

# 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	Genome structure and evolutionary history of frankincense producing <i>Boswellia sacra</i> . <i>IScience</i> , 2022, 25, 104574.	1.9	3
2	Nitrogen Fertilization Reduces Nitrogen Fixation Activity of Diverse Diazotrophs in Switchgrass Roots. <i>Phytobiomes Journal</i> , 2021, 5, 80-87.	1.4	33
3	Integration of high-density genetic mapping with transcriptome analysis uncovers numerous agronomic QTL and reveals candidate genes for the control of tillering in sorghum. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	4
4	Genome sequence and genetic diversity analysis of an under-domesticated orphan crop, white fonio ( <i>Digitaria exilis</i> ). <i>GigaScience</i> , 2021, 10, .	3.3	23
5	Sample Sequence Analysis Uncovers Recurrent Horizontal Transfers of Transposable Elements among Grasses. <i>Molecular Biology and Evolution</i> , 2021, 38, 3664-3675.	3.5	10
6	Black Tea Quality is Highly Affected during Processing by its Leaf Surface Microbiome. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 7115-7126.	2.4	19
7	Integrated Genomic Analyses From Low-Depth Sequencing Help Resolve Phylogenetic Incongruence in the Bamboos (Poaceae: Bambusoideae). <i>Frontiers in Plant Science</i> , 2021, 12, 725728.	1.7	5
8	<i>Aegilops tauschii</i> genome assembly Aet v5.0 features greater sequence contiguity and improved annotation. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	19
9	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	13.7	106
10	Allopolyploidy and genomic differentiation in holocentric species of the <i>Eleocharis montana</i> complex (Cyperaceae). <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	7
11	Discovery and characterization of tannase genes in plants: roles in hydrolysis of tannins. <i>New Phytologist</i> , 2020, 226, 1104-1116.	3.5	51
12	Exceptional subgenome stability and functional divergence in the allotetraploid Ethiopian cereal teff. <i>Nature Communications</i> , 2020, 11, 884.	5.8	101
13	5Gs for crop genetic improvement. <i>Current Opinion in Plant Biology</i> , 2020, 56, 190-196.	3.5	134
14	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
15	Culturing better tea research. <i>Nature</i> , 2019, 566, S5-S5.	13.7	4
16	The bracteatus pineapple genome and domestication of clonally propagated crops. <i>Nature Genetics</i> , 2019, 51, 1549-1558.	9.4	60
17	Genome sequence of <i>Malaria oleifera</i> , a tree with great value for nervonic acid production. <i>GigaScience</i> , 2019, 8, .	3.3	36
18	Lateral transfers of large DNA fragments spread functional genes among grasses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4416-4425.	3.3	94

