

Jeffrey L Bennetzen

List of Publications by Year in descending order

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200
papers

33,205
citations

8159

76
h-index

4323

173
g-index

214
all docs

214
docs citations

214
times ranked

22950
citing authors

#	ARTICLE	IF	CITATIONS
1	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
2	A unified classification system for eukaryotic transposable elements. <i>Nature Reviews Genetics</i> , 2007, 8, 973-982.	7.7	2,396
3	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. <i>Science</i> , 2008, 319, 64-69.	6.0	1,712
4	The genome of woodland strawberry (<i>Fragaria vesca</i>). <i>Nature Genetics</i> , 2011, 43, 109-116.	9.4	1,091
5	Plant Retrotransposons. <i>Annual Review of Genetics</i> , 1999, 33, 479-532.	3.2	1,029
6	The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by Vernalization. <i>Science</i> , 2004, 303, 1640-1644.	6.0	999
7	The paleontology of intergene retrotransposons of maize. <i>Nature Genetics</i> , 1998, 20, 43-45.	9.4	953
8	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , 2012, 30, 555-561.	9.4	864
9	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	2.4	832
10	The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. <i>Science</i> , 2011, 332, 960-963.	6.0	794
11	Draft genome sequence of <i>Camellia sinensis</i> var. <i>sinensis</i> provides insights into the evolution of the tea genome and tea quality. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4151-E4158.	3.3	730
12	Rapid recent growth and divergence of rice nuclear genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12404-12410.	3.3	674
13	Transposable element contributions to plant gene and genome evolution. , 2000, 42, 251-269.		643
14	Genome Size Reduction through Illegitimate Recombination Counteracts Genome Expansion in <i>Arabidopsis</i> . <i>Genome Research</i> , 2002, 12, 1075-1079.	2.4	634
15	Mechanisms of Recent Genome Size Variation in Flowering Plants. <i>Annals of Botany</i> , 2005, 95, 127-132.	1.4	598
16	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	18.7	563
17	Analyses of LTR-Retrotransposon Structures Reveal Recent and Rapid Genomic DNA Loss in Rice. <i>Genome Research</i> , 2004, 14, 860-869.	2.4	488
18	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	9.4	472

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19	Promoter mutations of an essential gene for pollen development result in disease resistance in rice. <i>Genes and Development</i> , 2006, 20, 1250-1255.	2.7	457
20	Close Split of Sorghum and Maize Genome Progenitors. <i>Genome Research</i> , 2004, 14, 1916-1923.	2.4	443
21	The Contributions of Transposable Elements to the Structure, Function, and Evolution of Plant Genomes. <i>Annual Review of Plant Biology</i> , 2014, 65, 505-530.	8.6	436
22	De novo genome sequencing and comparative genomics of date palm (<i>Phoenix dactylifera</i>). <i>Nature Biotechnology</i> , 2011, 29, 521-527.	9.4	356
23	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	9.4	356
24	Foxtail Millet: A Sequence-Driven Grass Model System. <i>Plant Physiology</i> , 2009, 149, 137-141.	2.3	337
25	Exceptional Diversity, Non-Random Distribution, and Rapid Evolution of Retroelements in the B73 Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000732.	1.5	322
26	Transposable elements, gene creation and genome rearrangement in flowering plants. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 621-627.	1.5	314
27	Analysis of retrotransposon structural diversity uncovers properties and propensities in angiosperm genome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17638-17643.	3.3	294
28	Comparative Sequence Analysis of Plant Nuclear Genomes: Microcolinearity and Its Many Exceptions. <i>Plant Cell</i> , 2000, 12, 1021-1029.	3.1	261
29	Mechanisms and rates of genome expansion and contraction in flowering plants. <i>Genetica</i> , 2002, 115, 29-36.	0.5	257
30	New reference genome sequences of hot pepper reveal the massive evolution of plant disease-resistance genes by retroduplication. <i>Genome Biology</i> , 2017, 18, 210.	3.8	255
31	The contributions of retroelements to plant genome organization, function and evolution. <i>Trends in Microbiology</i> , 1996, 4, 347-353.	3.5	233
32	Comparative Sequence Analysis of Colinear Barley and Rice Bacterial Artificial Chromosomes. <i>Plant Physiology</i> , 2001, 125, 1342-1353.	2.3	204
33	Geographical Distribution and Diversity of Bacteria Associated with Natural Populations of <i>Drosophila melanogaster</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 3470-3479.	1.4	200
34	Assessment of genetic diversity in dent and popcorn (<i>Zea mays</i> L.) inbred lines using inter-simple sequence repeat (ISSR) amplification. <i>Molecular Breeding</i> , 1995, 1, 365-373.	1.0	190
35	Nucleotide sequence of the maize transposable element <i>Mul</i> . <i>Nucleic Acids Research</i> , 1984, 12, 5955-5967.	6.5	188
36	Gene Loss and Movement in the Maize Genome. <i>Genome Research</i> , 2004, 14, 1924-1931.	2.4	186

