

Steven B Cannon

List of Publications by Year in descending order

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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 sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	27.8	3,854
2	The roles of segmental and tandem gene duplication in the evolution of large gene families in <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2004, 4, 10.	3.6	1,523
3	The <i>Medicago</i> genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	27.8	1,166
4	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014, 46, 707-713.	21.4	1,159
5	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
6	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
7	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
8	SoyBase, the USDA-ARS soybean genetics and genomics database. <i>Nucleic Acids Research</i> , 2010, 38, D843-D846.	14.5	553
9	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	21.4	439
10	Identification and Characterization of Nucleotide-Binding Site-Leucine-Rich Repeat Genes in the Model Plant <i>Medicago truncatula</i> . <i>Plant Physiology</i> , 2008, 146, 5-21.	4.8	295
11	Legume genome evolution viewed through the <i>Medicago truncatula</i> and <i>Lotus japonicus</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14959-14964.	7.1	286
12	The genome of cowpea (<i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019, 98, 767-782.	5.7	264
13	Multiple Polyploidy Events in the Early Radiation of Nodulating and Nonnodulating Legumes. <i>Molecular Biology and Evolution</i> , 2015, 32, 193-210.	8.9	223
14	A reference-grade wild soybean genome. <i>Nature Communications</i> , 2019, 10, 1216.	12.8	183
15	A comprehensive draft genome sequence for lupin (<i>Lupinus angustifolius</i>), an emerging health food: insights into plant-microbe interactions and legume evolution. <i>Plant Biotechnology Journal</i> , 2017, 15, 318-330.	8.3	153
16	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
17	Differential Accumulation of Retroelements and Diversification of NB-LRR Disease Resistance Genes in Duplicated Regions following Polyploidy in the Ancestor of Soybean. <i>Plant Physiology</i> , 2008, 148, 1740-1759.	4.8	140
18	Diversity, Distribution, and Ancient Taxonomic Relationships Within the TIR and Non-TIR NBS-LRR Resistance Gene Subfamilies. <i>Journal of Molecular Evolution</i> , 2002, 54, 548-562.	1.8	126

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19	An analysis of synteny of <i>Arachis</i> with <i>Lotus</i> and <i>Medicago</i> sheds new light on the structure, stability and evolution of legume genomes.. <i>BMC Genomics</i> , 2009, 10, 45.	2.8	125
20	Three Sequenced Legume Genomes and Many Crop Species: Rich Opportunities for Translational Genomics. <i>Plant Physiology</i> , 2009, 151, 970-977.	4.8	122
21	A Nomadic Subtelomeric Disease Resistance Gene Cluster in Common Bean \hat{A} . <i>Plant Physiology</i> , 2009, 151, 1048-1065.	4.8	121
22	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
23	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	5.7	113
24	Uneven recombination rate and linkage disequilibrium across a reference SNP map for common bean (<i>Phaseolus vulgaris</i> L.). <i>PLoS ONE</i> , 2018, 13, e0189597.	2.5	108
25	Polyploidy Did Not Predate the Evolution of Nodulation in All Legumes. <i>PLoS ONE</i> , 2010, 5, e11630.	2.5	88
26	Highly syntenic regions in the genomes of soybean, <i>Medicago truncatula</i> , and <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2005, 5, 15.	3.6	86
27	Taking the First Steps towards a Standard for Reporting on Phylogenies: Minimum Information about a Phylogenetic Analysis (MIAPA). <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 231-237.	2.0	76
28	A review of breeding objectives, genomic resources, and marker-assisted methods in common bean (<i>Phaseolus vulgaris</i> L.). <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	72
29	Databases and Information Integration for the <i>Medicago truncatula</i> Genome and Transcriptome. <i>Plant Physiology</i> , 2005, 138, 38-46.	4.8	59
30	Genome-wide associations and epistatic interactions for internode number, plant height, seed weight and seed yield in soybean. <i>BMC Genomics</i> , 2019, 20, 527.	2.8	59
31	OrthoParaMap: distinguishing orthologs from paralogs by integrating comparative genome data and gene phylogenies. <i>BMC Bioinformatics</i> , 2003, 4, 35.	2.6	56
32	An ontology approach to comparative phenomics in plants. <i>Plant Methods</i> , 2015, 11, 10.	4.3	53
33	DiagHunter and GenoPix2D: programs for genomic comparisons, large-scale homology discovery and visualization. <i>Genome Biology</i> , 2003, 4, R68.	9.6	52
34	PeanutBase and Other Bioinformatic Resources for Peanut. , 2016, , 241-252.		46
35	A Roadmap for Functional Structural Variants in the Soybean Genome. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1307-1318.	1.8	42
36	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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37	Reconstruction of ancestral genome reveals chromosome evolution history for selected legume species. <i>New Phytologist</i> , 2019, 223, 2090-2103.	7.3	40
38	Evaluation of linkage disequilibrium, population structure, and genetic diversity in the U.S. peanut mini core collection. <i>BMC Genomics</i> , 2019, 20, 481.	2.8	39
39	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. <i>Scientific Data</i> , 2021, 8, 50.	5.3	38
40	Chromosome Visualization Tool: A Whole Genome Viewer. <i>International Journal of Plant Genomics</i> , 2011, 2011, 1-4.	2.2	37
41	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. <i>Plant Breeding</i> , 2017, 136, 548-561.	1.9	36
42	Dynamic transcriptome profiling of Bean Common Mosaic Virus (BCMV) infection in Common Bean (<i>Phaseolus vulgaris</i> L.). <i>BMC Genomics</i> , 2016, 17, 613.	2.8	30
43	The future of legume genetic data resources: Challenges, opportunities, and priorities. , 2019, 1, e16.		30
44	Phylogenomics of the genus <i>Glycine</i> sheds light on polyploid evolution and life-strategy transition. <i>Nature Plants</i> , 2022, 8, 233-244.	9.3	26
45	<i>Cercis</i> : A Non-polyploid Genomic Relic Within the Generally Polyploid Legume Family. <i>Frontiers in Plant Science</i> , 2019, 10, 345.	3.6	25
46	Venturing Beyond Beans and Peas: What Can We Learn from <i>Chamaecrista</i> ?. <i>Plant Physiology</i> , 2009, 151, 1041-1047.	4.8	23
47	Gene expression patterns are correlated with genomic and genic structure in soybean. <i>Genome</i> , 2011, 54, 10-18.	2.0	23
48	A Mechanism for Genome Size Reduction Following Genomic Rearrangements. <i>Frontiers in Genetics</i> , 2018, 9, 454.	2.3	23
49	Evaluating two different models of peanut's origin. <i>Nature Genetics</i> , 2020, 52, 557-559.	21.4	22
50	Legacy genetics of <i>Arachis cardenasii</i> in the peanut crop shows the profound benefits of international seed exchange. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	18
51	Genotypic Characterization of the U.S. Peanut Core Collection. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4013-4026.	1.8	14
52	Characterization and development mechanism of <i>Apios americana</i> tuber starch. <i>Carbohydrate Polymers</i> , 2016, 151, 198-205.	10.2	12
53	The legume information system and associated online genomic resources. , 2021, 3, e74.		12
54	The Model Legume Genomes. <i>Methods in Molecular Biology</i> , 2013, 1069, 1-14.	0.9	11

