

Andrew D Farmer

List of Publications by Year in descending order

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Version: 2024-02-01

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	Alfalfa (<i>Medicago sativa</i> L.) <i>pho2</i> mutant plants hyperaccumulate phosphate. <i>G3: Genes, Genomes, Genetics</i> , 2022, , .	1.8	10
2	Targeted Mutagenesis of Alfalfa. <i>Compendium of Plant Genomes</i> , 2021, , 271-283.	0.5	3
3	The legume information system and associated online genomic resources. , 2021, 3, e74.		12
4	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
5	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
6	Vision, challenges and opportunities for a Plant Cell Atlas. <i>ELife</i> , 2021, 10, .	6.0	31
7	Araport Lives: An Updated Framework for <i>Arabidopsis</i> Bioinformatics. <i>Plant Cell</i> , 2020, 32, 2683-2686.	6.6	28
8	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
9	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	21.4	439
10	The genome of cowpea (<i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019, 98, 767-782.	5.7	264
11	Genome Context Viewer: visual exploration of multiple annotated genomes using microsynteny. <i>Bioinformatics</i> , 2018, 34, 1562-1564.	4.1	26
12	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
13	A gapless genome sequence of the fungus <i>Botrytis cinerea</i> . <i>Molecular Plant Pathology</i> , 2017, 18, 75-89.	4.2	265
14	Exploring structural variation and gene family architecture with De Novo assemblies of 15 <i>Medicago</i> genomes. <i>BMC Genomics</i> , 2017, 18, 261.	2.8	87
15	Genome resources for climate-resilient cowpea, an essential crop for food security. <i>Plant Journal</i> , 2017, 89, 1042-1054.	5.7	199
16	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	6.0	1,547
17	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.	7.3	51
18	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

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19	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
20	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
21	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. <i>PLoS Genetics</i> , 2016, 12, e1005876.	3.5	77
22	The plant-specific protein FEHLSTART controls male meiotic entry, initializing meiotic synchronization in <i>A. rabidopsis</i> . <i>Plant Journal</i> , 2015, 84, 659-671.	5.7	25
23	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
24	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
25	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
26	Whole Genome Sequencing of Elite Rice Cultivars as a Comprehensive Information Resource for Marker Assisted Selection. <i>PLoS ONE</i> , 2015, 10, e0124617.	2.5	72
27	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
28	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
29	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
30	The transcriptome landscape of early maize meiosis. <i>BMC Plant Biology</i> , 2014, 14, 118.	3.6	66
31	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.	2.5	87
32	Development of an Alfalfa SNP Array and Its Use to Evaluate Patterns of Population Structure and Linkage Disequilibrium. <i>PLoS ONE</i> , 2014, 9, e84329.	2.5	71
33	Comparisons of De Novo Transcriptome Assemblers in Diploid and Polyploid Species Using Peanut (<i>Arachis</i> spp.) RNA-Seq Data. <i>PLoS ONE</i> , 2014, 9, e115055.	2.5	54
34	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
35	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
36	Phylogenetic Signal Variation in the Genomes of <i>Medicago</i> (Fabaceae). <i>Systematic Biology</i> , 2013, 62, 424-438.	5.6	51

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37	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
38	The fate of duplicated genes in a polyploid plant genome. <i>Plant Journal</i> , 2013, 73, 143-153.	5.7	243
39	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. <i>Molecular Genetics and Genomics</i> , 2013, 288, 195-203.	2.1	53
40	Keeping an Eye on Biology. <i>Science</i> , 2013, 339, 408-409.	12.6	3
41	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
42	A comparative transcriptomic study of an allotetraploid and its diploid progenitors illustrates the unique advantages and challenges of RNA-seq in plant species. <i>American Journal of Botany</i> , 2012, 99, 383-396.	1.7	80
43	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
44	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
45	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.	8.3	87
46	A high-density genetic map of <i>Arachis duranensis</i> , a diploid ancestor of cultivated peanut. <i>BMC Genomics</i> , 2012, 13, 469.	2.8	81
47	Prevalence of single nucleotide polymorphism among 27 diverse alfalfa genotypes as assessed by transcriptome sequencing. <i>BMC Genomics</i> , 2012, 13, 568.	2.8	52
48	Characterization of a set of novel meiotically-active promoters in <i>Arabidopsis</i> . <i>BMC Plant Biology</i> , 2012, 12, 104.	3.6	22
49	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
50	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
51	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
52	Identification of candidate genes in rice for resistance to sheath blight disease by whole genome sequencing. <i>Theoretical and Applied Genetics</i> , 2012, 124, 63-74.	3.6	58
53	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
54	Population Genomics of the Facultatively Mutualistic Bacteria <i>Sinorhizobium meliloti</i> and <i>S. medicae</i> . <i>PLoS Genetics</i> , 2012, 8, e1002868.	3.5	69

