

Susan R Mccouch

List of Publications by Year in descending order

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180
papers

28,404
citations

5782

84
h-index

6349

163
g-index

194
all docs

194
docs citations

194
times ranked

19627
citing authors

#	ARTICLE	IF	CITATIONS
1	Reap the crop wild relatives for breeding future crops. <i>Trends in Biotechnology</i> , 2022, 40, 412-431.	4.9	122
2	Can biochemical traits bridge the gap between genomics and plant performance? A study in rice under drought. <i>Plant Physiology</i> , 2022, 189, 1139-1152.	2.3	8
3	Development and validation of an optimized marker set for genomic selection in southern U.S. rice breeding programs. <i>Plant Genome</i> , 2022, 15, .	1.6	11
4	Phenotypic response of farmer-selected CWR-derived rice lines to salt stress in the Mekong Delta. <i>Crop Science</i> , 2021, 61, 201-218.	0.8	10
5	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.	0.8	26
6	Genetic mapping identifies a rice naringenin O-glucosyltransferase that influences insect resistance. <i>Plant Journal</i> , 2021, 106, 1401-1413.	2.8	15
7	Genetic architecture of root and shoot ionomes in rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 2613-2637.	1.8	9
8	Addressing Research Bottlenecks to Crop Productivity. <i>Trends in Plant Science</i> , 2021, 26, 607-630.	4.3	76
9	Association mapping and genetic dissection of drought-induced canopy temperature differences in rice. <i>Journal of Experimental Botany</i> , 2020, 71, 1614-1627.	2.4	33
10	Low Additive Genetic Variation in a Trait Under Selection in Domesticated Rice. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2435-2443.	0.8	9
11	A Coordinated Suite of Wild-Introgression Lines in Indica and Japonica Elite Backgrounds. <i>Frontiers in Plant Science</i> , 2020, 11, 564824.	1.7	4
12	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020, 13, 1341-1344.	3.9	50
13	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.	3.3	16
14	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.	1.1	51
15	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.	1.7	33
16	Bridging old and new: diversity and evaluation of high iron-associated stress response of rice cultivated in West Africa. <i>Journal of Experimental Botany</i> , 2020, 71, 4188-4200.	2.4	14
17	Multiple Small-Effect Alleles of Indica Origin Enhance High Iron-Associated Stress Tolerance in Rice Under Field Conditions in West Africa. <i>Frontiers in Plant Science</i> , 2020, 11, 604938.	1.7	10
18	Genome wide association studies for japonica rice resistance to blast in field and controlled conditions. <i>Rice</i> , 2020, 13, 71.	1.7	14

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19	A SWEET solution to rice blight. <i>Nature Biotechnology</i> , 2019, 37, 1280-1282.	9.4	20
20	Validation of Yield Component Traits Identified by Genome-Wide Association Mapping in a tropical japonica × tropical japonica Rice Biparental Mapping Population. <i>Plant Genome</i> , 2019, 12, 180021.	1.6	13
21	Integrating Molecular Markers and Environmental Covariates To Interpret Genotype by Environment Interaction in Rice (<i>Oryza sativa</i> L.) Grown in Subtropical Areas. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1519-1531.	0.8	59
22	Plant genetic resources for food and agriculture: opportunities and challenges emerging from the science and information technology revolution. <i>New Phytologist</i> , 2018, 217, 1407-1419.	3.5	85
23	Resistance to Multiple Temperate and Tropical Stem and Sheath Diseases of Rice. <i>Plant Genome</i> , 2018, 11, 170029.	1.6	11
24	Genome-Wide Association Study Using Historical Breeding Populations Discovers Genomic Regions Involved in High-Quality Rice. <i>Plant Genome</i> , 2018, 11, 170076.	1.6	26
25	An imputation platform to enhance integration of rice genetic resources. <i>Nature Communications</i> , 2018, 9, 3519.	5.8	65
26	Multi-environment Models Increase Prediction Accuracy of Complex Traits in Advanced Breeding Lines of Rice. <i>Crop Science</i> , 2018, 58, 1519-1530.	0.8	41
27	Ethylene-gibberellin signaling underlies adaptation of rice to periodic flooding. <i>Science</i> , 2018, 361, 181-186.	6.0	188
28	Genomic regions responsible for seminal and crown root lengths identified by 2D & 3D root system image analysis. <i>BMC Genomics</i> , 2018, 19, 273.	1.2	12
29	The buffering capacity of stems: genetic architecture of nonstructural carbohydrates in cultivated Asian rice, <i>Oryza sativa</i> L. <i>New Phytologist</i> , 2017, 215, 658-671.	3.5	31
30	Metabolomics and genomics combine to unravel the pathway for the presence of fragrance in rice. <i>Scientific Reports</i> , 2017, 7, 8767.	1.6	36
31	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017, 18, 541.	1.2	51
32	Large-scale deployment of a rice 6K SNP array for genetics and breeding applications. <i>Rice</i> , 2017, 10, 40.	1.7	97
33	<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</i>) <i>ETQq1 1 0784314 rgBT /Over</i>		
34	Genetic architecture of cold tolerance in rice (<i>Oryza sativa</i>) determined through high resolution genome-wide analysis. <i>PLoS ONE</i> , 2017, 12, e0172133.	1.1	107
35	Functional properties of an alternative, tissue-specific promoter for rice NADPH-dependent dihydroflavonol reductase. <i>PLoS ONE</i> , 2017, 12, e0183722.	1.1	8
36	Marker-assisted introgression of drought tolerance from wild ancestors into popular Indian rice varieties using a 7K Infinium SNP array. <i>Canadian Journal of Biotechnology</i> , 2017, 1, 205-205.	0.3	2

