

Susan R Mccouch

List of Publications by Year in descending order

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180
papers

28,404
citations

4960

84
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163
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194
all docs

194
docs citations

194
times ranked

17622
citing authors

#	ARTICLE	IF	CITATIONS
1	Seed Banks and Molecular Maps: Unlocking Genetic Potential from the Wild. <i>Science</i> , 1997, 277, 1063-1066.	12.6	2,011
2	Computational and Experimental Analysis of Microsatellites in Rice (<i>Oryza sativa</i> L.): Frequency, Length Variation, Transposon Associations, and Genetic Marker Potential. <i>Genome Research</i> , 2001, 11, 1441-1452.	5.5	1,285
3	Genome-wide association mapping reveals a rich genetic architecture of complex traits in <i>Oryza sativa</i> . <i>Nature Communications</i> , 2011, 2, 467.	12.8	1,230
4	Development and Mapping of 2240 New SSR Markers for Rice (<i>Oryza sativa</i> L.). <i>DNA Research</i> , 2002, 9, 199-207.	3.4	1,203
5	Genetic Structure and Diversity in <i>Oryza sativa</i> L.. <i>Genetics</i> , 2005, 169, 1631-1638.	2.9	988
6	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2012, 30, 105-111.	17.5	818
7	Not just a grain of rice: the quest for quality. <i>Trends in Plant Science</i> , 2009, 14, 133-139.	8.8	643
8	Next-generation phenotyping: requirements and strategies for enhancing our understanding of genotype-phenotype relationships and its relevance to crop improvement. <i>Theoretical and Applied Genetics</i> , 2013, 126, 867-887.	3.6	512
9	Caught Red-Handed: Rc Encodes a Basic Helix-Loop-Helix Protein Conditioning Red Pericarp in Rice. <i>Plant Cell</i> , 2006, 18, 283-294.	6.6	465
10	Feeding the future. <i>Nature</i> , 2013, 499, 23-24.	27.8	464
11	Identification of Trait-Improving Quantitative Trait Loci Alleles From a Wild Rice Relative, <i>Oryza rufipogon</i> . <i>Genetics</i> , 1998, 150, 899-909.	2.9	463
12	Mapping quantitative trait loci for yield, yield components and morphological traits in an advanced backcross population between <i>Oryza rufipogon</i> and the <i>Oryza sativa</i> cultivar Jefferson. <i>Theoretical and Applied Genetics</i> , 2003, 107, 479-493.	3.6	450
13	New insights into the history of rice domestication. <i>Trends in Genetics</i> , 2007, 23, 578-587.	6.7	443
14	Genomic Selection and Association Mapping in Rice (<i>Oryza sativa</i>): Effect of Trait Genetic Architecture, Training Population Composition, Marker Number and Statistical Model on Accuracy of Rice Genomic Selection in Elite, Tropical Rice Breeding Lines. <i>PLoS Genetics</i> , 2015, 11, e1004982.	3.5	425
15	Genome-Wide Patterns of Nucleotide Polymorphism in Domesticated Rice. <i>PLoS Genetics</i> , 2007, 3, e163.	3.5	406
16	The Complex History of the Domestication of Rice. <i>Annals of Botany</i> , 2007, 100, 951-957.	2.9	393
17	Three-Dimensional Root Phenotyping with a Novel Imaging and Software Platform. <i>Plant Physiology</i> , 2011, 156, 455-465.	4.8	380
18	Open access resources for genome-wide association mapping in rice. <i>Nature Communications</i> , 2016, 7, 10532.	12.8	371