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55	Whole-genome nucleotide diversity, recombination, and linkage disequilibrium in the model legume <i>Medicago truncatula</i> . Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E864-70.	7.1	220
56	Gene expression patterns are correlated with genomic and genic structure in soybean. Genome, 2011, 54, 10-18.	2.0	23
57	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
58	The Medicago genome provides insight into the evolution of rhizobial symbioses. Nature, 2011, 480, 520-524.	27.8	1,166
59	Large-scale transcriptome analysis in chickpea (<i>Cicer arietinum</i> L.), an orphan legume crop of the semi-arid tropics of Asia and Africa. Plant Biotechnology Journal, 2011, 9, 922-931.	8.3	250
60	Development and use of genic molecular markers (GMMs) for construction of a transcript map of chickpea (<i>Cicer arietinum</i> L.). Theoretical and Applied Genetics, 2011, 122, 1577-1589.	3.6	120
61	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.). BMC Plant Biology, 2011, 11, 56.	3.6	121
62	Prediction of novel miRNAs and associated target genes in Glycine max. BMC Bioinformatics, 2010, 11, S14.	2.6	108
63	High-throughput SNP discovery through deep resequencing of a reduced representation library to anchor and orient scaffolds in the soybean whole genome sequence. BMC Genomics, 2010, 11, 38.	2.8	242
64	RNA-Seq Atlas of Glycine max: A guide to the soybean transcriptome. BMC Plant Biology, 2010, 10, 160.	3.6	634
65	Meiosis-specific gene discovery in plants: RNA-Seq applied to isolated Arabidopsis male meiocytes. BMC Plant Biology, 2010, 10, 280.	3.6	133
66	Complementary genetic and genomic approaches help characterize the linkage group I seed protein QTL in soybean. BMC Plant Biology, 2010, 10, 41.	3.6	96
67	An integrated transcriptome atlas of the crop model Glycine max, and its use in comparative analyses in plants. Plant Journal, 2010, 63, no-no.	5.7	331
68	Genome, epigenome and RNA sequences of monozygotic twins discordant for multiple sclerosis. Nature, 2010, 464, 1351-1356.	27.8	463
69	Complete Transcriptome of the Soybean Root Hair Cell, a Single-Cell Model, and Its Alteration in Response to <i>Bradyrhizobium japonicum</i> Infection. Plant Physiology, 2010, 152, 541-552.	4.8	268
70	An Integrative Approach to Genomic Introgression Mapping. Plant Physiology, 2010, 154, 3-12.	4.8	45
71	Soybean root hairs: A valuable system to investigate plant biology at the cellular level. Plant Signaling and Behavior, 2010, 5, 419-421.	2.4	8
72	Polyploidy Did Not Predate the Evolution of Nodulation in All Legumes. PLoS ONE, 2010, 5, e11630.	2.5	88

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73	Venturing Beyond Beans and Peas: What Can We Learn from <i>Chamaecrista</i> ? Plant Physiology, 2009, 151, 1041-1047.	4.8	23
74	Transcriptome sequencing of malignant pleural mesothelioma tumors. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3521-3526.	7.1	143
75	Interoperability with Moby 1.0--It's better than sharing your toothbrush!. Briefings in Bioinformatics, 2008, 9, 220-231.	6.5	91
76	Genomic Convergence Analysis of Schizophrenia: mRNA Sequencing Reveals Altered Synaptic Vesicular Transport in Post-Mortem Cerebellum. PLoS ONE, 2008, 3, e3625.	2.5	106
77	The Generation Challenge Programme Platform: Semantic Standards and Workbench for Crop Science. International Journal of Plant Genomics, 2008, 2008, 1-6.	2.2	5
78	Management of High-Throughput DNA Sequencing Projects: Alpheus. Journal of Computer Science and Systems Biology, 2008, 01, 132.	0.0	65
79	Leveraging Model Legume Information to Find Candidate Genes for Soybean Sudden Death Syndrome Using the Legume Information System. , 2007, 406, 245-259.		6
80	Phytophthora functional genomics database (PFGD): functional genomics of phytophthora-plant interactions. Nucleic Acids Research, 2006, 34, D465-D470.	14.5	20
81	The Legume Information System (LIS): an integrated information resource for comparative legume biology. Nucleic Acids Research, 2004, 33, D660-D665.	14.5	104