

## List of Publications by Citations

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

98 papers	4,203 citations	35 h-index	63 g-index
101 ext. papers	5,499 ext. citations	6 avg, IF	4.88 L-index

#	Paper	IF	Citations
98	The genome sequences of <i>Arachis duranensis</i> and <i>Arachis ipaensis</i> , the diploid ancestors of cultivated peanut. <i>Nature Genetics</i> , <b>2016</b> , 48, 438-46	36.3	498
97	Achievements and prospects of genomics-assisted breeding in three legume crops of the semi-arid tropics. <i>Biotechnology Advances</i> , <b>2013</b> , 31, 1120-34	17.8	218
96	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , <b>2019</b> , 51, 877-884	36.3	211
95	Advances in <i>Arachis</i> genomics for peanut improvement. <i>Biotechnology Advances</i> , <b>2012</b> , 30, 639-51	17.8	195
94	The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. <i>Nature Genetics</i> , <b>2019</b> , 51, 865-876	36.3	188
93	Utility of EST-derived SSR in cultivated peanut ( <i>Arachis hypogaea</i> L.) and <i>Arachis</i> wild species. <i>BMC Plant Biology</i> , <b>2009</b> , 9, 35	5.3	136
92	A SSR-based composite genetic linkage map for the cultivated peanut ( <i>Arachis hypogaea</i> L.) genome. <i>BMC Plant Biology</i> , <b>2010</b> , 10, 17	5.3	107
91	An integrated genetic linkage map of cultivated peanut ( <i>Arachis hypogaea</i> L.) constructed from two RIL populations. <i>Theoretical and Applied Genetics</i> , <b>2012</b> , 124, 653-64	6	106
90	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> , <b>2017</b> , 7, 40577	4.9	102
89	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> , <b>2017</b> , 15, 927-941	11.6	101
88	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> , <b>2013</b> , 20, 173-84	4.5	99
87	Population structure and marker-trait association analysis of the US peanut ( <i>Arachis hypogaea</i> L.) mini-core collection. <i>Theoretical and Applied Genetics</i> , <b>2011</b> , 123, 1307-17	6	82
86	Peanut gene expression profiling in developing seeds at different reproduction stages during <i>Aspergillus parasiticus</i> infection. <i>BMC Developmental Biology</i> , <b>2008</b> , 8, 12	3.1	82
85	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> , <b>2012</b> , 7, e41213	3.7	80
84	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> , <b>2014</b> , 15, 133	2.6	79
83	Drought stress and preharvest aflatoxin contamination in agricultural commodity: genetics, genomics and proteomics. <i>Journal of Integrative Plant Biology</i> , <b>2008</b> , 50, 1281-91	8.3	77
82	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> , <b>2012</b> , 12, 10	5.3	76

81	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> , <b>2014</b> , 9, e105228	3.7	76
80	Simple sequence repeat markers for botanical varieties of cultivated peanut ( <i>Arachis hypogaea</i> L.). <i>Euphytica</i> , <b>2005</b> , 142, 131-136	2.1	73
79	Environmental influences on maize- <i>Aspergillus flavus</i> interactions and aflatoxin production. <i>Frontiers in Microbiology</i> , <b>2014</b> , 5, 40	5.7	71
78	Monitoring the expression of maize genes in developing kernels under drought stress using oligo-microarray. <i>Journal of Integrative Plant Biology</i> , <b>2010</b> , 52, 1059-74	8.3	66
77	Gene expression profiling and identification of resistance genes to <i>Aspergillus flavus</i> infection in peanut through EST and microarray strategies. <i>Toxins</i> , <b>2011</b> , 3, 737-53	4.9	57
76	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> , <b>2018</b> , 16, 1954-1967	11.6	56
75	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> , <b>2015</b> , 10, e0119454	3.7	51
74	Oxidative stress and carbon metabolism influence <i>Aspergillus flavus</i> transcriptome composition and secondary metabolite production. <i>Scientific Reports</i> , <b>2016</b> , 6, 38747	4.9	47
73	Deciphering drought-induced metabolic responses and regulation in developing maize kernels. <i>Plant Biotechnology Journal</i> , <b>2018</b> , 16, 1616	11.6	45
72	Resistance to <i>Aspergillus flavus</i> in maize and peanut: Molecular biology, breeding, environmental stress, and future perspectives. <i>Crop Journal</i> , <b>2015</b> , 3, 229-237	4.6	45
71	Gene expression profiling in peanut using high density oligonucleotide microarrays. <i>BMC Genomics</i> , <b>2009</b> , 10, 265	4.5	45
70	Responses of to Oxidative Stress Are Related to Fungal Development Regulator, Antioxidant Enzyme, and Secondary Metabolite Biosynthetic Gene Expression. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 2048	5.7	44
69	Molecular Mapping of Oil Content and Fatty Acids Using Dense Genetic Maps in Groundnut (L.). <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 794	6.2	42
68	Genetic Mapping and Quantitative Trait Loci Analysis for Disease Resistance Using F2 and F5 Generation-based Genetic Maps Derived from 'Jifrunner'×'GT-C20' in Peanut. <i>Plant Genome</i> , <b>2013</b> , 6, plantgenome2013.05.0018	4.4	41
67	Proteome analysis of <i>Aspergillus flavus</i> isolate-specific responses to oxidative stress in relationship to aflatoxin production capability. <i>Scientific Reports</i> , <b>2018</b> , 8, 3430	4.9	37
66	Comparative leaf proteomics of drought-tolerant and -susceptible peanut in response to water stress. <i>Journal of Proteomics</i> , <b>2016</b> , 143, 209-226	3.9	37
65	Analysis of Gene Expression Profiles in Leaf Tissues of Cultivated Peanuts and Development of EST-SSR Markers and Gene Discovery. <i>International Journal of Plant Genomics</i> , <b>2009</b> , 2009, 715605		37
64	Co-localization of major quantitative trait loci for pod size and weight to a 3.7cM interval on chromosome A05 in cultivated peanut ( <i>Arachis hypogaea</i> L.). <i>BMC Genomics</i> , <b>2017</b> , 18, 58	4.5	35