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19	Multi-parent advanced generation inter-cross (MAGIC) populations in rice: progress and potential for genetics research and breeding. <i>Rice</i> , 2013, 6, 11.	4.0	361
20	Harvesting the Promising Fruits of Genomics: Applying Genome Sequencing Technologies to Crop Breeding. <i>PLoS Biology</i> , 2014, 12, e1001883.	5.6	341
21	Genes from wild rice improve yield. <i>Nature</i> , 1996, 384, 223-224.	27.8	335
22	Genetic Architecture of Aluminum Tolerance in Rice (<i>Oryza sativa</i>) Determined through Genome-Wide Association Analysis and QTL Mapping. <i>PLoS Genetics</i> , 2011, 7, e1002221.	3.5	334
23	The Extent of Linkage Disequilibrium in Rice (<i>Oryza sativa</i> L.). <i>Genetics</i> , 2007, 177, 2223-2232.	2.9	331
24	Evolutionary History of <i>GS3</i> , a Gene Conferring Grain Length in Rice. <i>Genetics</i> , 2009, 182, 1323-1334.	2.9	305
25	Genome-wide prediction models that incorporate de novo GWAS are a powerful new tool for tropical rice improvement. <i>Heredity</i> , 2016, 116, 395-408.	2.6	296
26	The Rice Bacterial Blight Resistance Gene <i>xa5</i> Encodes a Novel Form of Disease Resistance. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 1348-1354.	2.6	290
27	The origin and evolution of fragrance in rice (<i>Oryza sativa</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14444-14449.	7.1	288
28	Microsatellite marker development, mapping and applications in rice genetics and breeding. <i>Plant Molecular Biology</i> , 1997, 35, 89-99.	3.9	284
29	Identification of quantitative trait loci for yield and yield components in an advanced backcross population derived from the <i>Oryza sativa</i> variety IR64 and the wild relative <i>O. rufipogon</i> . <i>Theoretical and Applied Genetics</i> , 2003, 107, 1419-1432.	3.6	255
30	Getting to the roots of it: Genetic and hormonal control of root architecture. <i>Frontiers in Plant Science</i> , 2013, 4, 186.	3.6	254
31	Genomic Diversity and Introgression in <i>O. sativa</i> Reveal the Impact of Domestication and Breeding on the Rice Genome. <i>PLoS ONE</i> , 2010, 5, e10780.	2.5	250
32	Selection Under Domestication: Evidence for a Sweep in the Rice Waxy Genomic Region. <i>Genetics</i> , 2006, 173, 975-983.	2.9	246
33	Global Dissemination of a Single Mutation Conferring White Pericarp in Rice. <i>PLoS Genetics</i> , 2007, 3, e133.	3.5	228
34	Bridging the genotyping gap: using genotyping by sequencing (GBS) to add high-density SNP markers and new value to traditional bi-parental mapping and breeding populations. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2699-2716.	3.6	228
35	Whole genome de novo assemblies of three divergent strains of rice, <i>Oryza sativa</i> , document novel gene space of aus and indica. <i>Genome Biology</i> , 2014, 15, 506.	8.8	228
36	Diversifying Selection in Plant Breeding. <i>PLoS Biology</i> , 2004, 2, e347.	5.6	215

