

Jeremy Schmutz

List of Publications by Year in descending order

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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	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	27.8	21,074
2	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 2006, 313, 1596-1604.	12.6	3,945
3	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	27.8	3,854
4	The <i>Sorghum bicolor</i> genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	27.8	2,642
5	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
6	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	27.8	1,685
7	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
8	The genomic basis of adaptive evolution in threespine sticklebacks. <i>Nature</i> , 2012, 484, 55-61.	27.8	1,600
9	The amphioxus genome and the evolution of the chordate karyotype. <i>Nature</i> , 2008, 453, 1064-1071.	27.8	1,496
10	The <i>Phaeodactylum</i> genome reveals the evolutionary history of diatom genomes. <i>Nature</i> , 2008, 456, 239-244.	27.8	1,458
11	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 2012, 336, 1715-1719.	12.6	1,424
12	Widespread Parallel Evolution in Sticklebacks by Repeated Fixation of Ectodysplasin Alleles. <i>Science</i> , 2005, 307, 1928-1933.	12.6	1,299
13	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
14	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
15	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	1,031
16	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008, 452, 88-92.	27.8	1,008
17	Insights into Land Plant Evolution Garnered from the <i>Marchantia polymorpha</i> Genome. <i>Cell</i> , 2017, 171, 287-304.e15.	28.9	973
18	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

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19	The genome of <i>Tetranychus urticae</i> reveals herbivorous pest adaptations. <i>Nature</i> , 2011, 479, 487-492.	27.8	897
20	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , 2012, 30, 555-561.	17.5	864
21	Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . <i>Nature</i> , 2016, 538, 336-343.	27.8	849
22	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
23	The <i>Trichoplax</i> genome and the nature of placozoans. <i>Nature</i> , 2008, 454, 955-960.	27.8	801
24	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
25	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	27.8	725
26	The Genome of the Western Clawed Frog <i>Xenopus tropicalis</i> . <i>Science</i> , 2010, 328, 633-636.	12.6	708
27	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
28	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
29	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
30	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
31	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
32	Genomic Analysis of Organismal Complexity in the Multicellular Green Alga <i>Volvox carteri</i> . <i>Science</i> , 2010, 329, 223-226.	12.6	536
33	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
34	The Plant Cell Wall "Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	12.6	512
35	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010, 28, 957-963.	17.5	490
36	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

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37	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
38	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
39	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
40	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	21.4	439
41	Widespread natural variation of DNA methylation within angiosperms. <i>Genome Biology</i> , 2016, 17, 194.	8.8	436
42	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
43	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
44	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
45	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
46	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. <i>PLoS Genetics</i> , 2009, 5, e1000618.	3.5	402
47	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. <i>Nature</i> , 2012, 492, 59-65.	27.8	377
48	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
49	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
50	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
51	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
52	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
53	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
54	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	27.8	332

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55	A role for a neo-sex chromosome in stickleback speciation. <i>Nature</i> , 2009, 461, 1079-1083.	27.8	327
56	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	27.8	314
57	Whole-genome sequencing and intensive analysis of the undomesticated soybean (<i>Glycine soja</i>) in America, 2010, 107, 22032-22037.	10.784314 7.1	107 299
58	A mosaic monoploid reference sequence for the highly complex genome of sugarcane. <i>Nature Communications</i> , 2018, 9, 2638.	12.8	299
59	The DNA sequence and biology of human chromosome 19. <i>Nature</i> , 2004, 428, 529-535.	27.8	298
60	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
61	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
62	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <i>Plant Journal</i> , 2013, 76, 718-727.	5.7	264
63	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
64	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
65	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	8.8	256
66	Deeply conserved synteny resolves early events in vertebrate evolution. <i>Nature Ecology and Evolution</i> , 2020, 4, 820-830.	7.8	250
67	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
68	Insights into the red algae and eukaryotic evolution from the genome of <i>Porphyra umbilicalis</i> (Bangiophyceae, Rhodophyta). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6361-E6370.	7.1	233
69	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	3.5	232
70	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
71	Comparative DNA Sequence Analysis of Mouse and Human Protocadherin Gene Clusters. <i>Genome Research</i> , 2001, 11, 389-404.	5.5	224
72	Hemichordate genomes and deuterostome origins. <i>Nature</i> , 2015, 527, 459-465.	27.8	217

