

Scott A Jackson

List of Publications by Year in descending order

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105
papers

17,193
citations

34105

52
h-index

27406

106
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114
all docs

114
docs citations

114
times ranked

14140
citing authors

#	ARTICLE	IF	CITATIONS
1	TAR30, a homolog of the canonical plant TTTAGGG telomeric repeat, is enriched in the proximal chromosome regions of peanut (<i>Arachis hypogaea</i> L.). <i>Chromosome Research</i> , 2022, 30, 77-90.	2.2	4
2	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
3	Fast neutron mutagenesis in soybean enriches for small indels and creates frameshift mutations. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	4
4	Genomic resources in plant breeding for sustainable agriculture. <i>Journal of Plant Physiology</i> , 2021, 257, 153351.	3.5	90
5	Ancient genomes reveal early Andean farmers selected common beans while preserving diversity. <i>Nature Plants</i> , 2021, 7, 123-128.	9.3	29
6	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	1.8	97
7	Validation of resistance to root-knot nematode incorporated in peanut from the wild relative <i>Arachis stenosperma</i> . <i>Agronomy Journal</i> , 2021, 113, 2293-2302.	1.8	7
8	Registration of GA-BatSten1 and GA-MagSten1, two induced allotetraploids derived from peanut wild relatives with superior resistance to leaf spots, rust, and root-knot nematode. <i>Journal of Plant Registrations</i> , 2021, 15, 372-378.	0.5	9
9	Advancing crop genomics from lab to field. <i>Nature Genetics</i> , 2021, 53, 595-601.	21.4	47
10	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	1.8	51
11	Registration of three peanut allotetraploid interspecific hybrids resistant to late leaf spot disease and tomato spotted wilt. <i>Journal of Plant Registrations</i> , 2021, 15, 562-572.	0.5	7
12	Genetic control and allele variation among soybean maturity groups 000 through IX. <i>Plant Genome</i> , 2021, 14, e20146.	2.8	4
13	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
14	ValSten: a new wild species derived allotetraploid for increasing genetic diversity of the peanut crop (<i>Arachis hypogaea</i> L.). <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1471-1485.	1.6	6
15	Development and Genetic Characterization of Peanut Advanced Backcross Lines That Incorporate Root-Knot Nematode Resistance From <i>Arachis stenosperma</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 785358.	3.6	5
16	Evolution of Homeologous Gene Expression in Polyploid Wheat. <i>Genes</i> , 2020, 11, 1401.	2.4	6
17	The Effects of Gene Duplication Modes on the Evolution of Regulatory Divergence in Wild and Cultivated Soybean. <i>Frontiers in Genetics</i> , 2020, 11, 601003.	2.3	9
18	Pod and Seed Trait QTL Identification To Assist Breeding for Peanut Market Preferences. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2297-2315.	1.8	22

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19	A Domestication-Associated Gene GmPRR3b Regulates the Circadian Clock and Flowering Time in Soybean. <i>Molecular Plant</i> , 2020, 13, 745-759.	8.3	86
20	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	5.7	113
21	Genome-Wide Reinforcement of DNA Methylation Occurs during Somatic Embryogenesis in Soybean. <i>Plant Cell</i> , 2019, 31, 2315-2331.	6.6	55
22	Heterochromatin evolution in <i>Arachis</i> investigated through genome-wide analysis of repetitive DNA. <i>Planta</i> , 2019, 249, 1405-1415.	3.2	13
23	Breeding crops to feed 10 billion. <i>Nature Biotechnology</i> , 2019, 37, 744-754.	17.5	577
24	Impact of Chromosomal Rearrangements on the Interpretation of Lupin Karyotype Evolution. <i>Genes</i> , 2019, 10, 259.	2.4	9
25	Machine learning and complex biological data. <i>Genome Biology</i> , 2019, 20, 76.	8.8	202
26	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	21.4	439
27	Genome-wide nucleotide patterns and potential mechanisms of genome divergence following domestication in maize and soybean. <i>Genome Biology</i> , 2019, 20, 74.	8.8	13
28	A new source of root-knot nematode resistance from <i>Arachis stenosperma</i> incorporated into allotetraploid peanut (<i>Arachis hypogaea</i>). <i>Scientific Reports</i> , 2019, 9, 17702.	3.3	20
29	Genic C-Methylation in Soybean Is Associated with Gene Paralogs Relocated to Transposable Element-Rich Pericentromeres. <i>Molecular Plant</i> , 2018, 11, 485-495.	8.3	19
30	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> , 2018, 16, 1954-1967.	8.3	90
31	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	21.4	413
32	Genetic and epigenetic divergence of duplicate genes in two legume species. <i>Plant, Cell and Environment</i> , 2018, 41, 2033-2044.	5.7	29
33	Horizontal Transfer of Non-LTR Retrotransposons from Arthropods to Flowering Plants. <i>Molecular Biology and Evolution</i> , 2018, 35, 354-364.	8.9	41
34	Parallel selection on a dormancy gene during domestication of crops from multiple families. <i>Nature Genetics</i> , 2018, 50, 1435-1441.	21.4	168
35	Genomic and epigenomic immunity in common bean: the unusual features of NB-LRR gene family. <i>DNA Research</i> , 2018, 25, 161-172.	3.4	71
36	Segmental allopolyploidy in action: Increasing diversity through polyploid hybridization and homoeologous recombination. <i>American Journal of Botany</i> , 2018, 105, 1053-1066.	1.7	42

