

Manish K Pandey

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4359667/publications.pdf>

Version: 2024-02-01

147
papers

7,839
citations

57758

44
h-index

62596

80
g-index

153
all docs

153
docs citations

153
times ranked

4521
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	21.4	439
2	The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. <i>Nature Genetics</i> , 2019, 51, 865-876.	21.4	398
3	Achievements and prospects of genomics-assisted breeding in three legume crops of the semi-arid tropics. <i>Biotechnology Advances</i> , 2013, 31, 1120-1134.	11.7	289
4	Advances in <i>Arachis</i> genomics for peanut improvement. <i>Biotechnology Advances</i> , 2012, 30, 639-651.	11.7	258
5	Legume Crops Phylogeny and Genetic Diversity for Science and Breeding. <i>Critical Reviews in Plant Sciences</i> , 2015, 34, 43-104.	5.7	248
6	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.	7.1	235
7	Metabolomics for Plant Improvement: Status and Prospects. <i>Frontiers in Plant Science</i> , 2017, 8, 1302.	3.6	210
8	QTL-seq approach identified genomic regions and diagnostic markers for rust and late leaf spot resistance in groundnut (<i>Arachis hypogaea</i>). <i>Plant Biotechnology Journal</i> , 2017, 15, 927-941.	8.3	198
9	Sequencing of Cultivated Peanut, <i>Arachis hypogaea</i> , Yields Insights into Genome Evolution and Oil Improvement. <i>Molecular Plant</i> , 2019, 12, 920-934.	8.3	185
10	Emerging Genomic Tools for Legume Breeding: Current Status and Future Prospects. <i>Frontiers in Plant Science</i> , 2016, 7, 455.	3.6	180
11	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 rgBT / Overlock 10	3.6	167
12	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, 1771-1781.	3.6	167
13	Toward the sequence-based breeding in legumes in the post-genome sequencing era. <i>Theoretical and Applied Genetics</i> , 2019, 132, 797-816.	3.6	147
14	Development and Evaluation of a High Density Genotyping <i>Axiom_Arachis</i> ™ Array with 580K SNPs for Accelerating Genetics and Breeding in Groundnut. <i>Scientific Reports</i> , 2017, 7, 40577.	3.3	144
15	Groundnut improvement: use of genetic and genomic tools. <i>Frontiers in Plant Science</i> , 2013, 4, 23.	3.6	139
16	Genomewide Association Studies for 50 Agronomic Traits in Peanut Using the <i>Reference Set</i> ™ Comprising 300 Genotypes from 48 Countries of the Semi-Arid Tropics of the World. <i>PLoS ONE</i> , 2014, 9, e105228.	2.5	124
17	Molecular breeding for introgression of fatty acid desaturase mutant alleles (<i>ahFAD2A</i> and <i>ahFAD2B</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10 203-213.	3.6	124
18	Identification of QTLs associated with oil content and mapping <i>FAD2</i> 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