63	Genetic Dissection of Novel QTLs for Resistance to Leaf Spots and Tomato Spotted Wilt Virus in Peanut (L.). <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 25	6.2	35
62	Mitigating Aflatoxin Contamination in Groundnut through A Combination of Genetic Resistance and Post-Harvest Management Practices. <i>Toxins</i> , <b>2019</b> , 11,	4.9	34
61	Genome-Wide Discovery of Microsatellite Markers from Diploid Progenitor Species, and , and Their Application in Cultivated Peanut (). <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 1209	6.2	34
60	Translational genomics for achieving higher genetic gains in groundnut. <i>Theoretical and Applied Genetics</i> , <b>2020</b> , 133, 1679-1702	6	31
59	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> , <b>2016</b> , 11, e0158452	3.7	31
58	Root Morphology and Gene Expression Analysis in Response to Drought Stress in Maize ( <i>Zea mays</i> ). <i>Plant Molecular Biology Reporter</i> , <b>2012</b> , 30, 360-369	1.7	28
57	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> , <b>2020</b> , 18, 1457-1471	11.6	28
56	Strategies in Prevention of Preharvest Aflatoxin Contamination in Peanuts: Aflatoxin Biosynthesis, Genetics and Genomics. <i>Peanut Science</i> , <b>2009</b> , 36, 11-20	0.3	27
55	Whole-genome resequencing-based QTL-seq identified AhTc1 gene encoding a R2R3-MYB transcription factor controlling peanut purple testa colour. <i>Plant Biotechnology Journal</i> , <b>2020</b> , 18, 96-105	11.6	27
54	Stress Sensitivity Is Associated with Differential Accumulation of Reactive Oxygen and Nitrogen Species in Maize Genotypes with Contrasting Levels of Drought Tolerance. <i>International Journal of Molecular Sciences</i> , <b>2015</b> , 16, 24791-819	6.3	26
53	Protein profiles reveal diverse responsive signaling pathways in kernels of two maize inbred lines with contrasting drought sensitivity. <i>International Journal of Molecular Sciences</i> , <b>2014</b> , 15, 18892-918	6.3	26
52	Comparative analysis of NBS-LRR genes and their response to <i>Aspergillus flavus</i> in <i>Arachis</i> . <i>PLoS ONE</i> , <b>2017</b> , 12, e0171181	3.7	26
51	Impact of Molecular Genetic Research on Peanut Cultivar Development. <i>Agronomy</i> , <b>2011</b> , 1, 3-17	3.6	25
50	Peanut ( <i>Arachis hypogaea</i> ) Expressed Sequence Tag Project: Progress and Application. <i>Comparative and Functional Genomics</i> , <b>2012</b> , 2012, 373768		25
49	Potential roles of WRKY transcription factors in regulating host defense responses during <i>Aspergillus flavus</i> infection of immature maize kernels. <i>Physiological and Molecular Plant Pathology</i> , <b>2015</b> , 89, 31-40	2.6	24
48	<i>Aspergillus flavus</i> infection triggered immune responses and host-pathogen cross-talks in groundnut during in-vitro seed colonization. <i>Scientific Reports</i> , <b>2017</b> , 7, 9659	4.9	24
47	Functional Biology and Molecular Mechanisms of Host-Pathogen Interactions for Aflatoxin Contamination in Groundnut (L.) and Maize (L.). <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 227	5.7	22
46	Molecular Basis of Root Nodule Symbiosis between and 'Crack-Entry' Legume Groundnut (L.). <i>Plants</i> , <b>2020</b> , 9,	4.5	21

