

# Rajeev Kumar Varshney

## List of Publications by Year in descending order

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657  
papers

49,662  
citations

1294

109  
h-index

3021

188  
g-index

691  
all docs

691  
docs citations

691  
times ranked

23560  
citing authors

#	ARTICLE	IF	CITATIONS
1	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, 411-422.	1.8	2,073
2	Genic microsatellite markers in plants: features and applications. <i>Trends in Biotechnology</i> , 2005, 23, 48-55.	4.9	1,543
3	Draft genome sequence of chickpea ( <i>Cicer arietinum</i> ) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013, 31, 240-246.	9.4	1,049
4	Genomic Selection in Plant Breeding: Methods, Models, and Perspectives. <i>Trends in Plant Science</i> , 2017, 22, 961-975.	4.3	1,004
5	Next-generation sequencing technologies and their implications for crop genetics and breeding. <i>Trends in Biotechnology</i> , 2009, 27, 522-530.	4.9	805
6	Draft genome sequence of pigeonpea ( <i>Cajanus cajan</i> ), an orphan legume crop of resource-poor farmers. <i>Nature Biotechnology</i> , 2012, 30, 83-89.	9.4	788
7	The genome sequences of <i>Arachis duranensis</i> and <i>Arachis ipaensis</i> , the diploid ancestors of cultivated peanut. <i>Nature Genetics</i> , 2016, 48, 438-446.	9.4	761
8	Title is missing!. <i>Euphytica</i> , 2000, 113, 163-185.	0.6	689
9	Genomics-assisted breeding for crop improvement. <i>Trends in Plant Science</i> , 2005, 10, 621-630.	4.3	579
10	Development and implementation of high-throughput SNP genotyping in barley. <i>BMC Genomics</i> , 2009, 10, 582.	1.2	570
11	Neglecting legumes has compromised human health and sustainable food production. <i>Nature Plants</i> , 2016, 2, 16112.	4.7	529
12	Feeding the future. <i>Nature</i> , 2013, 499, 23-24.	13.7	464
13	Genome sequence of mungbean and insights into evolution within <i>Vigna</i> species. <i>Nature Communications</i> , 2014, 5, 5443.	5.8	453
14	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	9.4	439
15	Review Molecular markers and their applications in wheat breeding. <i>Plant Breeding</i> , 1999, 118, 369-390.	1.0	403
16	The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. <i>Nature Genetics</i> , 2019, 51, 865-876.	9.4	398
17	Integrated genomics, physiology and breeding approaches for improving drought tolerance in crops. <i>Theoretical and Applied Genetics</i> , 2012, 125, 625-645.	1.8	397
18	Crop Breeding Chips and Genotyping Platforms: Progress, Challenges, and Perspectives. <i>Molecular Plant</i> , 2017, 10, 1047-1064.	3.9	380

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19	Drought or/and Heat-Stress Effects on Seed Filling in Food Crops: Impacts on Functional Biochemistry, Seed Yields, and Nutritional Quality. <i>Frontiers in Plant Science</i> , 2018, 9, 1705.	1.7	371
20	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	9.4	356
21	Plant growth promoting rhizobia: challenges and opportunities. <i>3 Biotech</i> , 2015, 5, 355-377.	1.1	350
22	Differentially expressed genes between drought-tolerant and drought-sensitive barley genotypes in response to drought stress during the reproductive stage. <i>Journal of Experimental Botany</i> , 2009, 60, 3531-3544.	2.4	349
23	Harvesting the Promising Fruits of Genomics: Applying Genome Sequencing Technologies to Crop Breeding. <i>PLoS Biology</i> , 2014, 12, e1001883.	2.6	341
24	Agricultural biotechnology for crop improvement in a variable climate: hope or hype?. <i>Trends in Plant Science</i> , 2011, 16, 363-371.	4.3	311
25	Recent history of artificial outcrossing facilitates whole-genome association mapping in elite inbred crop varieties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18656-18661.	3.3	309
26	A high density barley microsatellite consensus map with 775 SSR loci. <i>Theoretical and Applied Genetics</i> , 2007, 114, 1091-1103.	1.8	308
27	Genetic dissection of drought tolerance in chickpea ( <i>Cicer Arietinum</i> L.). <i>Theoretical and Applied Genetics</i> , 2014, 127, 445-462.	1.8	304
28	Comparative assessment of EST-SSR, EST-SNP and AFLP markers for evaluation of genetic diversity and conservation of genetic resources using wild, cultivated and elite barleys. <i>Plant Science</i> , 2007, 173, 638-649.	1.7	294
29	Achievements and prospects of genomics-assisted breeding in three legume crops of the semi-arid tropics. <i>Biotechnology Advances</i> , 2013, 31, 1120-1134.	6.0	289
30	Genome-wide association mapping: a case study in bread wheat ( <i>Triticum aestivum</i> L.). <i>Molecular Breeding</i> , 2011, 27, 37-58.	1.0	278
31	Interspecific transferability and comparative mapping of barley EST-SSR markers in wheat, rye and rice. <i>Plant Science</i> , 2005, 168, 195-202.	1.7	266
32	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.	2.7	264
33	Advances in <i>Arachis</i> genomics for peanut improvement. <i>Biotechnology Advances</i> , 2012, 30, 639-651.	6.0	258
34	Development of genic-SSR markers by deep transcriptome sequencing in pigeonpea [ <i>Cajanus cajan</i> (L.) Millspaugh]. <i>BMC Plant Biology</i> , 2011, 11, 17.	1.6	251
35	Large-scale transcriptome analysis in chickpea ( <i>Cicer arietinum</i> L.), an orphan legume crop of the semi-arid tropics of Asia and Africa. <i>Plant Biotechnology Journal</i> , 2011, 9, 922-931.	4.1	250
36	Can genomics boost productivity of orphan crops?. <i>Nature Biotechnology</i> , 2012, 30, 1172-1176.	9.4	248

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37	Legume Crops Phylogeny and Genetic Diversity for Science and Breeding. <i>Critical Reviews in Plant Sciences</i> , 2015, 34, 43-104.	2.7	248
38	Genome sequencing of the high oil crop sesame provides insight into oil biosynthesis. <i>Genome Biology</i> , 2014, 15, R39.	13.9	245
39	Designing Future Crops: Genomics-Assisted Breeding Comes of Age. <i>Trends in Plant Science</i> , 2021, 26, 631-649.	4.3	244
40	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. <i>Frontiers in Plant Science</i> , 2015, 6, 563.	1.7	243
41	A 1,000-loci transcript map of the barley genome: new anchoring points for integrative grass genomics. <i>Theoretical and Applied Genetics</i> , 2007, 114, 823-839.	1.8	239
42	Advances in cereal genomics and applications in crop breeding. <i>Trends in Biotechnology</i> , 2006, 24, 490-499.	4.9	236
43	Draft genome of the peanut A-genome progenitor ( <i>Arachis duranensis</i> ) provides insights into geocarpy, oil biosynthesis, and allergens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6785-6790.	3.3	235
44	MAGIC populations in crops: current status and future prospects. <i>Theoretical and Applied Genetics</i> , 2015, 128, 999-1017.	1.8	230
45	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, 716-732.	4.1	221
46	Global agricultural intensification during climate change: a role for genomics. <i>Plant Biotechnology Journal</i> , 2016, 14, 1095-1098.	4.1	221
47	The first SSR-based genetic linkage map for cultivated groundnut ( <i>Arachis hypogaea</i> L.). <i>Theoretical and Applied Genetics</i> , 2009, 118, 729-739.	1.8	219
48	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.	9.4	219
49	Identification, characterization and utilization of EST-derived genic microsatellite markers for genome analyses of coffee and related species. <i>Theoretical and Applied Genetics</i> , 2007, 114, 359-372.	1.8	218
50	Whole-genome resequencing of 292 pigeonpea accessions identifies genomic regions associated with domestication and agronomic traits. <i>Nature Genetics</i> , 2017, 49, 1082-1088.	9.4	218
51	Orphan legume crops enter the genomics era!. <i>Current Opinion in Plant Biology</i> , 2009, 12, 202-210.	3.5	212
52	Isolation and characterization of novel microsatellite markers and their application for diversity assessment in cultivated groundnut ( <i>Arachis hypogaea</i> ). <i>BMC Plant Biology</i> , 2008, 8, 55.	1.6	203
53	Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with <i>Medicago truncatula</i> genome. <i>Theoretical and Applied Genetics</i> , 2010, 120, 1415-1441.	1.8	200
54	A comprehensive resource of drought- and salinity- responsive ESTs for gene discovery and marker development in chickpea ( <i>Cicer arietinum</i> L.). <i>BMC Genomics</i> , 2009, 10, 523.	1.2	199

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55	<sc>QTL</sc>â€seq approach identified genomic regions and diagnostic markers for rust and late leaf spot resistance in groundnut (<i>Arachis hypogaea</i> L.). Plant Biotechnology Journal, 2017, 15, 927-941.	4.1	198
56	Salt sensitivity in chickpea. Plant, Cell and Environment, 2010, 33, 490-509.	2.8	194
57	AFLP-based molecular characterization of an elite germplasm collection of <i>Jatropha curcas</i> L., a biofuel plant. Plant Science, 2009, 176, 505-513.	1.7	189
58	Identification of several small main-effect QTLs and a large number of epistatic QTLs for drought tolerance related traits in groundnut ( <i>Arachis hypogaea</i> L.). Theoretical and Applied Genetics, 2011, 122, 1119-1132.	1.8	188
59	Transcriptome analyses reveal genotype- and developmental stage-specific molecular responses to drought and salinity stresses in chickpea. Scientific Reports, 2016, 6, 19228.	1.6	188
60	Genetic Dissection of Drought and Heat Tolerance in Chickpea through Genome-Wide and Candidate Gene-Based Association Mapping Approaches. PLoS ONE, 2014, 9, e96758.	1.1	187
61	Assessing genetic diversity for crop improvement. Current Opinion in Plant Biology, 2010, 13, 167-173.	3.5	186
62	Sequencing of Cultivated Peanut, <i>Arachis hypogaea</i> , Yields Insights into Genome Evolution and Oil Improvement. Molecular Plant, 2019, 12, 920-934.	3.9	185
63	A QTL study on late leaf spot and rust revealed one major QTL for molecular breeding for rust resistance in groundnut ( <i>Arachis hypogaea</i> L.). Theoretical and Applied Genetics, 2010, 121, 971-984.	1.8	182
64	Proline over-accumulation alleviates salt stress and protects photosynthetic and antioxidant enzyme activities in transgenic sorghum [ <i>Sorghum bicolor</i> (L.) Moench]. Plant Physiology and Biochemistry, 2015, 94, 104-113.	2.8	182
65	Genotyping-by-sequencing based intra-specific genetic map refines a QTL-hotspot region for drought tolerance in chickpea. Molecular Genetics and Genomics, 2015, 290, 559-571.	1.0	180
66	Emerging Genomic Tools for Legume Breeding: Current Status and Future Prospects. Frontiers in Plant Science, 2016, 7, 455.	1.7	180
67	QTLâ€seq for rapid identification of candidate genes for 100â€seed weight and root/total plant dry weight ratio under rainfed conditions in chickpea. Plant Biotechnology Journal, 2016, 14, 2110-2119.	4.1	177
68	Super-Pangenome by Integrating the Wild Side of a Species for Accelerated Crop Improvement. Trends in Plant Science, 2020, 25, 148-158.	4.3	177
69	Structural variations in plant genomes. Briefings in Functional Genomics, 2014, 13, 296-307.	1.3	176
70	Genetic structure, diversity, and allelic richness in composite collection and reference set in chickpea ( <i>Cicer arietinum</i> L.). BMC Plant Biology, 2008, 8, 106.	1.6	170
71	Quantitative trait locus analysis and construction of consensus genetic map for foliar disease resistance based on two recombinant inbred line populations in cultivated groundnut ( <i>Arachis</i> Tj ETQq1 1 0.784314.orgBT/Overlock 10	1.4	169
72	Marker-assisted introgression of a QTL region to improve rust resistance in three elite and popular varieties of peanut ( <i>Arachis hypogaea</i> L.). Theoretical and Applied Genetics, 2014, 127, 1771-1781.	1.8	167

