

Susan R Mccouch

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175
papers

21,863
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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	Seed banks and molecular maps: unlocking genetic potential from the wild. <i>Science</i> , 1997 , 277, 1063-6	33.3	1630
174	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
173	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
172	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
171	Genetic structure and diversity in <i>Oryza sativa</i> L. <i>Genetics</i> , 2005 , 169, 1631-8	4	737
170	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
169	Not just a grain of rice: the quest for quality. <i>Trends in Plant Science</i> , 2009 , 14, 133-9	13.1	466
168	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
167	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
166	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
165	Agriculture: Feeding the future. <i>Nature</i> , 2013 , 499, 23-4	50.4	363
164	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
163	Genome-wide patterns of nucleotide polymorphism in domesticated rice. <i>PLoS Genetics</i> , 2007 , 3, 1745-56		334
162	New insights into the history of rice domestication. <i>Trends in Genetics</i> , 2007 , 23, 578-87	8.5	328
161	Three-dimensional root phenotyping with a novel imaging and software platform. <i>Plant Physiology</i> , 2011 , 156, 455-65	6.6	306
160	The complex history of the domestication of rice. <i>Annals of Botany</i> , 2007 , 100, 951-7	4.1	302
159	Genes from wild rice improve yield. <i>Nature</i> , 1996 , 384, 223-224	50.4	289

158	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
157	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
156	Harvesting the promising fruits of genomics: applying genome sequencing technologies to crop breeding. <i>PLoS Biology</i> , 2014 , 12, e1001883	9.7	256
155	Microsatellite marker development, mapping and applications in rice genetics and breeding. <i>Plant Molecular Biology</i> , 1997 , 35, 89-99	4.6	252
154	Evolutionary history of GS3, a gene conferring grain length in rice. <i>Genetics</i> , 2009 , 182, 1323-34	4	242
153	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
152	The extent of linkage disequilibrium in rice (<i>Oryza sativa</i> L.). <i>Genetics</i> , 2007 , 177, 2223-32	4	238
151	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
150	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
149	Open access resources for genome-wide association mapping in rice. <i>Nature Communications</i> , 2016 , 7, 10532	17.4	229
148	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
147	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
146	Selection under domestication: evidence for a sweep in the rice waxy genomic region. <i>Genetics</i> , 2006 , 173, 975-83	4	201
145	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
144	Global dissemination of a single mutation conferring white pericarp in rice. <i>PLoS Genetics</i> , 2007 , 3, e1336	6	190
143	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
142	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
141	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

140	The Oryza 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 Oryza. <i>Genome Research</i> , 2006 , 16, 140-7	9.7	177
139	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
138	Whole genome de novo assemblies of three divergent strains of rice, Oryza sativa, document novel gene space of aus and indica. <i>Genome Biology</i> , 2014 , 15, 506	18.3	168
137	Comparative mapping in grasses. Wheat relationships. <i>Molecular Genetics and Genomics</i> , 1995 , 248, 744-54		166
136	Gramene: a bird's eye view of cereal genomes. <i>Nucleic Acids Research</i> , 2006 , 34, D717-23	20.1	162
135	Gramene, a tool for grass genomics. <i>Plant Physiology</i> , 2002 , 130, 1606-13	6.6	162
134	Diversifying selection in plant breeding. <i>PLoS Biology</i> , 2004 , 2, e347	9.7	160
133	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
132	Development of genome-wide SNP assays for rice. <i>Breeding Science</i> , 2010 , 60, 524-535	2	149
131	Gramene database in 2010: updates and extensions. <i>Nucleic Acids Research</i> , 2011 , 39, D1085-94	20.1	145
130	Tagging and combining bacterial blight resistance genes in rice using RAPD and RFLP markers. <i>Molecular Breeding</i> , 1995 , 1, 375-387	3.4	144
129	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
128	Identification of quantitative trait loci for grain quality in an advanced backcross population derived from the Oryza sativa variety IR64 and the wild relative O. rufipogon. <i>Theoretical and Applied Genetics</i> , 2003 , 107, 1433-41	6	140
127	Through the genetic bottleneck: O. rufipogon as a source of trait-enhancing alleles for O. sativa. <i>Euphytica</i> , 2007 , 154, 317-339	2.1	135
126	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
125	Genetic diversity analysis of traditional and improved Indonesian rice (Oryza sativa L.) germplasm using microsatellite markers. <i>Theoretical and Applied Genetics</i> , 2007 , 114, 559-68	6	133
124	Inferences on the genome structure of progenitor maize through comparative analysis of rice, maize and the domesticated panicoids. <i>Genetics</i> , 1999 , 153, 453-73	4	131
123	Gramene: a growing plant comparative genomics resource. <i>Nucleic Acids Research</i> , 2008 , 36, D947-53	20.1	130

122	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
121	Genomics of gene banks: A case study in rice. <i>American Journal of Botany</i> , 2012 , 99, 407-23	2.7	124
120	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
119	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
118	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
117	Anchor probes for comparative mapping of grass genera. <i>Theoretical and Applied Genetics</i> , 1998 , 97, 3566-69	3.6	115
116	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
115	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
114	LABA1, a Domestication Gene Associated with Long, Barbed Awns in Wild Rice. <i>Plant Cell</i> , 2015 , 27, 1875-88	5.8	111
113	Plant Ontology (PO): a Controlled Vocabulary of Plant Structures and Growth Stages. <i>Comparative and Functional Genomics</i> , 2005 , 6, 388-97		109
112	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
111	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
110	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
109	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
108	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
107	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
106	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
105	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

