

# Manish Roorkiwal

## List of Publications by Year in descending order

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Version: 2024-02-01

62  
papers

4,451  
citations

159585

30  
h-index

144013

57  
g-index

64  
all docs

64  
docs citations

64  
times ranked

3803  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Chromosome-length genome assemblies of six legume species provide insights into genome organization, evolution, and agronomic traits for crop improvement. <i>Journal of Advanced Research</i> , 2022, 42, 315-329.                | 9.5  | 20        |
| 2  | Agronomic Performance of Chickpea Affected by Drought Stress at Different Growth Stages. <i>Agronomy</i> , 2022, 12, 995.  | 3.0  | 12        |
| 3  | Genetic variation in <i>CaTIFY4b</i> contributes to drought adaptation in chickpea. <i>Plant Biotechnology Journal</i> , 2022, 20, 1701-1715.  | 8.3  | 23        |
| 4  | The Key to the Future Lies in the Past: Insights from Grain Legume Domestication and Improvement Should Inform Future Breeding Strategies. <i>Plant and Cell Physiology</i> , 2022, 63, 1554-1572.                                 | 3.1  | 13        |
| 5  | Development of a dense genetic map and QTL analysis for pod borer <i>Helicoverpa armigera</i> (H $\frac{1}{4}$ bner) resistance component traits in chickpea ( <i>Cicer arietinum</i> L.). <i>Plant Genome</i> , 2021, 14, e20071. | 2.8  | 16        |
| 6  | Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. <i>Scientific Data</i> , 2021, 8, 50.   | 5.3  | 38        |
| 7  | Construction of a high-density genetic map and QTL analysis for yield, yield components and agronomic traits in chickpea ( <i>Cicer arietinum</i> L.). <i>PLoS ONE</i> , 2021, 16, e0251669.                                       | 2.5  | 18        |
| 8  | 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        |
| 9  | Molecular Mechanisms and Biochemical Pathways for Micronutrient Acquisition and Storage in Legumes to Support Biofortification for Nutritional Security. <i>Frontiers in Plant Science</i> , 2021, 12, 682842.                     | 3.6  | 19        |
| 10 | Genome-wide transcriptome analysis and physiological variation modulates gene regulatory networks acclimating salinity tolerance in chickpea. <i>Environmental and Experimental Botany</i> , 2021, 187, 104478.                    | 4.2  | 17        |
| 11 | Rapid delivery systems for future food security. <i>Nature Biotechnology</i> , 2021, 39, 1179-1181.  | 17.5 | 17        |
| 12 | Fast-forward breeding for a food-secure world. <i>Trends in Genetics</i> , 2021, 37, 1124-1136.  | 6.7  | 82        |
| 13 | Breeding custom-designed crops for improved drought adaptation. <i>Genetics &amp; Genomics Next</i> , 2021, 2, e202100017.   | 1.5  | 48        |
| 14 | Introgression of <i>QTL-hotspot</i> region enhances drought tolerance and grain yield in three elite chickpea cultivars. <i>Plant Genome</i> , 2021, 14, e20076.   | 2.8  | 73        |
| 15 | The genetics of vigour-related traits in chickpea ( <i>Cicer arietinum</i> L.): insights from genomic data. <i>Theoretical and Applied Genetics</i> , 2021, 135, 107.  | 3.6  | 4         |
| 16 | Translational Chickpea Genomics Consortium to Accelerate Genetic Gains in Chickpea ( <i>Cicer arietinum</i> ) <a href="#">Tj ETQq0 0,0_rgBT /Oyerlock 10</a>   | 3.5  | 2         |
| 17 | Genome-wide identification and functional prediction of salt-stress related long non-coding RNAs (lncRNAs) in chickpea ( <i>Cicer arietinum</i> L.). <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 2605-2619.      | 3.1  | 12        |
| 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 | Genetic, Epigenetic, Genomic and Microbial Approaches to Enhance Salt Tolerance of Plants: A Comprehensive Review. <i>Biology</i> , 2021, 10, 1255.   | 2.8  | 10        |
| 20 | 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         |
| 21 | Super-Pangenome by Integrating the Wild Side of a Species for Accelerated Crop Improvement. <i>Trends in Plant Science</i> , 2020, 25, 148-158.   | 8.8  | 177       |
| 22 | Characterization of ASR gene and its role in drought tolerance in chickpea ( <i>Cicer arietinum</i> L.). <i>PLoS ONE</i> , 2020, 15, e0234550.  | 2.5  | 18        |
| 23 | Genetic Dissection and Identification of Candidate Genes for Salinity Tolerance Using Axiom <sup>®</sup> CicerSNP Array in Chickpea. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5058.                     | 4.1  | 38        |
| 24 | Multi-parent populations in crops: a toolbox integrating genomics and genetic mapping with breeding. <i>Heredity</i> , 2020, 125, 396-416.  | 2.6  | 124       |
| 25 | Integrating genomics for chickpea improvement: achievements and opportunities. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1703-1720.  | 3.6  | 82        |
| 26 | 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        |
| 27 | QTLian breeding for climate resilience in cereals: progress and prospects. <i>Functional and Integrative Genomics</i> , 2019, 19, 685-701.  | 3.5  | 34        |
| 28 | 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       |
| 29 | InDel markers: An extended marker resource for molecular breeding in chickpea. <i>PLoS ONE</i> , 2019, 14, e0213999.  | 2.5  | 43        |
| 30 | Mapping Quantitative Trait Loci for Carotenoid Concentration in Three F <sub>2</sub> Populations of Chickpea. <i>Plant Genome</i> , 2019, 12, 1-12.   | 2.8  | 13        |
| 31 | 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        |
| 32 | Genetic imprints of domestication for disease resistance, oil quality, and yield component traits in groundnut ( <i>Arachis hypogaea</i> L.). <i>Molecular Genetics and Genomics</i> , 2019, 294, 365-378.                    | 2.1  | 12        |
| 33 | Genetic diversity of root system architecture in response to drought stress in grain legumes. <i>Journal of Experimental Botany</i> , 2018, 69, 3267-3277.  | 4.8  | 124       |
| 34 | Molecular and phenotypic diversity among chickpea ( <i>Cicer arietinum</i> ) genotypes as a function of drought tolerance. <i>Crop and Pasture Science</i> , 2018, 69, 142.   | 1.5  | 14        |
| 35 | Development and evaluation of high-density Axiom <sup>®</sup> CicerSNP Array for high-resolution genetic mapping and breeding applications in chickpea. <i>Plant Biotechnology Journal</i> , 2018, 16, 890-901.               | 8.3  | 76        |
| 36 | Chickpea Genomics. , 2018, , 289-316.   |      | 1         |

