

Jeremy Schmutz

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1467445/publications.pdf>

Version: 2024-02-01

257
papers

85,187
citations

2544

96
h-index

677

254
g-index

295
all docs

295
docs citations

295
times ranked

72441
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.	9.8	25
2	Multiplex knockout of trichome-regulating MYB duplicates in hybrid poplar using a single gRNA. <i>Plant Physiology</i> , 2022, 189, 516-526.	4.8	18
3	The Common Bean <i>V</i> Gene Encodes Flavonoid 3- β -Hydroxylase: A Major Mutational Target for Flavonoid Diversity in Angiosperms. <i>Frontiers in Plant Science</i> , 2022, 13, 869582.	3.6	7
4	Habitat-adapted microbial communities mediate <i>Sphagnum</i> peatmoss resilience to warming. <i>New Phytologist</i> , 2022, 234, 2111-2125.	7.3	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.	9.3	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.	7.1	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.	10.3	9
8	Representing sex chromosomes in genome assemblies. <i>Cell Genomics</i> , 2022, 2, 100132.	6.5	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, .	4.1	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.	8.3	48
11	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	27.8	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, .	7.1	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.	8.9	54
14	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	6.6	180
15	Improved chromosome-level genome assembly and annotation of the seagrass, <i>Zostera marina</i> (eelgrass). <i>F1000Research</i> , 2021, 10, 289.	1.6	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.	5.5	21
17	The tepary bean genome provides insight into evolution and domestication under heat stress. <i>Nature Communications</i> , 2021, 12, 2638.	12.8	43
18	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	4.4	21

#	ARTICLE	IF	CITATIONS
19	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .	10.3	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.	2.8	24
21	Genomic variation within the maize stiff-stalk heterotic germplasm pool. <i>Plant Genome</i> , 2021, 14, e20114.	2.8	14
22	Four chromosome scale genomes and a pan-genome annotation to accelerate pecan tree breeding. <i>Nature Communications</i> , 2021, 12, 4125.	12.8	49
23	Plant single-cell solutions for energy and the environment. <i>Communications Biology</i> , 2021, 4, 962.	4.4	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.	3.5	10
25	Integrative genomics reveals paths to sex dimorphism in <i>Salix purpurea</i> L. <i>Horticulture Research</i> , 2021, 8, 170.	6.3	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, .	2.5	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.	8.3	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.	1.9	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.	5.7	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.	8.8	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.	17.5	103
32	Assembly of the threespine stickleback Y chromosome reveals convergent signatures of sex chromosome evolution. <i>Genome Biology</i> , 2020, 21, 177.	8.8	79
33	Genomic adaptations of the green alga <i>Dunaliella salina</i> to life under high salinity. <i>Algal Research</i> , 2020, 50, 101990.	4.6	18
34	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	27.8	314
35	Genome-wide quantitative trait loci detection for biofuel traits in switchgrass (<i>Panicum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	5.8	3
36	Sequencing and Analysis of the Sex Determination Region of <i>Populus trichocarpa</i> . <i>Genes</i> , 2020, 11, 843.	2.4	19

#	ARTICLE	IF	CITATIONS
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.	12.8	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.	7.3	17
39	Genome biology of the paleotetraploid perennial biomass crop <i>Miscanthus</i> . <i>Nature Communications</i> , 2020, 11, 5442.	12.8	67
40	Environmentally responsive QTL controlling surface wax load in switchgrass. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3119-3137.	3.6	11
41	Chloroplast genome sequences of <i>Carya illinoensis</i> from two distinct geographic populations. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	1.6	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, .	6.4	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.	2.2	34
44	Marker-free carotenoid-enriched rice generated through targeted gene insertion using CRISPR-Cas9. <i>Nature Communications</i> , 2020, 11, 1178.	12.8	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.	2.7	35
46	A willow sex chromosome reveals convergent evolution of complex palindromic repeats. <i>Genome Biology</i> , 2020, 21, 38.	8.8	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.	3.1	48
48	Deeply conserved synteny resolves early events in vertebrate evolution. <i>Nature Ecology and Evolution</i> , 2020, 4, 820-830.	7.8	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.	21.4	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.	2.9	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.	3.6	9
52	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	5.7	113
53	Mediation of plant-mycorrhizal interaction by a lectin receptor-like kinase. <i>Nature Plants</i> , 2019, 5, 676-680.	9.3	42
54	SoyCSN: Soybean context-specific network analysis and prediction based on tissue-specific transcriptome data. <i>Plant Direct</i> , 2019, 3, e00167.	1.9	18

