

Jiming Jiang

List of Publications by Year in descending order

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246
papers

32,035
citations

6254

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353
times ranked

19518
citing authors

#	ARTICLE	IF	CITATIONS
1	Phased, chromosome-scale genome assemblies of tetraploid potato reveal a complex genome, transcriptome, and predicted proteome landscape underpinning genetic diversity. <i>Molecular Plant</i> , 2022, 15, 520-536.	8.3	72
2	Updates on gene editing and its applications. <i>Plant Physiology</i> , 2022, 188, 1725-1730.	4.8	15
3	Chromosome-specific painting unveils chromosomal fusions and distinct allopolyploid species in the <i>Saccharum</i> complex. <i>New Phytologist</i> , 2022, 233, 1953-1965.	7.3	19
4	Preferential meiotic chromosome pairing among homologous chromosomes with cryptic sequence variation in tetraploid maize. <i>New Phytologist</i> , 2021, 229, 3294-3302.	7.3	19
5	Efficient Genome Editing in Potato Using a Hairy Root Transformation System. <i>Springer Protocols</i> , 2021, , 149-158.	0.3	0
6	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	27.8	144
7	Enhancer-mediated reporter gene expression in <i>Arabidopsis thaliana</i> : a forward genetic screen. <i>Plant Journal</i> , 2021, 106, 661-671.	5.7	4
8	Genomic editing of intronic enhancers unveils their role in fine-tuning tissue-specific gene expression in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2021, 33, 1997-2014.	6.6	43
9	The <i>Mitragyna speciosa</i> (Kratom) Genome: a resource for data-mining potent pharmaceuticals that impact human health. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	19
10	BAC- and oligo-FISH mapping reveals chromosome evolution among <i>Vigna angularis</i> , <i>V. unguiculata</i> , and <i>Phaseolus vulgaris</i> . <i>Chromosoma</i> , 2021, 130, 133-147.	2.2	17
11	Chorus2: design of genome-scale oligonucleotide-based probes for fluorescence <i>in situ</i> hybridization. <i>Plant Biotechnology Journal</i> , 2021, 19, 1967-1978.	8.3	31
12	Oligo-FISH barcode in beans: a new chromosome identification system. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3675-3686.	3.6	23
13	Megabase-scale presence-absence variation with <i>Tripsacum</i> origin was under selection during maize domestication and adaptation. <i>Genome Biology</i> , 2021, 22, 237.	8.8	21
14	LD-CNV: rapid and simple discovery of chromosomal translocations using linkage disequilibrium between copy number variable loci. <i>Genetics</i> , 2021, 219, .	2.9	5
15	Rapid Validation of Transcriptional Enhancers Using a Transient Reporter Assay. <i>Methods in Molecular Biology</i> , 2021, 2328, 253-259.	0.9	0
16	Sucrose promotes stem branching through cytokinin. <i>Plant Physiology</i> , 2021, 185, 1708-1721.	4.8	54
17	Dual-color oligo-FISH can reveal chromosomal variations and evolution in <i>Oryza</i> species. <i>Plant Journal</i> , 2020, 101, 112-121.	5.7	44
18	An extraordinarily stable karyotype of the woody <i>Populus</i> species revealed by chromosome painting. <i>Plant Journal</i> , 2020, 101, 253-264.	5.7	46