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|----|---|-----|-----------|
| 37 | 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        |
| 38 | Genomic Selection in Plant Breeding: Methods, Models, and Perspectives. <i>Trends in Plant Science</i> , 2017, 22, 961-975.   | 8.8 | 1,004     |
| 39 | Genomic Selection for Crop Improvement: An Introduction. , 2017, , 1-6.   |     | 8         |
| 40 | Current Status and Prospects of Genomic Selection in Legumes. , 2017, , 131-147.  |     | 7         |
| 41 | Advances in Chickpea Genomic Resources for Accelerating the Crop Improvement. <i>Compendium of Plant Genomes</i> , 2017, , 53-67.   | 0.5 | 3         |
| 42 | Emerging Genomic Tools for Legume Breeding: Current Status and Future Prospects. <i>Frontiers in Plant Science</i> , 2016, 7, 455.  | 3.6 | 180       |
| 43 | Genome-Enabled Prediction Models for Yield Related Traits in Chickpea. <i>Frontiers in Plant Science</i> , 2016, 7, 1666.   | 3.6 | 127       |
| 44 | 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       |
| 45 | 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        |
| 46 | 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       |
| 47 | Prioritization of candidate genes in a QTL-hotspot region for drought tolerance in chickpea ( <i>Cicer</i> ) Tj ETQq1 1.0784314 rgBT/Over   | 3.3 | 131       |
| 48 | Legume Crops Phylogeny and Genetic Diversity for Science and Breeding. <i>Critical Reviews in Plant Sciences</i> , 2015, 34, 43-104.  | 5.7 | 248       |
| 49 | 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       |
| 50 | 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        |
| 51 | 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       |
| 52 | 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        |
| 53 | Chickpea. , 2013, , 81-111.   |     | 16        |
| 54 | Single Nucleotide Polymorphism-based Genetic Diversity in the Reference Set of Peanut ( <i>Arachis</i> spp.) by Developing and Applying Cost-Effective Kompetitive Allele Specific Polymerase Chain Reaction Genotyping Assays. <i>Plant Genome</i> , 2013, 6, plantgenome2013.06.0019. | 2.8 | 65        |

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|----|---|-----|-----------|
| 55 | 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        |
| 56 | Legume Genomics: From Genomic Resources to Molecular Breeding. <i>Plant Genome</i> , 2013, 6, plantgenome2013.12.0002in.  | 2.8 | 12        |
| 57 | Purifying Selection Bias against Microsatellites in Gene Rich Segmental Duplications in the Rice Genome. <i>International Journal of Evolutionary Biology</i> , 2012, 2012, 1-8.  | 1.0 | 1         |
| 58 | 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        |
| 59 | A classification scoring schema to validate protein interactors. <i>Bioinformatics</i> , 2012, 8, 92-97.  | 0.5 | 13        |
| 60 | Mining functional microsatellites in legume unigenes. <i>Bioinformatics</i> , 2011, 7, 264-270.   | 0.5 | 9         |
| 61 | Genome-wide analysis of conservation and divergence of microsatellites in rice. <i>Molecular Genetics and Genomics</i> , 2009, 282, 205-215.  | 2.1 | 12        |
| 62 | Breeding customâ€designed crops for improved drought adaptation. <i>Genetics &amp; Genomics Next</i> , 0, , .  | 1.5 | 0         |