#	ARTICLE	IF	CITATIONS
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.	3.3	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.	3.6	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.	4.9	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.	5.6	13
59	Wavelet-Based Genomic Signal Processing for Centromere Identification and Hypothesis Generation. <i>Frontiers in Genetics</i> , 2019, 10, 487.	2.3	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.	8.8	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.	3.6	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.	2.8	73
63	Multi-Phenotype Association Decomposition: Unraveling Complex Gene-Phenotype Relationships. <i>Frontiers in Genetics</i> , 2019, 10, 417.	2.3	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.	7.1	75
65	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	21.4	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.	3.6	22
67	A chromosome-scale genome assembly and dense genetic map for <i>Xenopus tropicalis</i> . <i>Developmental Biology</i> , 2019, 452, 8-20.	2.0	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.	2.8	55
69	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , 2019, 20, 905.	2.8	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.	5.7	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.	5.7	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.	2.2	13

#	ARTICLE	IF	CITATIONS
73	Amplification and adaptation of centromeric repeats in polyploid switchgrass species. <i>New Phytologist</i> , 2018, 218, 1645-1657.	7.3	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.	21.4	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.	2.6	17
77	The Sphagnum Project: enabling ecological and evolutionary insights through a genus-level sequencing project. <i>New Phytologist</i> , 2018, 217, 16-25.	7.3	54
78	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018, 93, 515-533.	5.7	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.	5.7	431
80	Hardwood Tree Genomics: Unlocking Woody Plant Biology. <i>Frontiers in Plant Science</i> , 2018, 9, 1799.	3.6	50
81	The genomic landscape of molecular responses to natural drought stress in <i>Panicum hallii</i> . <i>Nature Communications</i> , 2018, 9, 5213.	12.8	101
82	Population genomics and climate adaptation of a C4 perennial grass, <i>Panicum hallii</i> (Poaceae). <i>BMC Genomics</i> , 2018, 19, 792.	2.8	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.	7.1	61
84	Extensive Genetic Diversity is Present within North American Switchgrass Germplasm. <i>Plant Genome</i> , 2018, 11, 170055.	2.8	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.	1.8	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, .	2.3	32
88	Assembly of the <i>Boechera retrofracta</i> Genome and Evolutionary Analysis of Apomixis-Associated Genes. <i>Genes</i> , 2018, 9, 185.	2.4	24
89	A mosaic monoploid reference sequence for the highly complex genome of sugarcane. <i>Nature Communications</i> , 2018, 9, 2638.	12.8	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.	7.3	112

#	ARTICLE	IF	CITATIONS
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.	2.1	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.	6.6	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.	3.5	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, .	6.0	120
95	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	27.8	332
96	Divergent cytosine DNA methylation patterns in single-cell, soybean root hairs. <i>New Phytologist</i> , 2017, 214, 808-819.	7.3	75
97	DNA methylation and gene expression regulation associated with vascularization in <i>Sorghum bicolor</i> . <i>New Phytologist</i> , 2017, 214, 1213-1229.	7.3	47
98	Sparse panicle1 is required for inflorescence development in <i>Setaria viridis</i> and maize. <i>Nature Plants</i> , 2017, 3, 17054.	9.3	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.	6.6	138
101	Young inversion with multiple linked QTLs under selection in a hybrid zone. <i>Nature Ecology and Evolution</i> , 2017, 1, 119.	7.8	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.	2.8	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.	28.9	973
105	Insights of biomass recalcitrance in natural <i>Populus trichocarpa</i> variants for biomass conversion. <i>Green Chemistry</i> , 2017, 19, 5467-5478.	9.0	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.	7.1	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.	12.8	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.	3.3	23