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19	Overexpression of a modified eIF4E regulates potato virus Y resistance at the transcriptional level in potato. <i>BMC Genomics</i> , 2020, 21, 18.	2.8	17
20	Construction of a chromosome-scale long-read reference genome assembly for potato. <i>GigaScience</i> , 2020, 9, .	6.4	150
21	Generation of a chromosome-scale genome assembly of the insect-repellent terpenoid-producing Lamiaceae species, <i>Callicarpa americana</i> . <i>GigaScience</i> , 2020, 9, .	6.4	21
22	A universal chromosome identification system for maize and wild <i>Zea</i> species. <i>Chromosome Research</i> , 2020, 28, 183-194.	2.2	26
23	First-generation genome editing in potato using hairy root transformation. <i>Plant Biotechnology Journal</i> , 2020, 18, 2201-2209.	8.3	38
24	Extraordinarily conserved chromosomal synteny of <i>Citrus</i> species revealed by chromosome-specific painting. <i>Plant Journal</i> , 2020, 103, 2225-2235.	5.7	33
25	Genome-wide MNase hypersensitivity assay unveils distinct classes of open chromatin associated with H3K27me3 and DNA methylation in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2020, 21, 24.	8.8	35
26	Fluorescent In Situ Hybridization Using Oligonucleotide-Based Probes. <i>Methods in Molecular Biology</i> , 2020, 2148, 71-83.	0.9	20
27	Meiotic crossovers characterized by haplotype-specific chromosome painting in maize. <i>Nature Communications</i> , 2019, 10, 4604.	12.8	40
28	Local Changes in Chromatin Accessibility and Transcriptional Networks Underlying the Nitrate Response in <i>Arabidopsis</i> Roots. <i>Molecular Plant</i> , 2019, 12, 1545-1560.	8.3	31
29	Whole-chromosome paints in maize reveal rearrangements, nuclear domains, and chromosomal relationships. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1679-1685.	7.1	95
30	Historical Meiotic Crossover Hotspots Fueled Patterns of Evolutionary Divergence in Rice. <i>Plant Cell</i> , 2019, 31, 645-662.	6.6	41
31	Cold stress induces enhanced chromatin accessibility and bivalent histone modifications H3K4me3 and H3K27me3 of active genes in potato. <i>Genome Biology</i> , 2019, 20, 123.	8.8	119
32	Genome-wide Inference of Somatic Translocation Events During Potato Dihaploid Production. <i>Plant Genome</i> , 2019, 12, 180079.	2.8	8
33	Residual Heterozygosity and Epistatic Interactions Underlie the Complex Genetic Architecture of Yield in Diploid Potato. <i>Genetics</i> , 2019, 212, 317-332.	2.9	20
34	Rapid validation of transcriptional enhancers using agrobacterium-mediated transient assay. <i>Plant Methods</i> , 2019, 15, 21.	4.3	13
35	Fluorescence in situ hybridization in plants: recent developments and future applications. <i>Chromosome Research</i> , 2019, 27, 153-165.	2.2	142
36	Proliferation of Regulatory DNA Elements Derived from Transposable Elements in the Maize Genome. <i>Plant Physiology</i> , 2018, 176, 2789-2803.	4.8	71

