

# Ming-Cheng Luo

## List of Publications by Year in descending order

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151  
papers

22,169  
citations

18436

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9553

142  
g-index

157  
all docs

157  
docs citations

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times ranked

15483  
citing authors

#	ARTICLE	IF	CITATIONS
1	Population genomic analysis of <i>Aegilops tauschii</i> identifies targets for bread wheat improvement. <i>Nature Biotechnology</i> , 2022, 40, 422-431.	9.4	102
2	<i>Myb10a</i> confers <i>PHS3D</i> resistance to pre-harvest sprouting by regulating <i>NCED</i> in ABA biosynthesis pathway of wheat. <i>New Phytologist</i> , 2021, 230, 1940-1952.	3.5	53
3	Co-located quantitative trait loci mediate resistance to <i>Agrobacterium tumefaciens</i> , <i>Phytophthora cinnamomi</i> , and <i>P. pini</i> in <i>Juglans microcarpa</i> – <i>J. regia</i> hybrids. <i>Horticulture Research</i> , 2021, 8, 111.	2.9	4
4	Optical maps refine the bread wheat <i>Triticum aestivum</i> cv. Chinese Spring genome assembly. <i>Plant Journal</i> , 2021, 107, 303-314.	2.8	237
5	<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
6	High molecular weight glutenin gene diversity in <i>Aegilops tauschii</i> demonstrates unique origin of superior wheat quality. <i>Communications Biology</i> , 2021, 4, 1242.	2.0	14
7	The improved assembly of 7DL chromosome provides insight into the structure and evolution of bread wheat. <i>Plant Biotechnology Journal</i> , 2020, 18, 732-742.	4.1	6
8	Computational Identification and Comparative Analysis of Conserved miRNAs and Their Putative Target Genes in the <i>Juglans regia</i> and <i>J. microcarpa</i> Genomes. <i>Plants</i> , 2020, 9, 1330.	1.6	1
9	Identification of candidate chromosome region of <i>Sbwm1</i> for Soil-borne wheat mosaic virus resistance in wheat. <i>Scientific Reports</i> , 2020, 10, 8119.	1.6	10
10	Reduced chromatin accessibility underlies gene expression differences in homologous chromosome arms of diploid <i>Aegilops tauschii</i> and hexaploid wheat. <i>GigaScience</i> , 2020, 9, .	3.3	23
11	A rare single nucleotide variant in <i>Pm5e</i> confers powdery mildew resistance in common wheat. <i>New Phytologist</i> , 2020, 228, 1011-1026.	3.5	92
12	A CNL protein in wild emmer wheat confers powdery mildew resistance. <i>New Phytologist</i> , 2020, 228, 1027-1037.	3.5	89
13	Introgression of perennial growth habit from <i>Lophopyrum elongatum</i> into wheat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2545-2554.	1.8	4
14	Genome-wide introgression from a bread wheat – <i>Lophopyrum elongatum</i> amphiploid into wheat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1227-1241.	1.8	7
15	A rare gain of function mutation in a wheat tandem kinase confers resistance to powdery mildew. <i>Nature Communications</i> , 2020, 11, 680.	5.8	119
16	An ancestral NB-LRR with duplicated 3'UTRs confers stripe rust resistance in wheat and barley. <i>Nature Communications</i> , 2019, 10, 4023.	5.8	84
17	Recombination between homoeologous chromosomes induced in durum wheat by the <i>Aegilops speltoides</i> <i>Su1-Ph1</i> suppressor. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3265-3276.	1.8	8
18	<i>Aegilops tauschii</i> Genome Sequence: A Framework for Meta-analysis of Wheat QTLs. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 841-853.	0.8	1

