

Rajeev Kumar Varshney

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

644 papers	34,185 citations	95 h-index	162 g-index
691 ext. papers	42,533 ext. citations	6 avg, IF	7.36 L-index

#	Paper	IF	Citations
644	Genetic Enhancement of Groundnut: Current Status and Future Prospects 2022 , 63-110		1
643	Analysis of Small RNA Sequencing Data in Plants.. <i>Methods in Molecular Biology</i> , 2022 , 2443, 497-509	1.4	1
642	Genomic insights into the genetic signatures of selection and seed trait loci in cultivated peanut. <i>Journal of Advanced Research</i> , 2022 ,	13	2
641	Discovery of Major Quantitative Trait Loci and Candidate Genes for Fresh Seed Dormancy in Groundnut. <i>Agronomy</i> , 2022 , 12, 404	3.6	1
640	Breeding More Crops in Less Time: A Perspective on Speed Breeding.. <i>Biology</i> , 2022 , 11,	4.9	6
639	Recent Advances in Genetics, Genomics, and Breeding for Nutritional Quality in Groundnut 2022 , 111-137		0
638	Root exudation of contrasting drought-stressed pearl millet genotypes conveys varying biological nitrification inhibition (BNI) activity.. <i>Biology and Fertility of Soils</i> , 2022 , 58, 291-306	6.1	5
637	Integration of Genomics Approaches in Abiotic Stress Tolerance in Groundnut (<i>Arachis hypogaea</i> L.): An Overview 2022 , 149-197		0
636	A Scintillating Journey of Genomics in Simplifying Complex Traits and Development of Abiotic Stress Resilient Chickpeas 2022 , 15-43		
635	Multilateral benefit-sharing from digital sequence information will support both science and biodiversity conservation.. <i>Nature Communications</i> , 2022 , 13, 1086	17.4	5
634	Using an incomplete block design to allocate lines to environments improves sparse genome-based prediction in plant breeding.. <i>Plant Genome</i> , 2022 , e20194	4.4	0
633	Towards the Development, Maintenance and Standardized Phenotypic Characterization of Single-Seed-Descent Genetic Resources for Chickpea.. <i>Current Protocols</i> , 2022 , 2, e371		0
632	Molecular mechanisms, genetic mapping, and genome editing for insect pest resistance in field crops.. <i>Theoretical and Applied Genetics</i> , 2022 , 1	6	0
631	Genetic mapping of tolerance to iron deficiency chlorosis in peanut (<i>Arachis hypogaea</i> L.). <i>Euphytica</i> , 2022 , 218, 1	2.1	1
630	Identification of Key Gene Networks and Deciphering Transcriptional Regulators Associated With Peanut Embryo Abortion Mediated by Calcium Deficiency.. <i>Frontiers in Plant Science</i> , 2022 , 13, 814015	6.2	1
629	Pangenomics in Microbial and Crop Research: Progress, Applications, and Perspectives.. <i>Genes</i> , 2022 , 13,	4.2	1
628	Breeding Drought-Tolerant Pearl Millet Using Conventional and Genomic Approaches: Achievements and Prospects.. <i>Frontiers in Plant Science</i> , 2022 , 13, 781524	6.2	2

627	Lipid profile variations in high oleic acid peanuts by following different cooking processes.. <i>Food Research International</i> , 2022 , 155, 110993	7	1
626	Moving Beyond DNA Sequence to Improve Plant Stress Responses.. <i>Frontiers in Genetics</i> , 2022 , 13, 8746485	4.5	2
625	Comprehensive evaluation of Chinese peanut mini-mini core collection and QTL mapping for aflatoxin resistance.. <i>BMC Plant Biology</i> , 2022 , 22, 207	5.3	1
624	Efficient Breeding of Crop Plants 2022 , 745-777		0
623	Agronomic Performance of Chickpea Affected by Drought Stress at Different Growth Stages. <i>Agronomy</i> , 2022 , 12, 995	3.6	1
622	Genome-Wide Identification and Expression of Gene Family Provide Insight Into Pod Development in Peanut (). <i>Frontiers in Plant Science</i> , 2022 , 13, 893278	6.2	
621	Genomic, morphological, and biochemical analyses of a multi-metal resistant but multi-drug susceptible strain of <i>Bordetella petrii</i> from hospital soil.. <i>Scientific Reports</i> , 2022 , 12, 8439	4.9	1
620	Advances in "Omics" Approaches for Improving Toxic Metals/Metalloids Tolerance in Plants.. <i>Frontiers in Plant Science</i> , 2021 , 12, 794373	6.2	9
619	Karyotype Differentiation in Cultivated Chickpea Revealed by Oligopainting Fluorescence Hybridization.. <i>Frontiers in Plant Science</i> , 2021 , 12, 791303	6.2	0
618	Impact of different cooking methods on the chemical profile of high-oleic acid peanut seeds.. <i>Food Chemistry</i> , 2021 , 379, 131970	8.5	1
617	Features and applications of haplotypes in crop breeding. <i>Communications Biology</i> , 2021 , 4, 1266	6.7	6
616	Genome-wide identification and functional prediction of salt- stress related long non-coding RNAs (lncRNAs) in chickpea (L.).. <i>Physiology and Molecular Biology of Plants</i> , 2021 , 27, 2605-2619	2.8	1
615	The Plant Genome special issue: Advances in genomic selection and application of machine learning in genomic prediction for crop improvement. <i>Plant Genome</i> , 2021 , 14, e20178	4.4	0
614	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	6.2	0
613	Chromatin spatial organization of wild type and mutant peanuts reveals high-resolution genomic architecture and interaction alterations. <i>Genome Biology</i> , 2021 , 22, 315	18.3	0
612	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021 , 599, 622-627	50.4	15
611	Genetic, Epigenetic, Genomic and Microbial Approaches to Enhance Salt Tolerance of Plants: A Comprehensive Review.. <i>Biology</i> , 2021 , 10,	4.9	2
610	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	6	1