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37	Active maize genes are unmodified and flanked by diverse classes of modified, highly repetitive DNA. <i>Genome</i> , 1994, 37, 565-576.	0.9	185
38	Consistent over-estimation of gene number in complex plant genomes. <i>Current Opinion in Plant Biology</i> , 2004, 7, 732-736.	3.5	176
39	The Unified Grass Genome: Synergy in Synteny. <i>Genome Research</i> , 1997, 7, 301-306.	2.4	169
40	Do genetic recombination and gene density shape the pattern of DNA elimination in rice long terminal repeat retrotransposons?. <i>Genome Research</i> , 2009, 19, 2221-2230.	2.4	169
41	A complex history of rearrangement in an orthologous region of the maize, sorghum, and rice genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12265-12270.	3.3	163
42	Transposable elements, genes and recombination in a 215-kb contig from wheat chromosome 5Am. <i>Functional and Integrative Genomics</i> , 2002, 2, 70-80.	1.4	153
43	Comparison of DNA Marker Technologies in Characterizing Plant Genome Diversity: Variability in Chinese Sorghums. <i>Crop Science</i> , 1996, 36, 1669-1676.	0.8	152
44	Isolation of the structural gene for alcohol dehydrogenase by genetic complementation in yeast. <i>Nature</i> , 1980, 283, 214-216.	13.7	148
45	Rapid diversification of five <i>Oryza</i> AA genomes associated with rice adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4954-62.	3.3	145
46	Patterns in grass genome evolution. <i>Current Opinion in Plant Biology</i> , 2007, 10, 176-181.	3.5	139
47	Recombination at the Rp1 locus of maize. <i>Molecular Genetics and Genomics</i> , 1991, 226, 377-82.	2.4	137
48	5Gs for crop genetic improvement. <i>Current Opinion in Plant Biology</i> , 2020, 56, 190-196.	3.5	134
49	Plant centromere organization: a dynamic structure with conserved functions. <i>Trends in Genetics</i> , 2007, 23, 134-139.	2.9	133
50	Distribution, diversity, evolution, and survival of <i>Helitrons</i> in the maize genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19922-19927.	3.3	133
51	Different Types and Rates of Genome Evolution Detected by Comparative Sequence Analysis of Orthologous Segments From Four Cereal Genomes. <i>Genetics</i> , 2002, 162, 1389-1400.	1.2	132
52	Transposable element origins of epigenetic gene regulation. <i>Current Opinion in Plant Biology</i> , 2011, 14, 156-161.	3.5	130
53	The genetic colinearity of rice and other cereals on the basis of genomic sequence analysis. <i>Current Opinion in Plant Biology</i> , 2003, 6, 128-133.	3.5	129
54	The evolution of nuclear genome structure in seed plants. <i>American Journal of Botany</i> , 2004, 91, 1709-1725.	0.8	129

