

# Jeremy Schmutz

## List of Publications by Year in descending order

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Version: 2024-02-01

257  
papers

85,187  
citations

2962

96  
h-index

788

254  
g-index

295  
all docs

295  
docs citations

295  
times ranked

80669  
citing authors

#	ARTICLE	IF	CITATIONS
1	Novel metabolic interactions and environmental conditions mediate the boreal peatmoss-cyanobacteria mutualism. <i>ISME Journal</i> , 2022, 16, 1074-1085.	4.4	25
2	Multiplex knockout of trichome-regulating MYB duplicates in hybrid poplar using a single gRNA. <i>Plant Physiology</i> , 2022, 189, 516-526.	2.3	18
3	The Common Bean <i>V</i> Gene Encodes Flavonoid 3- $\beta$ -Hydroxylase: A Major Mutational Target for Flavonoid Diversity in Angiosperms. <i>Frontiers in Plant Science</i> , 2022, 13, 869582.	1.7	7
4	Habitat-adapted microbial communities mediate <i>Sphagnum</i> peatmoss resilience to warming. <i>New Phytologist</i> , 2022, 234, 2111-2125.	3.5	18
5	Phylogenomics of the genus <i>Glycine</i> sheds light on polyploid evolution and life-strategy transition. <i>Nature Plants</i> , 2022, 8, 233-244.	4.7	26
6	A generalist-specialist trade-off between switchgrass cytotypes impacts climate adaptation and geographic range. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2118879119.	3.3	5
7	The recent evolutionary rescue of a staple crop depended on over half a century of global germplasm exchange. <i>Science Advances</i> , 2022, 8, eabj4633.	4.7	9
8	Representing sex chromosomes in genome assemblies. <i>Cell Genomics</i> , 2022, 2, 100132.	3.0	13
9	The Transcription Factor <i>Roc1</i> Is a Key Regulator of Cellulose Degradation in the Wood-Decaying Mushroom <i>Schizophyllum commune</i> . <i>MBio</i> , 2022, 13, .	1.8	10
10	Soybean ( <i>Glycine max</i> ) Haplotype Map (GmHapMap): a universal resource for soybean translational and functional genomics. <i>Plant Biotechnology Journal</i> , 2021, 19, 324-334.	4.1	48
11	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	13.7	144
12	Widespread polycistronic gene expression in green algae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	30
13	Extensive Genome-Wide Phylogenetic Discordance Is Due to Incomplete Lineage Sorting and Not Ongoing Introgression in a Rapidly Radiated Bryophyte Genus. <i>Molecular Biology and Evolution</i> , 2021, 38, 2750-2766.	3.5	54
14	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	3.1	180
15	Improved chromosome-level genome assembly and annotation of the seagrass, <i>Zostera marina</i> (eelgrass). <i>F1000Research</i> , 2021, 10, 289.	0.8	26
16	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. <i>Genome Research</i> , 2021, 31, 799-810.	2.4	21
17	The tepary bean genome provides insight into evolution and domestication under heat stress. <i>Nature Communications</i> , 2021, 12, 2638.	5.8	43
18	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	2.0	21