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37	QTL detection for rice grain quality traits using an interspecific backcross population derived from cultivated Asian (<i>O. sativa</i> L.) and African (<i>O. glaberrima</i> S.) rice. <i>Genome</i> , 2004, 47, 697-704.	2.0	208
38	Population Structure and Its Effect on Haplotype Diversity and Linkage Disequilibrium Surrounding the <i>xa5</i> Locus of Rice (<i>Oryza sativa</i> L.). <i>Genetics</i> , 2003, 165, 759-769.	2.9	204
39	Development of a Novel Aluminum Tolerance Phenotyping Platform Used for Comparisons of Cereal Aluminum Tolerance and Investigations into Rice Aluminum Tolerance Mechanisms. <i>Plant Physiology</i> , 2010, 153, 1678-1691.	4.8	199
40	The <i>Oryza</i> bacterial artificial chromosome library resource: Construction and analysis of 12 deep-coverage large-insert BAC libraries that represent the 10 genome types of the genus <i>Oryza</i> . <i>Genome Research</i> , 2005, 16, 140-147.	5.5	197
41	Ethylene-gibberellin signaling underlies adaptation of rice to periodic flooding. <i>Science</i> , 2018, 361, 181-186.	12.6	188
42	High-throughput two-dimensional root system phenotyping platform facilitates genetic analysis of root growth and development. <i>Plant, Cell and Environment</i> , 2013, 36, 454-466.	5.7	184
43	Comparative mapping in grasses. Wheat relationships. <i>Molecular Genetics and Genomics</i> , 1995, 248, 744-754.	2.4	183
44	Gramene database in 2010: updates and extensions. <i>Nucleic Acids Research</i> , 2011, 39, D1085-D1094.	14.5	182
45	Development of genome-wide SNP assays for rice. <i>Breeding Science</i> , 2010, 60, 524-535.	1.9	180
46	Tagging and combining bacterial blight resistance genes in rice using RAPD and RFLP markers. <i>Molecular Breeding</i> , 1995, 1, 375-387.	2.1	178
47	Fine Mapping of a Grain-Weight Quantitative Trait Locus in the Pericentromeric Region of Rice Chromosome 3. <i>Genetics</i> , 2004, 168, 2187-2195.	2.9	178
48	<i>LABA1</i> , a Domestication Gene Associated with Long, Barbed Awns in Wild Rice. <i>Plant Cell</i> , 2015, 27, 1875-1888.	6.6	178
49	Gramene, a Tool for Grass Genomics. <i>Plant Physiology</i> , 2002, 130, 1606-1613.	4.8	177
50	Gramene: a bird's eye view of cereal genomes. <i>Nucleic Acids Research</i> , 2006, 34, D717-D723.	14.5	177
51	Identification of quantitative trait loci for grain quality in an advanced backcross population derived from the <i>Oryza sativa</i> variety IR64 and the wild relative <i>O. rufipogon</i> . <i>Theoretical and Applied Genetics</i> , 2003, 107, 1433-1441.	3.6	171
52	Genetic diversity analysis of traditional and improved Indonesian rice (<i>Oryza sativa</i> L.) germplasm using microsatellite markers. <i>Theoretical and Applied Genetics</i> , 2007, 114, 559-568.	3.6	171
53	Genome-wide association and high-resolution phenotyping link <i>Oryza sativa</i> panicle traits to numerous trait-specific QTL clusters. <i>Nature Communications</i> , 2016, 7, 10527.	12.8	165
54	Through the genetic bottleneck: <i>O. rufipogon</i> as a source of trait-enhancing alleles for <i>O. sativa</i> . <i>Euphytica</i> , 2007, 154, 317-339.	1.2	163