104	Ethylene-gibberellin signaling underlies adaptation of rice to periodic flooding. <i>Science</i> , 2018 , 361, 181-186	3.6	89
103	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
102	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
101	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
100	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
99	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
98	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
97	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
96	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
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. <i>Genetics</i> , 2006 , 172, 2501-14	4	66
94	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
93	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
92	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
91	Large-scale deployment of a rice 6K SNP array for genetics and breeding applications. <i>Rice</i> , 2017 , 10, 40	5.8	60
90	Simple sequence repeat diversity in diploid and tetraploid <i>Coffea</i> species. <i>Genome</i> , 2004 , 47, 501-9	2.4	60
89	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
88	Gramene QTL database: development, content and applications. <i>Database: the Journal of Biological Databases and Curation</i> , 2009 , 2009, bap005	5	59
87	Development and GBS-genotyping of introgression lines (ILs) using two wild species of rice, and in a common recurrent parent, <i>cv. Curinga</i> . <i>Molecular Breeding</i> , 2015 , 35, 81	3.4	57

86	Registration of the Rice Diversity Panel 1 for Genomewide Association Studies. <i>Journal of Plant Registrations</i> , 2014 , 8, 109-116	0.7	56
85	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
84	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
83	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
82	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
81	Rice PHYC gene: structure, expression, map position and evolution. <i>Plant Molecular Biology</i> , 2000 , 44, 27-42	4.6	54
80	Genomic variation in rice: genesis of highly polymorphic linkage blocks during domestication. <i>PLoS Genetics</i> , 2006 , 2, e199	6	52
79	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
78	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
77	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
76	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
75	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
74	High-Resolution Inflorescence Phenotyping Using a Novel Image-Analysis Pipeline, PANorama. <i>Plant Physiology</i> , 2014 , 165, 479-495	6.6	47
73	Functional markers for xa5-mediated resistance in rice (<i>Oryza sativa</i> , L.). <i>Molecular Breeding</i> , 2007 , 19, 291-296	3.4	47
72	A graph-theoretic approach to comparing and integrating genetic, physical and sequence-based maps. <i>Genetics</i> , 2003 , 165, 2235-47	4	46
71	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
70	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
69	A universal core genetic map for rice. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 563-72	6	39

68	An imputation platform to enhance integration of rice genetic resources. <i>Nature Communications</i> , 2018 , 9, 3519	17.4	39
67	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017 , 18, 541	4.5	33
66	Transgressive Segregation of Tiller Angle in Rice Caused by Complementary Gene Action. <i>Crop Science</i> , 1998 , 38, 12-19	2.4	33
65	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
64	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
63	Genomics and synteny. <i>Plant Physiology</i> , 2001 , 125, 152-5	6.6	30
62	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
61	The Tyrosine Aminomutase TAM1 Is Required for Tyrosine Biosynthesis in Rice. <i>Plant Cell</i> , 2015 , 27, 1265-78	11.6	29
60	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
59	Multiple and independent origins of short seeded alleles of GS3 in rice. <i>Breeding Science</i> , 2013 , 63, 77-85		27
58	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
57	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
56	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
55	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
54	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
53	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
52	Evidence for divergence of response in Indica, Japonica, and wild rice to high CO ₂ × temperature interaction. <i>Global Change Biology</i> , 2016 , 22, 2620-32	11.4	24
51	N- and P-mediated seminal root elongation response in rice seedlings. <i>Plant and Soil</i> , 2014 , 375, 303-315	4.2	24

50	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
49	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
48	Integrating Molecular Markers and Environmental Covariates To Interpret Genotype by Environment Interaction in Rice (<i>L.</i>) Grown in Subtropical Areas. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 1519-1531	3.2	21
47	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
46	Reap the crop wild relatives for breeding future crops. <i>Trends in Biotechnology</i> , 2021 ,	15.1	21
45	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020 , 13, 1341-1344	14.4	21
44	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
43	Addressing Research Bottlenecks to Crop Productivity. <i>Trends in Plant Science</i> , 2021 , 26, 607-630	13.1	20
42	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
41	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
40	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
39	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
38	A SWEET solution to rice blight. <i>Nature Biotechnology</i> , 2019 , 37, 1280-1282	44.5	16
37	() contributes to natural variation in aluminum resistance in diverse genetic backgrounds of rice (). <i>Plant Direct</i> , 2017 , 1, e00014	3.3	14
36	A genetic map of an interspecific diploid pseudo testcross population of coffee. <i>Euphytica</i> , 2013 , 192, 305-323	2.1	14
35	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
34	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
33	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

32	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
31	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
30	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
29	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
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	4.5	10
27	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
26	Marker Assisted Breeding 2009 , 451-469		10
25	The genetic origin of fragrance in NERICA1. <i>Molecular Breeding</i> , 2010 , 26, 419-424	3.4	10
24	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
23	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
22	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
21	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
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