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19	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .	4.7	53
20	Genetic dissection of natural variation in oilseed traits of camelina by whole-genome resequencing and QTL mapping. <i>Plant Genome</i> , 2021, 14, e20110.	1.6	24
21	Genomic variation within the maize stiff-stalk heterotic germplasm pool. <i>Plant Genome</i> , 2021, 14, e20114.	1.6	14
22	Four chromosome scale genomes and a pan-genome annotation to accelerate pecan tree breeding. <i>Nature Communications</i> , 2021, 12, 4125.	5.8	49
23	Plant single-cell solutions for energy and the environment. <i>Communications Biology</i> , 2021, 4, 962.	2.0	23
24	Comparative Transcriptomics of Non-Embryogenic and Embryogenic Callus in Semi-Recalcitrant and Non-Recalcitrant Upland Cotton Lines. <i>Plants</i> , 2021, 10, 1775.	1.6	10
25	Integrative genomics reveals paths to sex dimorphism in <i>Salix purpurea</i> L. <i>Horticulture Research</i> , 2021, 8, 170.	2.9	12
26	The Ancient Salicoid Genome Duplication Event: A Platform for Reconstruction of De Novo Gene Evolution in <i>Populus trichocarpa</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	9
27	Overexpression of a <i>Prefoldin 2</i> subunit gene reduces biomass recalcitrance in the bioenergy crop <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2020, 18, 859-871.	4.1	17
28	Identification of functional single nucleotide polymorphism of <i>Populus trichocarpa</i> PtrEPSP-ATF and determination of its transcriptional effect. <i>Plant Direct</i> , 2020, 4, e00178.	0.8	4
29	PEATmoss ( <i>Physcomitrella</i> Expression Atlas Tool): a unified gene expression atlas for the model plant <i>Physcomitrella patens</i> . <i>Plant Journal</i> , 2020, 102, 165-177.	2.8	74
30	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial <i>Populus trichocarpa</i> . <i>Genome Biology</i> , 2020, 21, 259.	3.8	68
31	A genome resource for green millet <i>Setaria viridis</i> enables discovery of agronomically valuable loci. <i>Nature Biotechnology</i> , 2020, 38, 1203-1210.	9.4	103
32	Assembly of the threespine stickleback Y chromosome reveals convergent signatures of sex chromosome evolution. <i>Genome Biology</i> , 2020, 21, 177.	3.8	79
33	Genomic adaptations of the green alga <i>Dunaliella salina</i> to life under high salinity. <i>Algal Research</i> , 2020, 50, 101990.	2.4	18
34	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	13.7	314
35	Genome-wide quantitative trait loci detection for biofuel traits in switchgrass ( <i>Panicum</i> ) Tj ETQq1 1 0.784314,rgBT /Overlock 10	2.5	3
36	Sequencing and Analysis of the Sex Determination Region of <i>Populus trichocarpa</i> . <i>Genes</i> , 2020, 11, 843.	1.0	19

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37	Gradual polyploid genome evolution revealed by pan-genomic analysis of <i>Brachypodium hybridum</i> and its diploid progenitors. <i>Nature Communications</i> , 2020, 11, 3670.	5.8	67
38	<i>Arabidopsis</i> C-terminal binding protein <i>ANGUSTIFOLIA</i> modulates transcriptional co-regulation of <i>MYB46</i> and <i>WRKY33</i> . <i>New Phytologist</i> , 2020, 228, 1627-1639.	3.5	17
39	Genome biology of the paleotetraploid perennial biomass crop <i>Miscanthus</i> . <i>Nature Communications</i> , 2020, 11, 5442.	5.8	67
40	Environmentally responsive QTL controlling surface wax load in switchgrass. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3119-3137.	1.8	11
41	Chloroplast genome sequences of <i>Carya illinoensis</i> from two distinct geographic populations. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	9
42	Light-responsive expression atlas reveals the effects of light quality and intensity in <i>Kalanchoë fedtschenkoi</i> , a plant with crassulacean acid metabolism. <i>GigaScience</i> , 2020, 9, .	3.3	11
43	Genome Sequence of the Chestnut Blight Fungus <i>Cryphonectria parasitica</i> EP155: A Fundamental Resource for an Archetypical Invasive Plant Pathogen. <i>Phytopathology</i> , 2020, 110, 1180-1188.	1.1	34
44	Marker-free carotenoid-enriched rice generated through targeted gene insertion using CRISPR-Cas9. <i>Nature Communications</i> , 2020, 11, 1178.	5.8	204
45	Phylogenomics reveals convergent evolution of red-violet coloration in land plants and the origins of the anthocyanin biosynthetic pathway. <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106904.	1.2	35
46	A willow sex chromosome reveals convergent evolution of complex palindromic repeats. <i>Genome Biology</i> , 2020, 21, 38.	3.8	74
47	Optimizing genomic selection for blight resistance in American chestnut backcross populations: A trade-off with American chestnut ancestry implies resistance is polygenic. <i>Evolutionary Applications</i> , 2020, 13, 31-47.	1.5	48
48	Deeply conserved synteny resolves early events in vertebrate evolution. <i>Nature Ecology and Evolution</i> , 2020, 4, 820-830.	3.4	250
49	Genomic diversifications of five <i>Gossypium</i> allopolyploid species and their impact on cotton improvement. <i>Nature Genetics</i> , 2020, 52, 525-533.	9.4	249
50	Genetic Associations in Four Decades of Multi-environment Trials Reveal Agronomic Trait Evolution in Common Bean. <i>Genetics</i> , 2020, 215, 267-284.	1.2	26
51	Hybridization History and Repetitive Element Content in the Genome of a Homoploid Hybrid, <i>Yucca gloriosa</i> (Asparagaceae). <i>Frontiers in Plant Science</i> , 2020, 11, 573767.	1.7	9
52	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	2.8	113
53	Mediation of plant-mycorrhizal interaction by a lectin receptor-like kinase. <i>Nature Plants</i> , 2019, 5, 676-680.	4.7	42
54	SoyCSN: Soybean context-specific network analysis and prediction based on tissue-specific transcriptome data. <i>Plant Direct</i> , 2019, 3, e00167.	0.8	18

