

Robert M Stupar

List of Publications by Year in descending order

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81
papers

5,695
citations

81743

39
h-index

82410

72
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96
all docs

96
docs citations

96
times ranked

6630
citing authors

#	ARTICLE	IF	CITATIONS
1	Iron deficiency in soybean. <i>Crop Science</i> , 2022, 62, 36-52.	0.8	16
2	Protoplast Isolation, Transfection, and Gene Editing for Soybean (<i>Glycine max</i>). <i>Methods in Molecular Biology</i> , 2022, 2464, 173-186.	0.4	5
3	Fast neutron mutagenesis in soybean enriches for small indels and creates frameshift mutations. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	4
4	Development of <i>mPing</i> -based activation tags for crop insertional mutagenesis. <i>Plant Direct</i> , 2021, 5, e00300.	0.8	6
5	Dissecting nematode resistance regions in soybean revealed pleiotropic effect of soybean cyst and reniform nematode resistance genes. <i>Plant Genome</i> , 2021, 14, e20083.	1.6	12
6	Mining Fiskeby III and Mandarin (Ottawa) Expression Profiles to Understand Iron Stress Tolerant Responses in Soybean. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11032.	1.8	3
7	Similar Seed Composition Phenotypes Are Observed From CRISPR-Generated In-Frame and Knockout Alleles of a Soybean KASI Ortholog. <i>Frontiers in Plant Science</i> , 2020, 11, 1005.	1.7	11
8	Characterization of genetic heterogeneity within accessions in the USDA soybean germplasm collection. <i>Plant Genome</i> , 2020, 13, e20000.	1.6	8
9	Plant Genome Editing and the Relevance of Off-Target Changes. <i>Plant Physiology</i> , 2020, 183, 1453-1471.	2.3	68
10	Integration, abundance, and transmission of mutations and transgenes in a series of CRISPR/Cas9 soybean lines. <i>BMC Biotechnology</i> , 2020, 20, 10.	1.7	21
11	Identification of nodulation-related genes in <i>Medicago truncatula</i> using genome-wide association studies and co-expression networks. <i>Plant Direct</i> , 2020, 4, e00220.	0.8	4
12	Screening populations for copy number variation using genotyping-by-sequencing: a proof of concept using soybean fast neutron mutants. <i>BMC Genomics</i> , 2019, 20, 634.	1.2	20
13	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	2.8	113
14	Identification and characterization of a fast-neutron-induced mutant with elevated seed protein content in soybean. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2965-2983.	1.8	7
15	Functional analysis and development of a CRISPR/Cas9 allelic series for a CPR5 ortholog necessary for proper growth of soybean trichomes. <i>Scientific Reports</i> , 2019, 9, 14757.	1.6	28
16	Genomic changes and biochemical alterations of seed protein and oil content in a subset of fast neutron induced soybean mutants. <i>BMC Plant Biology</i> , 2019, 19, 420.	1.6	7
17	Whole-genome resequencing reveals the impact of the interaction of copy number variants of the <i>Rhg1</i> and <i>Rhg4</i> genes on broad-based resistance to soybean cyst nematode. <i>Plant Biotechnology Journal</i> , 2019, 17, 1595-1611.	4.1	65
18	Domestication in Real Time: The Curious Case of a Trigenomic Sunflower Population. <i>Agronomy</i> , 2019, 9, 704.	1.3	1

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19	Identification and Fine-Mapping of a Soybean Quantitative Trait Locus on Chromosome 5 Conferring Tolerance to Iron Deficiency Chlorosis. <i>Plant Genome</i> , 2019, 12, 190007.	1.6	14
20	Genome Editing in Soybean with CRISPR/Cas9. <i>Methods in Molecular Biology</i> , 2019, 1917, 217-234.	0.4	27
21	Soybean [<i>Glycine max</i> (L.) Merr.] Breeding: History, Improvement, Production and Future Opportunities. , 2019, , 431-516.		36
22	<sc>CRISPR</sc>/Cas9 and <sc>TALEN</sc>s generate heritable mutations for genes involved in small <sc>RNA</sc> processing of <i>Glycine max</i> and <i>Medicago truncatula</i>. <i>Plant Biotechnology Journal</i> , 2018, 16, 1125-1137.	4.1	147
23	The importance of genotype identity, genetic heterogeneity, and bioinformatic handling for properly assessing genomic variation in transgenic plants. <i>BMC Biotechnology</i> , 2018, 18, 38.	1.7	9
24	Neo-Domestication of an Interspecific Tetraploid <i>Helianthus annuus</i> – <i>Helianthus tuberosus</i> Population That Segregates for Perennial Habit. <i>Genes</i> , 2018, 9, 422.	1.0	10
25	Genetic Architecture of Soybean Yield and Agronomic Traits. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3367-3375.	0.8	98
26	Validating Genome-Wide Association Candidates Controlling Quantitative Variation in Nodulation. <i>Plant Physiology</i> , 2017, 173, 921-931.	2.3	71
27	Exploring structural variation and gene family architecture with De Novo assemblies of 15 <i>Medicago</i> genomes. <i>BMC Genomics</i> , 2017, 18, 261.	1.2	87
28	An Induced Chromosomal Translocation in Soybean Disrupts a <i>KASI</i> Ortholog and Is Associated with a High-Sucrose and Low-Oil Seed Phenotype. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1215-1223.	0.8	42
29	Structural Variation and the Soybean Genome. <i>Compendium of Plant Genomes</i> , 2017, , 57-72.	0.3	0
30	Transcriptomic basis of genome by genome variation in a legume-rhizobia mutualism. <i>Molecular Ecology</i> , 2017, 26, 6122-6135.	2.0	40
31	Dissecting the Genetic Basis of Local Adaptation in Soybean. <i>Scientific Reports</i> , 2017, 7, 17195.	1.6	37
32	Strategies for optimizing BioNano and Dovetail explored through a second reference quality assembly for the legume model, <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2017, 18, 578.	1.2	54
33	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017, 18, 541.	1.2	51
34	Fast neutron-induced structural rearrangements at a soybean NAP1 locus result in gnarled trichomes. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1725-1738.	1.8	35
35	MicroRNA Maturation and MicroRNA Target Gene Expression Regulation Are Severely Disrupted in Soybean <i>dicer-like1</i> Double Mutants. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 423-433.	0.8	23
36	Environmental Association Analyses Identify Candidates for Abiotic Stress Tolerance in <i>Glycine soja</i>, the Wild Progenitor of Cultivated Soybeans. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 835-843.	0.8	39