#	ARTICLE	IF	CITATIONS
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.	2.0	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.	2.8	14
111	Sequence-Based Introgression Mapping Identifies Candidate White Mold Tolerance Genes in Common Bean. <i>Plant Genome</i> , 2016, 9, plantgenome2015.09.0092.	2.8	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.	2.8	136
113	Transposable Elements versus the Fungal Genome: Impact on Whole-Genome Architecture and Transcriptional Profiles. <i>PLoS Genetics</i> , 2016, 12, e1006108.	3.5	177
114	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016, 26, 1577-1584.	3.9	175
115	Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. <i>BMC Genomics</i> , 2016, 17, 267.	2.8	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.	17.5	340
117	Widespread natural variation of DNA methylation within angiosperms. <i>Genome Biology</i> , 2016, 17, 194.	8.8	436
118	The Sphagnum Genome Project. <i>Advances in Botanical Research</i> , 2016, , 167-187.	1.1	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.	7.1	260
120	Empty Niches after Extinctions Increase Population Sizes of Modern Corals. <i>Current Biology</i> , 2016, 26, 3190-3194.	3.9	79
121	Genome-wide analysis of lectin receptor-like kinases in <i>Populus</i> . <i>BMC Genomics</i> , 2016, 17, 699.	2.8	72
122	Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . <i>Nature</i> , 2016, 538, 336-343.	27.8	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.	6.6	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.	2.8	137
126	The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. <i>Nature</i> , 2016, 530, 331-335.	27.8	460

#	ARTICLE	IF	CITATIONS
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.	8.3	78
128	Drought responsive gene expression regulatory divergence between upland and lowland ecotypes of a perennial C ₄ grass. <i>Genome Research</i> , 2016, 26, 510-518.	5.5	52
129	Evolving New Skeletal Traits by cis-Regulatory Changes in Bone Morphogenetic Proteins. <i>Cell</i> , 2016, 164, 45-56.	28.9	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.	3.9	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.	3.5	77
132	Genome Analysis of Planctomycetes Inhabiting Blades of the Red Alga <i>Porphyra umbilicalis</i> . <i>PLoS ONE</i> , 2016, 11, e0151883.	2.5	39
133	Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. <i>Plant Journal</i> , 2015, 84, 800-815.	5.7	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.	7.3	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.	2.8	8
136	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1. <i>Frontiers in Microbiology</i> , 2015, 6, 978.	3.5	83
137	Proteome profile of the endomembrane of developing coleoptiles from switchgrass (<i>Panicum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1 2.2 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.	3.3	102
139	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	8.8	256
140	The genetics of divergence and reproductive isolation between ecotypes of <i>Panicum hallii</i> . <i>New Phytologist</i> , 2015, 205, 402-414.	7.3	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.	5.7	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.	1.8	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
144	Hemichordate genomes and deuterostome origins. <i>Nature</i> , 2015, 527, 459-465.	27.8	217