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55	High Density Genetic Maps of Seashore Paspalum Using Genotyping-By-Sequencing and Their Relationship to The Sorghum Bicolor Genome. <i>Scientific Reports</i> , 2019, 9, 12183.	1.6	16
56	Finding New Cell Wall Regulatory Genes in <i>Populus trichocarpa</i> Using Multiple Lines of Evidence. <i>Frontiers in Plant Science</i> , 2019, 10, 1249.	1.7	13
57	Overexpression of a serine hydroxymethyltransferase increases biomass production and reduces recalcitrance in the bioenergy crop <i>Populus</i> . <i>Sustainable Energy and Fuels</i> , 2019, 3, 195-207.	2.5	27
58	High-density linkage map reveals QTL underlying growth traits in AP13–VS16 biparental population of switchgrass. <i>GCB Bioenergy</i> , 2019, 11, 672-690.	2.5	13
59	Wavelet-Based Genomic Signal Processing for Centromere Identification and Hypothesis Generation. <i>Frontiers in Genetics</i> , 2019, 10, 487.	1.1	11
60	Ancient polymorphisms contribute to genome-wide variation by long-term balancing selection and divergent sorting in <i>Boechera stricta</i> . <i>Genome Biology</i> , 2019, 20, 126.	3.8	30
61	Genome mapping of quantitative trait loci (QTL) controlling domestication traits of intermediate wheatgrass ( <i>Thinopyrum intermedium</i> ). <i>Theoretical and Applied Genetics</i> , 2019, 132, 2325-2351.	1.8	30
62	A new reference genome for <i>Sorghum bicolor</i> reveals high levels of sequence similarity between sweet and grain genotypes: implications for the genetics of sugar metabolism. <i>BMC Genomics</i> , 2019, 20, 420.	1.2	73
63	Multi-Phenotype Association Decomposition: Unraveling Complex Gene-Phenotype Relationships. <i>Frontiers in Genetics</i> , 2019, 10, 417.	1.1	20
64	QTL–environment interactions underlie adaptive divergence in switchgrass across a large latitudinal gradient. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12933-12941.	3.3	75
65	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	9.4	439
66	The Genetic Architecture of Shoot and Root Trait Divergence Between Mesic and Xeric Ecotypes of a Perennial Grass. <i>Frontiers in Plant Science</i> , 2019, 10, 366.	1.7	22
67	A chromosome-scale genome assembly and dense genetic map for <i>Xenopus tropicalis</i> . <i>Developmental Biology</i> , 2019, 452, 8-20.	0.9	43
68	The genome of the soybean cyst nematode ( <i>Heterodera glycines</i> ) reveals complex patterns of duplications involved in the evolution of parasitism genes. <i>BMC Genomics</i> , 2019, 20, 119.	1.2	55
69	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , 2019, 20, 905.	1.2	59
70	Enhancing microRNA167A expression in seed decreases the linolenic acid content and increases seed size in <i>Camelina sativa</i> . <i>Plant Journal</i> , 2019, 98, 346-358.	2.8	36
71	The <i>Physcomitrella patens</i> gene atlas project: large-scale RNA-seq based expression data. <i>Plant Journal</i> , 2018, 95, 168-182.	2.8	115
72	Exploring the loblolly pine ( <i>Pinus taeda</i> L.) genome by BAC sequencing and Cot analysis. <i>Gene</i> , 2018, 663, 165-177.	1.0	13