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37	Chromosome painting and comparative physical mapping of the sex chromosomes in <i>Populus tomentosa</i> and <i>Populus deltoides</i> . <i>Chromosoma</i> , 2018, 127, 313-321.	2.2	43
38	Amplification and adaptation of centromeric repeats in polyploid switchgrass species. <i>New Phytologist</i> , 2018, 218, 1645-1657.	7.3	30
39	Genome sequence of M6, a diploid inbred clone of the high-glycoalkaloid-producing tuber-bearing potato species <i>Solanum chacoense</i> , reveals residual heterozygosity. <i>Plant Journal</i> , 2018, 94, 562-570.	5.7	112
40	The unique epigenetic features of Pack-MULEs and their impact on chromosomal base composition and expression spectrum. <i>Nucleic Acids Research</i> , 2018, 46, 2380-2397.	14.5	14
41	Transcriptional and epigenetic adaptation of maize chromosomes in Oat-Maize addition lines. <i>Nucleic Acids Research</i> , 2018, 46, 5012-5028.	14.5	19
42	Extrachromosomal circular DNA-based amplification and transmission of herbicide resistance in crop weed <i>Amaranthus palmeri</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3332-3337.	7.1	159
43	Single molecule mtDNA fiber FISH for analyzing numtogenesis. <i>Analytical Biochemistry</i> , 2018, 552, 45-49.	2.4	10
44	Comparative Oligo-FISH Mapping: An Efficient and Powerful Methodology To Reveal Karyotypic and Chromosomal Evolution. <i>Genetics</i> , 2018, 208, 513-523.	2.9	146
45	Genome Reduction in Tetraploid Potato Reveals Genetic Load, Haplotype Variation, and Loci Associated With Agronomic Traits. <i>Frontiers in Plant Science</i> , 2018, 9, 944.	3.6	30
46	Genomics of Maize Centromeres. <i>Compendium of Plant Genomes</i> , 2018, , 59-80.	0.5	2
47	Chromosome painting in meiosis reveals pairing of specific chromosomes in polyploid <i>Solanum</i> species. <i>Chromosoma</i> , 2018, 127, 505-513.	2.2	57
48	Genome sequences of two diploid wild relatives of cultivated sweetpotato reveal targets for genetic improvement. <i>Nature Communications</i> , 2018, 9, 4580.	12.8	181
49	Constitutively Expressed RB Gene Confers a High Level but Unregulated Resistance to Potato Late Blight. <i>American Journal of Potato Research</i> , 2018, 95, 575-583.	0.9	2
50	Comparison of <i>Oryza sativa</i> and <i>Oryza brachyantha</i> Genomes Reveals Selection-Driven Gene Escape from the Centromeric Regions. <i>Plant Cell</i> , 2018, 30, 1729-1744.	6.6	22
51	Chromosome painting and its applications in cultivated and wild rice. <i>BMC Plant Biology</i> , 2018, 18, 110.	3.6	48
52	Application of MNase-Seq in the Global Mapping of Nucleosome Positioning in Plants. <i>Methods in Molecular Biology</i> , 2018, 1830, 353-366.	0.9	6
53	Towards genome-wide prediction and characterization of enhancers in plants. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 131-139.	1.9	53
54	Analysis of Ribosome-Associated mRNAs in Rice Reveals the Importance of Transcript Size and GC Content in Translation. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 203-219.	1.8	43

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55	Overexpression of StNF-YB3.1 reduces photosynthetic capacity and tuber production, and promotes ABA-mediated stomatal closure in potato (<i>Solanum tuberosum</i> L.). <i>Plant Science</i> , 2017, 261, 50-59.	3.6	21
56	Recurrent establishment of de novo centromeres in the pericentromeric region of maize chromosome 3. <i>Chromosome Research</i> , 2017, 25, 299-311.	2.2	17
57	Etiolated Stem Branching Is a Result of Systemic Signaling Associated with Sucrose Level. <i>Plant Physiology</i> , 2017, 175, 734-745.	4.8	24
58	Genome-wide mapping of DNase I hypersensitive sites reveals chromatin accessibility changes in <i>Arabidopsis</i> euchromatin and heterochromatin regions under extended darkness. <i>Scientific Reports</i> , 2017, 7, 4093.	3.3	19
59	Meiotic crossovers are associated with open chromatin and enriched with Stowaway transposons in potato. <i>Genome Biology</i> , 2017, 18, 203.	8.8	62
60	Genomic abundance is not predictive of tandem repeat localization in grass genomes. <i>PLoS ONE</i> , 2017, 12, e0177896.	2.5	5
61	Reinventing Potato as a Diploid Inbred Line-Based Crop. <i>Crop Science</i> , 2016, 56, 1412-1422.	1.8	176
62	Isolation and Proteomics Analysis of Barley Centromeric Chromatin Using PICCh. <i>Journal of Proteome Research</i> , 2016, 15, 1875-1882.	3.7	7
63	Chromatin-associated transcripts of tandemly repetitive DNA sequences revealed by RNA-FISH. <i>Chromosome Research</i> , 2016, 24, 467-480.	2.2	29
64	Silencing of vacuolar invertase and asparagine synthetase genes and its impact on acrylamide formation of fried potato products. <i>Plant Biotechnology Journal</i> , 2016, 14, 709-718.	8.3	50
65	Genome Reduction Uncovers a Large Dispensable Genome and Adaptive Role for Copy Number Variation in Asexually Propagated <i>Solanum tuberosum</i> . <i>Plant Cell</i> , 2016, 28, 388-405.	6.6	163
66	A Mutant eIF4E Confers Resistance to Potato Virus Y Strains and is Inherited in a Dominant Manner in the Potato Varieties Atlantic and Russet Norkotah. <i>American Journal of Potato Research</i> , 2016, 93, 64-71.	0.9	11
67	High-resolution tyramide-FISH mapping of markers tightly linked to the male-fertility restoration (Ms) locus of onion. <i>Theoretical and Applied Genetics</i> , 2016, 129, 535-545.	3.6	21
68	Gene Expression and Chromatin Modifications Associated with Maize Centromeres. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 183-192.	1.8	30
69	PlantDHS: a database for DNase I hypersensitive sites in plants. <i>Nucleic Acids Research</i> , 2016, 44, D1148-D1153.	14.5	86
70	Transposons play an important role in the evolution and diversification of centromeres among closely related species. <i>Frontiers in Plant Science</i> , 2015, 6, 216.	3.6	51
71	Stable Patterns of CENH3 Occupancy Through Maize Lineages Containing Genetically Similar Centromeres. <i>Genetics</i> , 2015, 200, 1105-1116.	2.9	20
72	Genome-Wide Nucleosome Occupancy and Positioning and Their Impact on Gene Expression and Evolution in Plants. <i>Plant Physiology</i> , 2015, 168, 1406-1416.	4.8	98