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55	Dynamic Evolution of <i>Oryza</i> Genomes Is Revealed by Comparative Genomic Analysis of a Genus-Wide Vertical Data Set. <i>Plant Cell</i> , 2009, 20, 3191-3209.	3.1	128
56	Identification of stress-responsive genes in an indica rice (<i>Oryza sativa</i> L.) using ESTs generated from drought-stressed seedlings. <i>Journal of Experimental Botany</i> , 2007, 58, 253-265.	2.4	127
57	<i>Brachypodium distachyon</i> and <i>Setaria viridis</i> : Model Genetic Systems for the Grasses. <i>Annual Review of Plant Biology</i> , 2015, 66, 465-485.	8.6	126
58	The genetic map of finger millet, <i>Eleusine coracana</i> . <i>Theoretical and Applied Genetics</i> , 2006, 114, 321-332.	1.8	124
59	Recombination, rearrangement, reshuffling, and divergence in a centromeric region of rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 383-388.	3.3	124
60	Population Structure and Diversity in Finger Millet (<i>Eleusine coracana</i>) Germplasm. <i>Tropical Plant Biology</i> , 2008, 1, 131-141.	1.0	122
61	High-Cot sequence analysis of the maize genome. <i>Plant Journal</i> , 2003, 34, 249-255.	2.8	120
62	The <i>zml</i> Gene of Maize Codes for Phytoene Synthase. <i>Genetics</i> , 1996, 143, 479-488.	1.2	120
63	Comparative sequence analysis of <i>MONOCULM1</i> -orthologous regions in 14 <i>Oryza</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2071-2076.	3.3	119
64	Sequence Organization and Conservation in <i>sh2/a1</i> -Homologous Regions of Sorghum and Rice. <i>Genetics</i> , 1998, 148, 435-443.	1.2	116
65	The Regulatory Regions Required for <i>B1</i> Paramutation and Expression Are Located Far Upstream of the Maize <i>b1</i> Transcribed Sequences. <i>Genetics</i> , 2002, 162, 917-930.	1.2	116
66	Do Plants Have a One-Way Ticket to Genomic Obesity?. <i>Plant Cell</i> , 1997, 9, 1509.	3.1	115
67	Pathogen corruption and site-directed recombination at a plant disease resistance gene cluster. <i>Genome Research</i> , 2008, 18, 1918-1923.	2.4	112
68	G Protein Activation without a GEF in the Plant Kingdom. <i>PLoS Genetics</i> , 2012, 8, e1002756.	1.5	110
69	Sequence Analysis of Bacterial Artificial Chromosome Clones from the Apospory-Specific Genomic Region of <i>Pennisetum</i> and <i>Cenchrus</i> . <i>Plant Physiology</i> , 2008, 147, 1396-1411.	2.3	107
70	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	18.7	106
71	Numerous small rearrangements of gene content, order and orientation differentiate grass genomes. <i>Plant Molecular Biology</i> , 2002, 48, 821-827.	2.0	105
72	Uneven chromosome contraction and expansion in the maize genome. <i>Genome Research</i> , 2006, 16, 1241-1251.	2.4	105

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73	Structure-based discovery and description of plant and animal <i>Helitrons</i> . Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12832-12837.	3.3	102
74	Exceptional subgenome stability and functional divergence in the allotetraploid Ethiopian cereal teff. Nature Communications, 2020, 11, 884.	5.8	101
75	Lateral transfers of large DNA fragments spread functional genes among grasses. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 4416-4425.	3.3	94
76	Regulatory mutants of the maize Adh1 gene caused by DNA insertions. Nature, 1982, 300, 542-544.	13.7	91
77	Covalent DNA modification and the regulation of Mutator element transposition in maize. Molecular Genetics and Genomics, 1987, 208, 45-51.	2.4	86
78	Analysis and mapping of randomly chosen bacterial artificial chromosome clones from hexaploid bread wheat. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 19243-19248.	3.3	86
79	Analysis of the chromosomal distribution of transposon-carrying T-DNAs in tomato using the inverse polymerase chain reaction. Molecular Genetics and Genomics, 1994, 242, 573-585.	2.4	82
80	Natural selection on gene function drives the evolution of LTR retrotransposon families in the rice genome. Genome Research, 2009, 19, 243-254.	2.4	82
81	THE RICE GENOME: Opening the Door to Comparative Plant Biology. Science, 2002, 296, 60-63.	6.0	76
82	Structural Analysis of the Maize Rp1 Complex Reveals Numerous Sites and Unexpected Mechanisms of Local Rearrangement. Plant Cell, 2002, 14, 3213-3223.	3.1	72
83	Gene loss and genome rearrangement in the plastids of five Hemiparasites in the family Orobanchaceae. BMC Plant Biology, 2018, 18, 30.	1.6	72
84	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 April 2010 – 31 May 2010. Molecular Ecology Resources, 2010, 10, 1098-1105.	2.2	71
85	Circular RNA architecture and differentiation during leaf bud to young leaf development in tea (<i>Camellia sinensis</i>). Planta, 2018, 248, 1417-1429.	1.6	71
86	Allele-specific and Mutator-associated instability at the Rpl disease-resistance locus of maize. Nature, 1988, 332, 369-370.	13.7	70
87	Genomic sequencing reveals gene content, genomic organization, and recombination relationships in barley. Functional and Integrative Genomics, 2002, 2, 51-59.	1.4	65
88	Gene identification in a complex chromosomal continuum by local genomic cross-referencing. Plant Journal, 1996, 10, 1163-1168.	2.8	63
89	Structural Domains and Matrix Attachment Regions along Colinear Chromosomal Segments of Maize and Sorghum. Plant Cell, 2000, 12, 249-264.	3.1	63
90	DNA Rearrangement in Orthologous Orp Regions of the Maize, Rice and Sorghum Genomes. Genetics, 2005, 170, 1209-1220.	1.2	62