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73	The use of microsatellites for detecting DNA polymorphism, genotype identification and genetic diversity in wheat. <i>Theoretical and Applied Genetics</i> , 2000, 100, 584-592.	1.8	164
74	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.	1.1	160
75	Exciting journey of 10 years from genomes to fields and markets: Some success stories of genomics-assisted breeding in chickpea, pigeonpea and groundnut. <i>Plant Science</i> , 2016, 242, 98-107.	1.7	155
76	Toward the sequence-based breeding in legumes in the post-genome sequencing era. <i>Theoretical and Applied Genetics</i> , 2019, 132, 797-816.	1.8	147
77	Large variation in salinity tolerance in chickpea is explained by differences in sensitivity at the reproductive stage. <i>Field Crops Research</i> , 2007, 104, 123-129.	2.3	146
78	Food Legumes and Rising Temperatures: Effects, Adaptive Functional Mechanisms Specific to Reproductive Growth Stage and Strategies to Improve Heat Tolerance. <i>Frontiers in Plant Science</i> , 2017, 8, 1658.	1.7	146
79	Understanding sheath blight resistance in rice: the road behind and the road ahead. <i>Plant Biotechnology Journal</i> , 2020, 18, 895-915.	4.1	146
80	A high-density consensus map of barley to compare the distribution of QTLs for partial resistance to <i>Puccinia hordei</i> and of defence gene homologues. <i>Theoretical and Applied Genetics</i> , 2007, 114, 487-500.	1.8	145
81	Evaluation of <i>Streptomyces</i> strains isolated from herbal vermicompost for their plant growth-promotion traits in rice. <i>Microbiological Research</i> , 2014, 169, 40-48.	2.5	144
82	Draft genome sequence of adzuki bean, <i>Vigna angularis</i> . <i>Scientific Reports</i> , 2015, 5, 8069.	1.6	144
83	Development and Evaluation of a High Density Genotyping <i>~Axiom_Arachis~</i> ™ Array with 58~%K SNPs for Accelerating Genetics and Breeding in Groundnut. <i>Scientific Reports</i> , 2017, 7, 40577.	1.6	144
84	Pre-breeding for diversification of primary gene pool and genetic enhancement of grain legumes. <i>Frontiers in Plant Science</i> , 2013, 4, 309.	1.7	141
85	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.	4.9	141
86	QTLs for chlorophyll and chlorophyll fluorescence parameters in barley under post-flowering drought. <i>Euphytica</i> , 2008, 163, 203-214.	0.6	140
87	Groundnut improvement: use of genetic and genomic tools. <i>Frontiers in Plant Science</i> , 2013, 4, 23.	1.7	139
88	Large-scale analysis of the barley transcriptome based on expressed sequence tags. <i>Plant Journal</i> , 2004, 40, 276-290.	2.8	137
89	More genomic resources for less-studied crops. <i>Trends in Biotechnology</i> , 2010, 28, 452-460.	4.9	135
90	Large genetic variation for heat tolerance in the reference collection of chickpea ( <i>Cicer arietinum</i> L.) germplasm. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 59-69.	0.4	134

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91	5Gs for crop genetic improvement. <i>Current Opinion in Plant Biology</i> , 2020, 56, 190-196.	3.5	134
92	Marker-Assisted Backcrossing to Introgress Resistance to Fusarium Wilt Race 1 and Ascochyta Blight in C 214, an Elite Cultivar of Chickpea. <i>Plant Genome</i> , 2014, 7, plantgenome2013.10.0035.	1.6	132
93	Prioritization of candidate genes in a QTL-hotspot region for drought tolerance in chickpea ( <i>Cicer</i> ) Tj ETQq1 1,0,784314,rgBT /O	1.6	131
94	Impact of Genomic Technologies on Chickpea Breeding Strategies. <i>Agronomy</i> , 2012, 2, 199-221.	1.3	128
95	Genome-Enabled Prediction Models for Yield Related Traits in Chickpea. <i>Frontiers in Plant Science</i> , 2016, 7, 1666.	1.7	127
96	Identification of quantitative trait loci for protein content, oil content and oil quality for groundnut ( <i>Arachis hypogaea</i> L.). <i>Field Crops Research</i> , 2011, 122, 49-59.	2.3	125
97	Potential of promotion of alleles by genome editing to improve quantitative traits in livestock breeding programs. <i>Genetics Selection Evolution</i> , 2015, 47, 55.	1.2	125
98	Pigeonpea genomics initiative (PGI): an international effort to improve crop productivity of pigeonpea ( <i>Cajanus cajan</i> L.). <i>Molecular Breeding</i> , 2010, 26, 393-408.	1.0	124
99	Genomewide Association Studies for 50 Agronomic Traits in Peanut Using the "Reference Set"™ Comprising 300 Genotypes from 48 Countries of the Semi-Arid Tropics of the World. <i>PLoS ONE</i> , 2014, 9, e105228.	1.1	124
100	Molecular breeding for introgression of fatty acid desaturase mutant alleles ( ahFAD2A and ahFAD2B) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 203-213.	1.7	124
101	Genetic diversity of root system architecture in response to drought stress in grain legumes. <i>Journal of Experimental Botany</i> , 2018, 69, 3267-3277.	2.4	124
102	Multi-parent populations in crops: a toolbox integrating genomics and genetic mapping with breeding. <i>Heredity</i> , 2020, 125, 396-416.	1.2	124
103	Current state-of-art of sequencing technologies for plant genomics research. <i>Briefings in Functional Genomics</i> , 2012, 11, 3-11.	1.3	123
104	Reap the crop wild relatives for breeding future crops. <i>Trends in Biotechnology</i> , 2022, 40, 412-431.	4.9	122
105	Analysis of BAC-end sequences (BESs) and development of BES-SSR markers for genetic mapping and hybrid purity assessment in pigeonpea ( <i>Cajanus</i> spp.). <i>BMC Plant Biology</i> , 2011, 11, 56.	1.6	121
106	Development and use of genic molecular markers (GMMs) for construction of a transcript map of chickpea ( <i>Cicer arietinum</i> L.). <i>Theoretical and Applied Genetics</i> , 2011, 122, 1577-1589.	1.8	120
107	Exploring plant growth-promotion actinomycetes from vermicompost and rhizosphere soil for yield enhancement in chickpea. <i>Brazilian Journal of Microbiology</i> , 2016, 47, 85-95.	0.8	119
108	Identification of candidate genome regions controlling disease resistance in <i>Arachis</i> . <i>BMC Plant Biology</i> , 2009, 9, 112.	1.6	118

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109	FastTrack Introgression of 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.	1.6	118
110	Identification of a microsatellite on chromosomes 6B and a STS on 7D of bread wheat showing an association with preharvest sprouting tolerance. <i>Theoretical and Applied Genetics</i> , 1999, 99, 336-340.	1.8	117
111	Identification of QTLs associated with oil content and mapping FAD2 genes and their relative contribution to oil quality in peanut ( <i>Arachis hypogaea</i> L.). <i>BMC Genetics</i> , 2014, 15, 133.	2.7	117
112	Identification and Comparative Analysis of Differential Gene Expression in Soybean Leaf Tissue under Drought and Flooding Stress Revealed by RNA-Seq. <i>Frontiers in Plant Science</i> , 2016, 7, 1044.	1.7	116
113	A microsatellite marker associated with a QTL for grain protein content on chromosome arm 2DL of bread wheat. <i>Theoretical and Applied Genetics</i> , 1999, 99, 341-345.	1.8	114
114	Genome-wide SNP Genotyping Resolves Signatures of Selection and Tetrasomic Recombination in Peanut. <i>Molecular Plant</i> , 2017, 10, 309-322.	3.9	114
115	Can omics deliver temperature resilient ready-to-grow crops?. <i>Critical Reviews in Biotechnology</i> , 2021, 41, 1209-1232.	5.1	114
116	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.	1.5	113
117	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	2.8	113
118	Proteomics and Metabolomics: Two Emerging Areas for Legume Improvement. <i>Frontiers in Plant Science</i> , 2015, 6, 1116.	1.7	112
119	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.	0.6	111
120	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.	4.1	109
121	Comparative genomics and prediction of conditionally dispensable sequences in legume-infecting <i>Fusarium oxysporum</i> formae speciales facilitates identification of candidate effectors. <i>BMC Genomics</i> , 2016, 17, 191.	1.2	109
122	Next-generation sequencing for identification of candidate genes for <i>Fusarium</i> wilt and sterility mosaic disease in pigeonpea ( <i>Cajanus cajan</i> ). <i>Plant Biotechnology Journal</i> , 2016, 14, 1183-1194.	4.1	108
123	Genetic mapping and BAC assignment of EST-derived SSR markers shows non-uniform distribution of genes in the barley genome. <i>Theoretical and Applied Genetics</i> , 2006, 113, 239-250.	1.8	107
124	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	13.7	106
125	Can genomics deliver climate-change ready crops?. <i>Current Opinion in Plant Biology</i> , 2018, 45, 205-211.	3.5	105
126	Genome sequencing of adzuki bean ( <i>Vigna angularis</i> ) provides insight into high starch and low fat accumulation and domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13213-13218.	3.3	104



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127	Genome-wide sequencing of longan ( <i>Dimocarpus longan</i> Lour.) provides insights into molecular basis of its polyphenol-rich characteristics. <i>GigaScience</i> , 2017, 6, 1-14.	3.3	103
128	Chickpea Improvement: Role of Wild Species and Genetic Markers. <i>Biotechnology and Genetic Engineering Reviews</i> , 2008, 25, 267-314.	2.4	102
129	Comparative analysis of the grain proteome fraction in barley genotypes with contrasting salinity tolerance during germination. <i>Plant, Cell and Environment</i> , 2010, 33, 211-222.	2.8	102
130	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.	1.6	102
131	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.	1.6	101
132	Genetic Patterns of Domestication in Pigeonpea ( <i>Cajanus cajan</i> (L.) Millsp.) and Wild <i>Cajanus</i> Relatives. <i>PLoS ONE</i> , 2012, 7, e39563.	1.1	101
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, 449-461.	1.5	99
134	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> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.3	95
135	Generation and Comparison of EST-Derived SSRs and SNPs in Barley ( <i>Hordeum Vulgare</i> L.). <i>Hereditas</i> , 2004, 135, 145-151.	0.5	95
136	Scope for improvement of yield under drought through the root traits in chickpea ( <i>Cicer arietinum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.3	95
137	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, 1325-1338.	1.8	94
138	Pearl millet [ <i>Pennisetum glaucum</i> (L.) R. Br.] consensus linkage map constructed using four RIL mapping populations and newly developed EST-SSRs. <i>BMC Genomics</i> , 2013, 14, 159.	1.2	94
139	Exploring genetic variation for salinity tolerance in chickpea using image-based phenotyping. <i>Scientific Reports</i> , 2017, 7, 1300.	1.6	94
140	Fine mapping and gene cloning in the post-NGS era: advances and prospects. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1791-1810.	1.8	94
141	Dissecting genomic hotspots underlying seed protein, oil, and sucrose content in an interspecific mapping population of soybean using high-density linkage mapping. <i>Plant Biotechnology Journal</i> , 2018, 16, 1939-1953.	4.1	93
142	Genome wide association analyses for drought tolerance related traits in barley ( <i>Hordeum vulgare</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.3	91
143	Genome-wide analysis and identification of genes related to potassium transporter families in rice ( <i>Oryza sativa</i> L.). <i>Plant Science</i> , 2007, 172, 708-721.	1.7	90
144	The first set of EST resource for gene discovery and marker development in pigeonpea ( <i>Cajanus cajan</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	90

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145	Assessment of ICCV 2016–2017 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.	1.0	90
146	High-density genetic map using whole-genome resequencing for fine mapping and candidate gene discovery for disease resistance in peanut. <i>Plant Biotechnology Journal</i> , 2018, 16, 1954-1967.	4.1	90
147	Genomic resources in plant breeding for sustainable agriculture. <i>Journal of Plant Physiology</i> , 2021, 257, 153351.	1.6	90
148	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.	1.8	89
149	An International Reference Consensus Genetic Map with 897 Marker Loci Based on 11 Mapping Populations for Tetraploid Groundnut ( <i>Arachis hypogaea</i> L.). <i>PLoS ONE</i> , 2012, 7, e41213.	1.1	89
150	EST-derived single nucleotide polymorphism markers for assembling genetic and physical maps of the barley genome. <i>Functional and Integrative Genomics</i> , 2008, 8, 223-233.	1.4	87
151	A Comprehensive Transcriptome Assembly of Pigeonpea ( <i>Cajanus cajan</i> L.) using Sanger and Second-Generation Sequencing Platforms. <i>Molecular Plant</i> , 2012, 5, 1020-1028.	3.9	87
152	Comprehensive Transcriptome Assembly of Chickpea ( <i>Cicer arietinum</i> L.) Using Sanger and Next Generation Sequencing Platforms: Development and Applications. <i>PLoS ONE</i> , 2014, 9, e86039.	1.1	87
153	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.	2.4	87
154	Haplotype analysis of key genes governing grain yield and quality traits across 3K <i>RG</i> panel reveals scope for the development of tailor-made rice with enhanced genetic gains. <i>Plant Biotechnology Journal</i> , 2019, 17, 1612-1622.	4.1	87
155	Comparative analysis of expressed sequence tags (ESTs) between drought-tolerant and -susceptible genotypes of chickpea under terminal drought stress. <i>BMC Plant Biology</i> , 2011, 11, 70.	1.6	86
156	Genomics-assisted breeding in four major pulse crops of developing countries: present status and prospects. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1263-1291.	1.8	86
157	RNA-Seq analysis revealed genes associated with drought stress response in kabuli chickpea ( <i>Cicer</i> ) Tj ETQq1 1 0.784314 rgBT/Overl	1.1	86
158	Defining the Transcriptome Assembly and Its Use for Genome Dynamics and Transcriptome Profiling Studies in Pigeonpea ( <i>Cajanus cajan</i> L.). <i>DNA Research</i> , 2011, 18, 153-164.	1.5	85
159	Oxidative stress and carbon metabolism influence <i>Aspergillus flavus</i> transcriptome composition and secondary metabolite production. <i>Scientific Reports</i> , 2016, 6, 38747.	1.6	85
160	Translational Genomics in Agriculture: Some Examples in Grain Legumes. <i>Critical Reviews in Plant Sciences</i> , 2015, 34, 169-194.	2.7	83
161	Integrating genomics for chickpea improvement: achievements and opportunities. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1703-1720.	1.8	82
162	Fast-forward breeding for a food-secure world. <i>Trends in Genetics</i> , 2021, 37, 1124-1136.	2.9	82