#	ARTICLE	IF	CITATIONS
19	Genome-wide SNP Genotyping Resolves Signatures of Selection and Tetrasomic Recombination in Peanut. <i>Molecular Plant</i> , 2017, 10, 309-322.	8.3	114
20	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.	3.4	113
21	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 ETQq1 1 0.784314 rgBT /Ove	3.6	87
22	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.	8.3	90
23	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.	2.5	89
24	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.	4.8	87
25	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.	3.6	86
26	Oxidative stress and carbon metabolism influence <i>Aspergillus flavus</i> transcriptome composition and secondary metabolite production. <i>Scientific Reports</i> , 2016, 6, 38747.	3.3	85
27	Genomic Tools in Groundnut Breeding Program: Status and Perspectives. <i>Frontiers in Plant Science</i> , 2016, 7, 289.	3.6	79
28	Development and deployment of a high-density linkage map identified quantitative trait loci for plant height in peanut (<i>Arachis hypogaea</i> L.). <i>Scientific Reports</i> , 2016, 6, 39478.	3.3	76
29	Genetic Mapping of QTLs Controlling Fatty Acids Provided Insights into the Genetic Control of Fatty Acid Synthesis Pathway in Peanut (<i>Arachis hypogaea</i> L.). <i>PLoS ONE</i> , 2015, 10, e0119454.	2.5	73
30	Mitigating Aflatoxin Contamination in Groundnut through A Combination of Genetic Resistance and Post-Harvest Management Practices. <i>Toxins</i> , 2019, 11, 315.	3.4	73
31	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.	3.5	72
32	Advances in genetics and molecular breeding of three legume crops of semi-arid tropics using next-generation sequencing and high-throughput genotyping technologies. <i>Journal of Biosciences</i> , 2012, 37, 811-820.	1.1	68
33	Molecular Mapping of Oil Content and Fatty Acids Using Dense Genetic Maps in Groundnut (<i>Arachis</i>) Tj ETQq1 1 0.784314 rgBT /Ove	3.6	87
34	Single Nucleotide Polymorphism-based Genetic Diversity in the Reference Set of Peanut (<i>Arachis</i> spp.) by Developing and Applying Cost-Effective Kompetitive Allele Specific Polymerase Chain Reaction Genotyping Assays. <i>Plant Genome</i> , 2013, 6, plantgenome2013.06.0019.	2.8	65
35	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.	8.3	65
36	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.	1.2	64

#	ARTICLE	IF	CITATIONS
37	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.	1.9	62
38	Different isoforms of starch-synthesizing enzymes controlling amylose and amylopectin content in rice (<i>Oryza sativa</i> L.). <i>Biotechnology Advances</i> , 2012, 30, 1697-1706.	11.7	60
39	Whole-genome resequencing-based QTL-seq identified candidate genes and molecular markers for fresh seed dormancy in groundnut. <i>Plant Biotechnology Journal</i> , 2020, 18, 992-1003.	8.3	60
40	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.	3.6	58
41	Translational genomics for achieving higher genetic gains in groundnut. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1679-1702.	3.6	58
42	Co-localization of major quantitative trait loci for pod size and weight to a 3.7-M interval on chromosome A05 in cultivated peanut (<i>Arachis hypogaea</i> L.). <i>BMC Genomics</i> , 2017, 18, 58.	2.8	54
43	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.	3.6	54
44	Thiourea, a ROS Scavenger, Regulates Source-to-Sink Relationship to Enhance Crop Yield and Oil Content in <i>Brassica juncea</i> (L.). <i>PLoS ONE</i> , 2013, 8, e73921.	2.5	53
45	Genetic Mapping and Quantitative Trait Loci Analysis for Disease Resistance Using F ₂ and F ₅ Generation-based Genetic Maps Derived from ‘Tifrunner’ × ‘GT20’ in Peanut. <i>Plant Genome</i> , 2013, 6, plantgenome2013.05.0018.		52
46	Discovery of genomic regions and candidate genes controlling shelling percentage using QTL-seq approach in cultivated peanut (<i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2019, 17, 1248-1260.	8.3	51
47	Development of a simple functional marker for fragrance in rice and its validation in Indian Basmati and non-Basmati fragrant rice varieties. <i>Molecular Breeding</i> , 2009, 24, 185-190.	2.1	48
48	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.	5.2	47
49	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.	2.5	46
50	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.	3.3	45
51	Development of a PCR-based SNP marker system for effective selection of kernel length and kernel elongation in rice. <i>Molecular Breeding</i> , 2010, 26, 735-740.	2.1	43
52	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.	3.6	42
53	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.	8.3	41
54	Deployment of Genetic and Genomic Tools Toward Gaining a Better Understanding of Rice- <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Interactions for Development of Durable Bacterial Blight Resistant Rice. <i>Frontiers in Plant Science</i> , 2020, 11, 1152.	3.6	41

