

Susan R Mccouch

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

175
papers

21,863
citations

75
h-index

147
g-index

194
ext. papers

25,581
ext. citations

7.2
avg, IF

6.66
L-index

#	Paper	IF	Citations
175	Reap the crop wild relatives for breeding future crops. <i>Trends in Biotechnology</i> , 2021 ,	15.1	21
174	Genetic mapping identifies a rice naringenin O-glucosyltransferase that influences insect resistance. <i>Plant Journal</i> , 2021 , 106, 1401-1413	6.9	6
173	Genetic architecture of root and shoot ionomes in rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2021 , 134, 2613-2637	6	1
172	Addressing Research Bottlenecks to Crop Productivity. <i>Trends in Plant Science</i> , 2021 , 26, 607-630	13.1	20
171	Phenotypic response of farmer-selected CWR-derived rice lines to salt stress in the Mekong Delta. <i>Crop Science</i> , 2021 , 61, 201-218	2.4	7
170	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	2.4	11
169	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	11.5	6
168	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	3.7	13
167	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	6.2	22
166	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	7	6
165	Genome wide association studies for japonica rice resistance to blast in field and controlled conditions. <i>Rice</i> , 2020 , 13, 71	5.8	6
164	Association mapping and genetic dissection of drought-induced canopy temperature differences in rice. <i>Journal of Experimental Botany</i> , 2020 , 71, 1614-1627	7	11
163	Low Additive Genetic Variation in a Trait Under Selection in Domesticated Rice. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 2435-2443	3.2	5
162	A Coordinated Suite of Wild-Introgression Lines in and Elite Backgrounds. <i>Frontiers in Plant Science</i> , 2020 , 11, 564824	6.2	3
161	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020 , 13, 1341-1344	14.4	21
160	Multiple Small-Effect Alleles of Origin Enhance High Iron-Associated Stress Tolerance in Rice Under Field Conditions in West Africa. <i>Frontiers in Plant Science</i> , 2020 , 11, 604938	6.2	1
159	Validation of Yield Component Traits Identified by Genome-Wide Association Mapping in a Rice Biparental Mapping Population. <i>Plant Genome</i> , 2019 , 12, 180021	4.4	9

158	Integrating Molecular Markers and Environmental Covariates To Interpret Genotype by Environment Interaction in Rice (L.) Grown in Subtropical Areas. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 1519-1531	3.2	21
157	A SWEET solution to rice blight. <i>Nature Biotechnology</i> , 2019 , 37, 1280-1282	44.5	16
156	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	9.8	59
155	Multienvironment Models Increase Prediction Accuracy of Complex Traits in Advanced Breeding Lines of Rice. <i>Crop Science</i> , 2018 , 58, 1519-1530	2.4	18
154	Ethylene-gibberellin signaling underlies adaptation of rice to periodic flooding. <i>Science</i> , 2018 , 361, 181-186	39.3	89
153	Genomic regions responsible for seminal and crown root lengths identified by 2D & 3D root system image analysis. <i>BMC Genomics</i> , 2018 , 19, 273	4.5	10
152	Resistance to Multiple Temperate and Tropical Stem and Sheath Diseases of Rice. <i>Plant Genome</i> , 2018 , 11, 170029	4.4	5
151	Genome-Wide Association Study Using Historical Breeding Populations Discovers Genomic Regions Involved in High-Quality Rice. <i>Plant Genome</i> , 2018 , 11, 170076	4.4	12
150	An imputation platform to enhance integration of rice genetic resources. <i>Nature Communications</i> , 2018 , 9, 3519	17.4	39
149	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	9.8	16
148	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017 , 18, 541	4.5	33
147	Large-scale deployment of a rice 6K SNP array for genetics and breeding applications. <i>Rice</i> , 2017 , 10, 40	5.8	60
146	() contributes to natural variation in aluminum resistance in diverse genetic backgrounds of rice (). <i>Plant Direct</i> , 2017 , 1, e00014	3.3	14
145	Metabolomics and genomics combine to unravel the pathway for the presence of fragrance in rice. <i>Scientific Reports</i> , 2017 , 7, 8767	4.9	25
144	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	3.7	75
143	Functional properties of an alternative, tissue-specific promoter for rice NADPH-dependent dihydroflavonol reductase. <i>PLoS ONE</i> , 2017 , 12, e0183722	3.7	5
142	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
141	Evidence for divergence of response in Indica, Japonica, and wild rice to high CO2 [temperature interaction. <i>Global Change Biology</i> , 2016 , 22, 2620-32	11.4	24