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73	The "dark matter"™ in the plant genomes: non-coding and unannotated DNA sequences associated with open chromatin. <i>Current Opinion in Plant Biology</i> , 2015, 24, 17-23.	7.1	49
74	Chromosome-Specific Painting in <i>Cucumis</i> Species Using Bulk Oligonucleotides. <i>Genetics</i> , 2015, 200, 771-779.	2.9	192
75	Evidence for Emergence of Sex-Determining Gene(s) in a Centromeric Region in <i>Vasconcellea parviflora</i> . <i>Genetics</i> , 2015, 199, 413-421.	2.9	23
76	Genome-Wide Prediction and Validation of Intergenic Enhancers in <i>Arabidopsis</i> Using Open Chromatin Signatures. <i>Plant Cell</i> , 2015, 27, 2415-2426.	6.6	136
77	Cytogenetic and Sequence Analyses of Mitochondrial DNA Insertions in Nuclear Chromosomes of Maize. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2229-2239.	1.8	16
78	Genome-Wide Mapping of DNase I Hypersensitive Sites in Plants. <i>Methods in Molecular Biology</i> , 2015, 1284, 71-89.	0.9	34
79	Open Chromatin in Plant Genomes. <i>Cytogenetic and Genome Research</i> , 2014, 143, 18-27.	1.1	19
80	Genome-Wide Nucleosome Positioning Is Orchestrated by Genomic Regions Associated with DNase I Hypersensitivity in Rice. <i>PLoS Genetics</i> , 2014, 10, e1004378.	3.5	33
81	Distinct Copy Number, Coding Sequence, and Locus Methylation Patterns Underlie Rhg1-Mediated Soybean Resistance to Soybean Cyst Nematode. <i>Plant Physiology</i> , 2014, 165, 630-647.	4.8	136
82	Maize centromeres expand and adopt a uniform size in the genetic background of oat. <i>Genome Research</i> , 2014, 24, 107-116.	5.5	77
83	Sugar metabolism, chip color, invertase activity, and gene expression during long-term cold storage of potato (<i>Solanum tuberosum</i>) tubers from wild-type and vacuolar invertase silencing lines of Katahdin. <i>BMC Research Notes</i> , 2014, 7, 801.	1.4	45
84	Molecular Cytogenetics of Papaya. , 2014, , 157-167.		2
85	Next-generation sequencing, FISH mapping and synteny-based modeling reveal mechanisms of decreasing dysploidy in <i>Cucumis</i> . <i>Plant Journal</i> , 2014, 77, 16-30.	5.7	90
86	Three Potato Centromeres Are Associated with Distinct Haplotypes with or Without Megabase-Sized Satellite Repeat Arrays. <i>Genetics</i> , 2014, 196, 397-401.	2.9	25
87	Boom-Bust Turnovers of Megabase-Sized Centromeric DNA in <i>Solanum</i> Species: Rapid Evolution of DNA Sequences Associated with Centromeres. <i>Plant Cell</i> , 2014, 26, 1436-1447.	6.6	73
88	Vacuolar Invertase Gene Silencing in Potato (<i>Solanum tuberosum</i> L.) Improves Processing Quality by Decreasing the Frequency of Sugar-End Defects. <i>PLoS ONE</i> , 2014, 9, e93381.	2.5	40
89	Whole-genome sequencing of <i>Oryza brachyantha</i> reveals mechanisms underlying <i>Oryza</i> genome evolution. <i>Nature Communications</i> , 2013, 4, 1595.	12.8	190
90	Interstitial telomeric repeats are enriched in the centromeres of chromosomes in <i>Solanum</i> species. <i>Chromosome Research</i> , 2013, 21, 5-13.	2.2	50

