Steven B Cannon

List of Publications by Year
in descending order

69 papers	14,932 citations	101543 36 h-index	110387 64 g-index
76 all docs	76 docs citations	76 times ranked	11801 citing authors

#	Article	IF	Citations
1	Genome-wide approaches delineate the additive, epistatic, and pleiotropic nature of variants controlling fatty acid composition in peanut (<i>Arachis hypogaea</i> L.). G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	5
2	Doing Genetic and Genomic Biology Using the Legume Information System and Associated Resources. Methods in Molecular Biology, 2022, 2443, 81-100.	0.9	6
3	Phylogenomics of the genus Glycine sheds light on polyploid evolution and life-strategy transition. Nature Plants, 2022, 8, 233-244.	9.3	26
4	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. Scientific Data, 2021, 8, 50.	5.3	38
5	The legume information system and associated online genomic resources. , 2021, 3, e74.		12
6	A better mousetrap to guard against anthracnose disease in bean. Journal of Experimental Botany, 2021, 72, 3487-3488.	4.8	0
7	An accumulation of genetic variation and selection across the disease-related genes during apple domestication. Tree Genetics and Genomes, 2021, 17, 1.	1.6	10
8	Predictions from algorithmic modeling result in better decisions than from data modeling for soybean iron deficiency chlorosis. PLoS ONE, 2021, 16, e0240948.	2.5	2
9	Legacy genetics of <i>Arachis cardenasii</i> in the peanut crop shows the profound benefits of international seed exchange. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	18
10	Dissecting the Root Phenotypic and Genotypic Variability of the Iowa Mung Bean Diversity Panel. Frontiers in Plant Science, 2021, 12, 808001.	3.6	4
11	Genotypic Characterization of the U.S. Peanut Core Collection. G3: Genes, Genomes, Genetics, 2020, 10, 4013-4026.	1.8	14
12	GCViT: a method for interactive, genome-wide visualization of resequencing and SNP array data. BMC Genomics, 2020, 21, 822.	2.8	4
13	Family-Specific Gains and Losses of Protein Domains in the Legume and Grass Plant Families. Evolutionary Bioinformatics, 2020, 16, 117693432093994.	1.2	2
14	The First Genetic Map for a Psoraleoid Legume (Bituminaria bituminosa) Reveals Highly Conserved Synteny with Phaseoloid Legumes. Plants, 2020, 9, 973.	3.5	2
15	Evaluating two different models of peanutâ€™s origin. Nature Genetics, 2020, 52, 557-559.	21.4	22
16	Chromosomal Structure, History, and Genomic Synteny Relationships in Lupinus. Compendium of Plant Genomes, 2020, , 87-94.	0.5	1
17	Construction and comparison of three referenceâ€quality genome assemblies for soybean. Plant Journal, 2019, 100, 1066-1082.	5.7	113
18	Cercis: A Non-polyploid Genomic Relic Within the Generally Polyploid Legume Family. Frontiers in Plant Science, 2019, 10, 345.	3.6	25

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19	Genome-wide associations and epistatic interactions for internode number, plant height, seed weight and seed yield in soybean. BMC Genomics, 2019, 20, 527.	2.8	59
20	Evaluation of linkage disequilibrium, population structure, and genetic diversity in the U.S. peanut mini core collection. BMC Genomics, 2019, 20, 481.	2.8	39
21	The genome sequence of segmental allotetraploid peanut Arachis hypogaea. Nature Genetics, 2019, 51, 877-884.	21.4	439
22	The genome of cowpea (<i>Vigna unguiculata</i> [L.] Walp.). Plant Journal, 2019, 98, 767-782.	5.7	264
23	Reconstruction of ancestral genome reveals chromosome evolution history for selected legume species. New Phytologist, 2019, 223, 2090-2103.	7.3	40
24	A reference-grade wild soybean genome. Nature Communications, 2019, 10, 1216.	12.8	183
25	A review of breeding objectives, genomic resources, and marker-assisted methods in common bean (Phaseolus vulgaris L.). Molecular Breeding, 2019, 39, 1.	2.1	72
26	The future of legume genetic data resources: Challenges, opportunities, and priorities. , 2019, 1, e16.		30
27	A transcriptome-SNP-derived linkage map of Apios americana (potato bean) provides insights about genome re-organization and synteny conservation in the phaseoloid legumes. Theoretical and Applied Genetics, 2018, 131, 333-351.	3.6	5
28	Ten quick tips for sharing open genomic data. PLoS Computational Biology, 2018, 14, e1006472.	3.2	8
29	A Mechanism for Genome Size Reduction Following Genomic Rearrangements. Frontiers in Genetics, 2018, 9, 454.	2.3	23
30	Uneven recombination rate and linkage disequilibrium across a reference SNP map for common bean (Phaseolus vulgaris L.). PLoS ONE, 2018, 13, e0189597.	2.5	108
31	Improving adaptation to drought stress in white pea bean (<i>Phaseolus vulgaris</i> L.): Genotypic effects on grain yield, yield components and pod harvest index. Plant Breeding, 2017, 136, 548-561.	1.9	36
32	A comprehensive draft genome sequence for lupin (<i>Lupinus angustifolius</i>), an emerging health food: insights into plant–microbe interactions and legume evolution. Plant Biotechnology Journal, 2017, 15, 318-330.	8.3	153
33	Genomics Resources for Peanut Improvement. Compendium of Plant Genomes, 2017, , 69-91.	0.5	7
34	Dynamic transcriptome profiling of Bean Common Mosaic Virus (BCMV) infection in Common Bean (Phaseolus vulgaris L.). BMC Genomics, 2016, 17, 613.	2.8	30
35	PeanutBase and Other Bioinformatic Resources for Peanut. , 2016, , 241-252.		46
36	Characterization and development mechanism of Apios americana tuber starch. Carbohydrate Polymers, 2016, 151, 198-205.	10.2	12