140	Dissection of the genetic architecture of rice resistance to the blast fungus <i>Magnaporthe oryzae</i> . <i>Molecular Plant Pathology</i> , 2016 , 17, 959-72	5.7	49
139	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	17.4	99
138	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	3.6	173
137	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	2.1	22
136	Genome-Wide Association Study for Traits Related to Plant and Grain Morphology, and Root Architecture in Temperate Rice Accessions. <i>PLoS ONE</i> , 2016 , 11, e0155425	3.7	56
135	Whole-genome characterization in pedigreed non-human primates using genotyping-by-sequencing (GBS) and imputation. <i>BMC Genomics</i> , 2016 , 17, 676	4.5	6
134	Transgressive Variation for Yield Components Measured throughout the Growth Cycle of Jefferson Rice (<i>Oryza sativa</i>) ID. <i>rufipogon</i> Introgression Lines. <i>Crop Science</i> , 2016 , 56, 2336-2347	2.4	2
133	Robust phenotyping strategies for evaluation of stem non-structural carbohydrates (NSC) in rice. <i>Journal of Experimental Botany</i> , 2016 , 67, 6125-6138	7	19
132	Open access resources for genome-wide association mapping in rice. <i>Nature Communications</i> , 2016 , 7, 10532	17.4	229
131	Population Dynamics Among six Major Groups of the <i>Oryza rufipogon</i> Species Complex, Wild Relative of Cultivated Asian Rice. <i>Rice</i> , 2016 , 9, 56	5.8	32
130	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	2.6	14
129	Redefining stress resistance genes and why it matters. <i>Journal of Experimental Botany</i> , 2016 , 67, 5588-5591	3	
128	When more is better: how data sharing would accelerate genomic selection of crop plants. <i>New Phytologist</i> , 2016 , 212, 814-826	9.8	51
127	Loss of function at RAE2, a previously unidentified EPFL, is required for awnlessness in cultivated Asian rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 8969-74	11.5	55
126	Evolving technologies for growing, imaging and analyzing 3D root system architecture of crop plants. <i>Journal of Integrative Plant Biology</i> , 2016 , 58, 230-41	8.3	30
125	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	6	277
124	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	3.7	105
123	LABA1, a Domestication Gene Associated with Long, Barbed Awns in Wild Rice. <i>Plant Cell</i> , 2015 , 27, 1875-88	5.8	111

122	The Tyrosine Aminomutase TAM1 Is Required for Tyrosine Biosynthesis in Rice. <i>Plant Cell</i> , 2015 , 27, 1265-78	11.6	29
121	Development and GBS-genotyping of introgression lines (ILs) using two wild species of rice, and in a common recurrent parent, cv. Curinga. <i>Molecular Breeding</i> , 2015 , 35, 81	3.4	57
120	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	2.1	30
119	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, 2267-74	3.2	21
118	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	3.7	10
117	N- and P-mediated seminal root elongation response in rice seedlings. <i>Plant and Soil</i> , 2014 , 375, 303-315	4.2	24
116	Variation in soil aluminium tolerance genes is associated with local adaptation to soils at the Park Grass Experiment. <i>Molecular Ecology</i> , 2014 , 23, 6058-72	5.7	18
115	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	5.8	9
114	Natural variation underlies alterations in Nramp aluminum transporter (NRAT1) 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, 6503-8	11.5	104
113	Registration of the Rice Diversity Panel 1 for Genomewide Association Studies. <i>Journal of Plant Registrations</i> , 2014 , 8, 109-116	0.7	56
112	Natural variation of rice strigolactone biosynthesis is associated with the deletion of two MAX1 orthologs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 2379-84	11.5	96
111	Harvesting the promising fruits of genomics: applying genome sequencing technologies to crop breeding. <i>PLoS Biology</i> , 2014 , 12, e1001883	9.7	256
110	High-Resolution Inflorescence Phenotyping Using a Novel Image-Analysis Pipeline, PANorama. <i>Plant Physiology</i> , 2014 , 165, 479-495	6.6	47
109	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	18.3	168
108	Whole genome de novo assemblies of three divergent strains of rice, <i>Oryza sativa</i> , document novel gene space of aus and indica 2014 , 15, 506		105
107	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	0.4	1
106	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, 2699-716	6	194
105	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	5.8	72