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37	Ensuring and exploiting genetic diversity in rice. Burleigh Dodds Series in Agricultural Science, 2017, , 3-26.	0.1	0
38	Whole-genome characterization in pedigreed non-human primates using genotyping-by-sequencing (GBS) and imputation. BMC Genomics, 2016, 17, 676.	1.2	9
39	Transgressive Variation for Yield Components Measured throughout the Growth Cycle of Jefferson Rice (<i>Oryza sativa</i>) Å— <i>O. rufipogon</i> Introgression Lines. Crop Science, 2016, 56, 2336-2347.	0.8	3
40	Robust phenotyping strategies for evaluation of stem non-structural carbohydrates (NSC) in rice. Journal of Experimental Botany, 2016, 67, 6125-6138.	2.4	31
41	Open access resources for genome-wide association mapping in rice. Nature Communications, 2016, 7, 10532.	5.8	371
42	Population Dynamics Among six Major Groups of the <i>Oryza rufipogon</i> Species Complex, Wild Relative of Cultivated Asian Rice. Rice, 2016, 9, 56.	1.7	80
43	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> . Acta Physiologiae Plantarum, 2016, 38, 1.	1.0	17
44	Redefining "stress resistance genes"™, and why it matters. Journal of Experimental Botany, 2016, 67, 5588-5591.	2.4	7
45	When more is better: how data sharing would accelerate genomic selection of crop plants. New Phytologist, 2016, 212, 814-826.	3.5	82
46	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.	3.3	94
47	Evolving technologies for growing, imaging and analyzing 3D root system architecture of crop plants. Journal of Integrative Plant Biology, 2016, 58, 230-241.	4.1	43
48	Evidence for divergence of response in <i>Indica</i> , <i>Japonica</i> , and wild rice to high CO ₂ Å— temperature interaction. Global Change Biology, 2016, 22, 2620-2632.	4.2	38
49	Dissection of the genetic architecture of rice resistance to the blast fungus <i>Magnaporthe oryzae</i> . Molecular Plant Pathology, 2016, 17, 959-972.	2.0	66
50	Genome-wide association and high-resolution phenotyping link <i>Oryza sativa</i> panicle traits to numerous trait-specific QTL clusters. Nature Communications, 2016, 7, 10527.	5.8	165
51	Genome-wide prediction models that incorporate de novo GWAS are a powerful new tool for tropical rice improvement. Heredity, 2016, 116, 395-408.	1.2	296
52	A genetic linkage map of coffee (<i>Coffea arabica</i> L.) and QTL for yield, plant height, and bean size. Tree Genetics and Genomes, 2016, 12, 1.	0.6	37
53	Genome-Wide Association Study for Traits Related to Plant and Grain Morphology, and Root Architecture in Temperate Rice Accessions. PLoS ONE, 2016, 11, e0155425.	1.1	80
54	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. G3: Genes, Genomes, Genetics, 2015, 5, 2267-2274.	0.8	31