609	Nutritional Significance and Antioxidant-Mediated Antiaging Effects of Finger Millet: Molecular Insights and Prospects. <i>Frontiers in Sustainable Food Systems</i> , 2021 , 5,	4.8	2
608	Multivariate genomic analysis and optimal contributions selection predicts high genetic gains in cooking time, iron, zinc, and grain yield in common beans in East Africa. <i>Plant Genome</i> , 2021 , 14, e20156	4.4	3
607	Reap the crop wild relatives for breeding future crops. <i>Trends in Biotechnology</i> , 2021 ,	15.1	21
606	Voices of biotech research. <i>Nature Biotechnology</i> , 2021 , 39, 281-286	44.5	1
605	Genetic Gains in Pearl Millet in India: Insights Into Historic Breeding Strategies and Future Perspective. <i>Frontiers in Plant Science</i> , 2021 , 12, 645038	6.2	6
604	Comprehensive analysis and identification of drought-responsive candidate NAC genes in three semi-arid tropics (SAT) legume crops. <i>BMC Genomics</i> , 2021 , 22, 289	4.5	1
603	Can omics deliver temperature resilient ready-to-grow crops?. <i>Critical Reviews in Biotechnology</i> , 2021 , 41, 1209-1232	9.4	41
602	Genomics and breeding innovations for enhancing genetic gain for climate resilience and nutrition traits. <i>Theoretical and Applied Genetics</i> , 2021 , 134, 1829-1843	6	10
601	Regulatory non-coding RNAs: a new frontier in regulation of plant biology. <i>Functional and Integrative Genomics</i> , 2021 , 21, 313-330	3.8	10
600	Global Transcriptome Profiling Identified Transcription Factors, Biological Process, and Associated Pathways for Pre-Harvest Aflatoxin Contamination in Groundnut. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021 , 7,	5.6	3
599	De novo full length transcriptome analysis of <i>Arachis glabrata</i> provides insights into gene expression dynamics in response to biotic and abiotic stresses. <i>Genomics</i> , 2021 , 113, 1579-1588	4.3	1
598	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	3.7	2
597	Systems biology for crop improvement. <i>Plant Genome</i> , 2021 , 14, e20098	4.4	15
596	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	6.2	4
595	Molecular mapping of dry root rot resistance genes in chickpea (<i>Cicer arietinum</i> L.). <i>Euphytica</i> , 2021 , 217, 1	2.1	1
594	Dissection of the Genetic Basis of Yield-Related Traits in the Chinese Peanut Mini-Core Collection Through Genome-Wide Association Studies. <i>Frontiers in Plant Science</i> , 2021 , 12, 637284	6.2	4
593	MAGIC lines in chickpea: development and exploitation of genetic diversity. <i>Euphytica</i> , 2021 , 217, 1	2.1	1
592	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	6.2	3