#	ARTICLE	IF	CITATIONS
55	Marker-assisted introgression of bacterial blight and blast resistance into <i>IR58025B</i> , an elite maintainer line of rice. <i>Plant Breeding</i> , 2013, 132, 586-594.	1.9	40
56	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.	1.9	40
57	Improvement of two traditional Basmati rice varieties for bacterial blight resistance and plant stature through morphological and marker-assisted selection. <i>Molecular Breeding</i> , 2013, 31, 239-246.	2.1	39
58	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.	3.6	39
59	Molecular Basis of Root Nodule Symbiosis between <i>Bradyrhizobium</i> and <i>Crack-Entry™</i> Legume Groundnut (<i>Arachis hypogaea</i> L.). <i>Plants</i> , 2020, 9, 276.	3.5	39
60	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.	3.5	39
61	<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.	3.3	38
62	Improving oil quality by altering levels of fatty acids through marker-assisted selection of <i>ahfad2</i> alleles in peanut (<i>Arachis hypogaea</i> L.). <i>Euphytica</i> , 2018, 214, 1.	1.2	38
63	Genetics, genomics and breeding of groundnut (<i>Arachis hypogaea</i> L.). <i>Plant Breeding</i> , 2019, 138, 425-444.	1.9	38
64	<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.	8.3	38
65	Sequencing Analysis of Genetic Loci for Resistance for Late Leaf Spot and Rust in Peanut (<i>Arachis</i>) Tj ETQq1 1 0.784314 rgBT/Overlook	3.6	37
66	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
67	Epigenetics and epigenomics: underlying mechanisms, relevance, and implications in crop improvement. <i>Functional and Integrative Genomics</i> , 2020, 20, 739-761.	3.5	37
68	Metabolomics Intervention Towards Better Understanding of Plant Traits. <i>Cells</i> , 2021, 10, 346.	4.1	35
69	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.	2.5	34
70	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.	3.6	34
71	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.	5.2	33
72	Marker-assisted improvement of a stable restorer line, <i>KMR3R</i> and its derived hybrid <i>KRH2</i> for bacterial blight resistance and grain quality. <i>Plant Breeding</i> , 2011, 130, 608-616.	1.9	31

#	ARTICLE	IF	CITATIONS
73	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.	1.9	31
74	Whitebacked planthopper <i>Sogatella furcifera</i> (Horváth) (Homoptera: Delphacidae) resistance in rice variety Sinna Sivappu. <i>Euphytica</i> , 2014, 200, 139-148.	1.2	29
75	Identification of quantitative trait loci for yield and yield related traits in groundnut (<i>Arachis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.2	29
76	Genome-based trait prediction in multi-environment breeding trials in groundnut. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3101-3117.	3.6	29
77	Genomics, genetics and breeding of tropical legumes for better livelihoods of smallholder farmers. <i>Plant Breeding</i> , 2019, 138, 487-499.	1.9	28
78	Transcriptome and metabolome reveal redirection of flavonoids in a white testa peanut mutant. <i>BMC Plant Biology</i> , 2020, 20, 161.	3.6	28
79	Improved Genetic Map Identified Major QTLs for Drought Tolerance- and Iron Deficiency Tolerance-Related Traits in Groundnut. <i>Genes</i> , 2021, 12, 37.	2.4	28
80	Genetic Variation and Association Mapping of Seed-Related Traits in Cultivated Peanut (<i>Arachis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4 2105.	3.6	27
81	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.	3.7	26
82	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.	3.3	25
83	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.	3.6	24
84	Combining High Oleic Acid Trait and Resistance to Late Leaf Spot and Rust Diseases in Groundnut (<i>Arachis hypogaea</i> L.). <i>Frontiers in Genetics</i> , 2020, 11, 514.	2.3	24
85	Time course of physiological, biochemical, and gene expression changes under short-term salt stress in <i>Brassica juncea</i> L.. <i>Crop Journal</i> , 2017, 5, 219-230.	5.2	22
86	Chemical intervention for enhancing growth and reducing grain arsenic accumulation in rice. <i>Environmental Pollution</i> , 2021, 276, 116719.	7.5	22
87	Development of NILs 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.	1.9	20
88	Genome-wide transcriptome and physiological analyses provide new insights into peanut drought response mechanisms. <i>Scientific Reports</i> , 2020, 10, 4071.	3.3	20
89	Chromosome-length genome assemblies of six legume species provide insights into genome organization, evolution, and agronomic traits for crop improvement. <i>Journal of Advanced Research</i> , 2022, 42, 315-329.	9.5	20
90	Recent Advances in Molecular Genetic Linkage Maps of Cultivated Peanut. <i>Peanut Science</i> , 2013, 40, 95-106.	0.1	19