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73	Amplification and adaptation of centromeric repeats in polyploid switchgrass species. <i>New Phytologist</i> , 2018, 218, 1645-1657.	3.5	30
74	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	9.4	413
75	Quantitative trait loci for cell wall composition traits measured using near-infrared spectroscopy in the model C4 perennial grass <i>Panicum hallii</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 25.	6.2	8
76	Annotation of the <i>Corymbia</i> terpene synthase gene family shows broad conservation but dynamic evolution of physical clusters relative to <i>Eucalyptus</i> . <i>Heredity</i> , 2018, 121, 87-104.	1.2	17
77	The Sphagnum Project: enabling ecological and evolutionary insights through a genus-level sequencing project. <i>New Phytologist</i> , 2018, 217, 16-25.	3.5	54
78	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018, 93, 515-533.	2.8	406
79	The <i>Sorghum bicolor</i> reference genome: improved assembly, gene annotations, a transcriptome atlas, and signatures of genome organization. <i>Plant Journal</i> , 2018, 93, 338-354.	2.8	431
80	Hardwood Tree Genomics: Unlocking Woody Plant Biology. <i>Frontiers in Plant Science</i> , 2018, 9, 1799.	1.7	50
81	The genomic landscape of molecular responses to natural drought stress in <i>Panicum hallii</i> . <i>Nature Communications</i> , 2018, 9, 5213.	5.8	101
82	Population genomics and climate adaptation of a C4 perennial grass, <i>Panicum hallii</i> (Poaceae). <i>BMC Genomics</i> , 2018, 19, 792.	1.2	9
83	Association mapping, transcriptomics, and transient expression identify candidate genes mediating plant-pathogen interactions in a tree. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11573-11578.	3.3	61
84	Extensive Genetic Diversity is Present within North American Switchgrass Germplasm. <i>Plant Genome</i> , 2018, 11, 170055.	1.6	35
85	A Variable Polyglutamine Repeat Affects Subcellular Localization and Regulatory Activity of a <i>Populus</i> ANGUSTIFOLIA Protein. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2631-2641.	0.8	9
86	Revealing the transcriptomic complexity of switchgrass by PacBio long-read sequencing. <i>Biotechnology for Biofuels</i> , 2018, 11, 170.	6.2	30
87	Pleiotropic and Epistatic Network-Based Discovery: Integrated Networks for Target Gene Discovery. <i>Frontiers in Energy Research</i> , 2018, 6, .	1.2	32
88	Assembly of the <i>Boechera retrofracta</i> Genome and Evolutionary Analysis of Apomixis-Associated Genes. <i>Genes</i> , 2018, 9, 185.	1.0	24
89	A mosaic monoploid reference sequence for the highly complex genome of sugarcane. <i>Nature Communications</i> , 2018, 9, 2638.	5.8	299
90	Genome-wide association studies and expression-based quantitative trait loci analyses reveal roles of HCT2 in caffeoylquinic acid biosynthesis and its regulation by defense-responsive transcription factors in <i>Populus</i> . <i>New Phytologist</i> , 2018, 220, 502-516.	3.5	112