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73	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
74	A roadmap for research on crassulacean acid metabolism (<scp>CAM</scp>) to enhance sustainable food and bioenergy production in a hotter, drier world. <i>New Phytologist</i> , 2015, 207, 491-504.	7.3	211
75	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
76	Marker-free carotenoid-enriched rice generated through targeted gene insertion using CRISPR-Cas9. <i>Nature Communications</i> , 2020, 11, 1178.	12.8	204
77	The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 46.	3.6	198
78	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
79	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	6.6	180
80	Transposable Elements versus the Fungal Genome: Impact on Whole-Genome Architecture and Transcriptional Profiles. <i>PLoS Genetics</i> , 2016, 12, e1006108.	3.5	177
81	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016, 26, 1577-1584.	3.9	175
82	Quality assessment of the human genome sequence. <i>Nature</i> , 2004, 429, 365-368.	27.8	172
83	Evolution of an Expanded Sex-Determining Locus in <i>Volvox</i> . <i>Science</i> , 2010, 328, 351-354.	12.6	159
84	The <i>Kalanchoe</i> genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. <i>Nature Communications</i> , 2017, 8, 1899.	12.8	159
85	The sequence and analysis of duplication-rich human chromosome 16. <i>Nature</i> , 2004, 432, 988-994.	27.8	156
86	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
87	The <i>Chlamydomonas</i> genome project: a decade on. <i>Trends in Plant Science</i> , 2014, 19, 672-680.	8.8	145
88	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	27.8	144
89	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
90	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

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91	Construction of high resolution genetic linkage maps to improve the soybean genome sequence assembly Glyma1.01. BMC Genomics, 2016, 17, 33.	2.8	137
92	Genome-Wide Association Study Identifies Candidate Loci Underlying Agronomic Traits in a Middle American Diversity Panel of Common Bean. Plant Genome, 2016, 9, plantgenome2016.02.0012.	2.8	136
93	Evolving New Skeletal Traits by cis -Regulatory Changes in Bone Morphogenetic Proteins. Cell, 2016, 164, 45-56.	28.9	132
94	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	5.5	125
95	The Aquilegia genome provides insight into adaptive radiation and reveals an extraordinarily polymorphic chromosome with a unique history. ELife, 2018, 7, .	6.0	120
96	Rapid Mapping of Zebrafish Mutations With SNPs and Oligonucleotide Microarrays. Genome Research, 2002, 12, 1929-1934.	5.5	117
97	The <i>Physcomitrella patens</i> gene atlas project: large-scale RNA-seq based expression data. Plant Journal, 2018, 95, 168-182.	5.7	115
98	Construction and comparison of three reference-quality genome assemblies for soybean. Plant Journal, 2019, 100, 1066-1082.	5.7	113
99	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> . New Phytologist, 2018, 220, 502-516.	7.3	112
100	A genome resource for green millet <i>Setaria viridis</i> enables discovery of agronomically valuable loci. Nature Biotechnology, 2020, 38, 1203-1210.	17.5	103
101	The DNA sequence and comparative analysis of human chromosome 5. Nature, 2004, 431, 268-274.	27.8	102
102	Updating algal evolutionary relationships through plastid genome sequencing: did alveolate plastids emerge through endosymbiosis of an ochrophyte?. Scientific Reports, 2015, 5, 10134.	3.3	102
103	Sequencing crop genomes: approaches and applications. New Phytologist, 2011, 191, 915-925.	7.3	101
104	The genomic landscape of molecular responses to natural drought stress in <i>Panicum hallii</i> . Nature Communications, 2018, 9, 5213.	12.8	101
105	Gene Conversion and the Evolution of Protocadherin Gene Cluster Diversity. Genome Research, 2004, 14, 354-366.	5.5	100
106	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. Plant Cell, 2016, 28, tpc.00091.2016.	6.6	98
107	Young inversion with multiple linked QTLs under selection in a hybrid zone. Nature Ecology and Evolution, 2017, 1, 119.	7.8	94
108	The Switchgrass Genome: Tools and Strategies. Plant Genome, 2011, 4, 273-282.	2.8	91