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37	Genomic variation and DNA repair associated with soybean transgenesis: a comparison to cultivars and mutagenized plants. <i>BMC Biotechnology</i> , 2016, 16, 41.	1.7	54
38	The Role of Deleterious Substitutions in Crop Genomes. <i>Molecular Biology and Evolution</i> , 2016, 33, 2307-2317.	3.5	83
39	Soybean (<i>Glycine max</i>) Mutant and Germplasm Resources: Current Status and Future Prospects. <i>Current Protocols in Plant Biology</i> , 2016, 1, 307-327.	2.8	9
40	Perennial Grain and Oilseed Crops. <i>Annual Review of Plant Biology</i> , 2016, 67, 703-729.	8.6	68
41	Modification of centromere structure: a promising approach for haploidline production in plant breeding. <i>Türk Tarım Ve Ormancılık Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2015, 39, 557-562.	0.8	12
42	Identical Substitutions in Magnesium Chelatase Paralogs Result in Chlorophyll-Deficient Soybean Mutants. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 123-131.	0.8	57
43	CRISPR/Cas mutagenesis of soybean and <i>Medicago truncatula</i> using a new web-tool and a modified Cas9 enzyme. <i>GM Crops and Food</i> , 2015, 6, 243-252.	2.0	162
44	The Reflective Plant Breeding Paradigm: A Robust System of Germplasm Development to Support Strategic Diversification of Agroecosystems. <i>Crop Science</i> , 2014, 54, 1939-1948.	0.8	35
45	Potential Use of Perennial Sunflower to Reduce Blackbird Damage to Sunflower. <i>Proceedings of the Vertebrate Pest Conference</i> , 2014, 26, .	0.1	2
46	Genome Resilience and Prevalence of Segmental Duplications Following Fast Neutron Irradiation of Soybean. <i>Genetics</i> , 2014, 198, 967-981.	1.2	53
47	A Roadmap for Functional Structural Variants in the Soybean Genome. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1307-1318.	0.8	42
48	To the reference and beyond: understanding variation in plant genomes. <i>Briefings in Functional Genomics</i> , 2014, 13, 255-256.	1.3	1
49	Evaluating an interspecific <i>Helianthus annuus</i> — <i>Helianthus tuberosus</i> population for use in a perennial sunflower breeding program. <i>Field Crops Research</i> , 2014, 155, 254-264.	2.3	21
50	Insights from the Soybean (<i>Glycine max</i> and <i>Glycine soja</i>) Genome. <i>Advances in Agronomy</i> , 2013, , 177-204.	2.4	13
51	A re-sequencing based assessment of genomic heterogeneity and fast neutron-induced deletions in a common bean cultivar. <i>Frontiers in Plant Science</i> , 2013, 4, 210.	1.7	18
52	Genomic Heterogeneity and Structural Variation in Soybean Near Isogenic Lines. <i>Frontiers in Plant Science</i> , 2013, 4, 104.	1.7	12
53	Targeted Mutagenesis for Functional Analysis of Gene Duplication in Legumes. <i>Methods in Molecular Biology</i> , 2013, 1069, 25-42.	0.4	20
54	Structural Variants in the Soybean Genome Localize to Clusters of Biotic Stress-Response Genes. <i>Plant Physiology</i> , 2012, 159, 1295-1308.	2.3	175