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91	Characterization of a large sex determination region in <i>Salix purpurea</i> L. (Salicaceae). <i>Molecular Genetics and Genomics</i> , 2018, 293, 1437-1452.	1.0	61
92	A 5-Enolpyruvylshikimate 3-Phosphate Synthase Functions as a Transcriptional Repressor in <i>Populus</i> . <i>Plant Cell</i> , 2018, 30, 1645-1660.	3.1	56
93	Preferential retention of genes from one parental genome after polyploidy illustrates the nature and scope of the genomic conflicts induced by hybridization. <i>PLoS Genetics</i> , 2018, 14, e1007267.	1.5	78
94	The <i>Aquilegia</i> genome provides insight into adaptive radiation and reveals an extraordinarily polymorphic chromosome with a unique history. <i>ELife</i> , 2018, 7, .	2.8	120
95	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	13.7	332
96	Divergent cytosine DNA methylation patterns in single-cell, soybean root hairs. <i>New Phytologist</i> , 2017, 214, 808-819.	3.5	75
97	DNA methylation and gene expression regulation associated with vascularization in <i>Sorghum bicolor</i> . <i>New Phytologist</i> , 2017, 214, 1213-1229.	3.5	47
98	Sparse panicle1 is required for inflorescence development in <i>Setaria viridis</i> and maize. <i>Nature Plants</i> , 2017, 3, 17054.	4.7	63
99	Draft Nuclear Genome Sequence of the Liquid Hydrocarbon-Accumulating Green Microalga <i>Botryococcus braunii</i> Race B (Showa). <i>Genome Announcements</i> , 2017, 5, .	0.8	21
100	The Sequences of 1504 Mutants in the Model Rice Variety Kitaake Facilitate Rapid Functional Genomic Studies. <i>Plant Cell</i> , 2017, 29, 1218-1231.	3.1	138
101	Young inversion with multiple linked QTLs under selection in a hybrid zone. <i>Nature Ecology and Evolution</i> , 2017, 1, 119.	3.4	94
102	The Peach v2.0 release: high-resolution linkage mapping and deep resequencing improve chromosome-scale assembly and contiguity. <i>BMC Genomics</i> , 2017, 18, 225.	1.2	342
103	Draft Nuclear Genome Sequence of the Halophilic and Beta-Carotene-Accumulating Green Alga <i>Dunaliella salina</i> Strain CCAP19/18. <i>Genome Announcements</i> , 2017, 5, .	0.8	83
104	Insights into Land Plant Evolution Garnered from the <i>Marchantia polymorpha</i> Genome. <i>Cell</i> , 2017, 171, 287-304.e15.	13.5	973
105	Insights of biomass recalcitrance in natural <i>Populus trichocarpa</i> variants for biomass conversion. <i>Green Chemistry</i> , 2017, 19, 5467-5478.	4.6	82
106	Insights into the red algae and eukaryotic evolution from the genome of <i>Porphyra umbilicalis</i> (Bangioophyceae, Rhodophyta). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6361-E6370.	3.3	233
107	The <i>Kalanchoë</i> genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. <i>Nature Communications</i> , 2017, 8, 1899.	5.8	159
108	Sub genome anchored physical frameworks of the allotetraploid Upland cotton ( <i>Gossypium hirsutum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tj 7, 15274.	1.6	23

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109	Genome organization of the <i>vg1</i> and <i>nodal3</i> gene clusters in the allotetraploid frog <i>Xenopus laevis</i> . <i>Developmental Biology</i> , 2017, 426, 236-244.	0.9	4
110	Identification, characterization, and gene expression analysis of nucleotide binding site (NB)-type resistance gene homologues in switchgrass. <i>BMC Genomics</i> , 2016, 17, 892.	1.2	14
111	Sequence-Based Introgression Mapping Identifies Candidate White Mold Tolerance Genes in Common Bean. <i>Plant Genome</i> , 2016, 9, plantgenome2015.09.0092.	1.6	10
112	Genome-Wide Association Study Identifies Candidate Loci Underlying Agronomic Traits in a Middle American Diversity Panel of Common Bean. <i>Plant Genome</i> , 2016, 9, plantgenome2016.02.0012.	1.6	136
113	Transposable Elements versus the Fungal Genome: Impact on Whole-Genome Architecture and Transcriptional Profiles. <i>PLoS Genetics</i> , 2016, 12, e1006108.	1.5	177
114	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016, 26, 1577-1584.	1.8	175
115	Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. <i>BMC Genomics</i> , 2016, 17, 267.	1.2	74
116	Sequencing wild and cultivated cassava and related species reveals extensive interspecific hybridization and genetic diversity. <i>Nature Biotechnology</i> , 2016, 34, 562-570.	9.4	340
117	Widespread natural variation of DNA methylation within angiosperms. <i>Genome Biology</i> , 2016, 17, 194.	3.8	436
118	The Sphagnum Genome Project. <i>Advances in Botanical Research</i> , 2016, , 167-187.	0.5	17
119	On the origin and evolutionary consequences of gene body DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9111-9116.	3.3	260
120	Empty Niches after Extinctions Increase Population Sizes of Modern Corals. <i>Current Biology</i> , 2016, 26, 3190-3194.	1.8	79
121	Genome-wide analysis of lectin receptor-like kinases in <i>Populus</i> . <i>BMC Genomics</i> , 2016, 17, 699.	1.2	72
122	Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . <i>Nature</i> , 2016, 538, 336-343.	13.7	849
123	Complete Genome Sequence of <i>Alkaliphilus metalliredigens</i> Strain QYMF, an Alkaliphilic and Metal-Reducing Bacterium Isolated from Borax-Contaminated Leachate Ponds. <i>Genome Announcements</i> , 2016, 4, .	0.8	10
124	Genetic analysis of <i>Physcomitrella patens</i> identifies ABSCISIC ACID NON-RESPONSIVE (ANR), a regulator of ABA responses unique to basal land plants and required for desiccation tolerance. <i>Plant Cell</i> , 2016, 28, tpc.00091.2016.	3.1	98
125	Construction of high resolution genetic linkage maps to improve the soybean genome sequence assembly Glyma1.01. <i>BMC Genomics</i> , 2016, 17, 33.	1.2	137
126	The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. <i>Nature</i> , 2016, 530, 331-335.	13.7	460