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19	Rapid evolution of $\hat{\pm}$ -gliadin gene family revealed by analyzing Gli-2 locus regions of wild emmer wheat. <i>Functional and Integrative Genomics</i> , 2019, 19, 993-1005.	1.4	28
20	A fine-scale genetic linkage map reveals genomic regions associated with economic traits in walnut ( <i>Juglans regia</i> ). <i>Plant Breeding</i> , 2019, 138, 635-646.	1.0	10
21	The genome of cowpea ( <i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019, 98, 767-782.	2.8	264
22	Sequencing a <i>Juglans regia</i> microcarpa hybrid yields high-quality genome assemblies of parental species. <i>Horticulture Research</i> , 2019, 6, 55.	2.9	67
23	Improved Genome Sequence of Wild Emmer Wheat Zavitan with the Aid of Optical Maps. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 619-624.	0.8	64
24	Integrated physical map of bread wheat chromosome arm 7DS to facilitate gene cloning and comparative studies. <i>New Biotechnology</i> , 2019, 48, 12-19.	2.4	9
25	Chromosome-scale pseudomolecules refined by optical, physical and genetic maps in flax. <i>Plant Journal</i> , 2018, 95, 371-384.	2.8	119
26	Dynamic Evolution of $\hat{\pm}$ -Gliadin Prolamin Gene Family in Homeologous Genomes of Hexaploid Wheat. <i>Scientific Reports</i> , 2018, 8, 5181.	1.6	68
27	Uncovering the dispersion history, adaptive evolution and selection of wheat in China. <i>Plant Biotechnology Journal</i> , 2018, 16, 280-291.	4.1	62
28	Molecular mapping of YrTZ2, a stripe rust resistance gene in wild emmer accession TZ-2 and its comparative analyses with <i>Aegilops tauschii</i> . <i>Journal of Integrative Agriculture</i> , 2018, 17, 1267-1275.	1.7	9
29	Structural variation and rates of genome evolution in the grass family seen through comparison of sequences of genomes greatly differing in size. <i>Plant Journal</i> , 2018, 95, 487-503.	2.8	31
30	Gene Duplication and Evolution Dynamics in the Homeologous Regions Harboring Multiple Prolamin and Resistance Gene Families in Hexaploid Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 673.	1.7	84
31	Optical and physical mapping with local finishing enables megabase-scale resolution of agronomically important regions in the wheat genome. <i>Genome Biology</i> , 2018, 19, 112.	3.8	41
32	Reassessment of the evolution of wheat chromosomes 4A, 5A, and 7B. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2451-2462.	1.8	66
33	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	6.0	768
34	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	6.0	2,424
35	Analysis of <i>Brachypodium</i> genomes with genome-wide optical maps. <i>Genome</i> , 2018, 61, 559-565.	0.9	6
36	Hybrid assembly of the large and highly repetitive genome of <i>Aegilops tauschii</i> , a progenitor of bread wheat, with the MaSuRCA mega-reads algorithm. <i>Genome Research</i> , 2017, 27, 787-792.	2.4	382

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37	Wheat Ms2 encodes for an orphan protein that confers male sterility in grass species. <i>Nature Communications</i> , 2017, 8, 15121.	5.8	97
38	New insights into structural organization and gene duplication in a 1.75â€Mb genomic region harboring the Î±â€gliadin gene family in <i>Aegilops tauschii</i> , the source of wheat D genome. <i>Plant Journal</i> , 2017, 92, 571-583.	2.8	29
39	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	13.7	563
40	Genome resources for climateâ€resilient cowpea, an essential crop for food security. <i>Plant Journal</i> , 2017, 89, 1042-1054.	2.8	199
41	Sequencing and comparative analyses of <i>Aegilops tauschii</i> chromosome arm 3DS reveal rapid evolution of Triticeae genomes. <i>Journal of Genetics and Genomics</i> , 2017, 44, 51-61.	1.7	25
42	Solar Radiation-Associated Adaptive SNP Genetic Differentiation in Wild Emmer Wheat, <i>Triticum dicoccoides</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 258.	1.7	12
43	A High-Density Genetic Map of Wild Emmer Wheat from the Karaca DaÄŸ Region Provides New Evidence on the Structure and Evolution of Wheat Chromosomes. <i>Frontiers in Plant Science</i> , 2017, 8, 1798.	1.7	33
44	Introgression of the <i>Aegilops speltoides</i> Su1-Ph1 Suppressor into Wheat. <i>Frontiers in Plant Science</i> , 2017, 8, 2163.	1.7	45
45	Identification and evaluation of resistance to powdery mildew and yellow rust in a wheat mapping population. <i>PLoS ONE</i> , 2017, 12, e0177905.	1.1	12
46	A wholeâ€genome, radiation hybrid mapping resource of hexaploid wheat. <i>Plant Journal</i> , 2016, 86, 195-207.	2.8	23
47	Rapid evolutionary dynamics in a 2.8â€Mb chromosomal region containing multiple prolamin and resistance gene families in <i>Aegilops tauschii</i> . <i>Plant Journal</i> , 2016, 87, 495-506.	2.8	33
48	BioNano genome mapping of individual chromosomes supports physical mapping and sequence assembly in complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016, 14, 1523-1531.	4.1	104
49	Genetic mapping of SrCad and SNP marker development for marker-assisted selection of Ug99 stem rust resistance in wheat. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1373-1382.	1.8	33
50	Optical Nano-mapping and Analysis of Plant Genomes. <i>Methods in Molecular Biology</i> , 2016, 1429, 103-117.	0.4	4
51	Validation and diagnostic marker development for a genetic region associated with wheat yellow mosaic virus resistance. <i>Euphytica</i> , 2016, 211, 91-101.	0.6	6
52	Analysis of tandem gene copies in maize chromosomal regions reconstructed from long sequence reads. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7949-7956.	3.3	50
53	Radiation hybrid maps of the D-genome of <i>Aegilops tauschii</i> and their application in sequence assembly of large and complex plant genomes. <i>BMC Genomics</i> , 2015, 16, 800.	1.2	31
54	Synteny analysis in Rosids with a walnut physical map reveals slow genome evolution in long-lived woody perennials. <i>BMC Genomics</i> , 2015, 16, 707.	1.2	83