#	ARTICLE	IF	CITATIONS
145	High-resolution genetic maps of <i>Eucalyptus</i> improve <i>Eucalyptus grandis</i> genome assembly. <i>New Phytologist</i> , 2015, 206, 1283-1296.	7.3	90
146	<i>Sphagnum</i> physiology in the context of changing climate: emergent influences of genomics, modelling and host-microbiome interactions on understanding ecosystem function. <i>Plant, Cell and Environment</i> , 2015, 38, 1737-1751.	5.7	60
147	Developing market class specific InDel markers from next generation sequence data in <i>Phaseolus vulgaris</i> L. <i>Frontiers in Plant Science</i> , 2014, 5, 185.	3.6	79
148	Complete Plastome Sequences from <i>Glycine syndetika</i> and Six Additional Perennial Wild Relatives of Soybean. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2023-2033.	1.8	26
149	Annotation and sequence diversity of transposable elements in common bean (<i>Phaseolus vulgaris</i>). <i>Frontiers in Plant Science</i> , 2014, 5, 339.	3.6	39
150	The <i>Spirodela polyrhiza</i> genome reveals insights into its neotenus reduction fast growth and aquatic lifestyle. <i>Nature Communications</i> , 2014, 5, 3311.	12.8	262
151	Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. <i>Nature Biotechnology</i> , 2014, 32, 656-662.	17.5	572
152	Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white-rot/brown-rot paradigm for wood decay fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9923-9928.	7.1	595
153	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	27.8	725
154	The <i>Chlamydomonas</i> genome project: a decade on. <i>Trends in Plant Science</i> , 2014, 19, 672-680.	8.8	145
155	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014, 46, 707-713.	21.4	1,159
156	Generation of Transcript Assemblies and Identification of Single Nucleotide Polymorphisms from Seven Lowland and Upland Cultivars of Switchgrass. <i>Plant Genome</i> , 2014, 7, plantgenome2013.12.0041.	2.8	6
157	An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. <i>Nature Genetics</i> , 2013, 45, 891-898.	21.4	350
158	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <i>Plant Journal</i> , 2013, 76, 718-727.	5.7	264
159	Identification and characterization of functional centromeres of the common bean. <i>Plant Journal</i> , 2013, 76, 47-60.	5.7	61
160	The high-quality draft genome of peach (<i>Prunus persica</i>) identifies unique patterns of genetic diversity, domestication and genome evolution. <i>Nature Genetics</i> , 2013, 45, 487-494.	21.4	1,081
161	The <i>Capsella rubella</i> genome and the genomic consequences of rapid mating system evolution. <i>Nature Genetics</i> , 2013, 45, 831-835.	21.4	374
162	A re-sequencing based assessment of genomic heterogeneity and fast neutron-induced deletions in a common bean cultivar. <i>Frontiers in Plant Science</i> , 2013, 4, 210.	3.6	18

#	ARTICLE	IF	CITATIONS
163	The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 46.	3.6	198
164	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	3.5	232
165	Correction for Morin et al., Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4146-4146.	7.1	4
166	Fine-scale variation in meiotic recombination in <i>Mimulus</i> inferred from population shotgun sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19478-19482.	7.1	190
167	Development of an integrated transcript sequence database and a gene expression atlas for gene discovery and analysis in switchgrass (<i>Panicum virgatum</i> L.). <i>Plant Journal</i> , 2013, 74, 160-173.	5.7	70
168	The genome sequence of the most widely cultivated cacao type and its use to identify candidate genes regulating pod color. <i>Genome Biology</i> , 2013, 14, r53.	8.8	225
169	Complete genome sequence of <i>Polynucleobacter necessarius</i> subsp. <i>asymbioticus</i> type strain (QLW-P1DMWA-1T). <i>Standards in Genomic Sciences</i> , 2012, 6, 74-83.	1.5	33
170	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17501-17506.	7.1	359
171	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. <i>Nature</i> , 2012, 492, 59-65.	27.8	377
172	The genome of the polar eukaryotic microalga <i>Coccomyxa subellipsoidea</i> reveals traits of cold adaptation. <i>Genome Biology</i> , 2012, 13, R39.	9.6	289
173	Genetic Architecture of Variation in the Lateral Line Sensory System of Threespine Sticklebacks. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1047-1056.	1.8	47
174	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. <i>New Phytologist</i> , 2012, 194, 1001-1013.	7.3	210
175	Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen <i>Phytophthora capsici</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 1350-1360.	2.6	264
176	Theria-specific Homeodomain and cis-Regulatory Element Evolution of the <i>Dlx4</i> Bigene Cluster in 12 Different Mammalian Species. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2012, 318, 639-650.	1.3	5
177	Identical Genomic Organization of Two Hemichordate Hox Clusters. <i>Current Biology</i> , 2012, 22, 2053-2058.	3.9	43
178	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012, 492, 423-427.	27.8	1,204
179	A Genome-Wide Survey of Switchgrass Genome Structure and Organization. <i>PLoS ONE</i> , 2012, 7, e33892.	2.5	50
180	The genomic basis of adaptive evolution in threespine sticklebacks. <i>Nature</i> , 2012, 484, 55-61.	27.8	1,600