591	Delineation of genotype-by-environment interactions for identification and validation of resistant genotypes in chickpea to fusarium wilt using GGE biplot. <i>Crop Protection</i> , 2021 , 144, 105571	2.7	4
590	Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. <i>Plant Genome</i> , 2021 , e20109	4.4	11
589	Designing Future Crops: Genomics-Assisted Breeding Comes of Age. <i>Trends in Plant Science</i> , 2021 , 26, 631-649	13.1	68
588	Single Seed-Based High-Throughput Genotyping and Rapid Generation Advancement for Accelerated Groundnut Genetics and Breeding Research. <i>Agronomy</i> , 2021 , 11, 1226	3.6	2
587	Molecular Genetic Diversity and Population Structure in Ethiopian Chickpea Germplasm Accessions. <i>Diversity</i> , 2021 , 13, 247	2.5	3
586	Single-cell RNA-seq describes the transcriptome landscape and identifies critical transcription factors in the leaf blade of the allotetraploid peanut (<i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2021 , 19, 2261-2276	11.6	4
585	Enhancing oleic acid content in two commercially released peanut varieties through marker-assisted backcross breeding. <i>Crop Science</i> , 2021 , 61, 2435	2.4	2
584	MutMap Approach Enables Rapid Identification of Candidate Genes and Development of Markers Associated With Early Flowering and Enhanced Seed Size in Chickpea (L.). <i>Frontiers in Plant Science</i> , 2021 , 12, 688694	6.2	0
583	High-Throughput Estimation of Crop Traits: A Review of Ground and Aerial Phenotyping Platforms. <i>IEEE Geoscience and Remote Sensing Magazine</i> , 2021 , 9, 200-231	8.9	61
582	Natural polymorphisms in a pair of NSP2 homoeologs can cause loss of nodulation in peanut. <i>Journal of Experimental Botany</i> , 2021 , 72, 1104-1118	7	3
581	A diagnostic marker kit for Fusarium wilt and sterility mosaic diseases resistance in pigeonpea. <i>Theoretical and Applied Genetics</i> , 2021 , 134, 367-379	6	7
580	The celery genome sequence reveals sequential paleo-polyploidizations, karyotype evolution and resistance gene reduction in apiaceae. <i>Plant Biotechnology Journal</i> , 2021 , 19, 731-744	11.6	13
579	Sigma Factor Modulation for Cyanobacterial Metabolic Engineering. <i>Trends in Microbiology</i> , 2021 , 29, 266-277	12.4	6
578	Soybean transporter database: A comprehensive database for identification and exploration of natural variants in soybean transporter genes. <i>Physiologia Plantarum</i> , 2021 , 171, 756-770	4.6	7
577	Genetic diversity and population structure of groundnut (L.) accessions using phenotypic traits and SSR markers: implications for rust resistance breeding. <i>Genetic Resources and Crop Evolution</i> , 2021 , 68, 581-604	2	7
576	Fatty acid desaturase-2 (ahFAD2) mutant alleles in peanut (<i>Arachis hypogaea</i> L.) pre-breeding lines: an insight into the source, features, discourse, and selection of novel pre-breeding lines. <i>Genetic Resources and Crop Evolution</i> , 2021 , 68, 529-549	2	2
575	Genomics: Shaping Legume Improvement 2021 , 49-89		1
574	Innovation Platform for Catalyzing Access to Seed of Improved Legume Varieties to Smallholder Farmers 2021 , 199-205		

573	Population Genomics of Peanut. <i>Population Genomics</i> , 2021 , 1	1.4	2
572	Groundnut Kernel Transcriptome 2021 , 528-543		
571	Genomic resources in plant breeding for sustainable agriculture. <i>Journal of Plant Physiology</i> , 2021 , 257, 153351	3.6	24
570	Identification of microRNAs and their gene targets in cytoplasmic male sterile and fertile maintainer lines of pigeonpea. <i>Planta</i> , 2021 , 253, 59	4.7	5
569	Genomics-assisted lentil breeding: Current status and future strategies 2021 , 3, e71		5
568	Metabolomics Intervention Towards Better Understanding of Plant Traits. <i>Cells</i> , 2021 , 10,	7.9	17
567	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. <i>Scientific Data</i> , 2021 , 8, 50	8.2	13
566	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	3.8	6
565	Key Regulators of Sucrose Metabolism Identified through Comprehensive Comparative Transcriptome Analysis in Peanuts. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	3
564	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	5.9	4
563	Major QTLs and Potential Candidate Genes for Heat Stress Tolerance Identified in Chickpea (L.). <i>Frontiers in Plant Science</i> , 2021 , 12, 655103	6.2	9
562	Spatial distribution of proteins and metabolites in developing wheat grain and their differential regulatory response during the grain filling process. <i>Plant Journal</i> , 2021 , 107, 669-687	6.9	5
561	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	3.7	2
560	Characterization of heterosis and genomic prediction-based establishment of heterotic patterns for developing better hybrids in pigeonpea. <i>Plant Genome</i> , 2021 , 14, e20125	4.4	2
559	Rapid delivery systems for future food security. <i>Nature Biotechnology</i> , 2021 , 39, 1179-1181	44.5	4
558	Transcriptome analysis reveals key genes associated with root-lesion nematode <i>Pratylenchus thornei</i> resistance in chickpea. <i>Scientific Reports</i> , 2021 , 11, 17491	4.9	4
557	Genotyping-by-Sequencing Based Genetic Mapping Identified Major and Consistent Genomic Regions for Productivity and Quality Traits in Peanut. <i>Frontiers in Plant Science</i> , 2021 , 12, 668020	6.2	4
556	The INCREASE project: Intelligent Collections of food-legume genetic resources for European agrofood systems. <i>Plant Journal</i> , 2021 , 108, 646-660	6.9	5