104	Multi-parent advanced generation inter-cross (MAGIC) populations in rice: progress and potential for genetics research and breeding. <i>Rice</i> , 2013 , 6, 11	5.8	237
103	A genetic map of an interspecific diploid pseudo testcross population of coffee. <i>Euphytica</i> , 2013 , 192, 305-323	2.1	14
102	High-throughput two-dimensional root system phenotyping platform facilitates genetic analysis of root growth and development. <i>Plant, Cell and Environment</i> , 2013 , 36, 454-66	8.4	133
101	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, 867-87	6	398
100	Validation of yield-enhancing quantitative trait loci from a low-yielding wild ancestor of rice. <i>Molecular Breeding</i> , 2013 , 32, 101-120	3.4	27
99	Agriculture: Feeding the future. <i>Nature</i> , 2013 , 499, 23-4	50.4	363
98	Multiple and independent origins of short seeded alleles of GS3 in rice. <i>Breeding Science</i> , 2013 , 63, 77-85		27
97	Getting to the roots of it: Genetic and hormonal control of root architecture. <i>Frontiers in Plant Science</i> , 2013 , 4, 186	6.2	179
96	Genomics of gene banks: A case study in rice. <i>American Journal of Botany</i> , 2012 , 99, 407-23	2.7	124
95	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	3.7	20
94	High-throughput single nucleotide polymorphism genotyping for breeding applications in rice using the BeadXpress platform. <i>Molecular Breeding</i> , 2012 , 29, 875-886	3.4	117
93	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2011 , 30, 105-11	44.5	635
92	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	4.2	80
91	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	4.5	13
90	Three-dimensional root phenotyping with a novel imaging and software platform. <i>Plant Physiology</i> , 2011 , 156, 455-65	6.6	306
89	Genome-wide association mapping reveals a rich genetic architecture of complex traits in <i>Oryza sativa</i> . <i>Nature Communications</i> , 2011 , 2, 467	17.4	875
88	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	2.4	64
87	Gramene database in 2010: updates and extensions. <i>Nucleic Acids Research</i> , 2011 , 39, D1085-94	20.1	145

86	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	6	278
85	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	6.9	66
84	The Gramene Genetic Diversity Module: a resource for genotype-phenotype association analysis in grass species. <i>Nature Precedings</i> , 2010 ,		2
83	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, 1678-91	6.6	143
82	ALCHEMY: a reliable method for automated SNP genotype calling for small batch sizes and highly homozygous populations. <i>Bioinformatics</i> , 2010 , 26, 2952-60	7.2	45
81	Development of genome-wide SNP assays for rice. <i>Breeding Science</i> , 2010 , 60, 524-535	2	149
80	A universal core genetic map for rice. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 563-72	6	39
79	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	6	25
78	Genetic Analysis of Water Use Efficiency in Rice (<i>Oryza sativa</i> L.) at the Leaf Level. <i>Rice</i> , 2010 , 3, 72-86	5.8	25
77	Development of a Research Platform for Dissecting Phenotype-Genotype Associations in Rice (<i>Oryza</i> spp.). <i>Rice</i> , 2010 , 3, 205-217	5.8	62
76	Identification of quantitative trait loci for physical and chemical properties of rice grain. <i>Plant Biotechnology Reports</i> , 2010 , 4, 61-73	2.5	11
75	The genetic origin of fragrance in NERICA1. <i>Molecular Breeding</i> , 2010 , 26, 419-424	3.4	10
74	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	3.7	209
73	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, 14444-9	11.5	225
72	Gramene QTL database: development, content and applications. <i>Database: the Journal of Biological Databases and Curation</i> , 2009 , 2009, bap005	5	59
71	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	2.1	25
70	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	5.8	25
69	Leaf-level water use efficiency determined by carbon isotope discrimination in rice seedlings: genetic variation associated with population structure and QTL mapping. <i>Theoretical and Applied Genetics</i> , 2009 , 118, 1065-81	6	77