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163	Comprehensive tissue-specific proteome analysis of drought stress responses in Pennisetum glaucum (L.) R. Br. (Pearl millet). Journal of Proteomics, 2016, 143, 122-135.	1.2	81
164	Genomic Tools in Groundnut Breeding Program: Status and Perspectives. Frontiers in Plant Science, 2016, 7, 289.	1.7	79
165	Trait associations in the pangenome of pigeon pea (<i>Cajanus cajan</i>). Plant Biotechnology Journal, 2020, 18, 1946-1954.	4.1	79
166	Root traits confer grain yield advantages under terminal drought in chickpea ( Cicer arietinum L.). Field Crops Research, 2017, 201, 146-161.	2.3	78
167	A western Sahara centre of domestication inferred from pearl millet genomes. Nature Ecology and Evolution, 2018, 2, 1377-1380.	3.4	78
168	PANOMICS meets germplasm. Plant Biotechnology Journal, 2020, 18, 1507-1525.	4.1	78
169	Identification of eight chromosomes and a microsatellite marker on 1AS associated with QTL for grain weight in bread wheat. Theoretical and Applied Genetics, 2000, 100, 1290-1294.	1.8	77
170	Recent breeding programs enhanced genetic diversity in both desi and kabuli varieties of chickpea (Cicer arietinum L.). Scientific Reports, 2016, 6, 38636.	1.6	77
171	High-resolution skim genotyping by sequencing reveals the distribution of crossovers and gene conversions in Cicer arietinum and Brassica napus. Theoretical and Applied Genetics, 2015, 128, 1039-1047.	1.8	76
172	Development and deployment of a high-density linkage map identified quantitative trait loci for plant height in peanut (Arachis hypogaea L.). Scientific Reports, 2016, 6, 39478.	1.6	76
173	Development and evaluation of high-density Axiom <sup>®</sup> <i>Cicer</i> SNP </i> Array for high-resolution genetic mapping and breeding applications in chickpea. Plant Biotechnology Journal, 2018, 16, 890-901.	4.1	76
174	Deep sequencing analysis of the transcriptomes of peanut aerial and subterranean young pods identifies candidate genes related to early embryo abortion. Plant Biotechnology Journal, 2013, 11, 115-127.	4.1	75
175	Genomics-assisted breeding for drought tolerance in chickpea. Functional Plant Biology, 2014, 41, 1178.	1.1	75
176	Adapting legume crops to climate change using genomic approaches. Plant, Cell and Environment, 2019, 42, 6-19.	2.8	74
177	Genetic Mapping of QTLs Controlling Fatty Acids Provided Insights into the Genetic Control of Fatty Acid Synthesis Pathway in Peanut (Arachis hypogaea L.). PLoS ONE, 2015, 10, e0119454.	1.1	73
178	Molecular Mapping of QTLs for Heat Tolerance in Chickpea. International Journal of Molecular Sciences, 2018, 19, 2166.	1.8	73
179	Mitigating Aflatoxin Contamination in Groundnut through A Combination of Genetic Resistance and Post-Harvest Management Practices. Toxins, 2019, 11, 315.	1.5	73
180	Introgression of a QTL hotspot region enhances drought tolerance and grain yield in three elite chickpea cultivars. Plant Genome, 2021, 14, e20076.	1.6	73

#	ARTICLE	IF	CITATIONS
181	Transferability and polymorphism of barley EST-SSR markers used for phylogenetic analysis in <i>Hordeum chilense</i> . <i>BMC Plant Biology</i> , 2008, 8, 97.	1.6	72
182	Novel Genomic Tools and Modern Genetic and Breeding Approaches for Crop Improvement. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2009, 18, 127-138.	0.9	72
183	Genetic relationships among seven sections of genus <i>Arachis</i> studied by using SSR markers. <i>BMC Plant Biology</i> , 2010, 10, 15.	1.6	72
184	Responses of <i>Aspergillus flavus</i> to Oxidative Stress Are Related to Fungal Development Regulator, Antioxidant Enzyme, and Secondary Metabolite Biosynthetic Gene Expression. <i>Frontiers in Microbiology</i> , 2016, 7, 2048.	1.5	72
185	The RNA-Seq-based high resolution gene expression atlas of chickpea ( <i>Cicer arietinum</i> L.) reveals dynamic spatio-temporal changes associated with growth and development. <i>Plant, Cell and Environment</i> , 2018, 41, 2209-2225.	2.8	72
186	Genomic interventions for sustainable agriculture. <i>Plant Biotechnology Journal</i> , 2020, 18, 2388-2405.	4.1	71
187	Male sterility systems in pigeonpea and their role in enhancing yield. <i>Plant Breeding</i> , 2010, 129, 125-134.	1.0	70
188	Analytical and Decision Support Tools for Genomics-Assisted Breeding. <i>Trends in Plant Science</i> , 2016, 21, 354-363.	4.3	70
189	Novel SSR Markers for Polymorphism Detection in Pigeonpea ( <i>Cajanus</i> spp.). <i>Plant Breeding</i> , 2010, 129, 142-148.	1.0	69
190	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.	0.5	68
191	Integrated breeding approaches for improving drought and heat adaptation in chickpea ( <i>Cicer</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 1.0 68	1.0	68
192	Two key genomic regions harbour QTLs for salinity tolerance in ICCV 2 JG 11 derived chickpea ( <i>Cicer</i> ) Tj ETQq0 0.0 rgBT /O 1.6 67	1.6	67
193	Indel-seq: a fast forward genetics approach for identification of trait-associated putative candidate genomic regions and its application in pigeonpea ( <i>Cajanus cajan</i> ). <i>Plant Biotechnology Journal</i> , 2017, 15, 906-914.	4.1	67
194	Molecular Mapping of Oil Content and Fatty Acids Using Dense Genetic Maps in Groundnut ( <i>Arachis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 1.7 67	1.7	67
195	Evaluation and Validation of Housekeeping Genes as Reference for Gene Expression Studies in Pigeonpea ( <i>Cajanus cajan</i> ) Under Drought Stress Conditions. <i>PLoS ONE</i> , 2015, 10, e0122847.	1.1	67
196	Integrated transcriptome, small RNA and degradome sequencing approaches provide insights into <i>Ascochyta</i> blight resistance in chickpea. <i>Plant Biotechnology Journal</i> , 2019, 17, 914-931.	4.1	66
197	Features and applications of haplotypes in crop breeding. <i>Communications Biology</i> , 2021, 4, 1266.	2.0	66
198	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.	1.6	65

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199	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.	4.1	65
200	QTL mapping for late leaf spot and rust resistance using an improved genetic map and extensive phenotypic data on a recombinant inbred line population in peanut ( <i>Arachis hypogaea</i> L.). <i>Euphytica</i> , 2016, 209, 147-156.	0.6	64
201	Highly informative genic and genomic SSR markers to facilitate molecular breeding in cultivated groundnut ( <i>Arachis hypogaea</i> ). <i>Plant Breeding</i> , 2012, 131, 139-147.	1.0	62
202	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.	1.0	62
203	The celery genome sequence reveals sequential paleopolyploidizations, karyotype evolution and resistance gene reduction in apiales. <i>Plant Biotechnology Journal</i> , 2021, 19, 731-744.	4.1	62
204	The first genetic map of pigeon pea based on diversity arrays technology (DArT) markers. <i>Journal of Genetics</i> , 2011, 90, 103-109.	0.4	61
205	Marker-assisted introgression of resistance to fusarium wilt race 2 in Pusa 256, an elite cultivar of desi chickpea. <i>Molecular Genetics and Genomics</i> , 2017, 292, 1237-1245.	1.0	61
206	Differential Regulation of Genes Involved in Root Morphogenesis and Cell Wall Modification is Associated with Salinity Tolerance in Chickpea. <i>Scientific Reports</i> , 2018, 8, 4855.	1.6	61
207	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.	1.6	61
208	Superior haplotypes for haplotype-based breeding for drought tolerance in pigeonpea ( <i>Cajanus</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf	4.1	61
209	Genetic mapping and quantitative trait locus analysis of resistance to sterility mosaic disease in pigeonpea [ <i>Cajanus cajan</i> (L.) Millsp.]. <i>Field Crops Research</i> , 2011, 123, 53-61.	2.3	60
210	Phenotyping Chickpeas and Pigeonpeas for Adaptation to Drought. <i>Frontiers in Physiology</i> , 2012, 3, 179.	1.3	60
211	Whole-genome resequencing-based <i>scp</i> QTL <i>seq</i> identified candidate genes and molecular markers for fresh seed dormancy in groundnut. <i>Plant Biotechnology Journal</i> , 2020, 18, 992-1003.	4.1	60
212	Mapping QTL for resistance to botrytis grey mould in chickpea. <i>Euphytica</i> , 2011, 182, 1-9.	0.6	59
213	Candidate gene analysis for determinacy in pigeonpea ( <i>Cajanus</i> spp.). <i>Theoretical and Applied Genetics</i> , 2014, 127, 2663-2678.	1.8	59
214	Shoot traits and their relevance in terminal drought tolerance of chickpea ( <i>Cicer arietinum</i> L.). <i>Field Crops Research</i> , 2016, 197, 10-27.	2.3	59
215	New Hypervariable SSR Markers for Diversity Analysis, Hybrid Purity Testing and Trait Mapping in Pigeonpea [ <i>Cajanus cajan</i> (L.) Millspaugh]. <i>Frontiers in Plant Science</i> , 2017, 8, 377.	1.7	59
216	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.	1.6	59

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217	Single nucleotide polymorphisms in rye ( <i>Secale cereale</i> L.): discovery, frequency, and applications for genome mapping and diversity studies. <i>Theoretical and Applied Genetics</i> , 2007, 114, 1105-1116.	1.8	58
218	Genomic tools and germplasm diversity for chickpea improvement. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 45-58.	0.4	58
219	Cytoplasmic Male Sterility-Associated Chimeric Open Reading Frames Identified by Mitochondrial Genome Sequencing of Four <i>Cajanus</i> Genotypes. <i>DNA Research</i> , 2013, 20, 485-495.	1.5	58
220	Resistance to <i>Aspergillus flavus</i> in maize and peanut: Molecular biology, breeding, environmental stress, and future perspectives. <i>Crop Journal</i> , 2015, 3, 229-237.	2.3	58
221	Genome-Wide Discovery of Microsatellite Markers from Diploid Progenitor Species, <i>Arachis duranensis</i> and <i>A. ipaensis</i> , and Their Application in Cultivated Peanut ( <i>A. hypogaea</i> ). <i>Frontiers in Plant Science</i> , 2017, 8, 1209.	1.7	58
222	Translational genomics for achieving higher genetic gains in groundnut. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1679-1702.	1.8	58
223	Genetic Diversity and Demographic History of <i>Cajanus</i> spp. Illustrated from Genome-Wide SNPs. <i>PLoS ONE</i> , 2014, 9, e88568.	1.1	58
224	Identification and validation of a core set of informative genic SSR and SNP markers for assaying functional diversity in barley. <i>Molecular Breeding</i> , 2008, 22, 1-13.	1.0	57
225	Genomics-assisted breeding for boosting crop improvement in pigeonpea ( <i>Cajanus cajan</i> ). <i>Frontiers in Plant Science</i> , 2015, 6, 50.	1.7	57
226	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.	4.1	56
227	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.	1.6	55
228	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
229	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.	1.6	55
230	Gene expression atlas of pigeonpea and its application to gain insights into genes associated with pollen fertility implicated in seed formation. <i>Journal of Experimental Botany</i> , 2017, 68, 2037-2054.	2.4	55
231	Genomics-assisted breeding for pigeonpea improvement. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1721-1737.	1.8	55
232	A chromosomal genomics approach to assess and validate the <i>desi</i> and <i>kabuli</i> draft chickpea genome assemblies. <i>Plant Biotechnology Journal</i> , 2014, 12, 778-786.	4.1	54
233	Co-localization of major quantitative trait loci for pod size and weight to a 3.7 cM interval on chromosome A05 in cultivated peanut ( <i>Arachis hypogaea</i> L.). <i>BMC Genomics</i> , 2017, 18, 58.	1.2	54
234	Genetic Dissection of Novel QTLs for Resistance to Leaf Spots and Tomato Spotted Wilt Virus in Peanut ( <i>Arachis hypogaea</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 25.	1.7	54