555	Fast-forward breeding for a food-secure world. <i>Trends in Genetics</i> , 2021 , 37, 1124-1136	8.5	15
554	Global gene expression analysis of pigeonpea with male sterility conditioned by A cytoplasm. <i>Plant Genome</i> , 2021 , 14, e20132	4.4	6
553	Breeding custom-designed crops for improved drought adaptation. <i>Genetics & Genomics Next</i> , 2021 , 2, e202100017	1.2	1
552	Widely targeted metabolomics characterizes the dynamic changes of chemical profile in postharvest peanut sprouts grown under the dark and light conditions. <i>LWT - Food Science and Technology</i> , 2021 , 152, 112283	5.4	3
551	A Cross-Case Analysis of Innovation Platform Experiences in Seven Countries in West and East Africa and South Asia 2021 , 185-197		
550	Genetic Enhancement in Major Food Legumes: An Overview 2021 , 1-6		
549	Introgression of "QTL-hotspot" region enhances drought tolerance and grain yield in three elite chickpea cultivars. <i>Plant Genome</i> , 2021 , 14, e20076	4.4	21
548	General Context of Smallholder Farmers' Access to Seed of Improved Legume Varieties and Innovation Platform Perspectives 2021 , 1-7		
547	Hybrid Breeding in Food Legumes with Special Reference to Pigeonpea, Faba bean, and Soybean 2021 , 123-148		1
546	Aerially Applied Zinc Oxide Nanoparticle Affects Reproductive Components and Seed Quality in Fully Grown Bean Plants (L.). <i>Frontiers in Plant Science</i> , 2021 , 12, 808141	6.2	2
545	A New Deep Learning Calibration Method Enhances Genome-Based Prediction of Continuous Crop Traits.. <i>Frontiers in Genetics</i> , 2021 , 12, 798840	4.5	0
544	Pangenomics in crop improvement-from coding structural variations to finding regulatory variants with pangenome graphs.. <i>Plant Genome</i> , 2021 , e20177	4.4	2
543	Translational Pigeonpea Genomics Consortium for Accelerating Genetic Gains in Pigeonpea (Cajanus cajan L.). <i>Agronomy</i> , 2020 , 10, 1289	3.6	7
542	Genome-Wide SNP Discovery and Mapping QTLs for Seed Iron and Zinc Concentrations in Chickpea (L.). <i>Frontiers in Nutrition</i> , 2020 , 7, 559120	6.2	11
541	Reply to: Evaluating two different models of peanut's origin. <i>Nature Genetics</i> , 2020 , 52, 560-563	36.3	4
540	G x E interactions in QTL introgression lines of Spanish-type groundnut (Arachis hypogaea L.). <i>Euphytica</i> , 2020 , 216, 1	2.1	1
539	Superior haplotypes for haplotype-based breeding for drought tolerance in pigeonpea (Cajanus cajan L.). <i>Plant Biotechnology Journal</i> , 2020 , 18, 2482-2490	11.6	25
538	Molecular and Physiological Alterations in Chickpea under Elevated CO2 Concentrations. <i>Plant and Cell Physiology</i> , 2020 , 61, 1449-1463	4.9	6