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91	Fluorescence in Situ Hybridization Techniques for Cytogenetic and Genomic Analyses. <i>Methods in Molecular Biology</i> , 2013, 956, 13-27.	0.9	5
92	Copy number variation in potato “ an asexually propagated autotetraploid species. <i>Plant Journal</i> , 2013, 75, 80-89.	5.7	39
93	Keep Up with Critical Fields. , 2013, , 211-211.		0
94	Insertional Mutagenesis Using <i>Tnt1</i> Retrotransposon in Potato. <i>Plant Physiology</i> , 2013, 163, 21-29.	4.8	30
95	Persistent whole-chromosome aneuploidy is generally associated with nascent allohexaploid wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3447-3452.	7.1	180
96	The <i>CentO</i> satellite confers translational and rotational phasing on cenH3 nucleosomes in rice centromeres. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4875-83.	7.1	80
97	High-resolution mapping of open chromatin in the rice genome. <i>Genome Research</i> , 2012, 22, 151-162.	5.5	205
98	Strong epigenetic similarity between maize centromeric and pericentromeric regions at the level of small RNAs, DNA methylation and H3 chromatin modifications. <i>Nucleic Acids Research</i> , 2012, 40, 1550-1560.	14.5	45
99	Genome-Wide Identification of Regulatory DNA Elements and Protein-Binding Footprints Using Signatures of Open Chromatin in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2012, 24, 2719-2731.	6.6	204
100	Sequencing papaya X and Y chromosomes reveals molecular basis of incipient sex chromosome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13710-13715.	7.1	264
101	Repeatless and Repeat-Based Centromeres in Potato: Implications for Centromere Evolution. <i>Plant Cell</i> , 2012, 24, 3559-3574.	6.6	221
102	Copy Number Variation of Multiple Genes at <i>Rhg1</i> Mediates Nematode Resistance in Soybean. <i>Science</i> , 2012, 338, 1206-1209.	12.6	535
103	Construction of physical maps for the sex-specific regions of papaya sex chromosomes. <i>BMC Genomics</i> , 2012, 13, 176.	2.8	39
104	Genomic in situ hybridization reveals both auto- and allopolyploid origins of different North and Central American hexaploid potato (<i>Solanum</i> sect. <i>Petota</i>) species. <i>Genome</i> , 2012, 55, 407-415.	2.0	32
105	Centromeres: Sequences, Structure, and Biology. , 2012, , 59-70.		5
106	DNA and Chromatin Fiber-Based Plant Cytogenetics. , 2012, , 121-130.		1
107	Genome of papaya, a fast growing tropical fruit tree. <i>Tree Genetics and Genomes</i> , 2012, 8, 445-462.	1.6	21
108	Stable integration of an engineered megabase repeat array into the maize genome. <i>Plant Journal</i> , 2012, 70, 357-365.	5.7	17

