

# Andrew D Farmer

## List of Publications by Year in descending order

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81  
papers

13,823  
citations

34105

52  
h-index

64796

79  
g-index

86  
all docs

86  
docs citations

86  
times ranked

16125  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	6.0	1,547
2	The Medicago genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	27.8	1,166
3	Draft genome sequence of chickpea ( <i>Cicer arietinum</i> ) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013, 31, 240-246.	17.5	1,049
4	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.	17.5	788
5	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.	21.4	761
6	RNA-Seq Atlas of <i>Glycine max</i> : A guide to the soybean transcriptome. <i>BMC Plant Biology</i> , 2010, 10, 160.	3.6	634
7	Genome, epigenome and RNA sequences of monozygotic twins discordant for multiple sclerosis. <i>Nature</i> , 2010, 464, 1351-1356.	27.8	463
8	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	21.4	439
9	An integrated transcriptome atlas of the crop model <i>Glycine max</i> , and its use in comparative analyses in plants. <i>Plant Journal</i> , 2010, 63, no-no.	5.7	331
10	Transcriptome and Metabolite Profiling of the Infection Cycle of <i>Zymoseptoria tritici</i> on Wheat Reveals a Biphasic Interaction with Plant Immunity Involving Differential Pathogen Chromosomal Contributions and a Variation on the Hemibiotrophic Lifestyle Definition. <i>Plant Physiology</i> , 2015, 167, 1158-1185.	4.8	301
11	Complete Transcriptome of the Soybean Root Hair Cell, a Single-Cell Model, and Its Alteration in Response to <i>Bradyrhizobium japonicum</i> Infection. <i>Plant Physiology</i> , 2010, 152, 541-552.	4.8	268
12	A gapless genome sequence of the fungus <i>Botrytis cinerea</i> . <i>Molecular Plant Pathology</i> , 2017, 18, 75-89.	4.2	265
13	The genome of cowpea ( <i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019, 98, 767-782.	5.7	264
14	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.	8.3	250
15	The fate of duplicated genes in a polyploid plant genome. <i>Plant Journal</i> , 2013, 73, 143-153.	5.7	243
16	High-throughput SNP discovery through deep resequencing of a reduced representation library to anchor and orient scaffolds in the soybean whole genome sequence. <i>BMC Genomics</i> , 2010, 11, 38.	2.8	242
17	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.	8.3	221
18	Whole-genome nucleotide diversity, recombination, and linkage disequilibrium in the model legume <i>Medicago truncatula</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E864-70.	7.1	220

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19	Genome resources for climate-resilient cowpea, an essential crop for food security. <i>Plant Journal</i> , 2017, 89, 1042-1054.	5.7	199
20	Comparative genomics of the core and accessory genomes of 48 <i>Sinorhizobium</i> strains comprising five genospecies. <i>Genome Biology</i> , 2013, 14, R17.	9.6	164
21	Candidate Genes and Genetic Architecture of Symbiotic and Agronomic Traits Revealed by Whole-Genome, Sequence-Based Association Genetics in <i>Medicago truncatula</i> . <i>PLoS ONE</i> , 2013, 8, e65688.	2.5	156
22	Single-nucleus RNA and ATAC sequencing reveals the impact of chromatin accessibility on gene expression in <i>Arabidopsis</i> roots at the single-cell level. <i>Molecular Plant</i> , 2021, 14, 372-383.	8.3	153
23	Legume information system (LegumeInfo.org): a key component of a set of federated data resources for the legume family. <i>Nucleic Acids Research</i> , 2016, 44, D1181-D1188.	14.5	152
24	Transcriptome sequencing of malignant pleural mesothelioma tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3521-3526.	7.1	143
25	A high-throughput SNP marker system for parental polymorphism screening, and diversity analysis in common bean ( <i>Phaseolus vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 535-548.	3.6	139
26	Meiosis-specific gene discovery in plants: RNA-Seq applied to isolated <i>Arabidopsis</i> male meiocytes. <i>BMC Plant Biology</i> , 2010, 10, 280.	3.6	133
27	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.	3.6	121
28	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.	3.6	120
29	Comprehensive characterization and RNA-Seq profiling of the HD-Zip transcription factor family in soybean ( <i>Glycine max</i> ) during dehydration and salt stress. <i>BMC Genomics</i> , 2014, 15, 950.	2.8	120
30	Prediction of novel miRNAs and associated target genes in <i>Glycine max</i> . <i>BMC Bioinformatics</i> , 2010, 11, S14.	2.6	108
31	Genome and secretome analysis of the hemibiotrophic fungal pathogen, <i>Moniliophthora roreri</i> , which causes frosty pod rot disease of cacao: mechanisms of the biotrophic and necrotrophic phases. <i>BMC Genomics</i> , 2014, 15, 164.	2.8	107
32	Genomic Convergence Analysis of Schizophrenia: mRNA Sequencing Reveals Altered Synaptic Vesicular Transport in Post-Mortem Cerebellum. <i>PLoS ONE</i> , 2008, 3, e3625.	2.5	106
33	The Legume Information System (LIS): an integrated information resource for comparative legume biology. <i>Nucleic Acids Research</i> , 2004, 33, D660-D665.	14.5	104
34	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.	3.6	102
35	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.	3.4	99
36	Complementary genetic and genomic approaches help characterize the linkage group I seed protein QTL in soybean. <i>BMC Plant Biology</i> , 2010, 10, 41.	3.6	96