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37	Development and Evaluation of a High Density Genotyping <i>~</i> Axiom_Arachis [™] Array with 58â€‰%K SNPs for Accelerating Genetics and Breeding in Groundnut. <i>Scientific Reports</i> , 2017, 7, 40577.	3.3	144
38	Divergent cytosine DNA methylation patterns in singleâ€‰cell, soybean root hairs. <i>New Phytologist</i> , 2017, 214, 808-819.	7.3	75
39	Genome-wide SNP Genotyping Resolves Signatures of Selection and Tetrasomic Recombination in Peanut. <i>Molecular Plant</i> , 2017, 10, 309-322.	8.3	114
40	Epigenomics: dissecting hybridization and polyploidization. <i>Genome Biology</i> , 2017, 18, 117.	8.8	21
41	Comprehensive definition of genome features in <i>Spirodela polyrhiza</i> by highâ€‰depth physical mapping and shortâ€‰read <i><sc>DNA</sc></i> sequencing strategies. <i>Plant Journal</i> , 2017, 89, 617-635.	5.7	115
42	Genome resources for climateâ€‰resilient cowpea, an essential crop for food security. <i>Plant Journal</i> , 2017, 89, 1042-1054.	5.7	199
43	Application of Genomic, Transcriptomic, and Metabolomic Technologies in <i>Arachis</i> Species. , 2016, , 209-240.		3
44	Crowdsourcing the nodulation gene network discovery environment. <i>BMC Bioinformatics</i> , 2016, 17, 223.	2.6	5
45	Dynamics of a Novel Highly Repetitive CACTA Family in Common Bean (<i>Phaseolus vulgaris</i>). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2091-2101.	1.8	5
46	Highly distinct chromosomal structures in cowpea (<i>Vigna unguiculata</i>), as revealed by molecular cytogenetic analysis. <i>Chromosome Research</i> , 2016, 24, 197-216.	2.2	27
47	Widespread natural variation of DNA methylation within angiosperms. <i>Genome Biology</i> , 2016, 17, 194.	8.8	436
48	Construction of high resolution genetic linkage maps to improve the soybean genome sequence assembly Glyma1.01. <i>BMC Genomics</i> , 2016, 17, 33.	2.8	137
49	Landscape and evolutionary dynamics of terminal repeat retrotransposons in miniature in plant genomes. <i>Genome Biology</i> , 2016, 17, 7.	8.8	50
50	Evolution of plant genome architecture. <i>Genome Biology</i> , 2016, 17, 37.	8.8	331
51	Rice: The First Crop Genome. <i>Rice</i> , 2016, 9, 14.	4.0	66
52	Fluorescence <i><i>In Situ</i></i> Hybridization (FISH)-Based Karyotyping Reveals Rapid Evolution of Centromeric and Subtelomeric Repeats in Common Bean (<i>Phaseolus vulgaris</i>) and Relatives. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1013-1022.	1.8	27
53	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
54	Gene Network Reconstruction by Integration of Prior Biological Knowledge. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1075-1079.	1.8	39

