in Agrifood Systems. <i>Patterns</i> , 2020, 1, 100105.	5.9	53
29	Complete genome sequence of sixteen plant growth promoting <i>Streptomyces</i> strains. <i>Scientific Reports</i> , 2020, 10, 10294.	3.3	33
30	Fine-Mapping of Sorghum Stay-Green QTL on Chromosome10 Revealed Genes Associated with Delayed Senescence. <i>Genes</i> , 2020, 11, 1026.	2.4	20
31	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
32	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
33	Translational Pigeonpea Genomics Consortium for Accelerating Genetic Gains in Pigeonpea ( <i>Cajanus</i> ) Tj ETQq1 1 0,784314,rgBT /Ove	3.0	2
34	Multiple Genome Wide Association Mapping Models Identify Quantitative Trait Nucleotides for Brown Planthopper ( <i>Nilaparvata lugens</i> ) Resistance in MAGIC Indica Population of Rice. <i>Vaccines</i> , 2020, 8, 608.	4.4	7
35	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
36	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

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37	Identification of quantitative trait loci associated with iron deficiency chlorosis resistance in groundnut ( <i>Arachis hypogaea</i> ). <i>Plant Breeding</i> , 2020, 139, 790-803.	1.9	6
38	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
39	A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. <i>Plant Genome</i> , 2020, 13, e20009.	2.8	54
40	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
41	BrAPI – an application programming interface for plant breeding applications. <i>Bioinformatics</i> , 2019, 35, 4147-4155.	4.1	82
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.)	0.0	0
43	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
44	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
45	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
46	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
47	Genetic variability, genotype × 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
48	Current Status and Future Prospects of Next-Generation Data Management and Analytical Decision Support Tools for Enhancing Genetic Gains in Crops. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2018, 164, 277-292.	1.1	4
49	Identification of Ideal Locations and Stable High Biomass Sorghum Genotypes in semiarid Tropics. <i>Sugar Tech</i> , 2018, 20, 323-335.	1.8	4
50	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
51	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
52	Phenotypic and molecular diversity-based prediction of heterosis in pearl millet ( <i>Pennisetum glaucum</i> )	5.2	28
53	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
54	Molecular Evidence for Two Domestication Events in the Pea Crop. <i>Genes</i> , 2018, 9, 535.	2.4	42

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55	Survey of Fungal Foliar and Panicle Diseases of Sorghum in Important Agroecological Zones of Tanzania and Uganda. <i>Plant Health Progress</i> , 2018, 19, 265-271.	1.4	6
56	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
57	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
58	Phenotypic Data from Inbred Parents Can Improve Genomic Prediction in Pearl Millet Hybrids. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2513-2522.	1.8	41
59	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
60	Molecular Mapping of QTLs for Heat Tolerance in Chickpea. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2166.	4.1	73
61	Mapping Grain Iron and Zinc Content Quantitative Trait Loci in an Iniadi-Derived Immortal Population of Pearl Millet. <i>Genes</i> , 2018, 9, 248.	2.4	61
62	Genetic diversity and association mapping of Ethiopian and exotic finger millet accessions. <i>Crop and Pasture Science</i> , 2018, 69, 879.	1.5	19
63	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
64	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
65	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
66	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
67	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
68	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
69	Occurrence of aflatoxins and its management in diverse cropping systems of central Tanzania. <i>Mycotoxin Research</i> , 2017, 33, 323-331.	2.3	55
70	Genomic diversity and macroecology of the crop wild relatives of domesticated pea. <i>Scientific Reports</i> , 2017, 7, 17384.	3.3	59
71	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
72	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

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73	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
74	Emerging Genomic Tools for Legume Breeding: Current Status and Future Prospects. <i>Frontiers in Plant Science</i> , 2016, 7, 455.	3.6	180
75	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
76	Genome-Enabled Prediction Models for Yield Related Traits in Chickpea. <i>Frontiers in Plant Science</i> , 2016, 7, 1666.	3.6	127
77	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
78	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
79	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
80	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
81	Combining ability of some sorghum lines for dry lands and sub-humid environments of East Africa. <i>African Journal of Agricultural Research</i> Vol Pp, 2015, 10, 2048-2060.	0.5	4
82	Identification of quantitative trait loci for yield and yield related traits in groundnut ( <i>Arachis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 T	1.2	29
83	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
84	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
85	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
86	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
87	An Integrated SNP Mining and Utilization (ISMU) Pipeline for Next Generation Sequencing Data. <i>PLoS ONE</i> , 2014, 9, e101754.	2.5	10
88	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
89	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
90	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

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91	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
92	Plant growth-promoting activities of <i>Streptomyces</i> spp. in sorghum and rice. <i>SpringerPlus</i> , 2013, 2, 574.	1.2	79
93	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
94	The Ontologies Community of Practice: An Initiative by the CGIAR Platform for Big Data in Agriculture. <i>SSRN Electronic Journal</i> , 0, , .	0.4	4