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109	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
110	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. <i>Nature</i> , 2005, 434, 724-731.	27.8	85
111	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
112	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
113	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
114	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
115	Empty Niches after Extinctions Increase Population Sizes of Modern Corals. <i>Current Biology</i> , 2016, 26, 3190-3194.	3.9	79
116	Assembly of the threespine stickleback Y chromosome reveals convergent signatures of sex chromosome evolution. <i>Genome Biology</i> , 2020, 21, 177.	8.8	79
117	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
118	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
119	Evolutionary constraint facilitates interpretation of genetic variation in resequenced human genomes. <i>Genome Research</i> , 2010, 20, 301-310.	5.5	77
120	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
121	Divergent cytosine DNA methylation patterns in single-cell, soybean root hairs. <i>New Phytologist</i> , 2017, 214, 808-819.	7.3	75
122	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
123	Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. <i>BMC Genomics</i> , 2016, 17, 267.	2.8	74
124	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
125	A willow sex chromosome reveals convergent evolution of complex palindromic repeats. <i>Genome Biology</i> , 2020, 21, 38.	8.8	74
126	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

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127	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
128	Genome-wide analysis of lectin receptor-like kinases in <i>Populus</i> . <i>BMC Genomics</i> , 2016, 17, 699.	2.8	72
129	Coelacanth genome sequence reveals the evolutionary history of vertebrate genes. <i>Genome Research</i> , 2004, 14, 2397-2405.	5.5	70
130	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
131	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
132	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
133	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
134	Genome biology of the paleotetraploid perennial biomass crop <i>Miscanthus</i> . <i>Nature Communications</i> , 2020, 11, 5442.	12.8	67
135	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
136	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
137	New Genomic Tools for Molecular Studies of Evolutionary Change in Threespine Sticklebacks. <i>Behaviour</i> , 2004, 141, 1331-1344.	0.8	64
138	Sparse panicle1 is required for inflorescence development in <i>Setaria viridis</i> and maize. <i>Nature Plants</i> , 2017, 3, 17054.	9.3	63
139	Identification and characterization of functional centromeres of the common bean. <i>Plant Journal</i> , 2013, 76, 47-60.	5.7	61
140	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
141	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
142	The genetic basis of divergent pigment patterns in juvenile threespine sticklebacks. <i>Heredity</i> , 2011, 107, 155-166.	2.6	60
143	<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
144	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , 2019, 20, 905.	2.8	59

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145	Integrating microarray analysis and the soybean genome to understand the soybeans iron deficiency response. <i>BMC Genomics</i> , 2009, 10, 376.	2.8	56
146	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
147	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
148	The Sphagnome Project: enabling ecological and evolutionary insights through a genus-level sequencing project. <i>New Phytologist</i> , 2018, 217, 16-25.	7.3	54
149	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
150	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .	10.3	53
151	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
152	Extensive Linkage Disequilibrium, a Common 16.7-Kilobase Deletion, and Evidence of Balancing Selection in the Human Protocadherin 1± Cluster. <i>American Journal of Human Genetics</i> , 2003, 72, 621-635.	6.2	51
153	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
154	A Genome-Wide Survey of Switchgrass Genome Structure and Organization. <i>PLoS ONE</i> , 2012, 7, e33892.	2.5	50
155	Hardwood Tree Genomics: Unlocking Woody Plant Biology. <i>Frontiers in Plant Science</i> , 2018, 9, 1799.	3.6	50
156	Four chromosome scale genomes and a pan-genome annotation to accelerate pecan tree breeding. <i>Nature Communications</i> , 2021, 12, 4125.	12.8	49
157	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
158	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
159	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
160	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
161	Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. <i>Plant Journal</i> , 2015, 84, 800-815.	5.7	47
162	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