45	Effects of Hydrogen Peroxide on Different Toxigenic and Atoxigenic Isolates of <i>Aspergillus flavus</i> . <i>Toxins</i> , <b>2015</b> , 7, 2985-99	4.9	21
44	<i>Arachis hypogaea</i> gene expression atlas for fastigiata subspecies of cultivated groundnut to accelerate functional and translational genomics applications. <i>Plant Biotechnology Journal</i> , <b>2020</b> , 18, 2187-2200	11.6	19
43	Epigenetics and epigenomics: underlying mechanisms, relevance, and implications in crop improvement. <i>Functional and Integrative Genomics</i> , <b>2020</b> , 20, 739-761	3.8	18
42	Recent Advances in Molecular Genetic Linkage Maps of Cultivated Peanut. <i>Peanut Science</i> , <b>2013</b> , 40, 95-106	10.6	17
41	Metabolomics Intervention Towards Better Understanding of Plant Traits. <i>Cells</i> , <b>2021</b> , 10,	7.9	17
40	Identification and Characterization of a Multigene Family Encoding Germin-Like Proteins in Cultivated Peanut ( <i>Arachis hypogaea</i> L.). <i>Plant Molecular Biology Reporter</i> , <b>2011</b> , 29, 389-403	1.7	15
39	Expression analysis of stress-related genes in kernels of different maize ( <i>Zea mays</i> L.) inbred lines with different resistance to aflatoxin contamination. <i>Toxins</i> , <b>2011</b> , 3, 538-50	4.9	15
38	Evaluation of maize inbred lines for resistance to pre-harvest aflatoxin and fumonisin contamination in the field. <i>Crop Journal</i> , <b>2017</b> , 5, 259-264	4.6	14
37	Proteomic analysis of peanut seed storage proteins and genetic variation in a potential peanut allergen. <i>Protein and Peptide Letters</i> , <b>2008</b> , 15, 567-77	1.9	14
36	Variability in Field Response of Peanut Genotypes from the U.S. and China to Tomato Spotted Wilt Virus and Leaf Spots. <i>Peanut Science</i> , <b>2012</b> , 39, 30-37	0.3	13
35	Genetic linkage maps of white birches ( <i>Betula platyphylla</i> Suk. and <i>B. pendula</i> Roth) based on RAPD and AFLP markers. <i>Molecular Breeding</i> , <b>2011</b> , 27, 347-356	3.4	13
34	Integrated small RNA and mRNA expression profiles reveal miRNAs and their target genes in response to <i>Aspergillus flavus</i> growth in peanut seeds. <i>BMC Plant Biology</i> , <b>2020</b> , 20, 215	5.3	12
33	Identification of Resistance to Aflatoxin Accumulation and Yield Potential in Maize Hybrids in the Southeast Regional Aflatoxin Trials (SERAT). <i>Crop Science</i> , <b>2017</b> , 57, 202-215	2.4	11
32	Identification of expressed resistance gene analogs from peanut ( <i>Arachis hypogaea</i> L.) expressed sequence tags. <i>Journal of Integrative Plant Biology</i> , <b>2013</b> , 55, 453-61	8.3	11
31	A Note on Development of a Low-cost and High-throughput SSR-based Genotyping Method in Peanut ( <i>Arachis hypogaea</i> L.). <i>Peanut Science</i> , <b>2011</b> , 38, 122-127	0.3	11
30	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> , <b>2016</b> , 58, 452-65	8.3	11
29	Classical and Molecular Approaches for Mapping of Genes and Quantitative Trait Loci in Peanut. <i>Compendium of Plant Genomes</i> , <b>2017</b> , 93-116	0.8	10
28	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> , <b>2019</b> , 9, 18246	4.9	10