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55	Single Nucleotide Polymorphism Identification in Polyploids: A Review, Example, and Recommendations. <i>Molecular Plant</i> , 2015, 8, 831-846.	8.3	159
56	Identification of QTLs for Rust Resistance in the Peanut Wild Species <i>Arachis magna</i> and the Development of KASP Markers for Marker-Assisted Selection. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1403-1413.	1.8	57
57	A Comparative Epigenomic Analysis of Polyploidy-Derived Genes in Soybean and Common Bean. <i>Plant Physiology</i> , 2015, 168, 1433-1447.	4.8	88
58	Gene Networks in Plant Biology: Approaches in Reconstruction and Analysis. <i>Trends in Plant Science</i> , 2015, 20, 664-675.	8.8	73
59	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015, 16, 538.	2.8	86
60	Transcriptomic changes due to water deficit define a general soybean response and accession-specific pathways for drought avoidance. <i>BMC Plant Biology</i> , 2015, 15, 26.	3.6	47
61	A new approach for annotation of transposable elements using small RNA mapping. <i>Nucleic Acids Research</i> , 2015, 43, e84-e84.	14.5	28
62	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> , 2014, 9, e105228.	2.5	124
63	Genome sequence of mungbean and insights into evolution within <i>Vigna</i> species. <i>Nature Communications</i> , 2014, 5, 5443.	12.8	453
64	Annotation and sequence diversity of transposable elements in common bean (<i>Phaseolus vulgaris</i>). <i>Frontiers in Plant Science</i> , 2014, 5, 339.	3.6	39
65	An RNA-Seq based gene expression atlas of the common bean. <i>BMC Genomics</i> , 2014, 15, 866.	2.8	142
66	Assessing epigenetic variation in the plant methylome. <i>Briefings in Functional Genomics</i> , 2014, 13, 318-327.	2.7	24
67	Widespread and frequent horizontal transfers of transposable elements in plants. <i>Genome Research</i> , 2014, 24, 831-838.	5.5	177
68	Concerted evolution of <i>D1</i> and <i>D2</i> to regulate chlorophyll degradation in soybean. <i>Plant Journal</i> , 2014, 77, 700-712.	5.7	69
69	De novo assembly of soybean wild relatives for pan-genome analysis of diversity and agronomic traits. <i>Nature Biotechnology</i> , 2014, 32, 1045-1052.	17.5	535
70	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
71	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
72	Identification and characterization of functional centromeres of the common bean. <i>Plant Journal</i> , 2013, 76, 47-60.	5.7	61

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73	Whole-genome sequencing of <i>Oryza brachyantha</i> reveals mechanisms underlying <i>Oryza</i> genome evolution. <i>Nature Communications</i> , 2013, 4, 1595.	12.8	190
74	The fate of duplicated genes in a polyploid plant genome. <i>Plant Journal</i> , 2013, 73, 143-153.	5.7	243
75	The Subtelomeric khipu Satellite Repeat from <i>Phaseolus vulgaris</i> : Lessons Learned from the Genome Analysis of the Andean Genotype G19833. <i>Frontiers in Plant Science</i> , 2013, 4, 109.	3.6	39
76	Cytogenetics of Legumes in the Phaseoloid Clade. <i>Plant Genome</i> , 2013, 6, plantgenome2013.03.0004.	2.8	19
77	Use of Wild Relatives and Closely Related Species to Adapt Common Bean to Climate Change. <i>Agronomy</i> , 2013, 3, 433-461.	3.0	108
78	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
79	A Highly Conserved, Small LTR Retrotransposon that Preferentially Targets Genes in Grass Genomes. <i>PLoS ONE</i> , 2012, 7, e32010.	2.5	54
80	Integration of the Draft Sequence and Physical Map as a Framework for Genomic Research in Soybean (<i>Glycine max</i> (L.) Merr.) and Wild Soybean (<i>Glycine soja</i> Sieb. and Zucc.). <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 321-329.	1.8	9
81	Functional and Structural Divergence of an Unusual LTR Retrotransposon Family in Plants. <i>PLoS ONE</i> , 2012, 7, e48595.	2.5	11
82	Sequencing crop genomes: approaches and applications. <i>New Phytologist</i> , 2011, 191, 915-925.	7.3	101
83	Molecular and Cytological Characterization of Centromeric Retrotransposons in a Wild Relative of Rice, <i>Oryza granulata</i> . <i>Tropical Plant Biology</i> , 2011, 4, 217-227.	1.9	1
84	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	27.8	3,854
85	Orthologous Comparisons of the Hd1 Region across Genera Reveal Hd1 Gene Lability within Diploid <i>Oryza</i> Species and Disruptions to Microsynteny in <i>Sorghum</i> . <i>Molecular Biology and Evolution</i> , 2010, 27, 2487-2506.	8.9	31
86	Structural and Functional Divergence of a 1-Mb Duplicated Region in the Soybean (<i>Glycine max</i>) Genome and Comparison to an Orthologous Region from <i>Phaseolus vulgaris</i> . <i>Plant Cell</i> , 2010, 22, 2545-2561.	6.6	60
87	Whole-genome sequencing and intensive analysis of the undomesticated soybean (<i>Glycine soja</i>) in America, 2010, 107, 22032-22037.	7.1	299
88	Molecular and Chromosomal Evidence for Allopolyploidy in Soybean. <i>Plant Physiology</i> , 2009, 151, 1167-1174.	4.8	135
89	Comparative sequence analysis of <i>MONOCULM1</i> -orthologous regions in 14 <i>Oryza</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2071-2076.	7.1	119
90	Do genetic recombination and gene density shape the pattern of DNA elimination in rice long terminal repeat retrotransposons?. <i>Genome Research</i> , 2009, 19, 2221-2230.	5.5	169