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55	De Novo Transcriptome Assembly and Identification of Gene Candidates for Rapid Evolution of Soil Al Tolerance in <i>Anthoxanthum odoratum</i> at the Long-Term Park Grass Experiment. <i>PLoS ONE</i> , 2015, 10, e0124424.	1.1	11
56	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.	1.5	425
57	Genome-Wide Association Mapping for Yield and Other Agronomic Traits in an Elite Breeding Population of Tropical Rice (<i>Oryza sativa</i>). <i>PLoS ONE</i> , 2015, 10, e0119873.	1.1	157
58	<i>LABA1</i> , a Domestication Gene Associated with Long, Barbed Awns in Wild Rice. <i>Plant Cell</i> , 2015, 27, 1875-1888.	3.1	178
59	The Tyrosine Aminomutase TAM1 Is Required for β^2 -Tyrosine Biosynthesis in Rice. <i>Plant Cell</i> , 2015, 27, 1265-1278.	3.1	38
60	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. <i>Molecular Breeding</i> , 2015, 35, 81.	1.0	77
61	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.	0.6	39
62	Registration of the Rice Diversity Panel 1 for Genomewide Association Studies. <i>Journal of Plant Registrations</i> , 2014, 8, 109-116.	0.4	73
63	Natural variation of rice strigolactone biosynthesis is associated with the deletion of two <i>MAX1</i> orthologs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2379-2384.	3.3	138
64	Harvesting the Promising Fruits of Genomics: Applying Genome Sequencing Technologies to Crop Breeding. <i>PLoS Biology</i> , 2014, 12, e1001883.	2.6	341
65	New Horizons for Plant Translational Research. <i>PLoS Biology</i> , 2014, 12, e1001880.	2.6	10
66	High-Resolution Inflorescence Phenotyping Using a Novel Image-Analysis Pipeline, PANorama. <i>Plant Physiology</i> , 2014, 165, 479-495.	2.3	63
67	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.	3.8	228
68	N- and P-mediated seminal root elongation response in rice seedlings. <i>Plant and Soil</i> , 2014, 375, 303-315.	1.8	34
69	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.	2.0	20
70	Nuclear and chloroplast diversity and phenotypic distribution of rice (<i>Oryza sativa</i> L.) germplasm from the democratic people's republic of Korea (DPRK; North Korea). <i>Rice</i> , 2014, 7, 7.	1.7	14
71	Natural variation underlies alterations in Nramp aluminum transporter (<i>NRAT1</i>) expression and function that play a key role in rice aluminum tolerance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6503-6508.	3.3	160
72	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.	13.9	123

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73	Segregation analysis of molecular markers in a population derived from <i>Coffea liberica</i> Hiern x <i>C. eugenioides</i> L.. <i>Acta Agronomica</i> , 2014, 63, 153-163.	0.0	1
74	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.	1.8	228
75	A genome scale metabolic network for rice and accompanying analysis of tryptophan, auxin and serotonin biosynthesis regulation under biotic stress. <i>Rice</i> , 2013, 6, 15.	1.7	101
76	Multi-parent advanced generation inter-cross (MAGIC) populations in rice: progress and potential for genetics research and breeding. <i>Rice</i> , 2013, 6, 11.	1.7	361
77	A genetic map of an interspecific diploid pseudo testcross population of coffee. <i>Euphytica</i> , 2013, 192, 305-323.	0.6	17
78	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.	2.8	184
79	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.	1.8	512
80	Validation of yield-enhancing quantitative trait loci from a low-yielding wild ancestor of rice. <i>Molecular Breeding</i> , 2013, 32, 101-120.	1.0	34
81	Feeding the future. <i>Nature</i> , 2013, 499, 23-24.	13.7	464
82	Multiple and independent origins of short seeded alleles of <i>GS3</i> in rice. <i>Breeding Science</i> , 2013, 63, 77-85.	0.9	44
83	Getting to the roots of it: Genetic and hormonal control of root architecture. <i>Frontiers in Plant Science</i> , 2013, 4, 186.	1.7	254
84	Crop Technologies for the Coming Decade. , 2013, , 169-200.		1
85	Genomics of gene banks: A case study in rice. <i>American Journal of Botany</i> , 2012, 99, 407-423.	0.8	152
86	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2012, 30, 105-111.	9.4	818
87	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.	1.1	23
88	High-throughput single nucleotide polymorphism genotyping for breeding applications in rice using the BeadXpress platform. <i>Molecular Breeding</i> , 2012, 29, 875-886.	1.0	139
89	Three-Dimensional Root Phenotyping with a Novel Imaging and Software Platform. <i>Plant Physiology</i> , 2011, 156, 455-465.	2.3	380
90	Genome-wide association mapping reveals a rich genetic architecture of complex traits in <i>Oryza sativa</i> . <i>Nature Communications</i> , 2011, 2, 467.	5.8	1,230