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55	Natural variation underlies alterations in Nramp aluminum transporter (<i>NRAT1</i>) expression and function that play a key role in rice aluminum tolerance. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6503-6508.	7.1	160
56	Genetic analysis of Indian aromatic and quality rice (<i>Oryza sativa</i> L.) germplasm using panels of fluorescently-labeled microsatellite markers. Theoretical and Applied Genetics, 2004, 109, 965-977.	3.6	158
57	Genome-Wide Association Mapping for Yield and Other Agronomic Traits in an Elite Breeding Population of Tropical Rice (<i>Oryza sativa</i>). PLoS ONE, 2015, 10, e0119873.	2.5	157
58	Inferences on the Genome Structure of Progenitor Maize Through Comparative Analysis of Rice, Maize and the Domesticated Panicoids. Genetics, 1999, 153, 453-473.	2.9	154
59	Genomics of gene banks: A case study in rice. American Journal of Botany, 2012, 99, 407-423.	1.7	152
60	Gramene: a growing plant comparative genomics resource. Nucleic Acids Research, 2007, 36, D947-D953.	14.5	151
61	The Population Structure of African Cultivated Rice <i>Oryza glaberrima</i> (Steud.). Genetics, 2005, 169, 1639-1647.	2.9	145
62	Fine mapping of a yield-enhancing QTL cluster associated with transgressive variation in an <i>Oryza sativa</i> × <i>O. rufipogon</i> cross. Theoretical and Applied Genetics, 2008, 116, 613-622.	3.6	142
63	High-throughput single nucleotide polymorphism genotyping for breeding applications in rice using the BeadXpress platform. Molecular Breeding, 2012, 29, 875-886.	2.1	139
64	Comparative evaluation of within-cultivar variation of rice (<i>Oryza sativa</i> L.) using microsatellite and RFLP markers. Genome, 1997, 40, 370-378.	2.0	138
65	Natural variation of rice strigolactone biosynthesis is associated with the deletion of two <i>MAX1</i> orthologs. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2379-2384.	7.1	138
66	Population Structure and Breeding Patterns of 145 U.S. Rice Cultivars Based on SSR Marker Analysis. Crop Science, 2005, 45, 66-76.	1.8	135
67	The Plant Ontology Database: a community resource for plant structure and developmental stages controlled vocabulary and annotations. Nucleic Acids Research, 2008, 36, D449-D454.	14.5	135
68	Plant Ontology (PO): a Controlled Vocabulary of Plant Structures and Growth Stages. Comparative and Functional Genomics, 2005, 6, 388-397.	2.0	129
69	Anchor probes for comparative mapping of grass genera. Theoretical and Applied Genetics, 1998, 97, 356-369.	3.6	123
70	Whole genome de novo assemblies of three divergent strains of rice, <i>Oryza sativa</i> , document novel gene space of aus and indica. Genome Biology, 2014, 15, 506.	9.6	123
71	Cloning and mapping of variety-specific rice genomic DNA sequences: amplified fragment length polymorphisms (AFLP) from silver-stained Polyacrylamide gels. Genome, 1996, 39, 373-378.	2.0	122
72	Reap the crop wild relatives for breeding future crops. Trends in Biotechnology, 2022, 40, 412-431.	9.3	122

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73	Development and Mapping of 2240 New SSR Markers for Rice (<i>Oryza sativa</i> L.) (Supplement). DNA Research, 2002, 9, 257-279.	3.4	121
74	Characterization and Mapping of a Shattering Mutant in Rice That Corresponds to a Block of Domestication Genes. Genetics, 2006, 173, 995-1005.	2.9	108
75	Genetic architecture of cold tolerance in rice (<i>Oryza sativa</i>) determined through high resolution genome-wide analysis. PLoS ONE, 2017, 12, e0172133.	2.5	107
76	A genome scale metabolic network for rice and accompanying analysis of tryptophan, auxin and serotonin biosynthesis regulation under biotic stress. Rice, 2013, 6, 15.	4.0	101
77	Genotype and environment effects on rice (<i>Oryza sativa</i> L.) grain arsenic concentration in Bangladesh. Plant and Soil, 2011, 338, 367-382.	3.7	99
78	Large-scale deployment of a rice 6ÅK SNP array for genetics and breeding applications. Rice, 2017, 10, 40.	4.0	97
79	Gramene QTL database: development, content and applications. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap005.	3.0	95
80	Loss of function at <i>RAE2</i> , a previously unidentified EPFL, is required for awnlessness in cultivated Asian rice. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8969-8974.	7.1	94
81	The Plant Structure Ontology, a Unified Vocabulary of Anatomy and Morphology of a Flowering Plant. Plant Physiology, 2007, 143, 587-599.	4.8	91
82	Integrated map of AFLP, SSLP and RFLP markers using a recombinant inbred population of rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.6	90
83	Inactivation of the CTD phosphatase-like gene <i>OsCPL1</i> enhances the development of the abscission layer and seed shattering in rice. Plant Journal, 2010, 61, 96-106.	5.7	89
84	Microsatellites and microsynteny in the chloroplast genomes of <i>Oryza</i> and eight other Gramineae species. Theoretical and Applied Genetics, 2000, 100, 1257-1266.	3.6	86
85	Leaf-level water use efficiency determined by carbon isotope discrimination in rice seedlings: genetic variation associated with population structure and QTL mapping. Theoretical and Applied Genetics, 2009, 118, 1065-1081.	3.6	85
86	Plant genetic resources for food and agriculture: opportunities and challenges emerging from the science and information technology revolution. New Phytologist, 2018, 217, 1407-1419.	7.3	85
87	A Rice Diversity Panel Evaluated for Genetic and Agro-Morphological Diversity between Subpopulations and its Geographic Distribution. Crop Science, 2011, 51, 2021-2035.	1.8	83
88	When more is better: how data sharing would accelerate genomic selection of crop plants. New Phytologist, 2016, 212, 814-826.	7.3	82
89	A Marker-Based Approach to Broadening the Genetic Base of Rice in the USA. Crop Science, 2004, 44, 1947-1959.	1.8	80
90	Population Dynamics Among six Major Groups of the <i>Oryza rufipogon</i> Species Complex, Wild Relative of Cultivated Asian Rice. Rice, 2016, 9, 56.	4.0	80