68	Marker Assisted Breeding 2009 , 451-469		10
67	Evolutionary history of GS3, a gene conferring grain length in rice. <i>Genetics</i> , 2009 , 182, 1323-34	4	242
66	Not just a grain of rice: the quest for quality. <i>Trends in Plant Science</i> , 2009 , 14, 133-9	13.1	466
65	The Plant Ontology Database: a community resource for plant structure and developmental stages controlled vocabulary and annotations. <i>Nucleic Acids Research</i> , 2008 , 36, D449-54	20.1	115
64	Gramene: a growing plant comparative genomics resource. <i>Nucleic Acids Research</i> , 2008 , 36, D947-53	20.1	130
63	Fine mapping of a yield-enhancing QTL cluster associated with transgressive variation in an <i>Oryza sativa</i> x <i>O. rufipogon</i> cross. <i>Theoretical and Applied Genetics</i> , 2008 , 116, 613-22	6	117
62	Identification of Quantitative Trait Loci in Rice for Yield, Yield Components, and Agronomic Traits across Years and Locations. <i>Crop Science</i> , 2007 , 47, 2403-2417	2.4	49
61	New insights into the history of rice domestication. <i>Trends in Genetics</i> , 2007 , 23, 578-87	8.5	328
60	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, 559-68	6	133
59	Functional markers for xa5-mediated resistance in rice (<i>Oryza sativa</i> , L.). <i>Molecular Breeding</i> , 2007 , 19, 291-296	3.4	47
58	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	2.1	135
57	The extent of linkage disequilibrium in rice (<i>Oryza sativa</i> L.). <i>Genetics</i> , 2007 , 177, 2223-32	4	238
56	Global dissemination of a single mutation conferring white pericarp in rice. <i>PLoS Genetics</i> , 2007 , 3, e133 6		190
55	Genome-wide patterns of nucleotide polymorphism in domesticated rice. <i>PLoS Genetics</i> , 2007 , 3, 1745-56		334
54	The plant structure ontology, a unified vocabulary of anatomy and morphology of a flowering plant. <i>Plant Physiology</i> , 2007 , 143, 587-99	6.6	79
53	Use of Naturally Occurring Alleles for Crop Improvement 2007 , 107-147		3
52	The complex history of the domestication of rice. <i>Annals of Botany</i> , 2007 , 100, 951-7	4.1	302
51	Caught red-handed: Rc encodes a basic helix-loop-helix protein conditioning red pericarp in rice. <i>Plant Cell</i> , 2006 , 18, 283-94	11.6	362

50	Genomic variation in rice: genesis of highly polymorphic linkage blocks during domestication. <i>PLoS Genetics</i> , 2006 , 2, e199	6	52
49	Characterization and mapping of a shattering mutant in rice that corresponds to a block of domestication genes. <i>Genetics</i> , 2006 , 173, 995-1005	4	63
48	Selection under domestication: evidence for a sweep in the rice waxy genomic region. <i>Genetics</i> , 2006 , 173, 975-83	4	201
47	Substitution mapping of <i>dth1.1</i> , a flowering-time quantitative trait locus (QTL) associated with transgressive variation in rice, reveals multiple sub-QTL. <i>Genetics</i> , 2006 , 172, 2501-14	4	66
46	Gramene: a bird's eye view of cereal genomes. <i>Nucleic Acids Research</i> , 2006 , 34, D717-23	20.1	162
45	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> , 2006 , 32, 1089-1105	2.7	25
44	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> , 2006 , 16, 140-7	9.7	177
43	Genetic structure and diversity in <i>Oryza sativa</i> L. <i>Genetics</i> , 2005 , 169, 1631-8	4	737
42	The population structure of African cultivated rice <i>oryza glaberrima</i> (Steud.): evidence for elevated levels of linkage disequilibrium caused by admixture with <i>O. sativa</i> and ecological adaptation. <i>Genetics</i> , 2005 , 169, 1639-47	4	117
41	Plant Ontology (PO): a Controlled Vocabulary of Plant Structures and Growth Stages. <i>Comparative and Functional Genomics</i> , 2005 , 6, 388-97		109
40	How can we use genomics to improve cereals with rice as a reference genome?. <i>Plant Molecular Biology</i> , 2005 , 59, 7-26	4.6	51
39	Population Structure and Breeding Patterns of 145 U.S. Rice Cultivars Based on SSR Marker Analysis. <i>Crop Science</i> , 2005 , 45, 66-76	2.4	106
38	Global dissemination of a single mutation conferring white pericarp in rice. <i>PLoS Genetics</i> , 2005 , preprint, e133	6	
37	A Marker-Based Approach to Broadening the Genetic Base of Rice in the USA. <i>Crop Science</i> , 2004 , 44, 1947-1959	2.4	67
36	Fine mapping of a grain-weight quantitative trait locus in the pericentromeric region of rice chromosome 3. <i>Genetics</i> , 2004 , 168, 2187-95	4	152
35	Diversifying selection in plant breeding. <i>PLoS Biology</i> , 2004 , 2, e347	9.7	160
34	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, 965-77	6	129
33	Simple sequence repeat diversity in diploid and tetraploid <i>Coffea</i> species. <i>Genome</i> , 2004 , 47, 501-9	2.4	60