#	ARTICLE	IF	CITATIONS
235	A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. <i>Plant Genome</i> , 2020, 13, e20009.	1.6	54
236	Genic Molecular Markers in Plants: Development and Applications. , 2007, , 13-29.		53
237	Identification of ERF genes in peanuts and functional analysis of AhERF008 and AhERF019 in abiotic stress response. <i>Functional and Integrative Genomics</i> , 2014, 14, 467-477.	1.4	53
238	High throughput sequencing of small RNA component of leaves and inflorescence revealed conserved and novel miRNAs as well as phasiRNA loci in chickpea. <i>Plant Science</i> , 2015, 235, 46-57.	1.7	53
239	A Combined Comparative Transcriptomic, Metabolomic, and Anatomical Analyses of Two Key Domestication Traits: Pod Dehiscence and Seed Dormancy in Pea ( <i>Pisum sp.</i> ). <i>Frontiers in Plant Science</i> , 2017, 8, 542.	1.7	53
240	Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. <i>Plant Genome</i> , 2022, 15, e20109.	1.6	53
241	Genetic Mapping and Quantitative Trait Loci Analysis for Disease Resistance Using F <sub>2</sub> and F <sub>5</sub> Generation-based Genetic Maps Derived from "Tifrunner" – "GT20"™ in Peanut. <i>Plant Genome</i> , 2013, 6, plantgenome2013.05.0018.		52
242	Application of SSR markers for molecular characterization of hybrid parents and purity assessment of ICPH 2438 hybrid of pigeonpea [ <i>Cajanus cajan</i> (L.) Millspaugh]. <i>Molecular Breeding</i> , 2010, 26, 371-380.	1.0	51
243	Multiple post-domestication origins of <i>kabuli</i> chickpea through allelic variation in a diversification-associated transcription factor. <i>New Phytologist</i> , 2016, 211, 1440-1451.	3.5	51
244	Discovery of genomic regions and candidate genes controlling shelling percentage using <i>scp&gt;QTL&lt;/scp&gt;</i> approach in cultivated peanut ( <i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2019, 17, 1248-1260.	4.1	51
245	Marker-trait association study for protein content in chickpea ( <i>Cicer arietinum</i> L.). <i>Journal of Genetics</i> , 2015, 94, 279-286.	0.4	50
246	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020, 13, 1341-1344.	3.9	50
247	Multiple Resistant and Nutritionally Dense Germplasm Identified from Mini Core Collection in Peanut. <i>Crop Science</i> , 2014, 54, 679-693.	0.8	49
248	Integrated physical, genetic and genome map of chickpea ( <i>Cicer arietinum</i> L.). <i>Functional and Integrative Genomics</i> , 2014, 14, 59-73.	1.4	49
249	Regulatory non-coding RNAs: a new frontier in regulation of plant biology. <i>Functional and Integrative Genomics</i> , 2021, 21, 313-330.	1.4	49
250	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.	4.1	49
251	Selection and Validation of Housekeeping Genes as Reference for Gene Expression Studies in Pigeonpea ( <i>Cajanus cajan</i> ) under Heat and Salt Stress Conditions. <i>Frontiers in Plant Science</i> , 2015, 6, 1071.	1.7	48
252	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.	1.6	48

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253	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.	1.7	48
254	Genomics, genetics and breeding of common bean in Africa: A review of tropical legume project. <i>Plant Breeding</i> , 2019, 138, 401-414.	1.0	48
255	Systems biology for crop improvement. <i>Plant Genome</i> , 2021, 14, e20098.	1.6	48
256	Breeding custom-designed crops for improved drought adaptation. <i>Genetics &amp; Genomics Next</i> , 2021, 2, e202100017.	0.8	48
257	Allelic relationships of flowering time genes in chickpea. <i>Euphytica</i> , 2015, 203, 295-308.	0.6	47
258	The CarERF genes in chickpea ( <i>Cicer arietinum</i> L.) and the identification of CarERF116 as abiotic stress responsive transcription factor. <i>Functional and Integrative Genomics</i> , 2015, 15, 27-46.	1.4	47
259	Modelling predicts that soybean is poised to dominate crop production across Africa. <i>Plant, Cell and Environment</i> , 2019, 42, 373-385.	2.8	47
260	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.	2.3	47
261	Advances in Omics Approaches for Improving Toxic Metals/Metalloids Tolerance in Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 794373.	1.7	47
262	ICPH 2671 – the world's first commercial food legume hybrid. <i>Plant Breeding</i> , 2013, 132, 479-485.	1.0	46
263	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.	1.7	46
264	Mapping Quantitative Trait Loci of Resistance to Tomato Spotted Wilt Virus and Leaf Spots in a Recombinant Inbred Line Population of Peanut ( <i>Arachis hypogaea</i> L.) from SunOleic 97R and NC94022. <i>PLoS ONE</i> , 2016, 11, e0158452.	1.1	46
265	Traits of relevance to improve yield under terminal drought stress in chickpea ( <i>C. arietinum</i> L.). <i>Field Crops Research</i> , 2013, 145, 88-95.	2.3	45
266	Genome wide transcriptome profiling of <i>Fusarium oxysporum</i> f. sp. <i>ciceris</i> conidial germination reveals new insights into infection-related genes. <i>Scientific Reports</i> , 2016, 6, 37353.	1.6	45
267	Development of AhMITE1 markers through genome-wide analysis in peanut ( <i>Arachis hypogaea</i> L.). <i>BMC Research Notes</i> , 2018, 11, 10.	0.6	45
268	Proteome analysis of <i>Aspergillus flavus</i> isolate-specific responses to oxidative stress in relationship to aflatoxin production capability. <i>Scientific Reports</i> , 2018, 8, 3430.	1.6	45
269	Partitioning coefficient – A trait that contributes to drought tolerance in chickpea. <i>Field Crops Research</i> , 2013, 149, 354-365.	2.3	44
270	Physiological and Proteomic Signatures Reveal Mechanisms of Superior Drought Resilience in Pearl Millet Compared to Wheat. <i>Frontiers in Plant Science</i> , 2020, 11, 600278.	1.7	44



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271	Dissection of the Barley 2L1.0 Region Carrying the <i>Lr21</i> Quantitative Resistance Gene to Leaf Rust Using Near-Isogenic Lines (NIL) and subNIL. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 1604-1615.	1.4	43
272	Molecular Plant Breeding: Methodology and Achievements. <i>Methods in Molecular Biology</i> , 2009, 513, 283-304.	0.4	43
273	InDel markers: An extended marker resource for molecular breeding in chickpea. <i>PLoS ONE</i> , 2019, 14, e0213999.	1.1	43
274	Flow-cytometric analysis of reactive oxygen species in peripheral blood mononuclear cells of patients with thyroid dysfunction. <i>Cytometry Part B - Clinical Cytometry</i> , 2006, 70B, 20-23.	0.7	42
275	Application of Genomics to Molecular Breeding of Wheat and Barley. <i>Advances in Genetics</i> , 2007, 58, 121-155.	0.8	42
276	Consistent Variation Across Soil Types in Salinity Resistance of a Diverse Range of Chickpea ( <i>Cicer</i> ) Genotypes. <i>Plant Breeding</i> , 2017, 136, 107-115.	1.7	42
277	Functional genomics to study stress responses in crop legumes: progress and prospects. <i>Functional Plant Biology</i> , 2013, 40, 1221.	1.1	42
278	Genotyping-by-sequencing based genetic mapping reveals large number of epistatic interactions for stem rot resistance in groundnut. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1001-1016.	1.8	42
279	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.	1.1	42
280	Progress in the utilization of <i>Cajanus platycarpus</i> (Benth.) Maesen in pigeonpea improvement. <i>Plant Breeding</i> , 2011, 130, 507-514.	1.0	41
281	Phenotypic Data from Inbred Parents Can Improve Genomic Prediction in Pearl Millet Hybrids. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2513-2522.	0.8	41
282	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.	4.1	41
283	Breeding More Crops in Less Time: A Perspective on Speed Breeding. <i>Biology</i> , 2022, 11, 275.	1.3	41
284	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.	1.2	40
285	Foliar fungal disease-resistant introgression lines of groundnut ( <i>Arachis hypogaea</i> L.) record higher pod and haulm yield in multilocation testing. <i>Plant Breeding</i> , 2016, 135, 355-366.	1.0	40
286	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.	0.6	40
287	Progress in understanding drought tolerance: from alleles to cropping systems. <i>Journal of Experimental Botany</i> , 2018, 69, 3175-3179.	2.4	40
288	Variation in carbon isotope discrimination and its relationship with harvest index in the reference collection of chickpea germplasm. <i>Functional Plant Biology</i> , 2013, 40, 1350.	1.1	39

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289	Identification and Validation of Selected Universal Stress Protein Domain Containing Drought-Responsive Genes in Pigeonpea ( <i>Cajanus cajan</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 1065.	1.7	39
290	Transcriptome Analysis of a New Peanut Seed Coat Mutant for the Physiological Regulatory Mechanism Involved in Seed Coat Cracking and Pigmentation. <i>Frontiers in Plant Science</i> , 2016, 7, 1491.	1.7	39
291	First-generation HapMap in <i>Cajanus</i> spp. reveals untapped variations in parental lines of mapping populations. <i>Plant Biotechnology Journal</i> , 2016, 14, 1673-1681.	4.1	39
292	Genotypic variation in soil water use and root distribution and their implications for drought tolerance in chickpea. <i>Functional Plant Biology</i> , 2017, 44, 235.	1.1	39
293	Genetic variations of HvP5CS1 and their association with drought tolerance related traits in barley ( <i>Hordeum vulgare</i> L.). <i>Scientific Reports</i> , 2017, 7, 7870.	1.6	39
294	Molecular Basis of Root Nodule Symbiosis between Bradyrhizobium and "Crack-Entry" Legume Groundnut ( <i>Arachis hypogaea</i> L.). <i>Plants</i> , 2020, 9, 276.	1.6	39
295	Functional Biology and Molecular Mechanisms of Host-Pathogen Interactions for Aflatoxin Contamination in Groundnut ( <i>Arachis hypogaea</i> L.) and Maize ( <i>Zea mays</i> L.). <i>Frontiers in Microbiology</i> , 2020, 11, 227.	1.5	39
296	Inheritance of protein content and its relationships with seed size, grain yield and other traits in chickpea. <i>Euphytica</i> , 2016, 209, 253-260.	0.6	38
297	<i>Aspergillus flavus</i> infection triggered immune responses and host-pathogen cross-talks in groundnut during in-vitro seed colonization. <i>Scientific Reports</i> , 2017, 7, 9659.	1.6	38
298	Genome Sequencing and Analysis of the Peanut B-Genome Progenitor ( <i>Arachis ipaensis</i> ). <i>Frontiers in Plant Science</i> , 2018, 9, 604.	1.7	38
299	Improving oil quality by altering levels of fatty acids through marker-assisted selection of ahfad2 alleles in peanut ( <i>Arachis hypogaea</i> L.). <i>Euphytica</i> , 2018, 214, 1.	0.6	38
300	Genetics, genomics and breeding of groundnut ( <i>Arachis hypogaea</i> L.). <i>Plant Breeding</i> , 2019, 138, 425-444.	1.0	38
301	Genome-wide analysis of epigenetic and transcriptional changes associated with heterosis in pigeonpea. <i>Plant Biotechnology Journal</i> , 2020, 18, 1697-1710.	4.1	38
302	Genetic Dissection and Identification of Candidate Genes for Salinity Tolerance Using Axiom®CicerSNP Array in Chickpea. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5058.	1.8	38
303	<i>Arachis hypogaea</i> gene expression atlas for <i>fastigiata</i> subspecies of cultivated groundnut to accelerate functional and translational genomics applications. <i>Plant Biotechnology Journal</i> , 2020, 18, 2187-2200.	4.1	38
304	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. <i>Scientific Data</i> , 2021, 8, 50.	2.4	38
305	Major QTLs and Potential Candidate Genes for Heat Stress Tolerance Identified in Chickpea ( <i>Cicer</i> ) Tj ETQq1 1 0.784314 rgBT /Overlook	1.7	38
306	STMS markers for grain protein content and their validation using near-isogenic lines in bread wheat. <i>Plant Breeding</i> , 2001, 120, 273-278.	1.0	37