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55	Evaluation of Phenotypic Variation in a Collection of <i>Apios americana</i> : An Edible Tuberos Legume. <i>Crop Science</i> , 2015, 55, 712-726.	1.8	10
56	An accumulation of genetic variation and selection across the disease-related genes during apple domestication. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	1.6	10
57	Ten quick tips for sharing open genomic data. <i>PLoS Computational Biology</i> , 2018, 14, e1006472.	3.2	8
58	Genomics Resources for Peanut Improvement. <i>Compendium of Plant Genomes</i> , 2017, , 69-91.	0.5	7
59	Doing Genetic and Genomic Biology Using the Legume Information System and Associated Resources. <i>Methods in Molecular Biology</i> , 2022, 2443, 81-100.	0.9	6
60	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
61	Genome-wide approaches delineate the additive, epistatic, and pleiotropic nature of variants controlling fatty acid composition in peanut (<i>Arachis hypogaea</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	5
62	GCViT: a method for interactive, genome-wide visualization of resequencing and SNP array data. <i>BMC Genomics</i> , 2020, 21, 822.	2.8	4
63	Dissecting the Root Phenotypic and Genotypic Variability of the Iowa Mung Bean Diversity Panel. <i>Frontiers in Plant Science</i> , 2021, 12, 808001.	3.6	4
64	SoyBase and the Legume Information System: Accessing Information about the Soybean and Other Legume Genomes. , 2012, , 53-66.		3
65	Family-Specific Gains and Losses of Protein Domains in the Legume and Grass Plant Families. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432093994.	1.2	2
66	The First Genetic Map for a Psoraleoid Legume (<i>Bituminaria bituminosa</i>) Reveals Highly Conserved Synteny with Phaseoloid Legumes. <i>Plants</i> , 2020, 9, 973.	3.5	2
67	Predictions from algorithmic modeling result in better decisions than from data modeling for soybean iron deficiency chlorosis. <i>PLoS ONE</i> , 2021, 16, e0240948.	2.5	2
68	Chromosomal Structure, History, and Genomic Synteny Relationships in <i>Lupinus</i> . <i>Compendium of Plant Genomes</i> , 2020, , 87-94.	0.5	1
69	A better mousetrap to guard against anthracnose disease in bean. <i>Journal of Experimental Botany</i> , 2021, 72, 3487-3488.	4.8	0