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37	Interoperability with Moby 1.0–It's better than sharing your toothbrush!. Briefings in Bioinformatics, 2008, 9, 220-231.	6.5	91
38	Polyploidy Did Not Predate the Evolution of Nodulation in All Legumes. PLoS ONE, 2010, 5, e11630.	2.5	88
39	A Comprehensive Transcriptome Assembly of Pigeonpea ( <i>Cajanus cajan</i> L.) using Sanger and Second-Generation Sequencing Platforms. Molecular Plant, 2012, 5, 1020-1028.	8.3	87
40	Comprehensive Transcriptome Assembly of Chickpea ( <i>Cicer arietinum</i> L.) Using Sanger and Next Generation Sequencing Platforms: Development and Applications. PLoS ONE, 2014, 9, e86039.	2.5	87
41	Exploring structural variation and gene family architecture with De Novo assemblies of 15 <i>Medicago</i> genomes. BMC Genomics, 2017, 18, 261.	2.8	87
42	Defining the Transcriptome Assembly and Its Use for Genome Dynamics and Transcriptome Profiling Studies in Pigeonpea ( <i>Cajanus cajan</i> L.). DNA Research, 2011, 18, 153-164.	3.4	85
43	A high-density genetic map of <i>Arachis duranensis</i> , a diploid ancestor of cultivated peanut. BMC Genomics, 2012, 13, 469.	2.8	81
44	A comparative transcriptomic study of an allotetraploid and its diploid progenitors illustrates the unique advantages and challenges of RNA-seq in plant species. American Journal of Botany, 2012, 99, 383-396.	1.7	80
45	Combating a Global Threat to a Clonal Crop: Banana Black Sigatoka Pathogen <i>Pseudocercospora fijiensis</i> (Synonym <i>Mycosphaerella fijiensis</i> ) Genomes Reveal Clues for Disease Control. PLoS Genetics, 2016, 12, e1005876.	3.5	77
46	Whole Genome Sequencing of Elite Rice Cultivars as a Comprehensive Information Resource for Marker Assisted Selection. PLoS ONE, 2015, 10, e0124617.	2.5	72
47	Development of an Alfalfa SNP Array and Its Use to Evaluate Patterns of Population Structure and Linkage Disequilibrium. PLoS ONE, 2014, 9, e84329.	2.5	71
48	Population Genomics of the Facultatively Mutualistic Bacteria <i>Sinorhizobium meliloti</i> and <i>S. medicae</i> . PLoS Genetics, 2012, 8, e1002868.	3.5	69
49	The transcriptome landscape of early maize meiosis. BMC Plant Biology, 2014, 14, 118.	3.6	66
50	Management of High-Throughput DNA Sequencing Projects: Alpheus. Journal of Computer Science and Systems Biology, 2008, 01, 132.	0.0	65
51	Identification of candidate genes in rice for resistance to sheath blight disease by whole genome sequencing. Theoretical and Applied Genetics, 2012, 124, 63-74.	3.6	58
52	Comparisons of De Novo Transcriptome Assemblers in Diploid and Polyploid Species Using Peanut ( <i>Arachis</i> spp.) RNA-Seq Data. PLoS ONE, 2014, 9, e115055.	2.5	54
53	Comparative genomic analysis of two <i>Burkholderia glumae</i> strains from different geographic origins reveals a high degree of plasticity in genome structure associated with genomic islands. Molecular Genetics and Genomics, 2013, 288, 195-203.	2.1	53
54	Prevalence of single nucleotide polymorphism among 27 diverse alfalfa genotypes as assessed by transcriptome sequencing. BMC Genomics, 2012, 13, 568.	2.8	52