#	ARTICLE	IF	CITATIONS
91	Peg Biology: Deciphering the Molecular Regulations Involved During Peanut Peg Development. <i>Frontiers in Plant Science</i> , 2019, 10, 1289.	3.6	19
92	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.	3.6	19
93	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.	1.8	18
94	Carbohydrate, glutathione, and polyamine metabolism are central to <i>Aspergillus flavus</i> oxidative stress responses over time. <i>BMC Microbiology</i> , 2019, 19, 209.	3.3	18
95	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.	3.6	18
96	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.	2.3	17
97	Identification and Evaluation of Single-Nucleotide Polymorphisms in Allotetraploid Peanut (<i>Arachis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock <i>Frontiers in Plant Science</i> , 2015, 6, 1068.	3.6	16
98	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.	8.5	15
99	Harnessing Genetic Diversity of Wild <i>Arachis</i> Species for Genetic Enhancement of Cultivated Peanut. <i>Crop Science</i> , 2017, 57, 1121-1131.	1.8	15
100	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> , Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 377 Td	1.8	15
101	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.	2.1	15
102	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.	1.8	15
103	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.	3.5	15
104	Identification of Two Novel Peanut Genotypes Resistant to Aflatoxin Production and Their SNP Markers Associated with Resistance. <i>Toxins</i> , 2020, 12, 156.	3.4	15
105	Climate-Smart Groundnuts for Achieving High Productivity and Improved Quality: Current Status, Challenges, and Opportunities. , 2019, , 133-172.		14
106	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.	8.3	14
107	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.	3.6	14
108	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.	4.1	14

#	ARTICLE	IF	CITATIONS
109	Key Regulators of Sucrose Metabolism Identified through Comprehensive Comparative Transcriptome Analysis in Peanuts. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7266.	4.1	14
110	Chromatin spatial organization of wild type and mutant peanuts reveals high-resolution genomic architecture and interaction alterations. <i>Genome Biology</i> , 2021, 22, 315.	8.8	13
111	Genetic imprints of domestication for disease resistance, oil quality, and yield component traits in groundnut (<i>Arachis hypogaea</i> L.). <i>Molecular Genetics and Genomics</i> , 2019, 294, 365-378.	2.1	12
112	Discovery of Major Quantitative Trait Loci and Candidate Genes for Fresh Seed Dormancy in Groundnut. <i>Agronomy</i> , 2022, 12, 404.	3.0	12
113	Comprehensive evaluation of Chinese peanut mini-mini core collection and QTL mapping for aflatoxin resistance. <i>BMC Plant Biology</i> , 2022, 22, 207.	3.6	12
114	Thiourea mediates alleviation of UV-B stress-induced damage in the Indian mustard (<i>Brassica</i>). <i>Journal of Plant Physiology</i> , 2021, 159, 110-115.	2.1	11
115	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.	2.9	11
116	Single Seed-Based High-Throughput Genotyping and Rapid Generation Advancement for Accelerated Groundnut Genetics and Breeding Research. <i>Agronomy</i> , 2021, 11, 1226.	3.0	11
117	Genetic diversity and distinctness based on morphological and SSR markers in peanut. <i>Agronomy Journal</i> , 2021, 113, 4648-4660.	1.8	11
118	Classical and Molecular Approaches for Mapping of Genes and Quantitative Trait Loci in Peanut. <i>Compendium of Plant Genomes</i> , 2017, , 93-116.	0.5	10
119	Thiourea and hydrogen peroxide priming improved K ⁺ retention and source-sink relationship for mitigating salt stress in rice. <i>Scientific Reports</i> , 2021, 11, 3000.	3.3	10
120	Global Transcriptome Profiling Identified Transcription Factors, Biological Process, and Associated Pathways for Pre-Harvest Aflatoxin Contamination in Groundnut. <i>Journal of Fungi (Basel)</i> , 2021, 7, 10297.	0.0	10
121	Genomic insights into the genetic signatures of selection and seed trait loci in cultivated peanut. <i>Journal of Advanced Research</i> , 2022, 42, 237-248.	9.5	10
122	Transcriptional reprogramming and enhanced photosynthesis drive inducible salt tolerance in sugarcane mutant line M4209. <i>Journal of Experimental Botany</i> , 2020, 71, 6159-6173.	4.8	9
123	Groundnut Entered Post-genome Sequencing Era: Opportunities and Challenges in Translating Genomic Information from Genome to Field. , 2018, , 199-209.		8
124	Peanut Seed Coat Acts as a Physical and Biochemical Barrier against <i>Aspergillus flavus</i> Infection. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 1000.	3.5	8
125	Arsenic and cadmium induced macronutrient deficiencies trigger contrasting gene expression changes in rice. <i>Environmental Pollution</i> , 2022, 300, 118923.	7.5	8
126	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.	3.6	8

