

Rajeev Kumar Varshney

List of Publications by Citations

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

#	Paper	IF	Citations
644	Exploiting EST databases for the development and characterization of gene-derived SSR-markers in barley (<i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2003 , 106, 411-22	6	1633
643	Genic microsatellite markers in plants: features and applications. <i>Trends in Biotechnology</i> , 2005 , 23, 48-55	5.1	1315
642	Draft genome sequence of chickpea (<i>Cicer arietinum</i>) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013 , 31, 240-6	44.5	781
641	Next-generation sequencing technologies and their implications for crop genetics and breeding. <i>Trends in Biotechnology</i> , 2009 , 27, 522-30	15.1	692
640	Draft genome sequence of pigeonpea (<i>Cajanus cajan</i>), an orphan legume crop of resource-poor farmers. <i>Nature Biotechnology</i> , 2011 , 30, 83-9	44.5	587
639	Genomic Selection in Plant Breeding: Methods, Models, and Perspectives. <i>Trends in Plant Science</i> , 2017 , 22, 961-975	13.1	548
638	The development and use of microsatellite markers for genetic analysis and plant breeding with emphasis on bread wheat. <i>Euphytica</i> , 2000 , 113, 163-185	2.1	524
637	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, 438-46	36.3	498
636	Development and implementation of high-throughput SNP genotyping in barley. <i>BMC Genomics</i> , 2009 , 10, 582	4.5	477
635	Genomics-assisted breeding for crop improvement. <i>Trends in Plant Science</i> , 2005 , 10, 621-30	13.1	454
634	Agriculture: Feeding the future. <i>Nature</i> , 2013 , 499, 23-4	50.4	363
633	Neglecting legumes has compromised human health and sustainable food production. <i>Nature Plants</i> , 2016 , 2, 16112	11.5	344
632	Molecular markers and their applications in wheat breeding. <i>Plant Breeding</i> , 1999 , 118, 369-390	2.4	337
631	Integrated genomics, physiology and breeding approaches for improving drought tolerance in crops. <i>Theoretical and Applied Genetics</i> , 2012 , 125, 625-45	6	299
630	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, 3531-44	7	280
629	Genome sequence of mungbean and insights into evolution within <i>Vigna</i> species. <i>Nature Communications</i> , 2014 , 5, 5443	17.4	274
628	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, 18656-61	11.5	266

627	Agricultural biotechnology for crop improvement in a variable climate: hope or hype?. <i>Trends in Plant Science</i> , 2011 , 16, 363-71	13.1	265
626	A high density barley microsatellite consensus map with 775 SSR loci. <i>Theoretical and Applied Genetics</i> , 2007 , 114, 1091-103	6	264
625	Harvesting the promising fruits of genomics: applying genome sequencing technologies to crop breeding. <i>PLoS Biology</i> , 2014 , 12, e1001883	9.7	256
624	In silico analysis on frequency and distribution of microsatellites in ESTs of some cereal species. <i>Cellular and Molecular Biology Letters</i> , 2002 , 7, 537-46	8.1	251
623	Plant growth promoting rhizobia: challenges and opportunities. <i>3 Biotech</i> , 2015 , 5, 355-377	2.8	248
622	Interspecific transferability and comparative mapping of barley EST-SSR markers in wheat, rye and rice. <i>Plant Science</i> , 2005 , 168, 195-202	5.3	235
621	Genetic dissection of drought tolerance in chickpea (<i>Cicer arietinum</i> L.). <i>Theoretical and Applied Genetics</i> , 2014 , 127, 445-62	6	229
620	Crop Breeding Chips and Genotyping Platforms: Progress, Challenges, and Perspectives. <i>Molecular Plant</i> , 2017 , 10, 1047-1064	14.4	229
619	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	5.3	225
618	Achievements and prospects of genomics-assisted breeding in three legume crops of the semi-arid tropics. <i>Biotechnology Advances</i> , 2013 , 31, 1120-34	17.8	218
617	Genome-wide association mapping: a case study in bread wheat (<i>Triticum aestivum</i> L.). <i>Molecular Breeding</i> , 2011 , 27, 37-58	3.4	216
616	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, 922-31	11.6	213
615	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019 , 51, 877-884	36.3	211
614	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, 823-39	6	203
613	Advances in cereal genomics and applications in crop breeding. <i>Trends in Biotechnology</i> , 2006 , 24, 490-9	15.1	203
612	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017 , 35, 969-976	44.5	197
611	Advances in <i>Arachis</i> genomics for peanut improvement. <i>Biotechnology Advances</i> , 2012 , 30, 639-51	17.8	195
610	Can genomics boost productivity of orphan crops?. <i>Nature Biotechnology</i> , 2012 , 30, 1172-6	44.5	192