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19	Phoenix phylogeny, and analysis of genetic variation in a diverse collection of date palm (Phoenix) Tj ETQq1 1 0.784314 rgBT /Overlo	1.8	27
20	Draft genome sequence of <i>Camellia sinensis</i> var. <i>sinensis</i> provides insights into the evolution of the tea genome and tea quality. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4151-E4158.	3.3	730
21	Discovery of Lineage-Specific Genome Change in Rice Through Analysis of Resequencing Data. Genetics, 2018, 209, 617-626.	1.2	4
22	Distinguishing friends, foes, and freeloaders in giant genomes. Current Opinion in Genetics and Development, 2018, 49, 49-55.	1.5	19
23	Relationships between Gene Structure and Genome Instability in Flowering Plants. Molecular Plant, 2018, 11, 407-413.	3.9	10
24	The Hardy Rubber Tree Genome Provides Insights into the Evolution of Polyisoprene Biosynthesis. Molecular Plant, 2018, 11, 429-442.	3.9	62
25	Maize Transposable Element Dynamics. Compendium of Plant Genomes, 2018, , 49-58.	0.3	1
26	Birth and Death of LTR-Retrotransposons in <i>Aegilops tauschii</i> . Genetics, 2018, 210, 1039-1051.	1.2	14
27	Analysis of retrotransposon abundance, diversity and distribution in holocentric <i>Eleocharis</i> (Cyperaceae) genomes. Annals of Botany, 2018, 122, 279-290.	1.4	17
28	Species-Associated Differences in the Below-Ground Microbiomes of Wild and Domesticated <i>Setaria</i> . Frontiers in Plant Science, 2018, 9, 1183.	1.7	31
29	Comparative genome-wide characterization leading to simple sequence repeat marker development for <i>Nicotiana</i> . BMC Genomics, 2018, 19, 500.	1.2	46
30	Gene loss and genome rearrangement in the plastids of five Hemiparasites in the family Orobanchaceae. BMC Plant Biology, 2018, 18, 30.	1.6	72
31	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
32	Integrating transcriptome and microRNA analysis identifies genes and microRNAs for AHO-induced systemic acquired resistance in <i>N. tabacum</i> . Scientific Reports, 2017, 7, 12504.	1.6	36
33	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. Nature Biotechnology, 2017, 35, 969-976.	9.4	356
34	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . Nature, 2017, 551, 498-502.	18.7	563
35	New reference genome sequences of hot pepper reveal the massive evolution of plant disease-resistance genes by retroduplication. Genome Biology, 2017, 18, 210.	3.8	255
36	LTR Retrotransposon Dynamics and Specificity in <i>Setaria italica</i> . Plant Genetics and Genomics: Crops and Models, 2017, , 149-158.	0.3	3

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37	Developmental programmed cell death during asymmetric microsporogenesis in holocentric species of <i>Rhynchospora</i> (Cyperaceae). <i>Journal of Experimental Botany</i> , 2016, 67, 5391-5401.	2.4	13
38	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
39	<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
40	Adaptive Evolution of Signaling Partners. <i>Molecular Biology and Evolution</i> , 2015, 32, 998-1007.	3.5	17
41	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	9.4	472
42	Recurrent Loss of Specific Introns during Angiosperm Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004843.	1.5	26
43	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
44	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
45	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
46	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
47	Variation in allelic expression associated with a recombination hotspot in <i>Zea mays</i> . <i>Plant Journal</i> , 2014, 79, 375-384.	2.8	13
48	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
49	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
50	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
51	The genome of the pear ( <i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	2.4	832
52	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 October 2012–30 November 2012. <i>Molecular Ecology Resources</i> , 2013, 13, 341-343.	2.2	33
53	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
54	Fine-Mapping and Identification of a Candidate Gene Underlying the <i>d2</i> Dwarfing Phenotype in Pearl Millet, <i>Cenchrus americanus</i> (L.) Morrone. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 563-572.	0.8	20

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55	G Protein Activation without a GEF in the Plant Kingdom. PLoS Genetics, 2012, 8, e1002756.	1.5	110
56	Dynamic Gene Copy Number Variation in Collinear Regions of Grass Genomes. Molecular Biology and Evolution, 2012, 29, 861-871.	3.5	24
57	High-Throughput Discovery of Mutations in Tef Semi-Dwarfing Genes by Next-Generation Sequencing Analysis. Genetics, 2012, 192, 819-829.	1.2	48
58	Centromere retention and loss during the descent of maize from a tetraploid ancestor. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 21004-21009.	3.3	38
59	Genomic Characterization for Parasitic Weeds of the Genus <i>Striga</i> by Sample Sequence Analysis. Plant Genome, 2012, 5, .	1.6	15
60	Reference genome sequence of the model plant Setaria. Nature Biotechnology, 2012, 30, 555-561.	9.4	864
61	Zea. , 2011, , 457-488.		1
62	The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. Science, 2011, 332, 960-963.	6.0	794
63	The Genomes of All Angiosperms: A Call for a Coordinated Global Census. Journal of Botany, 2011, 2011, 1-10.	1.2	10
64	The genome of woodland strawberry ( <i>Fragaria vesca</i> ). Nature Genetics, 2011, 43, 109-116.	9.4	1,091
65	De novo genome sequencing and comparative genomics of date palm ( <i>Phoenix dactylifera</i> ). Nature Biotechnology, 2011, 29, 521-527.	9.4	356
66	Transposable element origins of epigenetic gene regulation. Current Opinion in Plant Biology, 2011, 14, 156-161.	3.5	130
67	Epigenetics of the epigenome. Current Opinion in Plant Biology, 2011, 14, 113-115.	3.5	15
68	Plant Genetics for Study of the Roles of Root Exudates and Microbes in the Soil. , 2011, , 99-111.		0
69	Genetic Diversity of a Parasitic Weed, <i>Striga hermonthica</i> , on Sorghum and Pearl Millet in Mali. Tropical Plant Biology, 2011, 4, 91-98.	1.0	16
70	Spatio-temporal patterns of genome evolution in allotetraploid species of the genus <i>Oryza</i> . Plant Journal, 2010, 63, 430-442.	2.8	48
71	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
72	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