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307	Imputation of Single Nucleotide Polymorphism Genotypes in Biparental, Backcross, and Topcross Populations with a Hidden Markov Model. <i>Crop Science</i> , 2015, 55, 1934-1946.	0.8	37
308	Sequencing Analysis of Genetic Loci for Resistance for Late Leaf Spot and Rust in Peanut ( <i>Arachis</i> ) Tj ETQq0 0 0 rgBT/Overlock, 10 Tf 50	1.7	37
309	Genome-Wide Identification and Analysis of Arabidopsis Sodium Proton Antiporter (NHX) and Human Sodium Proton Exchanger (NHE) Homologs in <i>Sorghum bicolor</i> . <i>Genes</i> , 2018, 9, 236.	1.0	37
310	Deciphering the genetic basis of root morphology, nutrient uptake, yield, and yield-related traits in rice under dry direct-seeded cultivation systems. <i>Scientific Reports</i> , 2019, 9, 9334.	1.6	37
311	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.	2.7	37
312	Epigenetics and epigenomics: underlying mechanisms, relevance, and implications in crop improvement. <i>Functional and Integrative Genomics</i> , 2020, 20, 739-761.	1.4	37
313	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.	1.1	37
314	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.	1.6	36
315	Identification and characterization of expressed sequence tags-derived simple sequence repeats markers from robusta coffee variety 'CxR' (an interspecific hybrid of <i>Coffea canephora</i> x <i>Coffea</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	1.4	35
316	Simple sequence repeat-based diversity in elite pigeonpea genotypes for developing mapping populations to map resistance to <i>Fusarium</i> wilt and sterility mosaic disease. <i>Plant Breeding</i> , 2010, 129, 135-141.	1.0	35
317	Pigeonpea composite collection and identification of germplasm for use in crop improvement programmes. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 97-108.	0.4	35
318	Evolving Molecular Marker Technologies in Plants: From RFLPs to GBS. , 2013, , 229-247.		35
319	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.	1.6	35
320	Metabolomics Intervention Towards Better Understanding of Plant Traits. <i>Cells</i> , 2021, 10, 346.	1.8	35
321	Genetic Gains in Pearl Millet in India: Insights Into Historic Breeding Strategies and Future Perspective. <i>Frontiers in Plant Science</i> , 2021, 12, 645038.	1.7	35
322	Molecular Genetics and Breeding of Grain Legume Crops for the Semi-Arid Tropics. , 2007, , 207-241.		35
323	Characterization of microsatellites and development of chromosome specific STMS markers in bread wheat. <i>Plant Molecular Biology Reporter</i> , 2000, 18, 5-16.	1.0	34
324	Features of SNP and SSR diversity in a set of ICARDA barley germplasm collection. <i>Molecular Breeding</i> , 2010, 26, 229-242.	1.0	34

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325	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, 186-192.	0.8	34
326	Characterization and mapping of Dt1 locus which co-segregates with CcTFL1 for growth habit in pigeonpea. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1773-1784.	1.8	34
327	Gene/QTL discovery for Anthracnose in common bean ( <i>Phaseolus vulgaris</i> L.) from North-western Himalayas. <i>PLoS ONE</i> , 2018, 13, e0191700.	1.1	34
328	QTLian breeding for climate resilience in cereals: progress and prospects. <i>Functional and Integrative Genomics</i> , 2019, 19, 685-701.	1.4	34
329	Steady expression of high oleic acid in peanut bred by marker-assisted backcrossing for fatty acid desaturase mutant alleles and its effect on seed germination along with other seedling traits. <i>PLoS ONE</i> , 2019, 14, e0226252.	1.1	34
330	Advances in Crop Improvement and Delivery Research for Nutritional Quality and Health Benefits of Groundnut ( <i>Arachis hypogaea</i> L.). <i>Frontiers in Plant Science</i> , 2020, 11, 29.	1.7	34
331	An integrated research framework combining genomics, systems biology, physiology, modelling and breeding for legume improvement in response to elevated CO <sub>2</sub> under climate change scenario. <i>Current Plant Biology</i> , 2020, 22, 100149.	2.3	34
332	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.	2.8	34
333	Multilateral benefit-sharing from digital sequence information will support both science and biodiversity conservation. <i>Nature Communications</i> , 2022, 13, 1086.	5.8	34
334	Isolation and sequence analysis of DREB2A homologues in three cereal and two legume species. <i>Plant Science</i> , 2009, 177, 460-467.	1.7	33
335	Characterization of AhMITE1 transposition and its association with the mutational and evolutionary origin of botanical types in peanut ( <i>Arachis</i> spp.). <i>Plant Systematics and Evolution</i> , 2011, 291, 153-158.	0.3	33
336	CicArMiSatDB: the chickpea microsatellite database. <i>BMC Bioinformatics</i> , 2014, 15, 212.	1.2	33
337	Phylogenetic diversity of <i>Mesorhizobium</i> in chickpea. <i>Journal of Biosciences</i> , 2014, 39, 513-517.	0.5	33
338	Diversification of primary gene pool through introgression of resistance to foliar diseases from synthetic amphidiploids to cultivated groundnut ( <i>Arachis hypogaea</i> L.). <i>Crop Journal</i> , 2014, 2, 110-119.	2.3	33
339	Complete genome sequence of sixteen plant growth promoting <i>Streptomyces</i> strains. <i>Scientific Reports</i> , 2020, 10, 10294.	1.6	33
340	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.	1.7	33
341	A database of simple sequence repeats from cereal and legume expressed sequence tags mined in silico: survey and evaluation. <i>In Silico Biology</i> , 2006, 6, 607-20.	0.4	33
342	Pangenomics in crop improvement—from coding structural variations to finding regulatory variants with pangenome graphs. <i>Plant Genome</i> , 2022, 15, e20177.	1.6	33

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343	Gene Expression and Yeast Two-Hybrid Studies of 1R-MYB Transcription Factor Mediating Drought Stress Response in Chickpea ( <i>Cicer arietinum</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 1117.	1.7	32
344	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.	2.3	32
345	Surveying the genome and constructing a high-density genetic map of napiergrass ( <i>Cenchrus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.6	32
346	Resistance to Plant-Parasitic Nematodes in Chickpea: Current Status and Future Perspectives. <i>Frontiers in Plant Science</i> , 2019, 10, 966.	1.7	32
347	Genomics and breeding innovations for enhancing genetic gain for climate resilience and nutrition traits. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1829-1843.	1.8	32
348	High level of natural variation in a groundnut ( <i>Arachis hypogaea</i> L.) germplasm collection assayed by selected informative SSR markers. <i>Plant Breeding</i> , 2009, 128, 486-494.	1.0	31
349	Identification of two major quantitative trait locus for fresh seed dormancy using the diversity arrays technology and diversity arrays technology-seq based genetic map in Spanish-type peanuts. <i>Plant Breeding</i> , 2016, 135, 367-375.	1.0	31
350	Vernalization response in chickpea is controlled by a major QTL. <i>Euphytica</i> , 2016, 207, 453-461.	0.6	31
351	An Axiom <i>Cajanus</i> 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.	1.2	31
352	Genetic molecular markers to accelerate genetic gains in crops. <i>BioTechniques</i> , 2020, 69, 158-160.	0.8	31
353	Comparative Root Transcriptomics Provide Insights into Drought Adaptation Strategies in Chickpea ( <i>Cicer arietinum</i> L.). <i>International Journal of Molecular Sciences</i> , 2020, 21, 1781.	1.8	31
354	Identification and Characterization of Toxigenic <i>Fusaria</i> Associated with Sorghum Grain Mold Complex in India. <i>Mycopathologia</i> , 2011, 171, 223-230.	1.3	30
355	Single feature polymorphisms (SFPs) for drought tolerance in pigeonpea ( <i>Cajanus</i> spp.). <i>Functional and Integrative Genomics</i> , 2011, 11, 651-657.	1.4	30
356	Transcriptome-wide sequencing provides insights into geocarpy in peanut ( <i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2016, 14, 1215-1224.	4.1	30
357	Overexpression of a Plasma Membrane Bound Na <sup>+</sup> /H <sup>+</sup> Antiporter-Like Protein (SbNHXP) Confers Salt Tolerance and Improves Fruit Yield in Tomato by Maintaining Ion Homeostasis. <i>Frontiers in Plant Science</i> , 2016, 7, 2027.	1.7	30
358	Identification of quantitative trait loci for yield and yield related traits in groundnut ( <i>Arachis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 If 50 142 T	0.6	29
359	Validation of markers linked to late leaf spot and rust resistance, and selection of superior genotypes among diverse recombinant inbred lines and backcross lines in peanut ( <i>Arachis hypogaea</i> L.). <i>Euphytica</i> , 2015, 204, 343-351.	0.6	29
360	Evaluation of <i>Streptomyces</i> sp. obtained from herbal vermicompost for broad spectrum of plant growth-promoting activities in chickpea. <i>Organic Agriculture</i> , 2015, 5, 123-133.	1.2	29

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361	Molecular mapping and inheritance of restoration of fertility (Rf) in A4 hybrid system in pigeonpea ( <i>Cajanus cajan</i> (L.) Millsp.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 1605-1614.	1.8	29
362	Genome-based trait prediction in multi-environment breeding trials in groundnut. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3101-3117.	1.8	29
363	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.	1.6	29
364	The INCREASE project: Intelligent Collections of food legume genetic resources for European agrofood systems. <i>Plant Journal</i> , 2021, 108, 646-660.	2.8	29
365	Genetics of ascochyta blight resistance in chickpea. <i>Euphytica</i> , 2010, 171, 337-343.	0.6	28
366	Comparative transcriptome analysis of aerial and subterranean pods development provides insights into seed abortion in peanut. <i>Plant Molecular Biology</i> , 2014, 85, 395-409.	2.0	28
367	Association of nad7a Gene with Cytoplasmic Male Sterility in Pigeonpea. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.11.0084.	1.6	28
368	The Role of Vegetables and Legumes in Assuring Food, Nutrition, and Income Security for Vulnerable Groups in Sub-Saharan Africa. <i>World Medical and Health Policy</i> , 2015, 7, 187-210.	0.9	28
369	Use of immature seed germination and single seed descent for rapid genetic gains in pigeonpea. <i>Plant Breeding</i> , 2017, 136, 954-957.	1.0	28
370	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.	0.6	28
371	Genomics, genetics and breeding of tropical legumes for better livelihoods of smallholder farmers. <i>Plant Breeding</i> , 2019, 138, 487-499.	1.0	28
372	Transcriptome and metabolome reveal redirection of flavonoids in a white testa peanut mutant. <i>BMC Plant Biology</i> , 2020, 20, 161.	1.6	28
373	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.	2.3	28
374	Improved Genetic Map Identified Major QTLs for Drought Tolerance- and Iron Deficiency Tolerance-Related Traits in Groundnut. <i>Genes</i> , 2021, 12, 37.	1.0	28
375	In silico development of simple sequence repeat markers within the aeschynomenoid/dalbergoid and genistoid clades of the Leguminosae family and their transferability to <i>Arachis hypogaea</i> , groundnut. <i>Plant Science</i> , 2008, 174, 51-60.	1.7	27
376	Single Nucleotide Polymorphisms in HSP17.8 and Their Association with Agronomic Traits in Barley. <i>PLoS ONE</i> , 2013, 8, e56816.	1.1	27
377	Mini Core Collection as a Resource to Identify New Sources of Variation. <i>Crop Science</i> , 2013, 53, 2506-2517.	0.8	27
378	Genetic Variation and Association Mapping of Seed-Related Traits in Cultivated Peanut ( <i>Arachis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6 2105.	1.7	27

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379	Technological perspectives for plant breeding. <i>Theoretical and Applied Genetics</i> , 2019, 132, 555-557.	1.8	27
380	Development of sequence-based markers for seed protein content in pigeonpea. <i>Molecular Genetics and Genomics</i> , 2019, 294, 57-68.	1.0	27
381	Gene-Based Marker Systems in Plants: High Throughput Approaches for Marker Discovery and Genotyping. , 2010, , 119-142.		26
382	Characterisation and genetic diversity analysis of selected chickpea cultivars of nine countries using simple sequence repeat (SSR) markers. <i>Crop and Pasture Science</i> , 2011, 62, 177.	0.7	26
383	From Mendel's discovery on pea to today's plant genetics and breeding. <i>Theoretical and Applied Genetics</i> , 2016, 129, 2267-2280.	1.8	26
384	An Improved Enzyme-Linked Immunosorbent Assay (ELISA) Based Protocol Using Seeds for Detection of Five Major Peanut Allergens Ara h 1, Ara h 2, Ara h 3, Ara h 6, and Ara h 8. <i>Frontiers in Nutrition</i> , 2019, 6, 68.	1.6	26
385	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.	1.2	26
386	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.	4.1	26
387	Differential Physio-Biochemical and Metabolic Responses of Peanut ( <i>Arachis hypogaea</i> L.) under Multiple Abiotic Stress Conditions. <i>International Journal of Molecular Sciences</i> , 2022, 23, 660.	1.8	26
388	Laboratory Information Management Software for genotyping workflows: applications in high throughput crop genotyping. <i>BMC Bioinformatics</i> , 2006, 7, 383.	1.2	25
389	A recombination bin-map identified a major QTL for resistance to Tomato Spotted Wilt Virus in peanut ( <i>Arachis hypogaea</i> ). <i>Scientific Reports</i> , 2019, 9, 18246.	1.6	25
390	Pigeonpea improvement: An amalgam of breeding and genomic research. <i>Plant Breeding</i> , 2019, 138, 445-454.	1.0	25
391	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.	1.8	25
392	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.	1.1	25
393	Cross-amplification of EST-derived markers among 16 grass species. <i>Field Crops Research</i> , 2010, 118, 28-35.	2.3	24
394	Genome-Wide Discovery and Deployment of Insertions and Deletions Markers Provided Greater Insights on Species, Genomes, and Sections Relationships in the Genus <i>Arachis</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 2064.	1.7	24
395	Breeding pigeonpea cultivars for intercropping: synthesis and strategies. <i>Breeding Science</i> , 2018, 68, 159-167.	0.9	24
396	Molecular Markers: Principles and Methodology. , 2002, , 9-54.		23