#	ARTICLE	IF	CITATIONS
127	Identification and validation of novel alleles of rice blast resistant gene Pi54, and analysis of their nucleotide diversity in landraces and wild <i>Oryza</i> species. <i>Euphytica</i> , 2016, 209, 725-737.	1.2	7
128	Current Status and Prospects of Genomic Selection in Legumes. , 2017, , 131-147.		7
129	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.	1.9	7
130	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
131	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.	0.5	6
132	Identification of quantitative trait loci associated with iron deficiency chlorosis resistance in groundnut (<i>Arachis hypogaea</i>). <i>Plant Breeding</i> , 2020, 139, 790-803.	1.9	6
133	Enhancing oleic acid content in two commercially released peanut varieties through marker-assisted backcross breeding. <i>Crop Science</i> , 2021, 61, 2435-2443.	1.8	6
134	Nested Association Mapping (NAM) Populations: Present Status and Future Prospects in the Genomics Era. <i>Critical Reviews in Plant Sciences</i> , 2021, 40, 49-67.	5.7	6
135	Genomic regions associated with resistance to peanut bud necrosis disease (PBNB) in a recombinant inbred line (RIL) population. <i>Plant Breeding</i> , 2019, 138, 748-760.	1.9	5
136	Genetic mapping for grain quality and yield-attributed traits in Basmati rice using SSR-based genetic map. <i>Journal of Biosciences</i> , 2021, 46, 1.	1.1	5
137	Pest and diseases: Old and new threats – Modern breeding tools to tailor new crop cultivars. <i>S&Ceres</i> , 2013, 24, 261-273.	0.1	4
138	Recent Advances in Peanut Breeding and Genetics. , 2016, , 111-145.		4
139	Future Prospects for Peanut Improvement. <i>Compendium of Plant Genomes</i> , 2017, , 165-169.	0.5	3
140	Population Genomics of Peanut. <i>Population Genomics</i> , 2021, , 1.	0.5	3
141	The Peanut Genome: An Introduction. <i>Compendium of Plant Genomes</i> , 2017, , 1-6.	0.5	2
142	G×E interactions in QTL introgression lines of Spanish-type groundnut (<i>Arachis hypogaea</i> L.). <i>Euphytica</i> , 2020, 216, 1.	1.2	2
143	Groundnut. , 2014, , 161-173.		2
144	Genetic Enhancement of Groundnut: Current Status and Future Prospects. , 2022, , 63-110.		2

#	ARTICLE	IF	CITATIONS
145	Genetic mapping of tolerance to iron deficiency chlorosis in peanut (<i>Arachis hypogaea</i> L.). <i>Euphytica</i> , 2022, 218, 1.	1.2	2
146	Genome-wide identification of meiotic recombination hot spots detected by SLAF in peanut (<i>Arachis</i>) Tj ETQq0 0 0 ggBT /Overlock 10 Tf	3.3	0
147	Groundnut Kernel Transcriptome. , 2021, , 528-543.		0