#	ARTICLE	IF	CITATIONS
163	Complete genome sequence of <i>Rhodospirillum rubrum</i> type strain (S1T). <i>Standards in Genomic Sciences</i> , 2011, 4, 293-302.	1.5	44
164	Genome Sequence of the Verrucomicrobium <i>Opiritatus terrae</i> PB90-1, an Abundant Inhabitant of Rice Paddy Soil Ecosystems. <i>Journal of Bacteriology</i> , 2011, 193, 2367-2368.	2.2	44
165	Identical Genomic Organization of Two Hemichordate Hox Clusters. <i>Current Biology</i> , 2012, 22, 2053-2058.	3.9	43
166	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
167	The tepary bean genome provides insight into evolution and domestication under heat stress. <i>Nature Communications</i> , 2021, 12, 2638.	12.8	43
168	Bifurcation and Enhancement of Autonomous-Nonautonomous Retrotransposon Partnership through LTR Swapping in Soybean. <i>Plant Cell</i> , 2010, 22, 48-61.	6.6	42
169	Mediation of plant-mycorrhizal interaction by a lectin receptor-like kinase. <i>Nature Plants</i> , 2019, 5, 676-680.	9.3	42
170	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
171	Genome Analysis of Planctomycetes Inhabiting Blades of the Red Alga <i>Porphyra umbilicalis</i> . <i>PLoS ONE</i> , 2016, 11, e0151883.	2.5	39
172	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
173	Toward a Reference Sequence of the Soybean Genome: A Multiagency Effort. <i>Crop Science</i> , 2006, 46, S-55.	1.8	37
174	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
175	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
176	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
177	Extensive Genetic Diversity is Present within North American Switchgrass Germplasm. <i>Plant Genome</i> , 2018, 11, 170055.	2.8	35
178	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
179	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
180	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

#	ARTICLE	IF	CITATIONS
181	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
182	Pleiotropic and Epistatic Network-Based Discovery: Integrated Networks for Target Gene Discovery. <i>Frontiers in Energy Research</i> , 2018, 6, .	2.3	32
183	Amplification and adaptation of centromeric repeats in polyploid switchgrass species. <i>New Phytologist</i> , 2018, 218, 1645-1657.	7.3	30
184	Revealing the transcriptomic complexity of switchgrass by PacBio long-read sequencing. <i>Biotechnology for Biofuels</i> , 2018, 11, 170.	6.2	30
185	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
186	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
187	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
188	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
189	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
190	Genetic Associations in Four Decades of Multienvironment Trials Reveal Agronomic Trait Evolution in Common Bean. <i>Genetics</i> , 2020, 215, 267-284.	2.9	26
191	Improved chromosome-level genome assembly and annotation of the seagrass, <i>Zostera marina</i> (eelgrass). <i>F1000Research</i> , 2021, 10, 289.	1.6	26
192	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
193	Novel metabolic interactions and environmental conditions mediate the boreal peatmoss-cyanobacteria mutualism. <i>ISME Journal</i> , 2022, 16, 1074-1085.	9.8	25
194	Fowl sequence. <i>Nature</i> , 2004, 432, 679-680.	27.8	24
195	Assembly of the <i>Boechera retrofracta</i> Genome and Evolutionary Analysis of Apomixis-Associated Genes. <i>Genes</i> , 2018, 9, 185.	2.4	24
196	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
197	Sub genome anchored physical frameworks of the allotetraploid Upland cotton (<i>Gossypium hirsutum</i>) Tj ETQq1 1 0.784314 rgBT /Overl 7, 15274.	3.3	23
198	Plant single-cell solutions for energy and the environment. <i>Communications Biology</i> , 2021, 4, 962.	4.4	23

#	ARTICLE	IF	CITATIONS
199	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
200	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
201	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
202	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	4.4	21
203	Multi-Phenotype Association Decomposition: Unraveling Complex Gene-Phenotype Relationships. <i>Frontiers in Genetics</i> , 2019, 10, 417.	2.3	20
204	Sequencing and Analysis of the Sex Determination Region of <i>Populus trichocarpa</i> . <i>Genes</i> , 2020, 11, 843.	2.4	19
205	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
206	SoyCSN: Soybean context-specific network analysis and prediction based on tissue-specific transcriptome data. <i>Plant Direct</i> , 2019, 3, e00167.	1.9	18
207	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
208	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
209	Habitat-adapted microbial communities mediate <i>Sphagnum</i> peatmoss resilience to warming. <i>New Phytologist</i> , 2022, 234, 2111-2125.	7.3	18
210	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
211	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
212	The <i>Sphagnum</i> Genome Project. <i>Advances in Botanical Research</i> , 2016, , 167-187.	1.1	17
213	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
214	Overexpression of a <i>Prefoldin Î²</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
215	<i>Arabidopsis</i> C-terminal binding protein <i>ANGUSTIFOLIA</i> modulates transcriptional coregulation of <i>MYB46</i> and <i>WRKY33</i> . <i>New Phytologist</i> , 2020, 228, 1627-1639.	7.3	17
216	High Density Genetic Maps of Seashore <i>Paspalum</i> Using Genotyping-By-Sequencing and Their Relationship to The <i>Sorghum Bicolor</i> Genome. <i>Scientific Reports</i> , 2019, 9, 12183.	3.3	16