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109	Chromosome rearrangements during domestication of cucumber as revealed by high-density genetic mapping and draft genome assembly. <i>Plant Journal</i> , 2012, 71, 895-906.	5.7	177
110	Genome sequence and analysis of the tuber crop potato. <i>Nature</i> , 2011, 475, 189-195.	27.8	1,912
111	Organization and Evolution of Subtelomeric Satellite Repeats in the Potato Genome. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 85-92.	1.8	75
112	Comparative FISH mapping of <i>Daucus</i> species (Apiaceae family). <i>Chromosome Research</i> , 2011, 19, 493-506.	2.2	42
113	Molecular and Cytological Characterization of Centromeric Retrotransposons in a Wild Relative of Rice, <i>Oryza granulata</i> . <i>Tropical Plant Biology</i> , 2011, 4, 217-227.	1.9	1
114	De novo assembly of potential linear artificial chromosome constructs capped with expansive telomeric repeats. <i>Plant Methods</i> , 2011, 7, 10.	4.3	4
115	Distinct DNA methylation patterns associated with active and inactive centromeres of the maize B chromosome. <i>Genome Research</i> , 2011, 21, 908-914.	5.5	65
116	Conservation and Purifying Selection of Transcribed Genes Located in a Rice Centromere. <i>Plant Cell</i> , 2011, 23, 2821-2830.	6.6	22
117	Euchromatic Subdomains in Rice Centromeres Are Associated with Genes and Transcription. <i>Plant Cell</i> , 2011, 23, 4054-4064.	6.6	51
118	Developing Cold-Chipping Potato Varieties by Silencing the Vacuolar Invertase Gene. <i>Crop Science</i> , 2011, 51, 981-990.	1.8	38
119	Super-Stretched Pachytene Chromosomes for Plant Molecular Cytogenetic Mapping. <i>Methods in Molecular Biology</i> , 2011, 701, 239-245.	0.9	1
120	Evolution of chromosome 6 of <i>Solanum</i> species revealed by comparative fluorescence in situ hybridization mapping. <i>Chromosoma</i> , 2010, 119, 435-442.	2.2	58
121	Centromere inactivation and epigenetic modifications of a plant chromosome with three functional centromeres. <i>Chromosoma</i> , 2010, 119, 553-563.	2.2	58
122	Integration of Genetic and Cytological Maps and Development of a Pachytene Chromosome-based Karyotype in Papaya. <i>Tropical Plant Biology</i> , 2010, 3, 166-170.	1.9	34
123	Genome-wide mapping of cytosine methylation revealed dynamic DNA methylation patterns associated with genes and centromeres in rice. <i>Plant Journal</i> , 2010, 63, 353-365.	5.7	112
124	Global sequence characterization of rice centromeric satellite based on oligomer frequency analysis in large-scale sequencing data. <i>Bioinformatics</i> , 2010, 26, 2101-2108.	4.1	43
125	Gene amplification confers glyphosate resistance in <i>Amaranthus palmeri</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1029-1034.	7.1	557
126	Suppression of the Vacuolar Invertase Gene Prevents Cold-Induced Sweetening in Potato. <i>Plant Physiology</i> , 2010, 154, 939-948.	4.8	165