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73	Gene Content and Distribution in the Nuclear Genome of <i>Fragaria vesca</i> . <i>Plant Genome</i> , 2009, 2, .	1.6	20
74	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000728.	1.5	39
75	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
76	Foxtail Millet: A Sequence-Driven Grass Model System. <i>Plant Physiology</i> , 2009, 149, 137-141.	2.3	337
77	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
78	Structure-based discovery and description of plant and animal <i>Helitrons</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12832-12837.	3.3	102
79	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
80	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
81	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
82	Biology and the beasts: individual investigator-driven research in the megaprojects era. <i>Trends in Genetics</i> , 2009, 25, 57-59.	2.9	3
83	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
84	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
85	The Future of Maize. , 2009, , 771-779.		2
86	Maize Genome Structure and Evolution. , 2009, , 179-199.		8
87	Grass Genomic Synteny Illuminates Plant Genome Function and Evolution. <i>Rice</i> , 2008, 1, 109-118.	1.7	25
88	Population Structure and Diversity in Finger Millet ( <i>Eleusine coracana</i> ) Germplasm. <i>Tropical Plant Biology</i> , 2008, 1, 131-141.	1.0	122
89	A universal classification of eukaryotic transposable elements implemented in Repbase. <i>Nature Reviews Genetics</i> , 2008, 9, 414-414.	7.7	5
90	Enchilada redux: how complete is your genome sequence?. <i>New Phytologist</i> , 2008, 179, 249-250.	3.5	15

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91	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
92	Methylation-sensitive linking libraries enhance gene-enriched sequencing of complex genomes and map DNA methylation domains. BMC Genomics, 2008, 9, 621.	1.2	11
93	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. Science, 2008, 319, 64-69.	6.0	1,712
94	Sequence Analysis of Bacterial Artificial Chromosome Clones from the Apospory-Specific Genomic Region of <i>Pennisetum</i> and <i>Cenchrus</i> . Plant Physiology, 2008, 147, 1396-1411.	2.3	107
95	Grass Genome Structure and Evolution. , 2008, 4, 41-56.		18
96	Pathogen corruption and site-directed recombination at a plant disease resistance gene cluster. Genome Research, 2008, 18, 1918-1923.	2.4	112
97	Evolutionary History and Positional Shift of a Rice Centromere. Genetics, 2007, 177, 1217-1220.	1.2	29
98	A GeneTrek analysis of the maize genome. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11844-11849.	3.3	59
99	Geographical Distribution and Diversity of Bacteria Associated with Natural Populations of <i>Drosophila melanogaster</i> . Applied and Environmental Microbiology, 2007, 73, 3470-3479.	1.4	200
100	Identification of stress-responsive genes in an indica rice ( <i>Oryza sativa</i> L.) using ESTs generated from drought-stressed seedlings. Journal of Experimental Botany, 2007, 58, 253-265.	2.4	127
101	A unified classification system for eukaryotic transposable elements. Nature Reviews Genetics, 2007, 8, 973-982.	7.7	2,396
102	Patterns in grass genome evolution. Current Opinion in Plant Biology, 2007, 10, 176-181.	3.5	139
103	Plant centromere organization: a dynamic structure with conserved functions. Trends in Genetics, 2007, 23, 134-139.	2.9	133
104	Fine mapping of the Pc locus of <i>Sorghum bicolor</i> , a gene controlling the reaction to a fungal pathogen and its host-selective toxin. Theoretical and Applied Genetics, 2007, 114, 961-970.	1.8	28
105	The genetic map of finger millet, <i>Eleusine coracana</i> . Theoretical and Applied Genetics, 2006, 114, 321-332.	1.8	124
106	The maize genome as a model for efficient sequence analysis of large plant genomes. Current Opinion in Plant Biology, 2006, 9, 149-156.	3.5	61
107	Promoter mutations of an essential gene for pollen development result in disease resistance in rice. Genes and Development, 2006, 20, 1250-1255.	2.7	457
108	Analysis of retrotransposon structural diversity uncovers properties and propensities in angiosperm genome evolution. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17638-17643.	3.3	294