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91	Genome-Wide Association Study for Traits Related to Plant and Grain Morphology, and Root Architecture in Temperate Rice Accessions. PLoS ONE, 2016, 11, e0155425.	2.5	80
92	Development and GBS-genotyping of introgression lines (ILs) using two wild species of rice, <i>O. meridionalis</i> and <i>O. rufipogon</i> , in a common recurrent parent, <i>O. sativa</i> cv. Curinga. Molecular Breeding, 2015, 35, 81.	2.1	77
93	Addressing Research Bottlenecks to Crop Productivity. Trends in Plant Science, 2021, 26, 607-630.	8.8	76
94	Development of a Research Platform for Dissecting Phenotype-Genotype Associations in Rice (<i>Oryza</i>) Tj ETQq0 0.0 rgBT /Overlock 10	4.0	75
95	Substitution Mapping of <i>dth1.1</i> , a Flowering-Time Quantitative Trait Locus (QTL) Associated With Transgressive Variation in Rice, Reveals Multiple Sub-QTL. Genetics, 2006, 172, 2501-2514.	2.9	73
96	Registration of the Rice Diversity Panel 1 for Genomewide Association Studies. Journal of Plant Registrations, 2014, 8, 109-116.	0.5	73
97	High resolution genetic mapping and candidate gene identification at the <i>xa5</i> locus for bacterial blight resistance in rice (<i>Oryza sativa</i> L.). Theoretical and Applied Genetics, 2003, 107, 62-73.	3.6	72
98	Design and Application of Microsatellite Marker Panels for Semiautomated Genotyping of Rice (<i>Oryza sativa</i> L.). Crop Science, 2002, 42, 2092-2099.	1.8	71
99	Simple sequence repeat diversity in diploid and tetraploid <i>Coffea</i> species. Genome, 2004, 47, 501-509.	2.0	71
100	Dissection of the genetic architecture of rice resistance to the blast fungus <i>Magnaporthe oryzae</i> . Molecular Plant Pathology, 2016, 17, 959-972.	4.2	66
101	An imputation platform to enhance integration of rice genetic resources. Nature Communications, 2018, 9, 3519.	12.8	65
102	Rice PHYC gene: structure, expression, map position and evolution. Plant Molecular Biology, 2000, 44, 27-42.	3.9	63
103	High-Resolution Inflorescence Phenotyping Using a Novel Image-Analysis Pipeline, PANorama. Plant Physiology, 2014, 165, 479-495.	4.8	63
104	Identification of Quantitative Trait Loci in Rice for Yield, Yield Components, and Agronomic Traits across Years and Locations. Crop Science, 2007, 47, 2403-2417.	1.8	60
105	A universal core genetic map for rice. Theoretical and Applied Genetics, 2010, 120, 563-572.	3.6	60
106	How Can We Use Genomics to Improve Cereals with Rice as a Reference Genome?. Plant Molecular Biology, 2005, 59, 7-26.	3.9	59
107	Integrating Molecular Markers and Environmental Covariates To Interpret Genotype by Environment Interaction in Rice (<i>Oryza sativa</i> L.) Grown in Subtropical Areas. G3: Genes, Genomes, Genetics, 2019, 9, 1519-1531.	1.8	59
108	Genomic Variation in Rice: Genesis of Highly Polymorphic Linkage Blocks during Domestication. PLoS Genetics, 2006, 2, e199.	3.5	57