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91	The Hardy Rubber Tree Genome Provides Insights into the Evolution of Polyisoprene Biosynthesis. <i>Molecular Plant</i> , 2018, 11, 429-442.	3.9	62
92	On the Tetraploid Origin of the Maize Genome. <i>Comparative and Functional Genomics</i> , 2004, 5, 281-284.	2.0	61
93	The maize genome as a model for efficient sequence analysis of large plant genomes. <i>Current Opinion in Plant Biology</i> , 2006, 9, 149-156.	3.5	61
94	The bracteatus pineapple genome and domestication of clonally propagated crops. <i>Nature Genetics</i> , 2019, 51, 1549-1558.	9.4	60
95	Gene enrichment in maize with hypomethylated partial restriction (HMPR) libraries. <i>Genome Research</i> , 2005, 15, 1441-1446.	2.4	59
96	A GeneTrek analysis of the maize genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11844-11849.	3.3	59
97	Structure and Evolution of the r/b Chromosomal Regions in Rice, Maize and Sorghum Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY542311, AF466202, AF466203, and AY542310.. <i>Genetics</i> , 2005, 169, 891-906.	1.2	51
98	Discovery and characterization of tannase genes in plants: roles in hydrolysis of tannins. <i>New Phytologist</i> , 2020, 226, 1104-1116.	3.5	51
99	Identification of a Pathogenicity Locus, rpfA, in <i>Erwinia carotovora</i> subsp. <i>carotovora</i> That Encodes a Two-Component Sensor-Regulator Protein. <i>Molecular Plant-Microbe Interactions</i> , 1997, 10, 407-415.	1.4	49
100	Spatio-temporal patterns of genome evolution in allotetraploid species of the genus <i>Oryza</i> . <i>Plant Journal</i> , 2010, 63, 430-442.	2.8	48
101	High-Throughput Discovery of Mutations in Tef Semi-Dwarfing Genes by Next-Generation Sequencing Analysis. <i>Genetics</i> , 2012, 192, 819-829.	1.2	48
102	Comparative genome-wide characterization leading to simple sequence repeat marker development for <i>Nicotiana</i> . <i>BMC Genomics</i> , 2018, 19, 500.	1.2	46
103	Selection and characterization of cadmium-resistant suspension cultures of the wild tomato <i>Lycopersicon peruvianum</i> . <i>Plant Cell Reports</i> , 1984, 3, 258-261.	2.8	42
104	Comparative Sequence Analysis of the Sorghum RphRegion and the Maize Rp1 Resistance Gene Complex. <i>Plant Physiology</i> , 2002, 130, 1728-1738.	2.3	42
105	Reply: A unified classification system for eukaryotic transposable elements should reflect their phylogeny. <i>Nature Reviews Genetics</i> , 2009, 10, 276-276.	7.7	41
106	Methylation-Spanning Linker Libraries Link Gene-Rich Regions and Identify Epigenetic Boundaries in Zea mays. <i>Genome Research</i> , 2002, 12, 1345-1349.	2.4	40
107	Genomic organization of the ribosomal DNA of sorghum and its close relatives. <i>Theoretical and Applied Genetics</i> , 1989, 77, 844-850.	1.8	39
108	Sequence composition and organization in the Sh2/A1-homologous region of rice. <i>Plant Molecular Biology</i> , 1996, 32, 999-1001.	2.0	39