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55	Phylogenetic Signal Variation in the Genomes of <i>Medicago</i> (Fabaceae). <i>Systematic Biology</i> , 2013, 62, 424-438.	5.6	51
56	Multiple post-domestication origins of <i>Cicer kabuli</i> chickpea through allelic variation in a diversification-associated transcription factor. <i>New Phytologist</i> , 2016, 211, 1440-1451.	7.3	51
57	Making a chocolate chip: development and evaluation of a 6K SNP array for <i>Theobroma cacao</i> . <i>DNA Research</i> , 2015, 22, 279-291.	3.4	46
58	An Integrative Approach to Genomic Introgression Mapping. <i>Plant Physiology</i> , 2010, 154, 3-12.	4.8	45
59	A genome-wide association and meta-analysis reveal regions associated with seed size in cowpea [ <i>Vigna unguiculata</i> (L.) Walp]. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3079-3087.	3.6	42
60	Genomics-assisted characterization of a breeding collection of <i>Apios americana</i> , an edible tuberous legume. <i>Scientific Reports</i> , 2016, 6, 34908.	3.3	40
61	The genome of a wild <i>Medicago</i> species provides insights into the tolerant mechanisms of legume forage to environmental stress. <i>BMC Biology</i> , 2021, 19, 96.	3.8	39
62	Genetic mapping of legume orthologs reveals high conservation of synteny between lentil species and the sequenced genomes of <i>Medicago</i> and chickpea. <i>Frontiers in Plant Science</i> , 2014, 5, 676.	3.6	38
63	Next-generation transcriptome sequencing, SNP discovery and validation in four market classes of peanut, <i>Arachis hypogaea</i> L.. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1169-1180.	2.1	38
64	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.	1.7	34
65	Vision, challenges and opportunities for a Plant Cell Atlas. <i>ELife</i> , 2021, 10, .	6.0	31
66	Ararport Lives: An Updated Framework for Arabidopsis Bioinformatics. <i>Plant Cell</i> , 2020, 32, 2683-2686.	6.6	28
67	Genome Context Viewer: visual exploration of multiple annotated genomes using microsynteny. <i>Bioinformatics</i> , 2018, 34, 1562-1564.	4.1	26
68	Identification and mapping of conserved ortholog set (COS) II sequences of cacao and their conversion to SNP markers for marker-assisted selection in <i>Theobroma cacao</i> and comparative genomics studies. <i>Tree Genetics and Genomes</i> , 2012, 8, 97-111.	1.6	25
69	The plant-specific protein FEHLSTART controls male meiotic entry, initializing meiotic synchronization in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2015, 84, 659-671.	5.7	25
70	Venturing Beyond Beans and Peas: What Can We Learn from <i>Chamaecrista</i> ? <i>Plant Physiology</i> , 2009, 151, 1041-1047.	4.8	23
71	Gene expression patterns are correlated with genomic and genic structure in soybean. <i>Genome</i> , 2011, 54, 10-18.	2.0	23
72	Characterization of a set of novel meiotically-active promoters in <i>Arabidopsis</i> . <i>BMC Plant Biology</i> , 2012, 12, 104.	3.6	22

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73	Phytophthora functional genomics database (PFGD): functional genomics of phytophthora-plant interactions. <i>Nucleic Acids Research</i> , 2006, 34, D465-D470.	14.5	20
74	The legume information system and associated online genomic resources. , 2021, 3, e74.		12
75	Alfalfa ( <i>Medicago sativa</i> ) <i>pho2</i> mutant plants hyperaccumulate phosphate. <i>G3: Genes, Genomes, Genetics</i> , 2022, , .	1.8	10
76	Soybean root hairs: A valuable system to investigate plant biology at the cellular level. <i>Plant Signaling and Behavior</i> , 2010, 5, 419-421.	2.4	8
77	Leveraging Model Legume Information to Find Candidate Genes for Soybean Sudden Death Syndrome Using the Legume Information System. , 2007, 406, 245-259.		6
78	A transcriptome-SNP-derived linkage map of <i>Apios americana</i> (potato bean) provides insights about genome re-organization and synteny conservation in the phaseoloid legumes. <i>Theoretical and Applied Genetics</i> , 2018, 131, 333-351.	3.6	5
79	The Generation Challenge Programme Platform: Semantic Standards and Workbench for Crop Science. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-6.	2.2	5
80	Keeping an Eye on Biology. <i>Science</i> , 2013, 339, 408-409.	12.6	3
81	Targeted Mutagenesis of Alfalfa. <i>Compendium of Plant Genomes</i> , 2021, , 271-283.	0.5	3