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397	Multilocus variable number tandem repeat analysis as a tool to discern genetic relationships among strains of <i>Yersinia enterocolitica</i> biovar 1A. <i>Journal of Applied Microbiology</i> , 2009, 107, 875-884.	1.4	23
398	Pigeonpea breeding in eastern and southern Africa: challenges and opportunities. <i>Plant Breeding</i> , 2016, 135, 148-154.	1.0	23
399	Genomics and Physiological Approaches for Root Trait Breeding to Improve Drought Tolerance in Chickpea ( <i>Cicer arietinum</i> L.). , 2011, , 233-250.		23
400	Genetic variation in <i>CaTIFY4b</i> contributes to drought adaptation in chickpea. <i>Plant Biotechnology Journal</i> , 2022, 20, 1701-1715.	4.1	23
401	A QTL analysis of aluminium tolerance in barley, using gene-based markers. <i>Cereal Research Communications</i> , 2009, 37, 531-540.	0.8	22
402	Assessing genetic diversity, allelic richness and genetic relationship among races in ICRISAT foxtail millet core collection. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2012, 10, 214-223.	0.4	22
403	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.	1.4	22
404	Genomics for greater efficiency in pigeonpea hybrid breeding. <i>Frontiers in Plant Science</i> , 2015, 6, 793.	1.7	22
405	A decade of Tropical Legumes projects: Development and adoption of improved varieties, creation of market demand to benefit smallholder farmers and empowerment of national programmes in sub-Saharan Africa and South Asia. <i>Plant Breeding</i> , 2019, 138, 379-388.	1.0	22
406	Genomics-assisted lentil breeding: Current status and future strategies. , 2021, 3, e71.		22
407	Genomic Designing of Pearl Millet: A Resilient Crop for Arid and Semi-arid Environments. , 2020, , 221-286.		22
408	Discovery of Putative Herbicide Resistance Genes and Its Regulatory Network in Chickpea Using Transcriptome Sequencing. <i>Frontiers in Plant Science</i> , 2017, 8, 958.	1.7	21
409	Development of <i>NIL</i> s from heterogeneous inbred families for validating the rust resistance QTL in peanut ( <i>Arachis hypogaea</i> L.). <i>Plant Breeding</i> , 2014, 133, 80-85.	1.0	20
410	Development of a High-Density Linkage Map and Tagging Leaf Spot Resistance in Pearl Millet Using Genotyping-by-Sequencing Markers. <i>Plant Genome</i> , 2016, 9, plantgenome2015.10.0106.	1.6	20
411	Widening the genetic base of cultivated gene pool following introgression from wild <i>Lens</i> taxa. <i>Plant Breeding</i> , 2018, 137, 470-485.	1.0	20
412	A SWEET solution to rice blight. <i>Nature Biotechnology</i> , 2019, 37, 1280-1282.	9.4	20
413	Origin of early maturing pigeonpea germplasm and its impact on adaptation and cropping systems. <i>Plant Breeding</i> , 2019, 138, 243-251.	1.0	20
414	Genome-wide transcriptome and physiological analyses provide new insights into peanut drought response mechanisms. <i>Scientific Reports</i> , 2020, 10, 4071.	1.6	20



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415	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.	4.4	20
416	Genetics of Fertility Restoration in A4 -Based, Diverse Maturing Hybrids of Pigeonpea [ <i>Cajanus cajan</i> (L.) Millsp.]. <i>Crop Science</i> , 2011, 51, 574-578.	0.8	19
417	Recent Advances in Molecular Genetic Linkage Maps of Cultivated Peanut. <i>Peanut Science</i> , 2013, 40, 95-106.	0.2	19
418	Mapping and identification of a <i>Cicer arietinum</i> NSP2 gene involved in nodulation pathway. <i>Theoretical and Applied Genetics</i> , 2014, 127, 481-488.	1.8	19
419	Peg Biology: Deciphering the Molecular Regulations Involved During Peanut Peg Development. <i>Frontiers in Plant Science</i> , 2019, 10, 1289.	1.7	19
420	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.	1.7	19
421	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.	1.7	19
422	Analysis of Genetic Diversity in <i>Pongamia</i> [ <i>Pongamia pinnata</i> (L) Pierre] using AFLP Markers. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2010, 19, 209-216.	0.9	18
423	Genomics of plant genetic resources: an introduction. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 151-154.	0.4	18
424	Differences between <i>Cajanus cajan</i> (L.) Millspaugh and <i>C. cajanifolius</i> (Haines) van der Maesen, the progenitor species of pigeonpea. <i>Genetic Resources and Crop Evolution</i> , 2012, 59, 411-417.	0.8	18
425	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.	1.6	18
426	Genome-based analysis of the transcriptome from mature chickpea root nodules. <i>Frontiers in Plant Science</i> , 2014, 5, 325.	1.7	18
427	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.	0.6	18
428	Analysis of genetic diversity and population structure of peanut cultivars and breeding lines from China, India and the US using simple sequence repeat markers. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 452-465.	4.1	18
429	Identification of low Ca <sup>2+</sup> stress-induced embryo apoptosis response genes in <i>Arachis hypogaea</i> by SSH-associated library lift (SSHaLL). <i>Plant Biotechnology Journal</i> , 2016, 14, 682-698.	4.1	18
430	Genomic and Transcriptomic Analysis Identified Gene Clusters and Candidate Genes for Oil Content in Peanut ( <i>Arachis hypogaea</i> L.). <i>Plant Molecular Biology Reporter</i> , 2018, 36, 518-529.	1.0	18
431	Genome-wide identification of microsatellite markers from cultivated peanut ( <i>Arachis hypogaea</i> L.). <i>BMC Genomics</i> , 2019, 20, 799.	1.2	18
432	Carbohydrate, glutathione, and polyamine metabolism are central to <i>Aspergillus flavus</i> oxidative stress responses over time. <i>BMC Microbiology</i> , 2019, 19, 209.	1.3	18

#	ARTICLE	IF	CITATIONS
433	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.	1.8	18
434	Characterization of ASR gene and its role in drought tolerance in chickpea ( <i>Cicer arietinum</i> L.). <i>PLoS ONE</i> , 2020, 15, e0234550.	1.1	18
435	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.	1.1	18
436	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.	1.7	18
437	Genomics-Assisted Crop Improvement: An Overview. , 2007, , 1-12.		18
438	A comparative assessment of genetic diversity in cultivated barley collected in different decades of the last century in Austria, Albania and India by using genomic and genic simple sequence repeat (SSR) markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2006, 4, 125-133.	0.4	17
439	Hypoallergen Peanut Lines Identified Through Large-Scale Phenotyping of Global Diversity Panel: Providing Hope Toward Addressing One of the Major Global Food Safety Concerns. <i>Frontiers in Genetics</i> , 2019, 10, 1177.	1.1	17
440	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.	1.6	17
441	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.	2.0	17
442	Rapid delivery systems for future food security. <i>Nature Biotechnology</i> , 2021, 39, 1179-1181.	9.4	17
443	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.	0.6	16
444	Chickpea. , 2013, , 81-111.		16
445	Advances in Chickpea Genomics. , 2014, , 73-94.		16
446	Population structure and linkage disequilibrium of ICRISAT foxtail millet ( <i>Setaria italica</i> (L.) ÂP. Beauv.) core collection. <i>Euphytica</i> , 2014, 196, 423-435.	0.6	16
447	Identification and Evaluation of Single-Nucleotide Polymorphisms in Allotetraploid Peanut ( <i>Arachis</i> Tj ETQq1 1 0.784314 rgBT /Overl... <i>Frontiers in Plant Science</i> , 2015, 6, 1068.	1.7	16
448	Assessing the prospects of <i>Streptomyces</i> sp. RP1A-12 in managing groundnut stem rot disease caused by <i>Sclerotium rolfsii</i> Sacc. <i>Journal of General Plant Pathology</i> , 2016, 82, 96-104.	0.6	16
449	Development of a dense genetic map and QTL analysis for pod borer <i>Helicoverpa armigera</i> (HÃ¼bner) resistance component traits in chickpea ( <i>Cicer arietinum</i> L.). <i>Plant Genome</i> , 2021, 14, e20071.	1.6	16
450	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.	1.1	16

#	ARTICLE	IF	CITATIONS
451	Breeding Drought-Tolerant Pearl Millet Using Conventional and Genomic Approaches: Achievements and Prospects. <i>Frontiers in Plant Science</i> , 2022, 13, 781524.	1.7	16
452	Low level of polymorphism detected by SSR probes in bread wheat. <i>Plant Breeding</i> , 1998, 117, 182-184.	1.0	15
453	From genome studies to agricultural biotechnology: closing the gap between basic plant science and applied agriculture. <i>Current Opinion in Plant Biology</i> , 2010, 13, 115-118.	3.5	15
454	Whole-genome scanning for mapping determinacy in Pigeonpea ( <i>Cajanus</i> spp.). <i>Plant Breeding</i> , 2013, 132, 472-478.	1.0	15
455	Identification of Expressed Resistance Gene Analogs from Peanut ( <i>Arachis hypogaea</i> L.) Expressed Sequence Tags. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 453-461.	4.1	15
456	Detection of a new QTL/gene for growth habit in chickpea CaLG1 using wide and narrow crosses. <i>Euphytica</i> , 2015, 204, 473-485.	0.6	15
457	Harnessing Genetic Diversity of Wild <i>Arachis</i> Species for Genetic Enhancement of Cultivated Peanut. <i>Crop Science</i> , 2017, 57, 1121-1131.	0.8	15
458	SSR markers associated to early leaf spot disease resistance through selective genotyping and single marker analysis in groundnut ( <i>Arachis hypogaea</i> L.). <i>Biotechnology Reports (Amsterdam)</i> , 2017, 10, 457-460.	1.0	15
459	Genome-Wide Identification, Characterization, and Expression Analysis of Small RNA Biogenesis Purveyors Reveal Their Role in Regulation of Biotic Stress Responses in Three Legume Crops. <i>Frontiers in Plant Science</i> , 2017, 8, 488.	1.7	15
460	Identification of main effect and epistatic quantitative trait loci for morphological and yield-related traits in peanut ( <i>Arachis hypogaea</i> L.). <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	15
461	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.	0.8	15
462	Identification of heterotic groups in South-Asian-bred hybrid parents of pearl millet. <i>Theoretical and Applied Genetics</i> , 2020, 133, 873-888.	1.8	15
463	Two New <i>Aspergillus flavus</i> 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.	0.8	15
464	Transcriptome Analysis Identified Coordinated Control of Key Pathways Regulating Cellular Physiology and Metabolism upon <i>Aspergillus flavus</i> Infection Resulting in Reduced Aflatoxin Production in Groundnut. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 370.	1.5	15
465	Molecular and Physiological Alterations in Chickpea under Elevated CO <sub>2</sub> Concentrations. <i>Plant and Cell Physiology</i> , 2020, 61, 1449-1463.	1.5	15
466	Identification of Two Novel Peanut Genotypes Resistant to Aflatoxin Production and Their SNP Markers Associated with Resistance. <i>Toxins</i> , 2020, 12, 156.	1.5	15
467	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.	2.4	15
468	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.	1.7	15

#	ARTICLE	IF	CITATIONS
469	Moving Beyond DNA Sequence to Improve Plant Stress Responses. <i>Frontiers in Genetics</i> , 2022, 13, 874648.	1.1	15
470	New eSSR and gSSR markers added to Australian barley maps. <i>Australian Journal of Agricultural Research</i> , 2006, 57, 953.	1.5	14
471	Next-generation sequencing technologies: opportunities and obligations in plant genomics. <i>Briefings in Functional Genomics</i> , 2012, 11, 1-2.	1.3	14
472	Comparative sequence analysis of nitrogen fixation-related genes in six legumes. <i>Frontiers in Plant Science</i> , 2013, 4, 300.	1.7	14
473	Mitochondrial SSRs and their utility in distinguishing wild species, CMS lines and maintainer lines in pigeonpea ( <i>Cajanus cajan</i> L.). <i>Euphytica</i> , 2015, 206, 737-746.	0.6	14
474	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.	0.7	14
475	Methodology: ssb-MASS: a single seed-based sampling strategy for marker-assisted selection in rice. <i>Plant Methods</i> , 2019, 15, 78.	1.9	14
476	Monitoring Changes in the Cultivation of Pigeonpea and Groundnut in Malawi Using Time Series Satellite Imagery for Sustainable Food Systems. <i>Remote Sensing</i> , 2019, 11, 1475.	1.8	14
477	Climate-Smart Groundnuts for Achieving High Productivity and Improved Quality: Current Status, Challenges, and Opportunities. , 2019, , 133-172.		14
478	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.	4.1	14
479	Multimiomics approach unravels fertility transition in a pigeonpea line for a two-line hybrid system. <i>Plant Genome</i> , 2020, 13, e20028.	1.6	14
480	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.	1.8	14
481	Comparative Transcriptome Analysis Identified Candidate Genes for Late Leaf Spot Resistance and Cause of Defoliation in Groundnut. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4491.	1.8	14
482	Key Regulators of Sucrose Metabolism Identified through Comprehensive Comparative Transcriptome Analysis in Peanuts. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7266.	1.8	14
483	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.	0.8	14
484	Generation and exploitation of EST-derived SSR markers for assaying molecular diversity in durum wheat populations. <i>Genetic Resources and Crop Evolution</i> , 2008, 55, 869-881.	0.8	13
485	Assessment and comparison of AFLP and SSR based molecular genetic diversity in Indian isolates of <i>Ascochyta rabiei</i> , a causal agent of <i>Ascochyta</i> blight in chickpea ( <i>Cicer arietinum</i> L.). <i>Mycological Progress</i> , 2009, 8, 87-97.	0.5	13
486	A comparative assessment of the utility of PCR-based marker systems in pearl millet. <i>Euphytica</i> , 2010, 174, 253-260.	0.6	13