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109	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000728.	1.5	39
110	Centromere retention and loss during the descent of maize from a tetraploid ancestor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21004-21009.	3.3	38
111	Integrating transcriptome and microRNA analysis identifies genes and microRNAs for AHO-induced systemic acquired resistance in <i>N. tabacum</i> . <i>Scientific Reports</i> , 2017, 7, 12504.	1.6	36
112	Genome sequence of <i>Malania oleifera</i> , a tree with great value for nervonic acid production. <i>GigaScience</i> , 2019, 8, .	3.3	36
113	The structure and evolution of angiosperm nuclear genomes. <i>Current Opinion in Plant Biology</i> , 1998, 1, 103-108.	3.5	35
114	Retrotransposons: central players in the structure, evolution and function of plant genomes. <i>Trends in Plant Science</i> , 2000, 5, 509-510.	4.3	35
115	Natural insertions in rice commonly form tandem duplications indicative of patch-mediated double-strand break induction and repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6684-6689.	3.3	34
116	The many hues of plant heterochromatin. <i>Genome Biology</i> , 2000, 1, reviews107.1.	13.9	33
117	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 October 2012â€“30 November 2012. <i>Molecular Ecology Resources</i> , 2013, 13, 341-343.	2.2	33
118	Nitrogen Fertilization Reduces Nitrogen Fixation Activity of Diverse Diazotrophs in Switchgrass Roots. <i>Phytobiomes Journal</i> , 2021, 5, 80-87.	1.4	33
119	Homologous recombination between plasmid DNA molecules in maize protoplasts. <i>Molecular Genetics and Genomics</i> , 1991, 230, 209-218.	2.4	32
120	Isolation of matrices from maize leaf nuclei: identification of a matrix-binding site adjacent to the <i>Adh1</i> gene. <i>Plant Molecular Biology</i> , 1993, 22, 1135-1143.	2.0	31
121	Species-Associated Differences in the Below-Ground Microbiomes of Wild and Domesticated <i>Setaria</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1183.	1.7	31
122	Evolutionary History and Positional Shift of a Rice Centromere. <i>Genetics</i> , 2007, 177, 1217-1220.	1.2	29
123	Young, intact and nested retrotransposons are abundant in the onion and asparagus genomes. <i>Annals of Botany</i> , 2013, 112, 881-889.	1.4	29
124	Genetic Diversity and Population Structure of Native and Introduced Date Palm (<i>Phoenix dactylifera</i>) Germplasm in the United Arab Emirates. <i>Tropical Plant Biology</i> , 2014, 7, 30-41.	1.0	29
125	The tea plant reference genome and improved gene annotation using long-read and paired-end sequencing data. <i>Scientific Data</i> , 2019, 6, 122.	2.4	29
126	Fine mapping of the <i>Pc</i> locus of <i>Sorghum bicolor</i> , a gene controlling the reaction to a fungal pathogen and its host-selective toxin. <i>Theoretical and Applied Genetics</i> , 2007, 114, 961-970.	1.8	28