537	Dissection of the genetic basis of oil content in Chinese peanut cultivars through association mapping. <i>BMC Genetics</i> , 2020 , 21, 60	2.6	2
536	Advances in Crop Improvement and Delivery Research for Nutritional Quality and Health Benefits of Groundnut (L.). <i>Frontiers in Plant Science</i> , 2020 , 11, 29	6.2	18
535	Comparative Root Transcriptomics Provide Insights into Drought Adaptation Strategies in Chickpea (L.). <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	13
534	PANOMICS meets germplasm. <i>Plant Biotechnology Journal</i> , 2020 , 18, 1507-1525	11.6	39
533	Arachis hypogaea gene expression atlas for fastigiata subspecies of cultivated groundnut to accelerate functional and translational genomics applications. <i>Plant Biotechnology Journal</i> , 2020 , 18, 2187-2200	11.6	19
532	Identification of quantitative trait loci associated with iron deficiency chlorosis resistance in groundnut (Arachis hypogaea). <i>Plant Breeding</i> , 2020 , 139, 790-803	2.4	3
531	Identification of Two Novel Peanut Genotypes Resistant to Aflatoxin Production and Their SNP Markers Associated with Resistance. <i>Toxins</i> , 2020 , 12,	4.9	8
530	Genome-wide transcriptome and physiological analyses provide new insights into peanut drought response mechanisms. <i>Scientific Reports</i> , 2020 , 10, 4071	4.9	13
529	High resolution mapping of restoration of fertility (Rf) by combining large population and high density genetic map in pigeonpea [Cajanus cajan (L.) Millsp]. <i>BMC Genomics</i> , 2020 , 21, 460	4.5	4
528	Multi-parent populations in crops: a toolbox integrating genomics and genetic mapping with breeding. <i>Heredity</i> , 2020 , 125, 396-416	3.6	53
527	Multomics approach unravels fertility transition in a pigeonpea line for a two-line hybrid system. <i>Plant Genome</i> , 2020 , 13, e20028	4.4	10
526	Trait associations in the pangenome of pigeon pea (Cajanus cajan). <i>Plant Biotechnology Journal</i> , 2020 , 18, 1946-1954	11.6	36
525	Seed protein content and its relationships with agronomic traits in pigeonpea is controlled by both main and epistatic effects QTLs. <i>Scientific Reports</i> , 2020 , 10, 214	4.9	8
524	Molecular Basis of Root Nodule Symbiosis between and 'Crack-Entry' Legume Groundnut (L.). <i>Plants</i> , 2020 , 9,	4.5	21
523	Genomics-assisted breeding for pigeonpea improvement. <i>Theoretical and Applied Genetics</i> , 2020 , 133, 1721-1737	6	32
522	Discovery of two novel and adjacent QTLs on chromosome B02 controlling resistance against bacterial wilt in peanut variety Zhonghua 6. <i>Theoretical and Applied Genetics</i> , 2020 , 133, 1133-1148	6	6
521	5Gs for crop genetic improvement. <i>Current Opinion in Plant Biology</i> , 2020 , 56, 190-196	9.9	64
520	Functional Biology and Molecular Mechanisms of Host-Pathogen Interactions for Aflatoxin Contamination in Groundnut (L.) and Maize (L.). <i>Frontiers in Microbiology</i> , 2020 , 11, 227	5.7	22

519	Integrating genomics for chickpea improvement: achievements and opportunities. <i>Theoretical and Applied Genetics</i> , 2020 , 133, 1703-1720	6	35
518	High-density SNP map facilitates fine mapping of QTLs and candidate genes discovery for <i>Aspergillus flavus</i> resistance in peanut (<i>Arachis hypogaea</i>). <i>Theoretical and Applied Genetics</i> , 2020 , 133, 2239-2257	6	9
517	Legume seed production for sustainable seed supply and crop productivity: case of groundnut in Tanzania and Uganda. <i>Journal of Crop Improvement</i> , 2020 , 34, 518-539	1.4	7
516	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	6.2	22
515	Translational genomics for achieving higher genetic gains in groundnut. <i>Theoretical and Applied Genetics</i> , 2020 , 133, 1679-1702	6	31
514	A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. <i>Plant Genome</i> , 2020 , 13, e20009	4.4	24
513	An integrated research framework combining genomics, systems biology, physiology, modelling and breeding for legume improvement in response to elevated CO under climate change scenario. <i>Current Plant Biology</i> , 2020 , 22, 100149	3.3	18
512	Unraveling candidate genomic regions responsible for delayed leaf senescence in rice. <i>PLoS ONE</i> , 2020 , 15, e0240591	3.7	2
511	Transcriptional responses of toxigenic and atoxigenic isolates of <i>Aspergillus flavus</i> to oxidative stress in aflatoxin-conducive and non-conducive media. <i>World Mycotoxin Journal</i> , 2020 , 13, 443-457	2.5	1
510	Improved Genetic Map Identified Major QTLs for Drought Tolerance- and Iron Deficiency Tolerance-Related Traits in Groundnut. <i>Genes</i> , 2020 , 12,	4.2	8
509	Breeding and Molecular Approaches for Evolving Drought-Tolerant Soybeans 2020 , 83-130		3
508	Genomic Designing of Pearl Millet: A Resilient Crop for Arid and Semi-arid Environments 2020 , 221-286		8
507	Fine mapping and gene cloning in the post-NGS era: advances and prospects. <i>Theoretical and Applied Genetics</i> , 2020 , 133, 1791-1810	6	50
506	Genome-wide expression quantitative trait locus analysis in a recombinant inbred line population for trait dissection in peanut. <i>Plant Biotechnology Journal</i> , 2020 , 18, 779-790	11.6	9
505	Whole-genome resequencing-based QTL-seq identified candidate genes and molecular markers for fresh seed dormancy in groundnut. <i>Plant Biotechnology Journal</i> , 2020 , 18, 992-1003	11.6	18
504	Improvement of three popular Indian groundnut varieties for foliar disease resistance and high oleic acid using SSR markers and SNP array in marker-assisted backcrossing. <i>Crop Journal</i> , 2020 , 8, 1-15	4.6	21
503	Genome-wide analysis of epigenetic and transcriptional changes associated with heterosis in pigeonpea. <i>Plant Biotechnology Journal</i> , 2020 , 18, 1697-1710	11.6	17
502	Identification of heterotic groups in South-Asian-bred hybrid parents of pearl millet. <i>Theoretical and Applied Genetics</i> , 2020 , 133, 873-888	6	6