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109	Functional markers for xa5-mediated resistance in rice (<i>Oryza sativa</i> , L.). <i>Molecular Breeding</i> , 2007, 19, 291-296.	2.1	54
110	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017, 18, 541.	2.8	51
111	An improved 7K SNP array, the C7AIR, provides a wealth of validated SNP markers for rice breeding and genetics studies. <i>PLoS ONE</i> , 2020, 15, e0232479.	2.5	51
112	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020, 13, 1341-1344.	8.3	50
113	A Graph-Theoretic Approach to Comparing and Integrating Genetic, Physical and Sequence-Based Maps. <i>Genetics</i> , 2003, 165, 2235-2247.	2.9	49
114	Fluorescent-labeled microsatellite panels useful for detecting allelic diversity in cultivated rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2002, 105, 449-457.	3.6	47
115	ALCHEMY: a reliable method for automated SNP genotype calling for small batch sizes and highly homozygous populations. <i>Bioinformatics</i> , 2010, 26, 2952-2960.	4.1	46
116	Multiple and independent origins of short seeded alleles of <i>GS3</i> in rice. <i>Breeding Science</i> , 2013, 63, 77-85.	1.9	44
117	Evolving technologies for growing, imaging and analyzing 3D root system architecture of crop plants. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 230-241.	8.5	43
118	Transgressive Segregation of Tiller Angle in Rice Caused by Complementary Gene Action. <i>Crop Science</i> , 1998, 38, 12-19.	1.8	42
119	Genetic Diversity of Isolated Populations of Indonesian Landraces of Rice (<i>Oryza sativa</i> L.) Collected in East Kalimantan on the Island of Borneo. <i>Rice</i> , 2009, 2, 80-92.	4.0	41
120	Multienvironment Models Increase Prediction Accuracy of Complex Traits in Advanced Breeding Lines of Rice. <i>Crop Science</i> , 2018, 58, 1519-1530.	1.8	41
121	Development of a SNP genotyping panel for detecting polymorphisms in <i>Oryza glaberrima</i> / <i>O. sativa</i> interspecific crosses. <i>Euphytica</i> , 2015, 201, 67-78.	1.2	39
122	Genomics and Syteny. <i>Plant Physiology</i> , 2001, 125, 152-155.	4.8	38
123	The Tyrosine Aminomutase TAM1 Is Required for $\hat{2}$ -Tyrosine Biosynthesis in Rice. <i>Plant Cell</i> , 2015, 27, 1265-1278.	6.6	38
124	Evidence for divergence of response in <i>Indica</i> , <i>Japonica</i> , and wild rice to high CO_2 — temperature interaction. <i>Global Change Biology</i> , 2016, 22, 2620-2632.	9.5	38
125	A genetic linkage map of coffee (<i>Coffea arabica</i> L.) and QTL for yield, plant height, and bean size. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	1.6	37
126	Metabolomics and genomics combine to unravel the pathway for the presence of fragrance in rice. <i>Scientific Reports</i> , 2017, 7, 8767.	3.3	36