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127	Identification of miniature inverted-repeat transposable elements (MITEs) and biogenesis of their siRNAs in the Solanaceae: New functional implications for MITEs. <i>Genome Research</i> , 2009, 19, 42-56.	5.5	152
128	Agrobacterium-Mediated Transient Gene Expression and Silencing: A Rapid Tool for Functional Gene Assay in Potato. <i>PLoS ONE</i> , 2009, 4, e5812.	2.5	111
129	Centromere repositioning in cucurbit species: Implication of the genomic impact from centromere activation and inactivation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14937-14941.	7.1	90
130	Structure and Evolution of Plant Centromeres. <i>Progress in Molecular and Subcellular Biology</i> , 2009, 48, 153-179.	1.6	14
131	Lineage-Specific Adaptive Evolution of the Centromeric Protein CENH3 in Diploid and Allotetraploid <i>Oryza</i> Species. <i>Molecular Biology and Evolution</i> , 2009, 26, 2877-2885.	8.9	59
132	Freedom Russet—A Dual Purpose Russet Potato Cultivar with Resistance to Common Scab and Good Fry Quality. <i>American Journal of Potato Research</i> , 2009, 86, 406-414.	0.9	2
133	Superstretched pachytene chromosomes for fluorescence <i>in situ</i> hybridization mapping and immunodetection of DNA methylation. <i>Plant Journal</i> , 2009, 59, 509-516.	5.7	46
134	A lineage-specific centromere retrotransposon in <i>Oryza brachyantha</i> . <i>Plant Journal</i> , 2009, 60, 820-831.	5.7	41
135	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	12.6	3,612
136	Higher Copy Numbers of the Potato <i>RB</i> Transgene Correspond to Enhanced Transcript and Late Blight Resistance Levels. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 437-446.	2.6	92
137	Correlation Between Transcript Abundance of the <i>RB</i> Gene and the Level of the <i>RB</i> -Mediated Late Blight Resistance in Potato. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 447-455.	2.6	64
138	Maize Centromere Structure and Evolution: Sequence Analysis of Centromeres 2 and 5 Reveals Dynamic Loci Shaped Primarily by Retrotransposons. <i>PLoS Genetics</i> , 2009, 5, e1000743.	3.5	168
139	Histone modifications associated with both A and B chromosomes of maize. <i>Chromosome Research</i> , 2008, 16, 1203-1214.	2.2	59
140	The draft genome of the transgenic tropical fruit tree papaya (<i>Carica papaya</i> Linnaeus). <i>Nature</i> , 2008, 452, 991-996.	27.8	964
141	Low X/Y divergence in four pairs of papaya sex-linked genes. <i>Plant Journal</i> , 2008, 53, 124-132.	5.7	78
142	Analysis of 90 Mb of the potato genome reveals conservation of gene structures and order with tomato but divergence in repetitive sequence composition. <i>BMC Genomics</i> , 2008, 9, 286.	2.8	37
143	Sgt1, but not Rar1, is essential for the RB-mediated broad-spectrum resistance to potato late blight. <i>BMC Plant Biology</i> , 2008, 8, 8.	3.6	65
144	Major cytogenetic landmarks and karyotype analysis in <i>Daucus carota</i> and other Apiaceae. <i>American Journal of Botany</i> , 2008, 95, 793-804.	1.7	41

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145	Allopolyploid speciation of the Mexican tetraploid potato species <i>Solanum stoloniferum</i> and <i>S. hjertingii</i> revealed by genomic in situ hybridization. <i>Genome</i> , 2008, 51, 714-720.	2.0	50
146	Chromatin Structure and Physical Mapping of Chromosome 6 of Potato and Comparative Analyses With Tomato. <i>Genetics</i> , 2008, 180, 1307-1317.	2.9	82
147	DNA methylation and heterochromatinization in the male-specific region of the primitive Y chromosome of papaya. <i>Genome Research</i> , 2008, 18, 1938-1943.	5.5	107
148	High-Resolution Mapping of Epigenetic Modifications of the Rice Genome Uncovers Interplay between DNA Methylation, Histone Methylation, and Gene Expression. <i>Plant Cell</i> , 2008, 20, 259-276.	6.6	281
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