#	ARTICLE	IF	CITATIONS
181	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 2012, 336, 1715-1719.	12.6	1,424
182	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , 2012, 30, 555-561.	17.5	864
183	A Genome-wide SNP Genotyping Array Reveals Patterns of Global and Repeated Species-Pair Divergence in Sticklebacks. <i>Current Biology</i> , 2012, 22, 83-90.	3.9	212
184	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9166-9171.	7.1	640
185	Comparative genomics of the social amoebae <i>Dictyostelium discoideum</i> and <i>Dictyostelium purpureum</i> . <i>Genome Biology</i> , 2011, 12, R20.	9.6	141
186	The <i>Selaginella</i> Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. <i>Science</i> , 2011, 332, 960-963.	12.6	794
187	Complete genome sequence of the filamentous gliding predatory bacterium <i>Herpetosiphon aurantiacus</i> type strain (114-95T). <i>Standards in Genomic Sciences</i> , 2011, 5, 356-370.	1.5	47
188	The genome of <i>Tetranychus urticae</i> reveals herbivorous pest adaptations. <i>Nature</i> , 2011, 479, 487-492.	27.8	897
189	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nature Biotechnology</i> , 2011, 29, 922-927.	17.5	428
190	The Switchgrass Genome: Tools and Strategies. <i>Plant Genome</i> , 2011, 4, 273-282.	2.8	91
191	Complete genome sequence of <i>Rhodospirillum rubrum</i> type strain (S1T). <i>Standards in Genomic Sciences</i> , 2011, 4, 293-302.	1.5	44
192	Complete genome sequence of <i>Tolumonas auensis</i> type strain (TA 4T). <i>Standards in Genomic Sciences</i> , 2011, 5, 112-120.	1.5	6
193	Complete genome sequence of the halophilic and highly halotolerant <i>Chromohalobacter salexigens</i> type strain (1H11T). <i>Standards in Genomic Sciences</i> , 2011, 5, 379-388.	1.5	35
194	Qualitative and quantitative resistances to leaf rust finely mapped within two nucleotide-binding site leucine-rich repeat (NBS-LRR)-rich genomic regions of chromosome 19 in poplar. <i>New Phytologist</i> , 2011, 192, 151-163.	7.3	37
195	Sequencing crop genomes: approaches and applications. <i>New Phytologist</i> , 2011, 191, 915-925.	7.3	101
196	The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , 2011, 43, 476-481.	21.4	814
197	The genetic basis of divergent pigment patterns in juvenile threespine sticklebacks. <i>Heredity</i> , 2011, 107, 155-166.	2.6	60
198	Genome Sequence of the Verrucomicrobium <i>Opitutus terrae</i> PB90-1, an Abundant Inhabitant of Rice Paddy Soil Ecosystems. <i>Journal of Bacteriology</i> , 2011, 193, 2367-2368.	2.2	44