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55	Genome Engineering of Crops with Designer Nucleases. <i>Plant Genome</i> , 2012, 5, 42-50.	1.6	102
56	Co-expression of soybean Dicer-like genes in response to stress and development. <i>Functional and Integrative Genomics</i> , 2012, 12, 671-682.	1.4	19
57	Breaking Tuber Dormancy in <i>Helianthus tuberosus</i> L. and Interspecific Hybrids of <i>Helianthus annuus</i> L. – <i>Helianthus tuberosus</i> . <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2012, 47, 1342-1346.	0.5	6
58	Targeted Mutagenesis of Duplicated Genes in Soybean with Zinc-Finger Nucleases. <i>Plant Physiology</i> , 2011, 156, 466-473.	2.3	260
59	Selection-free zinc-finger-nuclease engineering by context-dependent assembly (CoDA). <i>Nature Methods</i> , 2011, 8, 67-69.	9.0	480
60	The Composition and Origins of Genomic Variation among Individuals of the Soybean Reference Cultivar Williams 82. <i>Plant Physiology</i> , 2011, 155, 645-655.	2.3	137
61	Phenotypic and Genomic Analyses of a Fast Neutron Mutant Population Resource in Soybean. <i>Plant Physiology</i> , 2011, 156, 240-253.	2.3	175
62	Into the wild: The soybean genome meets its undomesticated relative. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21947-21948.	3.3	49
63	An Integrative Approach to Genomic Introgression Mapping. <i>Plant Physiology</i> , 2010, 154, 3-12.	2.3	45
64	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.	3.1	60
65	Transcriptome Analysis of the Barley-Deoxynivalenol Interaction: Evidence for a Role of Glutathione in Deoxynivalenol Detoxification. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 962-976.	1.4	140
66	Reciprocal Silencing, Transcriptional Bias and Functional Divergence of Homeologs in Polyploid Cotton (<i>Gossypium</i>). <i>Genetics</i> , 2009, 182, 503-517.	1.2	212
67	Gene expression analyses in maize inbreds and hybrids with varying levels of heterosis. <i>BMC Plant Biology</i> , 2008, 8, 33.	1.6	145
68	Phenotypic and Transcriptomic Changes Associated With Potato Autopolyploidization. <i>Genetics</i> , 2007, 176, 2055-2067.	1.2	208
69	Nonadditive Expression and Parent-of-Origin Effects Identified by Microarray and Allele-Specific Expression Profiling of Maize Endosperm. <i>Plant Physiology</i> , 2007, 145, 411-425.	2.3	64
70	Allele-Specific Expression Patterns Reveal Biases and Embryo-Specific Parent-of-Origin Effects in Hybrid Maize. <i>Plant Cell</i> , 2007, 19, 2391-2402.	3.1	157
71	Natural Variation for Alleles Under Epigenetic Control by the Maize Chromomethylase <i>Zmet2</i> . <i>Genetics</i> , 2007, 177, 749-760.	1.2	31
72	Allelic variation and heterosis in maize: How do two halves make more than a whole?. <i>Genome Research</i> , 2007, 17, 264-275.	2.4	306

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73	Cis-transcriptional Variation in Maize Inbred Lines B73 and Mo17 Leads to Additive Expression Patterns in the F1 Hybrid. <i>Genetics</i> , 2006, 173, 2199-2210.	1.2	253
74	Structural Diversity and Differential Transcription of the Patatin Multicopy Gene Family During Potato Tuber Development. <i>Genetics</i> , 2006, 172, 1263-1275.	1.2	38
75	Fluorescence In Situ Hybridization Analysis Reveals Multiple Loci of Knob-associated DNA Elements in One-knob and Knobless Maize Lines. <i>Journal of Histochemistry and Cytochemistry</i> , 2004, 52, 1113-1116.	1.3	24
76	The HECT ubiquitin-protein ligase (UPL) family in Arabidopsis: UPL3 has a specific role in trichome development. <i>Plant Journal</i> , 2003, 35, 729-742.	2.8	186
77	Molecular and Cytological Analyses of Large Tracks of Centromeric DNA Reveal the Structure and Evolutionary Dynamics of Maize Centromeres. <i>Genetics</i> , 2003, 163, 759-770.	1.2	155
78	Highly Condensed Potato Pericentromeric Heterochromatin Contains rDNA-Related Tandem Repeats. <i>Genetics</i> , 2002, 162, 1435-1444.	1.2	75
79	Instability of bacterial artificial chromosome (BAC) clones containing tandemly repeated DNA sequences. <i>Genome</i> , 2001, 44, 463-469.	0.9	38
80	A tandemly repeated DNA sequence is associated with both knob-like heterochromatin and a highly decondensed structure in the meiotic pachytene chromosomes of rice. <i>Chromosoma</i> , 2001, 110, 24-31.	1.0	59
81	Complex mtDNA constitutes an approximate 620-kb insertion on Arabidopsis thaliana chromosome 2: Implication of potential sequencing errors caused by large-unit repeats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 5099-5103.	3.3	207