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127	Validation of yield-enhancing quantitative trait loci from a low-yielding wild ancestor of rice. <i>Molecular Breeding</i> , 2013, 32, 101-120.	2.1	34
128	N- and P-mediated seminal root elongation response in rice seedlings. <i>Plant and Soil</i> , 2014, 375, 303-315.	3.7	34
129	Association mapping and genetic dissection of drought-induced canopy temperature differences in rice. <i>Journal of Experimental Botany</i> , 2020, 71, 1614-1627.	4.8	33
130	Strategies for Effective Use of Genomic Information in Crop Breeding Programs Serving Africa and South Asia. <i>Frontiers in Plant Science</i> , 2020, 11, 353.	3.6	33
131	Genetic Analysis of Water Use Efficiency in Rice (<i>Oryza sativa</i> L.) at the Leaf Level. <i>Rice</i> , 2010, 3, 72-86.	4.0	32
132	Convergent Loss of Awn in Two Cultivated Rice Species <i>Oryza sativa</i> and <i>Oryza glaberrima</i> Is Caused by Mutations in Different Loci. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2267-2274.	1.8	31
133	Robust phenotyping strategies for evaluation of stem non-structural carbohydrates (NSC) in rice. <i>Journal of Experimental Botany</i> , 2016, 67, 6125-6138.	4.8	31
134	The buffering capacity of stems: genetic architecture of nonstructural carbohydrates in cultivated Asian rice, <i>Oryza sativa</i> . <i>New Phytologist</i> , 2017, 215, 658-671.	7.3	31
135	<i>ALUMINUM RESISTANCE TRANSCRIPTION FACTOR 1</i> (<i>ART1</i>) contributes to natural variation in aluminum resistance in diverse genetic backgrounds of rice (<i>O. Tj ETQq1 1 0.784314 rgBT /Over</i>)		
136	The effects of resource availability and environmental conditions on genetic rankings for carbon isotope discrimination during growth in tomato and rice. <i>Functional Plant Biology</i> , 2005, 32, 1089.	2.1	27
137	Analysis of genetic structure in a sample of coffee (<i>Coffea arabica</i> L.) using fluorescent SSR markers. <i>Tree Genetics and Genomes</i> , 2009, 5, 435-446.	1.6	27
138	Marker Assisted Breeding. , 2009, , 451-469.		27
139	Dissection of a QTL reveals an adaptive, interacting gene complex associated with transgressive variation for flowering time in rice. <i>Theoretical and Applied Genetics</i> , 2010, 120, 895-908.	3.6	26
140	Genome-Wide Association Study Using Historical Breeding Populations Discovers Genomic Regions Involved in High-Quality Rice. <i>Plant Genome</i> , 2018, 11, 170076.	2.8	26
141	From bits to bites: Advancement of the Germinate platform to support prebreeding informatics for crop wild relatives. <i>Crop Science</i> , 2021, 61, 1538-1566.	1.8	26
142	PICARA, an Analytical Pipeline Providing Probabilistic Inference about A Priori Candidates Genes Underlying Genome-Wide Association QTL in Plants. <i>PLoS ONE</i> , 2012, 7, e46596.	2.5	23
143	Variation in soil aluminium tolerance genes is associated with local adaptation to soils at the Park Grass Experiment. <i>Molecular Ecology</i> , 2014, 23, 6058-6072.	3.9	20
144	A SWEET solution to rice blight. <i>Nature Biotechnology</i> , 2019, 37, 1280-1282.	17.5	20

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145	A genetic map of an interspecific diploid pseudo testcross population of coffee. <i>Euphytica</i> , 2013, 192, 305-323.	1.2	17
146	Identification of QTLs associated with agronomic performance under nitrogen-deficient conditions using chromosome segment substitution lines of a wild rice relative, <i>Oryza rufipogon</i> . <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	2.1	17
147	Identification of quantitative trait loci for physical and chemical properties of rice grain. <i>Plant Biotechnology Reports</i> , 2010, 4, 61-73.	1.5	16
148	A massively parallel barcoded sequencing pipeline enables generation of the first ORFeome and interactome map for rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11836-11842.	7.1	16
149	Genetic mapping identifies a rice naringenin <i>O</i> -glucosyltransferase that influences insect resistance. <i>Plant Journal</i> , 2021, 106, 1401-1413.	5.7	15
150	Exceptional lability of a genomic complex in rice and its close relatives revealed by interspecific and intraspecific comparison and population analysis. <i>BMC Genomics</i> , 2011, 12, 142.	2.8	14
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