501	Super-Pangenome by Integrating the Wild Side of a Species for Accelerated Crop Improvement. <i>Trends in Plant Science</i> , 2020 , 25, 148-158	13.1	87
500	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	6	13
499	Nested-association mapping (NAM)-based genetic dissection uncovers candidate genes for seed and pod weights in peanut (<i>Arachis hypogaea</i>). <i>Plant Biotechnology Journal</i> , 2020 , 18, 1457-1471	11.6	28
498	Understanding sheath blight resistance in rice: the road behind and the road ahead. <i>Plant Biotechnology Journal</i> , 2020 , 18, 895-915	11.6	49
497	Two New Reference Genomes Reveal a Large Insertion Potentially Contributing to Isolate Stress Tolerance and Aflatoxin Production. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 3515-3531	3.2	4
496	Epigenetics and epigenomics: underlying mechanisms, relevance, and implications in crop improvement. <i>Functional and Integrative Genomics</i> , 2020 , 20, 739-761	3.8	18
495	Characterization of ASR gene and its role in drought tolerance in chickpea (<i>Cicer arietinum</i> L.). <i>PLoS ONE</i> , 2020 , 15, e0234550	3.7	8
494	Complete genome sequence of sixteen plant growth promoting <i>Streptomyces</i> strains. <i>Scientific Reports</i> , 2020 , 10, 10294	4.9	15
493	Advances in genomics and molecular breeding for legume improvement 2020 , 129-139		3
492	Genetic Dissection and Identification of Candidate Genes for Salinity Tolerance Using Axiom Array in Chickpea. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	15
491	Global transcriptome analysis of subterranean pod and seed in peanut (<i>Arachis hypogaea</i> L.) unravels the complexity of fruit development under dark condition. <i>Scientific Reports</i> , 2020 , 10, 13050	4.9	1
490	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020 , 13, 1341-1344	14.4	21
489	Genomic interventions for sustainable agriculture. <i>Plant Biotechnology Journal</i> , 2020 , 18, 2388-2405	11.6	41
488	Analyzing Pathways of Nurturing Informal Seed Production into Formal Private Ventures for Sustainable Seed Delivery and Crop Productivity: Experiences from Ethiopia. <i>Sustainability</i> , 2020 , 12, 6828	3.6	2
487	Genome-based trait prediction in multi- environment breeding trials in groundnut. <i>Theoretical and Applied Genetics</i> , 2020 , 133, 3101-3117	6	19
486	Factors Influencing Preferences and Adoption of Improved Groundnut Varieties among Farmers in Tanzania. <i>Agronomy</i> , 2020 , 10, 1271	3.6	3
485	Genome-wide identification of meiotic recombination hot spots detected by SLAF in peanut (<i>Arachis hypogaea</i> L.). <i>Scientific Reports</i> , 2020 , 10, 13792	4.9	
484	Transcriptome Analysis Identified Coordinated Control of Key Pathways Regulating Cellular Physiology and Metabolism upon Infection Resulting in Reduced Aflatoxin Production in Groundnut. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020 , 6,	5.6	3