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91	A lineage-specific centromere retrotransposon in <i>Oryza brachyantha</i> . <i>Plant Journal</i> , 2009, 60, 820-831.	5.7	41
92	Three Sequenced Legume Genomes and Many Crop Species: Rich Opportunities for Translational Genomics. <i>Plant Physiology</i> , 2009, 151, 970-977.	4.8	122
93	BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean (<i>Phaseolus vulgaris</i> L.) Genome. <i>Tropical Plant Biology</i> , 2008, 1, 40-48.	1.9	70
94	Construction, alignment and analysis of 12 framework physical maps that represent the 10 genome types of the genus <i>Oryza</i> . <i>Genome Biology</i> , 2008, 9, R45.	9.6	82
95	Comparative Physical Mapping Between <i>Oryza sativa</i> (AA Genome Type) and <i>O. punctata</i> (BB Genome) Tj ETQq1 1.0,784314,rgBT /Over	2.9	49
96	Evolutionary dynamics of an ancient retrotransposon family provides insights into evolution of genome size in the genus <i>Oryza</i> . <i>Plant Journal</i> , 2007, 52, 342-351.	5.7	99
97	Gene duplication and paleopolyploidy in soybean and the implications for whole genome sequencing. <i>BMC Genomics</i> , 2007, 8, 330.	2.8	132
98	Integration of hybridization-based markers (overgos) into physical maps for comparative and evolutionary explorations in the genus <i>Oryza</i> and in <i>Sorghum</i> . <i>BMC Genomics</i> , 2006, 7, 199.	2.8	12
99	Toward a Reference Sequence of the Soybean Genome: A Multiagency Effort. <i>Crop Science</i> , 2006, 46, S-55.	1.8	37
100	Physical Mapping of Plant Chromosomes. , 2005, , 131-149.		1
101	Pericentromeric Regions of Soybean (<i>Glycine max</i> L. Merr.) Chromosomes Consist of Retroelements and Tandemly Repeated DNA and Are Structurally and Evolutionarily Labile. <i>Genetics</i> , 2005, 170, 1221-1230.	2.9	53
102	Preparation of Samples for Comparative Studies of Plant Chromosomes Using In Situ Hybridization Methods. <i>Methods in Enzymology</i> , 2005, 395, 443-460.	1.0	28
103	Cytogenomic Analyses Reveal the Structural Plasticity of the Chloroplast Genome in Higher Plants. <i>Plant Cell</i> , 2001, 13, 245-254.	6.6	125
104	Comparative Fluorescence in Situ Hybridization Mapping of a 431-kb <i>Arabidopsis thaliana</i> Bacterial Artificial Chromosome Contig Reveals the Role of Chromosomal Duplications in the Expansion of the <i>Brassica rapa</i> Genome. <i>Genetics</i> , 2000, 156, 833-838.	2.9	90
105	Retrotransposon-Related DNA Sequences in the Centromeres of Grass Chromosomes. <i>Genetics</i> , 1998, 150, 1615-1623.	2.9	161