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91	Genotype and environment effects on rice (<i>Oryza sativa</i> L.) grain arsenic concentration in Bangladesh. <i>Plant and Soil</i> , 2011, 338, 367-382.	1.8	99
92	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.	1.2	14
93	A Rice Diversity Panel Evaluated for Genetic and Agro-Morphological Diversity between Subpopulations and its Geographic Distribution. <i>Crop Science</i> , 2011, 51, 2021-2035.	0.8	83
94	Gramene database in 2010: updates and extensions. <i>Nucleic Acids Research</i> , 2011, 39, D1085-D1094.	6.5	182
95	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.	1.5	334
96	A universal core genetic map for rice. <i>Theoretical and Applied Genetics</i> , 2010, 120, 563-572.	1.8	60
97	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.	1.8	26
98	Genetic Analysis of Water Use Efficiency in Rice (<i>Oryza sativa</i> L.) at the Leaf Level. <i>Rice</i> , 2010, 3, 72-86.	1.7	32
99	Development of a Research Platform for Dissecting Phenotype-Genotype Associations in Rice (<i>Oryza</i>) Tj ETQq1 1.0.784314.rgBT /O	1.7	75
100	Identification of quantitative trait loci for physical and chemical properties of rice grain. <i>Plant Biotechnology Reports</i> , 2010, 4, 61-73.	0.9	16
101	The genetic origin of fragrance in NERICA1. <i>Molecular Breeding</i> , 2010, 26, 419-424.	1.0	10
102	Inactivation of the CTD phosphatase-like gene <i>OsCPL1</i> enhances the development of the abscission layer and seed shattering in rice. <i>Plant Journal</i> , 2010, 61, 96-106.	2.8	89
103	The Gramene Genetic Diversity Module: a resource for genotype-phenotype association analysis in grass species. <i>Nature Precedings</i> , 2010, , .	0.1	3
104	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.	2.3	199
105	ALCHEMY: a reliable method for automated SNP genotype calling for small batch sizes and highly homozygous populations. <i>Bioinformatics</i> , 2010, 26, 2952-2960.	1.8	46
106	Development of genome-wide SNP assays for rice. <i>Breeding Science</i> , 2010, 60, 524-535.	0.9	180
107	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.	1.1	250
108	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.	3.3	288

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109	Gramene QTL database: development, content and applications. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap005.	1.4	95
110	Analysis of genetic structure in a sample of coffee (<i>Coffea arabica</i> L.) using fluorescent SSR markers. Tree Genetics and Genomes, 2009, 5, 435-446.	0.6	27
111	Genetic Diversity of Isolated Populations of Indonesian Landraces of Rice (<i>Oryza sativa</i> L.) Collected in East Kalimantan on the Island of Borneo. Rice, 2009, 2, 80-92.	1.7	41
112	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.	1.8	85
113	Marker Assisted Breeding. , 2009, , 451-469.		27
114	Evolutionary History of <i>GS3</i> , a Gene Conferring Grain Length in Rice. Genetics, 2009, 182, 1323-1334.	1.2	305
115	Not just a grain of rice: the quest for quality. Trends in Plant Science, 2009, 14, 133-139.	4.3	643
116	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.	1.8	142
117	The Plant Ontology Database: a community resource for plant structure and developmental stages controlled vocabulary and annotations. Nucleic Acids Research, 2008, 36, D449-D454.	6.5	135
118	The Extent of Linkage Disequilibrium in Rice (<i>Oryza sativa</i> L.). Genetics, 2007, 177, 2223-2232.	1.2	331
119	Global Dissemination of a Single Mutation Conferring White Pericarp in Rice. PLoS Genetics, 2007, 3, e133.	1.5	228
120	Genome-Wide Patterns of Nucleotide Polymorphism in Domesticated Rice. PLoS Genetics, 2007, 3, e163.	1.5	406
121	The Plant Structure Ontology, a Unified Vocabulary of Anatomy and Morphology of a Flowering Plant. Plant Physiology, 2007, 143, 587-599.	2.3	91
122	Use of Naturally Occurring Alleles for Crop Improvement. , 2007, , 107-147.		3
123	The Complex History of the Domestication of Rice. Annals of Botany, 2007, 100, 951-957.	1.4	393
124	Identification of Quantitative Trait Loci in Rice for Yield, Yield Components, and Agronomic Traits across Years and Locations. Crop Science, 2007, 47, 2403-2417.	0.8	60
125	New insights into the history of rice domestication. Trends in Genetics, 2007, 23, 578-587.	2.9	443
126	Gramene: a growing plant comparative genomics resource. Nucleic Acids Research, 2007, 36, D947-D953.	6.5	151