#	ARTICLE	IF	CITATIONS
217	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
218	Genomic variation within the maize stiffâ€stalk heterotic germplasm pool. <i>Plant Genome</i> , 2021, 14, e20114.	2.8	14
219	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
220	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
221	Highâ€density linkage map reveals QTL underlying growth traits in AP13Ã—VS16 biparental population of switchgrass. <i>GCB Bioenergy</i> , 2019, 11, 672-690.	5.6	13
222	Representing sex chromosomes in genome assemblies. <i>Cell Genomics</i> , 2022, 2, 100132.	6.5	13
223	Integrative genomics reveals paths to sex dimorphism in <i>Salix purpurea</i> L. <i>Horticulture Research</i> , 2021, 8, 170.	6.3	12
224	Wavelet-Based Genomic Signal Processing for Centromere Identification and Hypothesis Generation. <i>Frontiers in Genetics</i> , 2019, 10, 487.	2.3	11
225	Environmentally responsive QTL controlling surface wax load in switchgrass. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3119-3137.	3.6	11
226	Light-responsive expression atlas reveals the effects of light quality and intensity in <i>KalanchoÃ« fedtschenkoi</i> , a plant with crassulacean acid metabolism. <i>GigaScience</i> , 2020, 9, .	6.4	11
227	Sequenceâ€Based Introgression Mapping Identifies Candidate White Mold Tolerance Genes in Common Bean. <i>Plant Genome</i> , 2016, 9, plantgenome2015.09.0092.	2.8	10
228	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
229	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
230	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
231	The Transcription Factor Roc1 Is a Key Regulator of Cellulose Degradation in the Wood-Decaying Mushroom <i>Schizophyllum commune</i> . <i>MBio</i> , 2022, 13, .	4.1	10
232	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
233	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
234	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

#	ARTICLE	IF	CITATIONS
235	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
236	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
237	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
238	Six is seventh. <i>Nature</i> , 2003, 425, 775-776.	27.8	8
239	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
240	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
241	The Common Bean V Gene Encodes Flavonoid 3-Hydroxylase: A Major Mutational Target for Flavonoid Diversity in Angiosperms. <i>Frontiers in Plant Science</i> , 2022, 13, 869582.	3.6	7
242	Complete genome sequence of <i>Tolomonas auensis</i> type strain (TA 4T). <i>Standards in Genomic Sciences</i> , 2011, 5, 112-120.	1.5	6
243	Proteome profile of the endomembrane of developing coleoptiles from switchgrass (<i>Panicum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 2.2 6		
244	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
245	Theria-specific Homeodomain and cis-Regulatory Element Evolution of the <i>Dlx3</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
246	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
247	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
248	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
249	Identification of functional single nucleotide polymorphism of <i>Populus trichocarpa</i> PtrEPSP-AT and determination of its transcriptional effect. <i>Plant Direct</i> , 2020, 4, e00178.	1.9	4
250	Genome-wide quantitative trait loci detection for biofuel traits in switchgrass (<i>Panicum</i>) Tj ETQq0 0 0 rgBT /Overlock 10.3 Tf 50 142 3.6		
251	Sequence Finishing. , 2004, 255, 333-342.		2
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	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
254	Assembly of DNA Sequencing Data. , 2004, 255, 319-332.		0
255	Quality Assessment of Finished BAC Sequences. , 2004, 255, 343-350.		0
256	The Draft Soybean Genome Sequence. , 2010, , 223-244.		0
257	Sequence and Assembly of the Soybean Genome. , 2008, , 101-112.		0