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109	Uneven chromosome contraction and expansion in the maize genome. <i>Genome Research</i> , 2006, 16, 1241-1251.	2.4	105
110	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
111	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
112	DNA Rearrangement in Orthologous Orp Regions of the Maize, Rice and Sorghum Genomes. <i>Genetics</i> , 2005, 170, 1209-1220.	1.2	62
113	Gene enrichment in maize with hypomethylated partial restriction (HMPCR) libraries. <i>Genome Research</i> , 2005, 15, 1441-1446.	2.4	59
114	Analysis and mapping of randomly chosen bacterial artificial chromosome clones from hexaploid bread wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 19243-19248.	3.3	86
115	Mechanisms of Recent Genome Size Variation in Flowering Plants. <i>Annals of Botany</i> , 2005, 95, 127-132.	1.4	598
116	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
117	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
118	Gene Loss and Movement in the Maize Genome. <i>Genome Research</i> , 2004, 14, 1924-1931.	2.4	186
119	Close Split of Sorghum and Maize Genome Progenitors. <i>Genome Research</i> , 2004, 14, 1916-1923.	2.4	443
120	Consistent over-estimation of gene number in complex plant genomes. <i>Current Opinion in Plant Biology</i> , 2004, 7, 732-736.	3.5	176
121	On the Tetraploid Origin of the Maize Genome. <i>Comparative and Functional Genomics</i> , 2004, 5, 281-284.	2.0	61
122	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
123	The evolution of nuclear genome structure in seed plants. <i>American Journal of Botany</i> , 2004, 91, 1709-1725.	0.8	129
124	The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by Vernalization. <i>Science</i> , 2004, 303, 1640-1644.	6.0	999
125	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
126	High-Cot sequence analysis of the maize genome. <i>Plant Journal</i> , 2003, 34, 249-255.	2.8	120



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127	Structure and evolution of the Cinfu retrotransposon family of maize. <i>Genome</i> , 2003, 46, 745-752.	0.9	26
128	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
129	Genomic Colinearity as a Tool for Plant Gene Isolation. , 2003, 236, 109-122.		8
130	Structural Analysis of the Maize Rp1 Complex Reveals Numerous Sites and Unexpected Mechanisms of Local Rearrangement. <i>Plant Cell</i> , 2002, 14, 3213-3223.	3.1	72
131	THE RICE GENOME: Opening the Door to Comparative Plant Biology. <i>Science</i> , 2002, 296, 60-63.	6.0	76
132	Exceptional haplotype variation in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9093-9095.	3.3	17
133	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
134	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
135	Genome Size Reduction through Illegitimate Recombination Counteracts Genome Expansion in Arabidopsis. <i>Genome Research</i> , 2002, 12, 1075-1079.	2.4	634
136	Frequent Genic Rearrangements in Two Regions of Grass Genomes Identified by Comparative Sequence Analysis. <i>Comparative and Functional Genomics</i> , 2002, 3, 165-166.	2.0	5
137	Genomic sequencing reveals gene content, genomic organization, and recombination relationships in barley. <i>Functional and Integrative Genomics</i> , 2002, 2, 51-59.	1.4	65
138	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
139	Divergent perspectives on GM food. <i>Nature Biotechnology</i> , 2002, 20, 1195-1196.	9.4	11
140	Numerous small rearrangements of gene content, order and orientation differentiate grass genomes. <i>Plant Molecular Biology</i> , 2002, 48, 821-827.	2.0	105
141	Mechanisms and rates of genome expansion and contraction in flowering plants. <i>Genetica</i> , 2002, 115, 29-36.	0.5	257
142	The Regulatory Regions Required for $\beta$ Paramutation and Expression Are Located Far Upstream of the Maize $\beta$ Transcribed Sequences. <i>Genetics</i> , 2002, 162, 917-930.	1.2	116
143	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
144	Arabidopsis arrives. <i>Nature Genetics</i> , 2001, 27, 3-5.	9.4	9