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127	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.	1.8	171
128	Functional markers for xa5-mediated resistance in rice (<i>Oryza sativa</i> , L.). <i>Molecular Breeding</i> , 2007, 19, 291-296.	1.0	54
129	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.	0.6	163
130	Gramene: a bird's eye view of cereal genomes. <i>Nucleic Acids Research</i> , 2006, 34, D717-D723.	6.5	177
131	Caught Red-Handed: Rc Encodes a Basic Helix-Loop-Helix Protein Conditioning Red Pericarp in Rice. <i>Plant Cell</i> , 2006, 18, 283-294.	3.1	465
132	Genomic Variation in Rice: Genesis of Highly Polymorphic Linkage Blocks during Domestication. <i>PLoS Genetics</i> , 2006, 2, e199.	1.5	57
133	Characterization and Mapping of a Shattering Mutant in Rice That Corresponds to a Block of Domestication Genes. <i>Genetics</i> , 2006, 173, 995-1005.	1.2	108
134	Selection Under Domestication: Evidence for a Sweep in the Rice Waxy Genomic Region. <i>Genetics</i> , 2006, 173, 975-983.	1.2	246
135	Substitution Mapping of dth1.1, a Flowering-Time Quantitative Trait Locus (QTL) Associated With Transgressive Variation in Rice, Reveals Multiple Sub-QTL. <i>Genetics</i> , 2006, 172, 2501-2514.	1.2	73
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.	1.1	27
137	Plant Ontology (PO): a Controlled Vocabulary of Plant Structures and Growth Stages. <i>Comparative and Functional Genomics</i> , 2005, 6, 388-397.	2.0	129
138	How Can We Use Genomics to Improve Cereals with Rice as a Reference Genome?. <i>Plant Molecular Biology</i> , 2005, 59, 7-26.	2.0	59
139	Population Structure and Breeding Patterns of 145 U.S. Rice Cultivars Based on SSR Marker Analysis. <i>Crop Science</i> , 2005, 45, 66-76.	0.8	135
140	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.	2.4	197
141	Genetic Structure and Diversity in <i>Oryza sativa</i> L.. <i>Genetics</i> , 2005, 169, 1631-1638.	1.2	988
142	The Population Structure of African Cultivated Rice <i>Oryza glaberrima</i> (Steud.). <i>Genetics</i> , 2005, 169, 1639-1647.	1.2	145
143	Global dissemination of a single mutation conferring white pericarp in rice. <i>PLoS Genetics</i> , 2005, preprint, e133.	1.5	1
144	A Marker-Based Approach to Broadening the Genetic Base of Rice in the USA. <i>Crop Science</i> , 2004, 44, 1947-1959.	0.8	80

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145	Fine Mapping of a Grain-Weight Quantitative Trait Locus in the Pericentromeric Region of Rice Chromosome 3. <i>Genetics</i> , 2004, 168, 2187-2195.	1.2	178
146	Diversifying Selection in Plant Breeding. <i>PLoS Biology</i> , 2004, 2, e347.	2.6	215
147	Genetic analysis of Indian aromatic and quality rice (<i>Oryza sativa</i> L.) germplasm using panels of fluorescently-labeled microsatellite markers. <i>Theoretical and Applied Genetics</i> , 2004, 109, 965-977.	1.8	158
148	Simple sequence repeat diversity in diploid and tetraploid <i>Coffea</i> species. <i>Genome</i> , 2004, 47, 501-509.	0.9	71
149	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.	1.4	290
150	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.	0.9	208
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