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127	Genome-Wide Sequencing of 41 Rice ( <i>Oryza sativa</i> L.) Mutated Lines Reveals Diverse Mutations Induced by Fast-Neutron Irradiation. <i>Molecular Plant</i> , 2016, 9, 1078-1081.	3.9	78
128	Drought responsive gene expression regulatory divergence between upland and lowland ecotypes of a perennial C <sub>4</sub> grass. <i>Genome Research</i> , 2016, 26, 510-518.	2.4	52
129	Evolving New Skeletal Traits by cis-Regulatory Changes in Bone Morphogenetic Proteins. <i>Cell</i> , 2016, 164, 45-56.	13.5	132
130	Targeted Switchgrass BAC Library Screening and Sequence Analysis Identifies Predicted Biomass and Stress Response-Related Genes. <i>Bioenergy Research</i> , 2016, 9, 109-122.	2.2	10
131	Combating a Global Threat to a Clonal Crop: Banana Black Sigatoka Pathogen <i>Pseudocercospora fijiensis</i> (Synonym <i>Mycosphaerella fijiensis</i> ) Genomes Reveal Clues for Disease Control. <i>PLoS Genetics</i> , 2016, 12, e1005876.	1.5	77
132	Genome Analysis of Planctomycetes Inhabiting Blades of the Red Alga <i>Porphyra umbilicalis</i> . <i>PLoS ONE</i> , 2016, 11, e0151883.	1.1	39
133	Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. <i>Plant Journal</i> , 2015, 84, 800-815.	2.8	47
134	A roadmap for research on crassulacean acid metabolism (CAM) to enhance sustainable food and bioenergy production in a hotter, drier world. <i>New Phytologist</i> , 2015, 207, 491-504.	3.5	211
135	High-Density Single Nucleotide Polymorphism Linkage Maps of Lowland Switchgrass using Genotyping-by-Sequencing. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0065.	1.6	8
136	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1. <i>Frontiers in Microbiology</i> , 2015, 6, 978.	1.5	83
137	Proteome profile of the endomembrane of developing coleoptiles from switchgrass ( <i>Panicum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 1.3 6		
138	Updating algal evolutionary relationships through plastid genome sequencing: did alveolate plastids emerge through endosymbiosis of an ochrophyte?. <i>Scientific Reports</i> , 2015, 5, 10134.	1.6	102
139	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	3.8	256
140	The genetics of divergence and reproductive isolation between ecotypes of <i>Panicum hallii</i> . <i>New Phytologist</i> , 2015, 205, 402-414.	3.5	65
141	Sequencing of 15,622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015, 84, 216-227.	2.8	36
142	SNP Assay Development for Linkage Map Construction, Anchoring Whole-Genome Sequence, and Other Genetic and Genomic Applications in Common Bean. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2285-2290.	0.8	147
143	Complete Genome Sequence of <i>Anaeromyxobacter</i> sp. Fw109-5, an Anaerobic, Metal-Reducing Bacterium Isolated from a Contaminated Subsurface Environment. <i>Genome Announcements</i> , 2015, 3, .	0.8	17
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