#	ARTICLE	IF	CITATIONS
487	EST-SSR based estimates on functional genetic variation in a barley ( <i>Hordeum vulgare</i> L.) collection from Egypt. <i>Genetic Resources and Crop Evolution</i> , 2010, 57, 515-521.	0.8	13
488	Market-led options to scale up legume seeds in developing countries: Experiences from the Tropical Legumes Project. <i>Plant Breeding</i> , 2019, 138, 474-486.	1.0	13
489	Mapping Quantitative Trait Loci for Carotenoid Concentration in Three F <sub>2</sub> Populations of Chickpea. <i>Plant Genome</i> , 2019, 12, 1-12.	1.6	13
490	Genetic diversity and population structure of groundnut ( <i>Arachis hypogaea</i> L.) accessions using phenotypic traits and SSR markers: implications for rust resistance breeding. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 581-604.	0.8	13
491	Transcriptome analysis reveals key genes associated with root-lesion nematode <i>Pratylenchus thornei</i> resistance in chickpea. <i>Scientific Reports</i> , 2021, 11, 17491.	1.6	13
492	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.	1.6	13
493	Chromatin spatial organization of wild type and mutant peanuts reveals high-resolution genomic architecture and interaction alterations. <i>Genome Biology</i> , 2021, 22, 315.	3.8	13
494	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.	1.5	13
495	Legume Genomics: From Genomic Resources to Molecular Breeding. <i>Plant Genome</i> , 2013, 6, plantgenome2013.12.0002in.	1.6	12
496	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.	1.0	12
497	Translational Pigeonpea Genomics Consortium for Accelerating Genetic Gains in Pigeonpea ( <i>Cajanus</i> ) Tj ETQq1 1 0,784314 rsgBT /Over	1.8	12
498	Sigma Factor Modulation for Cyanobacterial Metabolic Engineering. <i>Trends in Microbiology</i> , 2021, 29, 266-277.	3.5	12
499	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.	2.6	12
500	Challenges and Strategies for Next Generation Sequencing (NGS) Data Analysis. <i>Journal of Computer Science and Systems Biology</i> , 2010, 03, .	0.0	12
501	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.	1.4	12
502	Discovery of Major Quantitative Trait Loci and Candidate Genes for Fresh Seed Dormancy in Groundnut. <i>Agronomy</i> , 2022, 12, 404.	1.3	12
503	Molecular mechanisms, genetic mapping, and genome editing for insect pest resistance in field crops. <i>Theoretical and Applied Genetics</i> , 2022, 135, 3875-3895.	1.8	12
504	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.	1.7	12

#	ARTICLE	IF	CITATIONS
505	Comprehensive evaluation of Chinese peanut mini-mini core collection and QTL mapping for aflatoxin resistance. <i>BMC Plant Biology</i> , 2022, 22, 207.	1.6	12
506	Agronomic Performance of Chickpea Affected by Drought Stress at Different Growth Stages. <i>Agronomy</i> , 2022, 12, 995.	1.3	12
507	Hoechst 33342 induces radiosensitization in malignant glioma cells via increase in mitochondrial reactive oxygen species. <i>Free Radical Research</i> , 2010, 44, 936-949.	1.5	11
508	Molecular genetics and genomics of abiotic stress responses. <i>Frontiers in Plant Science</i> , 2014, 5, 398.	1.7	11
509	Enhancement of the use and impact of germplasm in crop improvement. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S155-S159.	0.4	11
510	Deciphering Transcriptional Programming during Pod and Seed Development Using RNA-Seq in Pigeonpea ( <i>Cajanus cajan</i> ). <i>PLoS ONE</i> , 2016, 11, e0164959.	1.1	11
511	Public sector soybean ( <i>Glycine max</i> ) breeding: Advances in cultivar development in the African tropics. <i>Plant Breeding</i> , 2019, 138, 455-464.	1.0	11
512	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.	0.9	11
513	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.	1.4	11
514	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.	1.2	11
515	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.	1.3	11
516	Single Seed-Based High-Throughput Genotyping and Rapid Generation Advancement for Accelerated Groundnut Genetics and Breeding Research. <i>Agronomy</i> , 2021, 11, 1226.	1.3	11
517	Genetic diversity and distinctness based on morphological and SSR markers in peanut. <i>Agronomy Journal</i> , 2021, 113, 4648-4660.	0.9	11
518	Nutritional Significance and Antioxidant-Mediated Antiaging Effects of Finger Millet: Molecular Insights and Prospects. <i>Frontiers in Sustainable Food Systems</i> , 2021, 5, .	1.8	11
519	Impact of different cooking methods on the chemical profile of high-oleic acid peanut seeds. <i>Food Chemistry</i> , 2022, 379, 131970.	4.2	11
520	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.	1.6	11
521	SSR and SNP diversity in a barley germplasm collection. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2008, 6, 167-174.	0.4	10
522	Characterisation of pathogenic and molecular diversity in <i>Sclerospora graminicola</i> , the causal agent of pearl millet downy mildew. <i>Archives of Phytopathology and Plant Protection</i> , 2010, 43, 538-551.	0.6	10

#	ARTICLE	IF	CITATIONS
523	Pigeonpea. , 2013, , 181-202.		10
524	Development and use of molecular markers for crop improvement. Plant Breeding, 2013, 132, 431-432.	1.0	10
525	An Integrated SNP Mining and Utilization (ISMLU) Pipeline for Next Generation Sequencing Data. PLoS ONE, 2014, 9, e101754.	1.1	10
526	Annotation of Trait Loci on Integrated Genetic Maps of Arachis Species. , 2016, , 163-207.		10
527	Classical and Molecular Approaches for Mapping of Genes and Quantitative Trait Loci in Peanut. Compendium of Plant Genomes, 2017, , 93-116.	0.3	10
528	A diagnostic marker kit for Fusarium wilt and sterility mosaic diseases resistance in pigeonpea. Theoretical and Applied Genetics, 2021, 134, 367-379.	1.8	10
529	Identification of microRNAs and their gene targets in cytoplasmic male sterile and fertile maintainer lines of pigeonpea. Planta, 2021, 253, 59.	1.6	10
530	Global Transcriptome Profiling Identified Transcription Factors, Biological Process, and Associated Pathways for Pre-Harvest Aflatoxin Contamination in Groundnut. Journal of Fungi (Basel,) Tj ETQq0 0 0 rgBT /Overlap 10 Tf 50457 Td (	1.0	10
531	Genetic, Epigenetic, Genomic and Microbial Approaches to Enhance Salt Tolerance of Plants: A Comprehensive Review. Biology, 2021, 10, 1255.	1.3	10
532	Genomic insights into the genetic signatures of selection and seed trait loci in cultivated peanut. Journal of Advanced Research, 2022, 42, 237-248.	4.4	10
533	Comparative Flower Transcriptome Network Analysis Reveals DEGs Involved in Chickpea Reproductive Success during Salinity. Plants, 2022, 11, 434.	1.6	10
534	Cereal Genomics II. , 2013, , .		9
535	Legume biology: the basis for crop improvement. Functional Plant Biology, 2013, 40, v.	1.1	9
536	Draft Genome Report of Bacillus altitudinis SORB11, Isolated from the Indian Sector of the Southern Ocean. Genome Announcements, 2017, 5, .	0.8	9
537	Modern Genomic Tools for Pigeonpea Improvement: Status and Prospects. Compendium of Plant Genomes, 2017, , 41-54.	0.3	9
538	Factors Influencing Preferences and Adoption of Improved Groundnut Varieties among Farmers in Tanzania. Agronomy, 2020, 10, 1271.	1.3	9
539	QTL-seq for the identification of candidate genes for days to flowering and leaf shape in pigeonpea. Heredity, 2022, 128, 411-419.	1.2	9
540	Aerially Applied Zinc Oxide Nanoparticle Affects Reproductive Components and Seed Quality in Fully Grown Bean Plants (Phaseolus vulgaris L.). Frontiers in Plant Science, 2021, 12, 808141.	1.7	9

#	ARTICLE	IF	CITATIONS
541	Pangenomics in Microbial and Crop Research: Progress, Applications, and Perspectives. <i>Genes</i> , 2022, 13, 598.	1.0	9
542	A simple hybridization-based strategy for the generation of non-redundant EST collections—a case study in barley ( <i>Hordeum vulgare</i> L.). <i>Plant Science</i> , 2004, 167, 629-634.	1.7	8
543	Genomic Selection for Crop Improvement: An Introduction. , 2017, , 1-6.		8
544	Improving crop performance under drought “ cross-fertilization of disciplines. <i>Journal of Experimental Botany</i> , 2017, 68, 1393-1398.	2.4	8
545	Groundnut Entered Post-genome Sequencing Era: Opportunities and Challenges in Translating Genomic Information from Genome to Field. , 2018, , 199-209.		8
546	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.	1.6	8
547	Reply to: Evaluating two different models of peanut’s origin. <i>Nature Genetics</i> , 2020, 52, 560-563.	9.4	8
548	High resolution mapping of restoration of fertility (Rf) by combining large population and high density genetic map in pigeonpea [ <i>Cajanus cajan</i> (L.) Millsp]. <i>BMC Genomics</i> , 2020, 21, 460.	1.2	8
549	Molecular mapping of dry root rot resistance genes in chickpea ( <i>Cicer arietinum</i> L.). <i>Euphytica</i> , 2021, 217, 1.	0.6	8
550	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.	1.0	8
551	Peanut Seed Coat Acts as a Physical and Biochemical Barrier against <i>Aspergillus flavus</i> Infection. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 1000.	1.5	8
552	Genome-Wide Identification and Expression of FAR1 Gene Family Provide Insight Into Pod Development in Peanut ( <i>Arachis hypogaea</i> ). <i>Frontiers in Plant Science</i> , 2022, 13, 893278.	1.7	8
553	Cereal Genomics: An Overview. , 2004, , 1-18.		7
554	Perl module and PISE wrappers for the integrated analysis of sequence data and SNP features. <i>BMC Research Notes</i> , 2009, 2, 92.	0.6	7
555	Hoechst 33342 induced reactive oxygen species and impaired expression of cytochrome c oxidase subunit 1 leading to cell death in irradiated human cancer cells. <i>Molecular and Cellular Biochemistry</i> , 2011, 352, 281-292.	1.4	7
556	Development of a new CMS system in pigeonpea utilizing crosses with <i>Cajanus lanceolatus</i> (WV Fitzg) van der Maesen. <i>Euphytica</i> , 2015, 204, 289-302.	0.6	7
557	Draft Genome Sequence of the Nonpathogenic, Thermotolerant, and Exopolysaccharide-Producing <i>Bacillus anthracis</i> Strain PFAB2 from Panifala Hot Water Spring in West Bengal, India. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
558	Current Status and Prospects of Genomic Selection in Legumes. , 2017, , 131-147.		7



#	ARTICLE	IF	CITATIONS
559	A novel aphid resistance locus in cowpea identified by combining <sc>SSR</sc> and <sc>SNP</sc> markers. <i>Plant Breeding</i> , 2018, 137, 203-209.	1.0	7
560	Assessing variability for disease resistance and nutritional quality traits in an interspecific collection of groundnut (<i>Arachis hypogaea</i>). <i>Plant Breeding</i> , 2018, 137, 883-894.	1.0	7
561	Advances in genomics and molecular breeding for legume improvement. , 2020, , 129-139.		7
562	Dissection of the genetic basis of oil content in Chinese peanut cultivars through association mapping. <i>BMC Genetics</i> , 2020, 21, 60.	2.7	7
563	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.	0.8	7
564	Molecular Genetic Diversity and Population Structure in Ethiopian Chickpea Germplasm Accessions. <i>Diversity</i> , 2021, 13, 247.	0.7	7
565	Past and Future Milestones of Plant Breeding. <i>Trends in Plant Science</i> , 2021, 26, 530-538.	4.3	7
566	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.	1.7	7
567	Global gene expression analysis of pigeonpea with male sterility conditioned by A 2 cytoplasm. <i>Plant Genome</i> , 2021, 14, e20132.	1.6	7
568	Molecular and Genomic Characterization of PFAB2: A Non-virulent <i>Bacillus anthracis</i> Strain Isolated from an Indian Hot Spring. <i>Current Genomics</i> , 2020, 20, 491-507.	0.7	7
569	Cloning, Expression Pattern Analysis and Subcellular Localization of Resveratrol Synthase Gene in Peanut (&lt;i>Arachis hypogaea&lt;/i> L.). <i>American Journal of Plant Sciences</i> , 2014, 05, 3619-3631.	0.3	7
570	Identification of superior haplotypes in a diverse natural population for breeding desirable plant height in soybean. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2407-2422.	1.8	7
571	Organization of Retrotransposons and Microsatellites in Cereal Genomes. , 2004, , 83-118.		6
572	Functional Genomics for Tolerance to Abiotic Stress in Cereals. , 2004, , 483-514.		6
573	Wheat. , 2006, , 79-134.		6
574	Satellite imagery and household survey for tracking chickpea adoption in Andhra Pradesh, India. <i>International Journal of Remote Sensing</i> , 2016, 37, 1955-1972.	1.3	6
575	Botanical Description of Pigeonpea [ <i>Cajanus cajan</i> (L.) Millsp.]. <i>Compendium of Plant Genomes</i> , 2017, , 17-29.	0.3	6
576	The Chickpea Genome: An Introduction. <i>Compendium of Plant Genomes</i> , 2017, , 1-4.	0.3	6