609	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	5.3	191
608	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, 359-72	6	189
607	The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. <i>Nature Genetics</i> , 2019 , 51, 865-876	36.3	188
606	Large-scale development of cost-effective SNP marker assays for diversity assessment and genetic mapping in chickpea and comparative mapping in legumes. <i>Plant Biotechnology Journal</i> , 2012 , 10, 716-32	11.6	185
605	Orphan legume crops enter the genomics era!. <i>Current Opinion in Plant Biology</i> , 2009 , 12, 202-10	9.9	184
604	Genome sequencing of the high oil crop sesame provides insight into oil biosynthesis. <i>Genome Biology</i> , 2014 , 15, R39	18.3	179
603	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	6.2	179
602	The first SSR-based genetic linkage map for cultivated groundnut (<i>Arachis hypogaea</i> L.). <i>Theoretical and Applied Genetics</i> , 2009 , 118, 729-39	6	177
601	Legume Crops Phylogeny and Genetic Diversity for Science and Breeding. <i>Critical Reviews in Plant Sciences</i> , 2015 , 34, 43-104	5.6	172
600	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, 1415-41	6	172
599	MAGIC populations in crops: current status and future prospects. <i>Theoretical and Applied Genetics</i> , 2015 , 128, 999-1017	6	171
598	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	5.3	171
597	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	4.5	165
596	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. <i>Frontiers in Plant Science</i> , 2015 , 6, 563	6.2	161
595	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.). <i>Theoretical and Applied Genetics</i> , 2011 , 122, 1119-32	6	158
594	AFLP-based molecular characterization of an elite germplasm collection of <i>Jatropha curcas</i> L., a biofuel plant. <i>Plant Science</i> , 2009 , 176, 505-13	5.3	157
593	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	6	153
592	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, 6785-90	11.5	149

591	Salt sensitivity in chickpea. <i>Plant, Cell and Environment</i> , 2010 , 33, 490-509	8.4	146
590	Genetic dissection of drought and heat tolerance in chickpea through genome-wide and candidate gene-based association mapping approaches. <i>PLoS ONE</i> , 2014 , 9, e96758	3.7	146
589	Genetic structure, diversity, and allelic richness in composite collection and reference set in chickpea (<i>Cicer arietinum</i> L.). <i>BMC Plant Biology</i> , 2008 , 8, 106	5.3	142
588	Genotyping-by-sequencing based intra-specific genetic map refines a "QTL-hotspot" region for drought tolerance in chickpea. <i>Molecular Genetics and Genomics</i> , 2015 , 290, 559-71	3.1	140
587	Global agricultural intensification during climate change: a role for genomics. <i>Plant Biotechnology Journal</i> , 2016 , 14, 1095-8	11.6	138
586	Assessing genetic diversity for crop improvement. <i>Current Opinion in Plant Biology</i> , 2010 , 13, 167-73	9.9	137
585	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	6	136
584	Proline over-accumulation alleviates salt stress and protects photosynthetic and antioxidant enzyme activities in transgenic sorghum [<i>Sorghum bicolor</i> (L.) Moench]. <i>Plant Physiology and Biochemistry</i> , 2015 , 94, 104-13	5.4	135
583	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.). <i>Theoretical and Applied Genetics</i> , 2010 , 121, 971-84	6	135
582	Whole-genome resequencing of 292 pigeonpea accessions identifies genomic regions associated with domestication and agronomic traits. <i>Nature Genetics</i> , 2017 , 49, 1082-1088	36.3	134
581	Emerging Genomic Tools for Legume Breeding: Current Status and Future Prospects. <i>Frontiers in Plant Science</i> , 2016 , 7, 455	6.2	133
580	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	3.7	132
579	Structural variations in plant genomes. <i>Briefings in Functional Genomics</i> , 2014 , 13, 296-307	4.9	128
578	Large-scale analysis of the barley transcriptome based on expressed sequence tags. <i>Plant Journal</i> , 2004 , 40, 276-90	6.9	125
577	Marker-assisted introgression of a QTL region to improve rust resistance in three elite and popular varieties of peanut (<i>Arachis hypogaea</i> L.). <i>Theoretical and Applied Genetics</i> , 2014 , 127, 1771-81	6	118
576	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 hypogaea</i> L.). <i>Molecular Breeding</i> , 2012 , 30, 773-788	3.4	118
575	Evaluation of <i>Streptomyces</i> strains isolated from herbal vermicompost for their plant growth-promotion traits in rice. <i>Microbiological Research</i> , 2014 , 169, 40-8	5.3	117
574	Resequencing of 429 chickpea accessions from 45 countries provides insights into genome diversity, domestication and agronomic traits. <i>Nature Genetics</i> , 2019 , 51, 857-864	36.3	116