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145	Comparative Sequence Analysis of Colinear Barley and Rice Bacterial Artificial Chromosomes. <i>Plant Physiology</i> , 2001, 125, 1342-1353.	2.3	204
146	A framework genetic map of sorghum containing RFLP, SSR and morphological markers. <i>Advances in Cellular and Molecular Biology of Plants</i> , 2001, , 347-355.	0.2	7
147	Comparative mapping of plant chromosomes. <i>Advances in Cellular and Molecular Biology of Plants</i> , 2001, , 101-114.	0.2	2
148	National Science Foundation-sponsored workshop report. Maize genome sequencing project. <i>Plant Physiology</i> , 2001, 127, 1572-8.	2.3	27
149	Comparative Sequence Analysis of Plant Nuclear Genomes: Microcolinearity and Its Many Exceptions. <i>Plant Cell</i> , 2000, 12, 1021.	3.1	2
150	Transposable element contributions to plant gene and genome evolution. , 2000, 42, 251-269.		643
151	Structural Domains and Matrix Attachment Regions along Colinear Chromosomal Segments of Maize and Sorghum. <i>Plant Cell</i> , 2000, 12, 249.	3.1	0
152	Structural Domains and Matrix Attachment Regions along Colinear Chromosomal Segments of Maize and Sorghum. <i>Plant Cell</i> , 2000, 12, 249-264.	3.1	63
153	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
154	The many hues of plant heterochromatin. <i>Genome Biology</i> , 2000, 1, reviews107.1.	13.9	33
155	Comparative Sequence Analysis of Plant Nuclear Genomes: Microcolinearity and Its Many Exceptions. <i>Plant Cell</i> , 2000, 12, 1021-1029.	3.1	261
156	Transposable element contributions to plant gene and genome evolution. , 2000, , 251-269.		16
157	Plant genomics takes root, branches out. <i>Trends in Genetics</i> , 1999, 15, 85-87.	2.9	15
158	Plant Retrotransposons. <i>Annual Review of Genetics</i> , 1999, 33, 479-532.	3.2	1,029
159	The Grasses as a Single Genetic System. <i>Advances in Cellular and Molecular Biology of Plants</i> , 1999, , 387-394.	0.2	1
160	The paleontology of intergene retrotransposons of maize. <i>Nature Genetics</i> , 1998, 20, 43-45.	9.4	953
161	The structure and evolution of angiosperm nuclear genomes. <i>Current Opinion in Plant Biology</i> , 1998, 1, 103-108.	3.5	35
162	A Plant Genome Initiative. <i>Plant Cell</i> , 1998, 10, 488-493.	3.1	15

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163	A Plant Genome Initiative. <i>Plant Cell</i> , 1998, 10, 488.	3.1	1
164	Sequence Organization and Conservation in sh2/a1-Homologous Regions of Sorghum and Rice. <i>Genetics</i> , 1998, 148, 435-443.	1.2	116
165	Slow but Steady: Reduction of Genome Size through Biased Mutation [with Reply]. <i>Plant Cell</i> , 1997, 9, 1900.	3.1	10
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