#	ARTICLE	IF	CITATIONS
199	Genome Sequence of the Ethene- and Vinyl Chloride-Oxidizing Actinomycete <i>Nocardioides</i> sp. Strain JS614. <i>Journal of Bacteriology</i> , 2011, 193, 3399-3400.	2.2	17
200	The Plant Cell Wallâ€œDecomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	12.6	512
201	Finished Genome of the Fungal Wheat Pathogen <i>Mycosphaerella graminicola</i> Reveals Dispensome Structure, Chromosome Plasticity, and Stealth Pathogenesis. <i>PLoS Genetics</i> , 2011, 7, e1002070.	3.5	532
202	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	27.8	3,854
203	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	27.8	1,685
204	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010, 28, 957-963.	17.5	490
205	Evolutionary constraint facilitates interpretation of genetic variation in resequenced human genomes. <i>Genome Research</i> , 2010, 20, 301-310.	5.5	77
206	Complete HOX cluster characterization of the coelacanth provides further evidence for slow evolution of its genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3622-3627.	7.1	65
207	Adaptive Evolution of Pelvic Reduction in Sticklebacks by Recurrent Deletion of a <i>Pitx1</i> Enhancer. <i>Science</i> , 2010, 327, 302-305.	12.6	901
208	Bifurcation and Enhancement of Autonomous-Nonautonomous Retrotransposon Partnership through LTR Swapping in Soybean. <i>Plant Cell</i> , 2010, 22, 48-61.	6.6	42
209	The Genome of the Western Clawed Frog <i>Xenopus tropicalis</i> . <i>Science</i> , 2010, 328, 633-636.	12.6	708
210	Evolution of an Expanded Sex-Determining Locus in <i>Volvox</i> . <i>Science</i> , 2010, 328, 351-354.	12.6	159
211	Genomic Analysis of Organismal Complexity in the Multicellular Green Alga <i>Volvox carteri</i> . <i>Science</i> , 2010, 329, 223-226.	12.6	536
212	Whole-genome sequencing and intensive analysis of the undomesticated soybean (<i>Glycine soja</i>) in America, 2010, 107, 22032-22037.	7.1	299
213	The Draft Soybean Genome Sequence. , 2010, , 223-244.		0
214	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2009, 19, 2324-2333.	5.5	125
215	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. <i>PLoS Genetics</i> , 2009, 5, e1000618.	3.5	402
216	Integrating microarray analysis and the soybean genome to understand the soybeans iron deficiency response. <i>BMC Genomics</i> , 2009, 10, 376.	2.8	56

#	ARTICLE	IF	CITATIONS
217	The <i>Sorghum bicolor</i> genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	27.8	2,642
218	A role for a neo-sex chromosome in stickleback speciation. <i>Nature</i> , 2009, 461, 1079-1083.	27.8	327
219	Green Evolution and Dynamic Adaptations Revealed by Genomes of the Marine Picoeukaryotes <i>Micromonas</i> . <i>Science</i> , 2009, 324, 268-272.	12.6	591
220	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008, 452, 88-92.	27.8	1,003
221	The amphioxus genome and the evolution of the chordate karyotype. <i>Nature</i> , 2008, 453, 1064-1071.	27.8	1,496
222	The <i>Trichoplax</i> genome and the nature of placozoans. <i>Nature</i> , 2008, 454, 955-960.	27.8	801
223	The <i>Phaeodactylum</i> genome reveals the evolutionary history of diatom genomes. <i>Nature</i> , 2008, 456, 239-244.	27.8	1,458
224	A genetic linkage map for the ectomycorrhizal fungus <i>Laccaria bicolor</i> and its alignment to the whole-genome sequence assemblies. <i>New Phytologist</i> , 2008, 180, 316-328.	7.3	32
225	Microsatellite discovery from BAC end sequences and genetic mapping to anchor the soybean physical and genetic maps. <i>Genome</i> , 2008, 51, 294-302.	2.0	50
226	Sequence and Assembly of the Soybean Genome. , 2008, , 101-112.		0
227	The tiny eukaryote <i>Ostreococcus</i> provides genomic insights into the paradox of plankton speciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7705-7710.	7.1	563
228	Genome sequence of the lignocellulose-bioconverting and xylose-fermenting yeast <i>Pichia stipitis</i> . <i>Nature Biotechnology</i> , 2007, 25, 319-326.	17.5	449
229	A physical map of the highly heterozygous <i>Populus</i> genome: integration with the genome sequence and genetic map and analysis of haplotype variation. <i>Plant Journal</i> , 2007, 50, 1063-1078.	5.7	70
230	The <i>Chlamydomonas</i> Genome Reveals the Evolution of Key Animal and Plant Functions. <i>Science</i> , 2007, 318, 245-250.	12.6	2,354
231	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 2006, 313, 1596-1604.	12.6	3,945
232	Sequencing and analysis of 10,967 full-length cDNA clones from <i>Xenopus laevis</i> and <i>Xenopus tropicalis</i> reveals post-tetraploidization transcriptome remodeling. <i>Genome Research</i> , 2006, 16, 796-803.	5.5	73
233	Toward a Reference Sequence of the Soybean Genome: A Multiagency Effort. <i>Crop Science</i> , 2006, 46, S-55.	1.8	37
234	Widespread Parallel Evolution in Sticklebacks by Repeated Fixation of Ectodysplasin Alleles. <i>Science</i> , 2005, 307, 1928-1933.	12.6	1,299