573	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	5.5	116
572	Transcriptome analyses reveal genotype- and developmental stage-specific molecular responses to drought and salinity stresses in chickpea. <i>Scientific Reports</i> , 2016 , 6, 19228	4.9	114
571	More genomic resources for less-studied crops. <i>Trends in Biotechnology</i> , 2010 , 28, 452-60	15.1	112
570	QTL-seq for rapid identification of candidate genes for 100-seed weight and root/total plant dry weight ratio under rainfed conditions in chickpea. <i>Plant Biotechnology Journal</i> , 2016 , 14, 2110-2119	11.6	112
569	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, 1577-89	6	110
568	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	5.3	107
567	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	5.3	105
566	QTLs for chlorophyll and chlorophyll fluorescence parameters in barley under post-flowering drought. <i>Euphytica</i> , 2008 , 163, 203-214	2.1	105
565	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	6	103
564	Development and Evaluation of a High Density Genotyping 'Axiom_Arachis' Array with 58 K SNPs For Accelerating Genetics and Breeding in Groundnut. <i>Scientific Reports</i> , 2017 , 7, 40577	4.9	102
563	Current state-of-art of sequencing technologies for plant genomics research. <i>Briefings in Functional Genomics</i> , 2012 , 11, 3-11	4.9	102
562	QTL-seq approach identified genomic regions and diagnostic markers for rust and late leaf spot resistance in groundnut (<i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2017 , 15, 927-941	11.6	101
561	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	6	101
560	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	4.4	100
559	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	5.5	100
558	Sequencing of Cultivated Peanut, <i>Arachis hypogaea</i> , Yields Insights into Genome Evolution and Oil Improvement. <i>Molecular Plant</i> , 2019 , 12, 920-934	14.4	99
557	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, 173-84	4.5	99
556	Identification of candidate genome regions controlling disease resistance in <i>Arachis</i> . <i>BMC Plant Biology</i> , 2009 , 9, 112	5.3	98

555	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	3.4	98
554	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	1	97
553	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, 239-50	6	97
552	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	6.2	96
551	Prioritization of candidate genes in "QTL-hotspot" region for drought tolerance in chickpea (<i>Cicer arietinum</i> L.). <i>Scientific Reports</i> , 2015 , 5, 15296	4.9	96
550	Impact of Genomic Technologies on Chickpea Breeding Strategies. <i>Agronomy</i> , 2012 , 2, 199-221	3.6	96
549	Draft genome sequence of adzuki bean, <i>Vigna angularis</i> . <i>Scientific Reports</i> , 2015 , 5, 8069	4.9	95
548	Pre-breeding for diversification of primary gene pool and genetic enhancement of grain legumes. <i>Frontiers in Plant Science</i> , 2013 , 4, 309	6.2	93
547	Molecular breeding for introgression of fatty acid desaturase mutant alleles (ahFAD2A and ahFAD2B) enhances oil quality in high and low oil containing peanut genotypes. <i>Plant Science</i> , 2016 , 242, 203-213	5.3	89
546	Fast-Track 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	4.4	89
545	Super-Pangenome by Integrating the Wild Side of a Species for Accelerated Crop Improvement. <i>Trends in Plant Science</i> , 2020 , 25, 148-158	13.1	87
544	Large-scale development of cost-effective single-nucleotide polymorphism marker assays for genetic mapping in pigeonpea and comparative mapping in legumes. <i>DNA Research</i> , 2012 , 19, 449-61	4.5	86
543	An intra-specific consensus genetic map of pigeonpea [<i>Cajanus cajan</i> (L.) Millspaugh] derived from six mapping populations. <i>Theoretical and Applied Genetics</i> , 2012 , 125, 1325-38	6	85
542	Potential of promotion of alleles by genome editing to improve quantitative traits in livestock breeding programs. <i>Genetics Selection Evolution</i> , 2015 , 47, 55	4.9	84
541	Toward the sequence-based breeding in legumes in the post-genome sequencing era. <i>Theoretical and Applied Genetics</i> , 2019 , 132, 797-816	6	84
540	Molecular mapping of QTLs for resistance to Fusarium wilt (race 1) and Ascochyta blight in chickpea (<i>Cicer arietinum</i> L.). <i>Euphytica</i> , 2013 , 193, 121-133	2.1	81
539	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	3.7	80
538	Genome-Enabled Prediction Models for Yield Related Traits in Chickpea. <i>Frontiers in Plant Science</i> , 2016 , 7, 1666	6.2	80