483	A systematic dissection of the mechanisms underlying the natural variation of silique number in rapeseed (<i>Brassica napus</i> L.) germplasm. <i>Plant Biotechnology Journal</i> , 2020 , 18, 568-580	11.6	12
482	Transcriptome and metabolome reveal redirection of flavonoids in a white testa peanut mutant. <i>BMC Plant Biology</i> , 2020 , 20, 161	5.3	12
481	Development of a dense genetic map and QTL analysis for pod borer <i>Helicoverpa armigera</i> (Hßner) resistance component traits in chickpea (<i>Cicer arietinum</i> L.). <i>Plant Genome</i> , 2020 , 14, e20071	4.4	6
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477	Haplotype analysis of key genes governing grain yield and quality traits across 3K RG panel reveals scope for the development of tailor-made rice with enhanced genetic gains. <i>Plant Biotechnology Journal</i> , 2019 , 17, 1612-1622	11.6	43
476	Genomic Interventions to Improve Resilience of Pigeonpea in Changing Climate 2019 , 107-134		1
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474	Origin of early maturing pigeonpea germplasm and its impact on adaptation and cropping systems. <i>Plant Breeding</i> , 2019 , 138, 243-251	2.4	7
473	Genome-wide association study reveals significant genomic regions for improving yield, adaptability of rice under dry direct seeded cultivation condition. <i>BMC Genomics</i> , 2019 , 20, 471	4.5	13
472	QTLian breeding for climate resilience in cereals: progress and prospects. <i>Functional and Integrative Genomics</i> , 2019 , 19, 685-701	3.8	16
471	Next-generation sequencing identified genomic region and diagnostic markers for resistance to bacterial wilt on chromosome B02 in peanut (<i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2019 , 17, 2356-2369	11.6	17
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469	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	36.3	116
468	The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. <i>Nature Genetics</i> , 2019 , 51, 865-876	36.3	188
467	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019 , 51, 877-884	36.3	211
466	An "Axiom Cajanus SNP Array" based high density genetic map and QTL mapping for high-selfing flower and seed quality traits in pigeonpea. <i>BMC Genomics</i> , 2019 , 20, 235	4.5	22

465	Identification of genomic regions and diagnostic markers for resistance to aflatoxin contamination in peanut (<i>Arachis hypogaea</i> L.). <i>BMC Genetics</i> , 2019 , 20, 32	2.6	19
464	InDel markers: An extended marker resource for molecular breeding in chickpea. <i>PLoS ONE</i> , 2019 , 14, e0213999	3.7	23
463	Drought and heat stress-related proteins: an update about their functional relevance in imparting stress tolerance in agricultural crops. <i>Theoretical and Applied Genetics</i> , 2019 , 132, 1607-1638	6	45
462	Epistatic interactions of major effect drought QTLs with genetic background loci determine grain yield of rice under drought stress. <i>Scientific Reports</i> , 2019 , 9, 2616	4.9	26
461	Climate-Smart Groundnuts for Achieving High Productivity and Improved Quality: Current Status, Challenges, and Opportunities 2019 , 133-172		5
460	Genome sequence of <i>Jatropha curcas</i> L., a non-edible biodiesel plant, provides a resource to improve seed-related traits. <i>Plant Biotechnology Journal</i> , 2019 , 17, 517-530	11.6	35
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429	Modelling predicts that soybean is poised to dominate crop production across Africa. <i>Plant, Cell and Environment</i> , 2019 , 42, 373-385	8.4	25
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399	Chickpea Genomics 2018 , 289-316		0
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360	The Pigeonpea Genome: An Overview. <i>Compendium of Plant Genomes</i> , 2017 , 1-4	0.8	
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345	The Peanut Genome: An Introduction. <i>Compendium of Plant Genomes</i> , 2017 , 1-6	0.8	2
344	Future Prospects for Peanut Improvement. <i>Compendium of Plant Genomes</i> , 2017 , 165-169	0.8	3
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176	Comparative sequence analysis of nitrogen fixation-related genes in six legumes. <i>Frontiers in Plant Science</i> , 2013 , 4, 300	6.2	12
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171	Recent Advances in Molecular Genetic Linkage Maps of Cultivated Peanut. <i>Peanut Science</i> , 2013 , 40, 95-106	10.6	17
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160	Exploiting Genomic Resources for Efficient Conservation and Use of Chickpea, Groundnut, and Pigeonpea Collections for Crop Improvement. <i>Plant Genome</i> , 2013 , 6, plantgenome2013.05.0016	4.4	17