32	The rice bacterial blight resistance gene xa5 encodes a novel form of disease resistance. <i>Molecular Plant-Microbe Interactions</i> , 2004 , 17, 1348-54	3.6	239
31	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	2.4	179
30	High resolution genetic mapping and candidate gene identification at the xa5 locus for bacterial blight resistance in rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2003 , 107, 62-73	6	52
29	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, 479-93	6	392
28	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, 1419-32	6	229
27	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, 1433-41	6	140
26	A graph-theoretic approach to comparing and integrating genetic, physical and sequence-based maps. <i>Genetics</i> , 2003 , 165, 2235-47	4	46
25	Population structure and its effect on haplotype diversity and linkage disequilibrium surrounding the xa5 locus of rice (<i>Oryza sativa</i> L.). <i>Genetics</i> , 2003 , 165, 759-69	4	184
24	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	6	41
23	Gramene, a tool for grass genomics. <i>Plant Physiology</i> , 2002 , 130, 1606-13	6.6	162
22	Development and mapping of 2240 new SSR markers for rice (<i>Oryza sativa</i> L.) (supplement). <i>DNA Research</i> , 2002 , 9, 257-79	4.5	107
21	Design and Application of Microsatellite Marker Panels for Semiautomated Genotyping of Rice (<i>Oryza sativa</i> L.). <i>Crop Science</i> , 2002 , 42, 2092-2099	2.4	56
20	Development and mapping of 2240 new SSR markers for rice (<i>Oryza sativa</i> L.). <i>DNA Research</i> , 2002 , 9, 199-207	4.5	1009
19	Genomics and synteny. <i>Plant Physiology</i> , 2001 , 125, 152-5	6.6	30
18	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, 1441-52	9.7	1103
17	Rice PHYC gene: structure, expression, map position and evolution. <i>Plant Molecular Biology</i> , 2000 , 44, 27-42	4.6	54
16	Microsatellites and microsynteny in the chloroplast genomes of <i>Oryza</i> and eight other Gramineae species. <i>Theoretical and Applied Genetics</i> , 2000 , 100, 1257-1266	6	75
15	Algorithms for Constructing Comparative Maps. <i>Computational Biology</i> , 2000 , 243-261	0.7	5

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13	Anchor probes for comparative mapping of grass genera. <i>Theoretical and Applied Genetics</i> , 1998 , 97, 356-369	6	115
12	Integrated map of AFLP, SSLP and RFLP markers using a recombinant inbred population of rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 1998 , 97, 370-380	6	56
11	Transgressive Segregation of Tiller Angle in Rice Caused by Complementary Gene Action. <i>Crop Science</i> , 1998 , 38, 12-19	2.4	33
10	Identification of trait-improving quantitative trait loci alleles from a wild rice relative, <i>Oryza rufipogon</i> . <i>Genetics</i> , 1998 , 150, 899-909	4	392
9	Comparative evaluation of within-cultivar variation of rice (<i>Oryza sativa</i> L.) using microsatellite and RFLP markers. <i>Genome</i> , 1997 , 40, 370-8	2.4	114
8	Seed banks and molecular maps: unlocking genetic potential from the wild. <i>Science</i> , 1997 , 277, 1063-6	33.3	1630
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5	Cloning and mapping of variety-specific rice genomic DNA sequences: amplified fragment length polymorphisms (AFLP) from silver-stained polyacrylamide gels. <i>Genome</i> , 1996 , 39, 373-8	2.4	103
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3	Comparative mapping in grasses. Wheat relationships. <i>Molecular Genetics and Genomics</i> , 1995 , 248, 744-54		166
2	The Dynamics of Rice Domestication: A Balance between Gene Flow and Genetic Isolation	311-329	3
1	New whole genome de novo assemblies of three divergent strains of rice (<i>O. sativa</i>) documents novel gene space of aus and indica		5