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37	Genomics-assisted characterization of a breeding collection of Apios americana, an edible tuberous legume. Scientific Reports, 2016, 6, 34908.	3.3	40
38	Legume information system (LegumeInfo.org): a key component of a set of federated data resources for the legume family. Nucleic Acids Research, 2016, 44, D1181-D1188.	14.5	152
39	The genome sequences of Arachis duranensis and Arachis ipaensis, the diploid ancestors of cultivated peanut. Nature Genetics, 2016, 48, 438-446.	21.4	761
40	Evaluation of Phenotypic Variation in a Collection of <i>Apios americana</i>: An Edible Tuberous Legume. Crop Science, 2015, 55, 712-726.	1.8	10
41	An ontology approach to comparative phenomics in plants. Plant Methods, 2015, 11, 10.	4.3	53
42	Multiple Polyploidy Events in the Early Radiation of Nodulating and Nonnodulating Legumes. Molecular Biology and Evolution, 2015, 32, 193-210.	8.9	223
43	Comprehensive characterization and RNA-Seq profiling of the HD-Zip transcription factor family in soybean (Glycine max) during dehydration and salt stress. BMC Genomics, 2014, 15, 950.	2.8	120
44	A Roadmap for Functional Structural Variants in the Soybean Genome. G3: Genes, Genomes, Genetics, 2014, 4, 1307-1318.	1.8	42
45	A reference genome for common bean and genome-wide analysis of dual domestications. Nature Genetics, 2014, 46, 707-713.	21.4	1,159
46	Draft genome sequence of chickpea (Cicer arietinum) provides a resource for trait improvement. Nature Biotechnology, 2013, 31, 240-246.	17.5	1,049
47	The Model Legume Genomes. Methods in Molecular Biology, 2013, 1069, 1-14.	0.9	11
48	SoyBase and the Legume Information System: Accessing Information about the Soybean and Other Legume Genomes. , 2012, , 53-66.		3
49	Gene expression patterns are correlated with genomic and genic structure in soybean. Genome, 2011, 54, 10-18.	2.0	23
50	The Medicago genome provides insight into the evolution of rhizobial symbioses. Nature, 2011, 480, 520-524.	27.8	1,166
51	Chromosome Visualization Tool: A Whole Genome Viewer. International Journal of Plant Genomics, 2011, 2011, 1-4.	2.2	37
52	RNA-Seq Atlas of Glycine max: A guide to the soybean transcriptome. BMC Plant Biology, 2010, 10, 160.	3.6	634
53	Genome sequence of the palaeopolyploid soybean. Nature, 2010, 463, 178-183.	27.8	3,854
54	SoyBase, the USDA-ARS soybean genetics and genomics database. Nucleic Acids Research, 2010, 38, D843-D846.	14.5	553

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55	Polyploidy Did Not Predate the Evolution of Nodulation in All Legumes. PLoS ONE, 2010, 5, e11630.	2.5	88
56	Venturing Beyond Beans and Peas: What Can We Learn from *Chamaecrista*?. Plant Physiology, 2009, 151, 1041-1047.	4.8	23
57	A Nomadic Subtelomeric Disease Resistance Gene Cluster in Common Bean Â. Plant Physiology, 2009, 151, 1048-1065.	4.8	121
58	An analysis of synteny of Arachis with Lotus and Medicago sheds new light on the structure, stability and evolution of legume genomes.. BMC Genomics, 2009, 10, 45.	2.8	125
59	Three Sequenced Legume Genomes and Many Crop Species: Rich Opportunities for Translational Genomics. Plant Physiology, 2009, 151, 970-977.	4.8	122
60	Differential Accumulation of Retroelements and Diversification of NB-LRR Disease Resistance Genes in Duplicated Regions following Polyploidy in the Ancestor of Soybean Â. Plant Physiology, 2008, 148, 1740-1759.	4.8	140
61	Identification and Characterization of Nucleotide-Binding Site-Leucine-Rich Repeat Genes in the Model Plant *Medicago truncatula* Â. Plant Physiology, 2008, 146, 5-21.	4.8	295
62	Taking the First Steps towards a Standard for Reporting on Phylogenies: Minimum Information about a Phylogenetic Analysis (MIAPA). OMICS A Journal of Integrative Biology, 2006, 10, 231-237.	2.0	76
63	Legume genome evolution viewed through the Medicago truncatula and Lotus japonicus genomes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14959-14964.	7.1	286
64	Highly syntenic regions in the genomes of soybean, Medicago truncatula, and Arabidopsis thaliana. BMC Plant Biology, 2005, 5, 15.	3.6	86
65	Databases and Information Integration for the Medicago truncatula Genome and Transcriptome. Plant Physiology, 2005, 138, 38-46.	4.8	59
66	The roles of segmental and tandem gene duplication in the evolution of large gene families in Arabidopsis thaliana. BMC Plant Biology, 2004, 4, 10.	3.6	1,523
67	OrthoParaMap: distinguishing orthologs from paralogs by integrating comparative genome data and gene phylogenies. BMC Bioinformatics, 2003, 4, 35.	2.6	56
68	DiagHunter and GenoPix2D: programs for genomic comparisons, large-scale homology discovery and visualization. Genome Biology, 2003, 4, R68.	9.6	52
69	Diversity, Distribution, and Ancient Taxonomic Relationships Within the TIR and Non-TIR NBS-LRR Resistance Gene Subfamilies. Journal of Molecular Evolution, 2002, 54, 548-562.	1.8	126