537	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	2.6	79
536	Groundnut improvement: use of genetic and genomic tools. <i>Frontiers in Plant Science</i> , 2013 , 4, 23	6.2	79
535	Generation and comparison of EST-derived SSRs and SNPs in barley (<i>Hordeum vulgare</i> L.). <i>Hereditas</i> , 2001 , 135, 145-51	2.4	79
534	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, 153-64	4.5	78
533	The first set of EST resource for gene discovery and marker development in pigeonpea (<i>Cajanus cajan</i> L.). <i>BMC Plant Biology</i> , 2010 , 10, 45	5.3	78
532	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	6.2	78
531	Genome wide association analyses for drought tolerance related traits in barley (<i>Hordeum vulgare</i> L.). <i>Field Crops Research</i> , 2012 , 126, 171-180	5.5	77
530	Development and characterization of BAC-end sequence derived SSRs, and their incorporation into a new higher density genetic map for cultivated peanut (<i>Arachis hypogaea</i> L.). <i>BMC Plant Biology</i> , 2012 , 12, 10	5.3	76
529	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	4.5	76
528	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	3.7	76
527	Assessment of ICCV 2 62 chickpea progenies shows sensitivity of reproduction to salt stress and reveals QTL for seed yield and yield components. <i>Molecular Breeding</i> , 2012 , 30, 9-21	3.4	76
526	EST-derived single nucleotide polymorphism markers for assembling genetic and physical maps of the barley genome. <i>Functional and Integrative Genomics</i> , 2008 , 8, 223-33	3.8	76
525	Genome-wide SNP Genotyping Resolves Signatures of Selection and Tetrasomic Recombination in Peanut. <i>Molecular Plant</i> , 2017 , 10, 309-322	14.4	75
524	Comparative analysis of the grain proteome fraction in barley genotypes with contrasting salinity tolerance during germination. <i>Plant, Cell and Environment</i> , 2010 , 33, 211-22	8.4	75
523	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	5.3	74
522	Next-generation sequencing for identification of candidate genes for Fusarium wilt and sterility mosaic disease in pigeonpea (<i>Cajanus cajan</i>). <i>Plant Biotechnology Journal</i> , 2016 , 14, 1183-94	11.6	74
521	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	3.7	73
520	A comprehensive transcriptome assembly of Pigeonpea (<i>Cajanus cajan</i> L.) using sanger and second-generation sequencing platforms. <i>Molecular Plant</i> , 2012 , 5, 1020-8	14.4	73

519	Proteomics and Metabolomics: Two Emerging Areas for Legume Improvement. <i>Frontiers in Plant Science</i> , 2015 , 6, 1116	6.2	72
518	Quantitative trait locus analysis and construction of consensus genetic map for drought tolerance traits based on three recombinant inbred line populations in cultivated groundnut (<i>Arachis hypogaea</i> L.). <i>Molecular Breeding</i> , 2012 , 30, 757-772	3.4	72
517	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	3.7	72
516	Chickpea improvement: role of wild species and genetic markers. <i>Biotechnology and Genetic Engineering Reviews</i> , 2008 , 25, 267-313	4.1	71
515	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, 1563-77	11.6	71
514	Identification of eight chromosomes and a microsatellite marker on 1AS associated with QTL for grain weight in bread wheat. <i>Theoretical and Applied Genetics</i> , 2000 , 100, 1290-1294	6	70
513	Can genomics deliver climate-change ready crops?. <i>Current Opinion in Plant Biology</i> , 2018 , 45, 205-211	9.9	68
512	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	4.5	68
511	Designing Future Crops: Genomics-Assisted Breeding Comes of Age. <i>Trends in Plant Science</i> , 2021 , 26, 631-649	13.1	68
510	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 Suppl 1, 10	5.3	67
509	Genomics-assisted breeding in four major pulse crops of developing countries: present status and prospects. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 1263-91	6	67
508	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	5.3	67
507	Deep sequencing analysis of the transcriptomes of peanut aerial and subterranean young pods identifies candidate genes related to early embryo abortion. <i>Plant Biotechnology Journal</i> , 2013 , 11, 115-27	11.6	65
506	5Gs for crop genetic improvement. <i>Current Opinion in Plant Biology</i> , 2020 , 56, 190-196	9.9	64
505	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	7.6	63
504	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, 13213-8	11.5	62
503	Scope for improvement of yield under drought through the root traits in chickpea (<i>Cicer arietinum</i> L.). <i>Field Crops Research</i> , 2015 , 170, 47-54	5.5	62
502	Translational Genomics in Agriculture: Some Examples in Grain Legumes. <i>Critical Reviews in Plant Sciences</i> , 2015 , 34, 169-194	5.6	62

501	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	5.3	62
500	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	2.2	61
499	High-Throughput Estimation of Crop Traits: A Review of Ground and Aerial Phenotyping Platforms. <i>IEEE Geoscience and Remote Sensing Magazine</i> , 2021 , 9, 200-231	8.9	61
498	Genetic diversity of root system architecture in response to drought stress in grain legumes. <i>Journal of Experimental Botany</i> , 2018 , 69, 3267-3277	7	60
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21	Using an incomplete block design to allocate lines to environments improves sparse genome-based prediction in plant breeding.. <i>Plant Genome</i> , 2022 , e20194	4.4	o
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