159	Pest and diseases: Old and new threats [Modern breeding tools to tailor new crop cultivars. <i>Shheresse</i> , 2013 , 24, 261-273		4
158	Genomics in Agriculture and Food Processing 2013 , 45-70		3
157	Advances in Arachis genomics for peanut improvement. <i>Biotechnology Advances</i> , 2012 , 30, 639-51	17.8	195
156	Large-scale development of cost-effective SNP marker assays for diversity assessment and genetic mapping in chickpea and comparative mapping in legumes. <i>Plant Biotechnology Journal</i> , 2012 , 10, 716-32	11.6	185
155	Development and characterization of BAC-end sequence derived SSRs, and their incorporation into a new higher density genetic map for cultivated peanut (<i>Arachis hypogaea</i> L.). <i>BMC Plant Biology</i> , 2012 , 12, 10	5.3	76
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153	An intra-specific consensus genetic map of pigeonpea [<i>Cajanus cajan</i> (L.) Millspaugh] derived from six mapping populations. <i>Theoretical and Applied Genetics</i> , 2012 , 125, 1325-38	6	85
152	Coverage-based consensus calling (CbCC) of short sequence reads and comparison of CbCC results to identify SNPs in chickpea (<i>Cicer arietinum</i> ; Fabaceae), a crop species without a reference genome. <i>American Journal of Botany</i> , 2012 , 99, 186-92	2.7	29
151	Whole-genome scanning for mapping determinacy in Pigeonpea (<i>Cajanus</i> spp.). <i>Plant Breeding</i> , 2012 , 132, no-no	2.4	7
150	Current state-of-art of sequencing technologies for plant genomics research. <i>Briefings in Functional Genomics</i> , 2012 , 11, 3-11	4.9	102
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147	Identification of dominant and recessive genes for resistance to Fusarium wilt in pigeonpea and their implication in breeding hybrids. <i>Euphytica</i> , 2012 , 188, 221-227	2.1	13
146	Quantitative trait locus analysis and construction of consensus genetic map for drought tolerance traits based on three recombinant inbred line populations in cultivated groundnut (<i>Arachis hypogaea</i> L.). <i>Molecular Breeding</i> , 2012 , 30, 757-772	3.4	72
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143	Can genomics boost productivity of orphan crops?. <i>Nature Biotechnology</i> , 2012 , 30, 1172-6	44.5	192
142	Future Prospects of Molecular Markers in Plants 2012 , 169-190		8

141	Translational Root Genomics for Crop Improvement 2012 , 249-264		1
140	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, 811-20	2.3	58
139	Omics Techniques in Crop Research: An Overview 2012 , 289-300		0
138	Assessment of ICCV 2 \times G 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	3.4	76
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136	Genome wide association analyses for drought tolerance related traits in barley (<i>Hordeum vulgare</i> L.). <i>Field Crops Research</i> , 2012 , 126, 171-180	5.5	77
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133	Large-scale development of cost-effective single-nucleotide polymorphism marker assays for genetic mapping in pigeonpea and comparative mapping in legumes. <i>DNA Research</i> , 2012 , 19, 449-61	4.5	86
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117	Mapping QTL for resistance to botrytis grey mould in chickpea. <i>Euphytica</i> , 2011 , 182, 1-9	2.1	49
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19	Large-scale analysis of the barley transcriptome based on expressed sequence tags. <i>Plant Journal</i> , 2004 , 40, 276-90	6.9	125
18	A simple hybridization-based strategy for the generation of non-redundant EST collections—case study in barley (<i>Hordeum vulgare</i> L.). <i>Plant Science</i> , 2004 , 167, 629-634	5.3	6
17	Molecular Maps in Cereals: Methodology and Progress 2004 , 35-82		5
16	Exploiting EST databases for the development and characterization of gene-derived SSR-markers in barley (<i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2003 , 106, 411-22	6	1633

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14	In silico analysis on frequency and distribution of microsatellites in ESTs of some cereal species. <i>Cellular and Molecular Biology Letters</i> , 2002 , 7, 537-46	8.1	251
13	Generation and comparison of EST-derived SSRs and SNPs in barley (<i>Hordeum vulgare</i> L.). <i>Hereditas</i> , 2001 , 135, 145-51	2.4	79
12	STMS markers for grain protein content and their validation using near-isogenic lines in bread wheat. <i>Plant Breeding</i> , 2001 , 120, 273-278	2.4	33
11	Integrated physical maps of 2DL, 6BS and 7DL carrying loci for grain protein content and pre-harvest sprouting tolerance in bread wheat. <i>Cereal Research Communications</i> , 2001 , 29, 33-40	1.1	10
10	The development and use of microsatellite markers for genetic analysis and plant breeding with emphasis on bread wheat. <i>Euphytica</i> , 2000 , 113, 163-185	2.1	524
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