#	ARTICLE	IF	CITATIONS
577	History and Impact of the International Peanut Genome Initiative: The Exciting Journey Toward Peanut Whole-Genome Sequencing. <i>Compendium of Plant Genomes</i> , 2017, , 117-133.	0.3	6
578	Genetic diversity of <i>Jatropha curcas</i> collections from different islands in Indonesia. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2018, 16, 334-342.	0.4	6
579	<i>Plant Genetics and Molecular Biology: An Introduction. Advances in Biochemical Engineering/Biotechnology</i> , 2018, 164, 1-9.	0.6	6
580	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.	1.0	6
581	MAGIC lines in chickpea: development and exploitation of genetic diversity. <i>Euphytica</i> , 2021, 217, 1.	0.6	6
582	Enhancing oleic acid content in two commercially released peanut varieties through marker-assisted backcross breeding. <i>Crop Science</i> , 2021, 61, 2435-2443.	0.8	6
583	Characterization of heterosis and genomic prediction-based establishment of heterotic patterns for developing better hybrids in pigeonpea. <i>Plant Genome</i> , 2021, 14, e20125.	1.6	6
584	<i>Advances in Pigeonpea Genomics</i> . , 2014, , 95-110.		6
585	Next generation breeding in pulses: Present status and future directions. <i>Crop Breeding and Applied Biotechnology</i> , 2021, 21, .	0.1	6
586	Towards the Development, Maintenance and Standardized Phenotypic Characterization of Single-Seed-Descent Genetic Resources for Chickpea. <i>Current Protocols</i> , 2022, 2, e371.	1.3	6
587	Lipid profile variations in high oleic acid peanuts by following different cooking processes. <i>Food Research International</i> , 2022, 155, 110993.	2.9	6
588	A New Deep Learning Calibration Method Enhances Genome-Based Prediction of Continuous Crop Traits. <i>Frontiers in Genetics</i> , 2021, 12, 798840.	1.1	6
589	<i>Molecular Maps in Cereals: Methodology and Progress</i> . , 2004, , 35-82.		5
590	A SSR kit to study genetic diversity in chickpea ( <i>Cicer arietinum</i> L.). <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S118-S120.	0.4	5
591	Molecular Mapping of Genes and QTLs in Pigeonpea. <i>Compendium of Plant Genomes</i> , 2017, , 55-64.	0.3	5
592	Genomic regions associated with resistance to peanut bud necrosis disease (PBND) in a recombinant inbred line (RIL) population. <i>Plant Breeding</i> , 2019, 138, 748-760.	1.0	5
593	First Report of Pearl Millet Bacterial Leaf Blight Caused by <i>Pantoea stewartii</i> Subspecies <i>indologenes</i> in India. <i>Plant Disease</i> , 2021, 105, 3736.	0.7	5
594	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.	2.5	5

#	ARTICLE	IF	CITATIONS
595	<i>The Plant Genome</i> special issue: Advances in genomic selection and application of machine learning in genomic prediction for crop improvement. <i>Plant Genome</i> , 2021, 14, e20178.	1.6	5
596	Quantitative genetics and plant genomics: an overview. <i>Molecular Breeding</i> , 2010, 26, 133-134.	1.0	4
597	Pest and diseases: Old and new threats – Modern breeding tools to tailor new crop cultivars. <i>SÃ©cheresse</i> , 2013, 24, 261-273.	0.1	4
598	Genomics of plant genetic resources: a gateway to a new era of global food security. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S2-S5.	0.4	4
599	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.	1.6	4
600	Crop genetics research in Asia: improving food security and nutrition. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1339-1344.	1.8	4
601	Unraveling candidate genomic regions responsible for delayed leaf senescence in rice. <i>PLoS ONE</i> , 2020, 15, e0240591.	1.1	4
602	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.	1.8	4
603	A probit Analysis of Determinants of Adoption of Improved Sorghum Technologies Among Farmers in Tanzania. <i>Journal of Agricultural Science</i> , 2020, 13, 73.	0.1	4
604	Karyotype Differentiation in Cultivated Chickpea Revealed by Oligopainting Fluorescence in situ Hybridization. <i>Frontiers in Plant Science</i> , 2021, 12, 791303.	1.7	4
605	Using an incomplete block design to allocate lines to environments improves sparse genome-based prediction in plant breeding. <i>Plant Genome</i> , 2022, 15, e20194.	1.6	4
606	Efficient Breeding of Crop Plants. , 2022, , 745-777.		4
607	Introduction to Root Genomics. , 2011, , 1-10.		3
608	Evidence of a unique inter-allelic epistatic interaction for seed coat color in pigeonpea [ <i>Cajanus cajan</i> (L.) Millspaugh]. <i>Euphytica</i> , 2012, 186, 813-816.	0.6	3
609	Impact of Genomics on Chickpea Breeding. <i>Compendium of Plant Genomes</i> , 2017, , 125-134.	0.3	3
610	Advances in Chickpea Genomic Resources for Accelerating the Crop Improvement. <i>Compendium of Plant Genomes</i> , 2017, , 53-67.	0.3	3
611	Future Prospects for Peanut Improvement. <i>Compendium of Plant Genomes</i> , 2017, , 165-169.	0.3	3
612	Genomics: Shaping Legume Improvement. , 2021, , 49-89.		3

#	ARTICLE	IF	CITATIONS
613	Population Genomics of Peanut. <i>Population Genomics</i> , 2021, , 1.	0.2	3
614	Voices of biotech research. <i>Nature Biotechnology</i> , 2021, 39, 281-286.	9.4	3
615	Pigeonpea. , 2014, , 149-159.		3
616	Genomics in Agriculture and Food Processing. , 2013, , 45-70.		3
617	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.	0.8	3
618	Genomics, trait mapping and molecular breeding in pigeonpea and chickpea. <i>Indian Journal of Genetics and Plant Breeding</i> , 2016, 76, 504.	0.2	3
619	Molecular and morphological diversity in <i>Rhizoctonia bataticola</i> isolates causing dry root rot of chickpea ( <i>Cicer arietinum</i> L.) in India. <i>African Journal of Biotechnology</i> , 2012, 11, .	0.3	3
620	Technologies for Intensification of Production and Uses of Grain Legumes for Nutrition Security. <i>Proceedings of the Indian National Science Academy</i> , 2016, 82, .	0.5	3
621	Pigeonpea ( <i>Cajanus cajan</i> L. Millsp.): An Ideal Crop for Sustainable Agriculture. , 2019, , 409-429.		3
622	Breeding and Molecular Approaches for Evolving Drought-Tolerant Soybeans. , 2020, , 83-130.		3
623	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.	1.7	3
624	Designing chickpea for a hotter drier world. <i>Euphytica</i> , 2022, 218, .	0.6	3
625	An Integrated Pipeline of Open Source Software Adapted for Multi-CPU Architectures: Use in the Large-Scale Identification of Single Nucleotide Polymorphisms. <i>Comparative and Functional Genomics</i> , 2007, 2007, 1-7.	2.0	2
626	Sequencing Pigeonpea Genome. <i>Compendium of Plant Genomes</i> , 2017, , 93-97.	0.3	2
627	The Peanut Genome: An Introduction. <i>Compendium of Plant Genomes</i> , 2017, , 1-6.	0.3	2
628	G $\times$ E interactions in QTL introgression lines of Spanish-type groundnut ( <i>Arachis hypogaea</i> L.). <i>Euphytica</i> , 2020, 216, 1.	0.6	2
629	Hybrid Breeding in Food Legumes with Special Reference to Pigeonpea, Faba bean, and Soybean. , 2021, , 123-148.		2
630	Delineating investment opportunities for stakeholders in sorghum seed systems: a logit model perspective. <i>Agriculture and Food Security</i> , 2021, 10, .	1.6	2

#	ARTICLE	IF	CITATIONS
631	Groundnut. , 2014, , 161-173.		2
632	Translational Chickpea Genomics Consortium to Accelerate Genetic Gains in Chickpea ( <i>Cicer arietinum</i> ) Tj ETQq0 0,0,rgBT /Oyerlock 10	1.6	2
633	Genetic Enhancement of Groundnut: Current Status and Future Prospects. , 2022, , 63-110.		2
634	Genetic mapping of tolerance to iron deficiency chlorosis in peanut ( <i>Arachis hypogaea</i> L.). <i>Euphytica</i> , 2022, 218, 1.	0.6	2
635	Comprehensive transcriptomic analysis of two RIL parents with contrasting salt responsiveness identifies polyadenylated and nonâ€polyadenylated flower lncRNAs in chickpea. <i>Plant Biotechnology Journal</i> , 2022, , .	4.1	2
636	Estimating the potential to close yield gaps through increased efficiency of chickpea production in Ethiopia. <i>Food Security</i> , 0, , 1.	2.4	2
637	Editorial. <i>Journal of Biosciences</i> , 2012, 37, 807-810.	0.5	1
638	The Pigeonpea Genome: An Overview. <i>Compendium of Plant Genomes</i> , 2017, , 1-4.	0.3	1
639	Wide Crossing Technology for Pigeonpea Improvement. <i>Compendium of Plant Genomes</i> , 2017, , 31-39.	0.3	1
640	Whole-Genome Sequencing of Pigeonpea: Requirement, Background History, Current Status and Future Prospects for Crop Improvement. <i>Compendium of Plant Genomes</i> , 2017, , 81-91.	0.3	1
641	Future Prospects for Chickpea Research. <i>Compendium of Plant Genomes</i> , 2017, , 135-142.	0.3	1
642	Chickpea Genomics. , 2018, , 289-316.		1
643	Genomic Interventions to Improve Resilience of Pigeonpea in Changing Climate. , 2019, , 107-134.		1
644	Transcription Factors Evaluation in a Transcriptome Analysis on Chickpea ( <i>Cicer arietinum</i> L.) Under Drought Stress. <i>Journal of Crop Breeding</i> , 2019, 11, 133-141.	0.4	1
645	Analysis of Small RNA Sequencing Data in Plants. <i>Methods in Molecular Biology</i> , 2022, 2443, 497-509.	0.4	1
646	Cytogenetics to functional genomics: six decades journey of Professor P.K. Gupta. <i>Plant Biotechnology Journal</i> , 2022, , .	4.1	1
647	Cereal Genomics: Excitements, Challenges and Opportunities. , 2013, , 1-9.		0
648	Sequencing the Chickpea Genome. <i>Compendium of Plant Genomes</i> , 2017, , 117-123.	0.3	0

#	ARTICLE	IF	CITATIONS
649	Requirement of Whole-Genome Sequencing and Background History of the National and International Genome Initiatives. <i>Compendium of Plant Genomes</i> , 2017, , 107-115.	0.3	0
650	Genome-wide identification of meiotic recombination hot spots detected by SLAF in peanut ( <i>Arachis</i> ) Tj ETQq0 0 0 156 /Overlock 10 Tf		
651	Innovation Platform for Catalyzing Access to Seed of Improved Legume Varieties to Smallholder Farmers. , 2021, , 199-205.		0
652	Groundnut Kernel Transcriptome. , 2021, , 528-543.		0
653	Breeding customâ€designed crops for improved drought adaptation. <i>Genetics &amp; Genomics Next</i> , 0, , .	0.8	0
654	A Cross-Case Analysis of Innovation Platform Experiences in Seven Countries in West and East Africa and South Asia. , 2021, , 185-197.		0
655	General Context of Smallholder Farmersâ€™ Access to Seed of Improved Legume Varieties and Innovation Platform Perspectives. , 2021, , 1-7.		0
656	Aggravated food insecurity in COVID-19 era: quality seed flow of adapted and nutrient-dense varieties is central to the recovery equation in the drylands. <i>Technium: Romanian Journal of Applied Sciences and Technology</i> , 2020, 2, 62-65.	0.2	0
657	Genome-Wide Association Analysis of Yield-Related Traits of Soybean Using Haplotype-Based Framework. , 2021, 11, .		0