#	ARTICLE	IF	CITATIONS
235	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. <i>Nature</i> , 2005, 434, 724-731.	27.8	85
236	Sequence Finishing. , 2004, 255, 333-342.		2
237	Assembly of DNA Sequencing Data. , 2004, 255, 319-332.		0
238	Quality Assessment of Finished BAC Sequences. , 2004, 255, 343-350.		0
239	Coelacanth genome sequence reveals the evolutionary history of vertebrate genes. <i>Genome Research</i> , 2004, 14, 2397-2405.	5.5	70
240	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2004, 14, 2121-2127.	5.5	486
241	Quality assessment of the human genome sequence. <i>Nature</i> , 2004, 429, 365-368.	27.8	172
242	The DNA sequence and biology of human chromosome 19. <i>Nature</i> , 2004, 428, 529-535.	27.8	298
243	The DNA sequence and comparative analysis of human chromosome 5. <i>Nature</i> , 2004, 431, 268-274.	27.8	102
244	The sequence and analysis of duplication-rich human chromosome 16. <i>Nature</i> , 2004, 432, 988-994.	27.8	156
245	Fowl sequence. <i>Nature</i> , 2004, 432, 679-680.	27.8	24
246	The Master Sex-Determination Locus in Threespine Sticklebacks Is on a Nascent Y Chromosome. <i>Current Biology</i> , 2004, 14, 1416-1424.	3.9	367
247	Gene Conversion and the Evolution of Protocadherin Gene Cluster Diversity. <i>Genome Research</i> , 2004, 14, 354-366.	5.5	100
248	New Genomic Tools for Molecular Studies of Evolutionary Change in Threespine Sticklebacks. <i>Behaviour</i> , 2004, 141, 1331-1344.	0.8	64
249	Six is seventh. <i>Nature</i> , 2003, 425, 775-776.	27.8	8
250	Extensive Linkage Disequilibrium, a Common 16.7-Kilobase Deletion, and Evidence of Balancing Selection in the Human Protocadherin $\hat{1}\pm$ Cluster. <i>American Journal of Human Genetics</i> , 2003, 72, 621-635.	6.2	51
251	Coding potential of laboratory and clinical strains of human cytomegalovirus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 14976-14981.	7.1	450
252	Assessing the Quality of Finished Genomic Sequence. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2003, 68, 31-38.	1.1	2

#	ARTICLE	IF	CITATIONS
253	Rapid Mapping of Zebrafish Mutations With SNPs and Oligonucleotide Microarrays. <i>Genome Research</i> , 2002, 12, 1929-1934.	5.5	117
254	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16899-16903.	7.1	1,610
255	Comparative DNA Sequence Analysis of Mouse and Human Protocadherin Gene Clusters. <i>Genome Research</i> , 2001, 11, 389-404.	5.5	224
256	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	27.8	21,074
257	Re-evaluating the Systematics of <i>Dendrolycopodium</i> Using Restriction-Site Associated DNA-Sequencing. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1