27	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> , <b>2020</b> , 133, 2239-2257	6	9
26	Phenotypic evaluation of the Chinese mini-mini core collection of peanut ( <i>Arachis hypogaea</i> L.) and assessment for resistance to bacterial wilt disease caused by <i>Ralstonia solanacearum</i> . <i>Plant Genetic Resources: Characterisation and Utilisation</i> , <b>2013</b> , 11, 77-83	1	9
25	Annotation of Trait Loci on Integrated Genetic Maps of <i>Arachis</i> Species <b>2016</b> , 163-207		9
24	Evaluation of maize inbred lines and topcross progeny for resistance to pre-harvest aflatoxin contamination. <i>Crop Journal</i> , <b>2019</b> , 7, 118-125	4.6	8
23	Characterization of Simple Sequence Repeat (SSR) Markers and Genetic Relationships within Cultivated Peanut ( <i>Arachis hypogaea</i> L.). <i>Peanut Science</i> , <b>2011</b> , 38, 1-10	0.3	8
22	Comparison of gene expression profiles in cultivated peanut ( <i>Arachis hypogaea</i> ) under strong artificial selection. <i>Plant Breeding</i> , <b>2012</b> , 131, 620-630	2.4	7
21	Proteomic screening points to the potential importance of Ara h 3 basic subunit in allergenicity of peanut. <i>Inflammation and Allergy: Drug Targets</i> , <b>2008</b> , 7, 163-6		7
20	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> , <b>2019</b> , 294, 365-378	3.1	7
19	Peanut Resistance Gene Expression in Response to <i>Aspergillus flavus</i> Infection During Seed Germination. <i>Journal of Phytopathology</i> , <b>2015</b> , 163, 212-221	1.8	6
18	Draft Genome Sequences of One <i>Aspergillus parasiticus</i> Isolate and Nine <i>Aspergillus flavus</i> Isolates with Varying Stress Tolerance and Aflatoxin Production. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	6
17	Climate-Smart Groundnuts for Achieving High Productivity and Improved Quality: Current Status, Challenges, and Opportunities <b>2019</b> , 133-172		5
16	Genomics of Peanut, a Major Source of Oil and Protein <b>2008</b> , 421-440		5
15	Carbohydrate, glutathione, and polyamine metabolism are central to <i>Aspergillus flavus</i> oxidative stress responses over time. <i>BMC Microbiology</i> , <b>2019</b> , 19, 209	4.5	4
14	History and Impact of the International Peanut Genome Initiative: The Exciting Journey Toward Peanut Whole-Genome Sequencing. <i>Compendium of Plant Genomes</i> , <b>2017</b> , 117-133	0.8	4
13	Two New Reference Genomes Reveal a Large Insertion Potentially Contributing to Isolate Stress Tolerance and Aflatoxin Production. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 3515-3531	3.2	4
12	Transcriptome Analysis Identified Coordinated Control of Key Pathways Regulating Cellular Physiology and Metabolism upon Infection Resulting in Reduced Aflatoxin Production in Groundnut. <i>Journal of Fungi (Basel, Switzerland)</i> , <b>2020</b> , 6,	5.6	3
11	Global Transcriptome Profiling Identified Transcription Factors, Biological Process, and Associated Pathways for Pre-Harvest Aflatoxin Contamination in Groundnut. <i>Journal of Fungi (Basel, Switzerland)</i> , <b>2021</b> , 7,	5.6	3
10	Crop Stress and Aflatoxin Contamination: Perspectives and Prevention Strategies <b>2012</b> , 399-427		2

9	Sensitivity of Isolates from Peanut Seeds in Georgia to Azoxystrobin, a Quinone outside Inhibitor (QoI) Fungicide. <i>Journal of Fungi (Basel, Switzerland)</i> , <b>2021</b> , 7,	5.6	2
8	Evaluation of Elite Maize Inbred Lines for Reduced <i>Aspergillus flavus</i> Infection, Aflatoxin Accumulation, and Agronomic Traits. <i>Crop Science</i> , <b>2019</b> , 59, 2562-2571	2.4	2
7	Identification of QTLs for Seed Dormancy in Cultivated Peanut Using a Recombinant Inbred Line Mapping Population. <i>Plant Molecular Biology Reporter</i> , 1	1.7	2
6	Spatio-temporal patterns of <i>Aspergillus flavus</i> infection and aflatoxin B biosynthesis on maize kernels probed by SWIR hyperspectral imaging and synchrotron FTIR microspectroscopy.. <i>Food Chemistry</i> , <b>2022</b> , 382, 132340	8.5	1
5	Discovery of Major Quantitative Trait Loci and Candidate Genes for Fresh Seed Dormancy in Groundnut. <i>Agronomy</i> , <b>2022</b> , 12, 404	3.6	1
4	Chromatin spatial organization of wild type and mutant peanuts reveals high-resolution genomic architecture and interaction alterations. <i>Genome Biology</i> , <b>2021</b> , 22, 315	18.3	0
3	Lessons Learned: the Importance of Biological Curation. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10, e0047321	1.3	0
2	Recent Advances in Genetics, Genomics, and Breeding for Nutritional Quality in Groundnut <b>2022</b> , 111-137		0
1	De novo QTL-seq Identifies Loci Linked to Blanchability in Peanut ( <i>Arachis hypogaea</i> ) and Refines Previously Identified QTL with Low Coverage Sequence. <i>Agronomy</i> , <b>2021</b> , 11, 2201	3.6	0