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127	The State of DNA Modification within and Flanking Maize Transposable Elements. , 1988, , 237-250.		28
128	Phoenix phylogeny, and analysis of genetic variation in a diverse collection of date palm (Phoenix) Tj ETQq0 0 0 rgBT /Overlock, 10 Tf 50	1.8	27
129	National Science Foundation-sponsored workshop report. Maize genome sequencing project. Plant Physiology, 2001, 127, 1572-8.	2.3	27
130	Structure and evolution of the Cinful retrotransposon family of maize. Genome, 2003, 46, 745-752.	0.9	26
131	Recurrent Loss of Specific Introns during Angiosperm Evolution. PLoS Genetics, 2014, 10, e1004843.	1.5	26
132	Grass Genomic Synteny Illuminates Plant Genome Function and Evolution. Rice, 2008, 1, 109-118.	1.7	25
133	Dynamic Gene Copy Number Variation in Collinear Regions of Grass Genomes. Molecular Biology and Evolution, 2012, 29, 861-871.	3.5	24
134	Characterization of four dispersed repetitive DNA sequences from <i>Zea mays</i> and their use in constructing contiguous DNA fragments using YAC clones. Genome, 1996, 39, 811-817.	0.9	23
135	Discovery and assembly of repeat family pseudomolecules from sparse genomic sequence data using the Assisted Automated Assembler of Repeat Families (AAARF) algorithm. BMC Bioinformatics, 2008, 9, 235.	1.2	23
136	Genome sequence and genetic diversity analysis of an under-domesticated orphan crop, white fonio (<i>Digitaria exilis</i>). GigaScience, 2021, 10, .	3.3	23
137	Gene Content and Distribution in the Nuclear Genome of <i>Fragaria vesca</i> . Plant Genome, 2009, 2, .	1.6	20
138	Fine-Mapping and Identification of a Candidate Gene Underlying the <i>d2</i> Dwarfing Phenotype in Pearl Millet, <i>Cenchrus americanus</i> (L.) Morrone. G3: Genes, Genomes, Genetics, 2013, 3, 563-572.	0.8	20
139	Distinguishing friends, foes, and freeloaders in giant genomes. Current Opinion in Genetics and Development, 2018, 49, 49-55.	1.5	19
140	Black Tea Quality is Highly Affected during Processing by its Leaf Surface Microbiome. Journal of Agricultural and Food Chemistry, 2021, 69, 7115-7126.	2.4	19
141	<i>Aegilops tauschii</i> genome assembly Aet v5.0 features greater sequence contiguity and improved annotation. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	19
142	Grass Genome Structure and Evolution. , 2008, 4, 41-56.		18
143	Construction and Homologous Expression of a Maize Adh1 Based NcoI Cassette Vector. Plant Physiology, 1987, 85, 327-330.	2.3	17
144	Exceptional haplotype variation in maize. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9093-9095.	3.3	17

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145	Adaptive Evolution of Signaling Partners. <i>Molecular Biology and Evolution</i> , 2015, 32, 998-1007.	3.5	17
146	Analysis of retrotransposon abundance, diversity and distribution in holocentric <i>Eleocharis</i> (Cyperaceae) genomes. <i>Annals of Botany</i> , 2018, 122, 279-290.	1.4	17
147	Whole Plastome Sequences from Five Ginger Species Facilitate Marker Development and Define Limits to Barcode Methodology. <i>PLoS ONE</i> , 2014, 9, e108581.	1.1	17
148	Genetic Diversity of a Parasitic Weed, <i>Striga hermonthica</i> , on Sorghum and Pearl Millet in Mali. <i>Tropical Plant Biology</i> , 2011, 4, 91-98.	1.0	16
149	Transposable element contributions to plant gene and genome evolution. , 2000, , 251-269.		16
150	A Plant Genome Initiative. <i>Plant Cell</i> , 1998, 10, 488-493.	3.1	15
151	Plant genomics takes root, branches out. <i>Trends in Genetics</i> , 1999, 15, 85-87.	2.9	15
152	Enchilada redux: how complete is your genome sequence?. <i>New Phytologist</i> , 2008, 179, 249-250.	3.5	15
153	Epigenetics of the epigenome. <i>Current Opinion in Plant Biology</i> , 2011, 14, 113-115.	3.5	15
154	Genomic Characterization for Parasitic Weeds of the Genus <i>Striga</i> by Sample Sequence Analysis. <i>Plant Genome</i> , 2012, 5, .	1.6	15
155	Isolation and bioinformatic analysis of a novel transposable element, IS <i>Cbe</i> 4, from the hyperthermophilic bacterium, <i>Caldicellulosiruptor bescii</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2013, 40, 1443-1448.	1.4	15
156	Genomic Resources for Gene Discovery, Functional Genome Annotation, and Evolutionary Studies of Maize and Its Close Relatives. <i>Genetics</i> , 2013, 195, 723-737.	1.2	15
157	Teff, an Orphan Cereal in the <i>Chloridoideae</i> , Provides Insights into the Evolution of Storage Proteins in Grasses. <i>Genome Biology and Evolution</i> , 2016, 8, 1712-1721.	1.1	15
158	Matrix Attachment Regions and Transcribed Sequences within a Long Chromosomal Continuum Containing Maize <i>Adh1</i> . <i>Plant Cell</i> , 1995, 7, 1667.	3.1	14
159	Birth and Death of LTR-Retrotransposons in <i>Aegilops tauschii</i> . <i>Genetics</i> , 2018, 210, 1039-1051.	1.2	14
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