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55	Association of Agronomic Traits with SNP Markers in Durum Wheat ( <i>Triticum turgidum</i> L. durum) Tj ETQq1 1 0.784314 rgBT //Overloc	1.1	41
56	Dynamic evolution of resistance gene analogs in the orthologous genomic regions of powdery mildew resistance gene MlIW170 in <i>Triticum dicoccoides</i> and <i>Aegilops tauschii</i> . <i>Theoretical and Applied Genetics</i> , 2015, 128, 1617-1629.	1.8	21
57	Development of Microsatellite Markers in Tung Tree ( <i>Vernicia fordii</i> ) Using Cassava Genomic Sequences. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 893-904.	1.0	4
58	High-Density Genetic Linkage Map Construction and QTL Mapping of Grain Shape and Size in the Wheat Population Yanda1817 Å– Beinong6. <i>PLoS ONE</i> , 2015, 10, e0118144.	1.1	167
59	Development of a D genome specific marker resource for diploid and hexaploid wheat. <i>BMC Genomics</i> , 2015, 16, 646.	1.2	6
60	The wheat Sr50 gene reveals rich diversity at a cereal disease resistance locus. <i>Nature Plants</i> , 2015, 1, 15186.	4.7	209
61	Chromosomal genomics facilitates fine mapping of a Russian wheat aphid resistance gene. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1373-1383.	1.8	7
62	Sequencing of 15 Å622 geneâ€bearing BAC s clarifies the geneâ€dense regions of the barley genome. <i>Plant Journal</i> , 2015, 84, 216-227.	2.8	36
63	Genetic and physical mapping of powdery mildew resistance gene MlHLT in Chinese wheat landrace Hulutou. <i>Theoretical and Applied Genetics</i> , 2015, 128, 365-373.	1.8	48
64	Fine Physical and Genetic Mapping of Powdery Mildew Resistance Gene MlIW172 Originating from Wild Emmer ( <i>Triticum dicoccoides</i> ). <i>PLoS ONE</i> , 2014, 9, e100160.	1.1	36
65	Characterization of polyploid wheat genomic diversity using a highâ€density 90 Å000 single nucleotide polymorphism array. <i>Plant Biotechnology Journal</i> , 2014, 12, 787-796.	4.1	1,828
66	Identification of a robust molecular marker for the detection of the stem rust resistance gene Sr45 in common wheat. <i>Theoretical and Applied Genetics</i> , 2014, 127, 947-955.	1.8	62
67	Cassava genome from a wild ancestor to cultivated varieties. <i>Nature Communications</i> , 2014, 5, 5110.	5.8	230
68	Integrated physical, genetic and genome map of chickpea ( <i>Cicer arietinum</i> L.). <i>Functional and Integrative Genomics</i> , 2014, 14, 59-73.	1.4	49
69	Recent emergence of the wheat Lr34 multi-pathogen resistance: insights from haplotype analysis in wheat, rice, sorghum and <i>Aegilops tauschii</i> . <i>Theoretical and Applied Genetics</i> , 2013, 126, 663-672.	1.8	79
70	Draft genome sequence of chickpea ( <i>Cicer arietinum</i> ) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013, 31, 240-246.	9.4	1,049
71	Draft genome of the wheat A-genome progenitor <i>Triticum urartu</i> . <i>Nature</i> , 2013, 496, 87-90.	13.7	700
72	<i>Aegilops tauschii</i> single nucleotide polymorphisms shed light on the origins of wheat Dâ€genome genetic diversity and pinpoint the geographic origin of hexaploid wheat. <i>New Phytologist</i> , 2013, 198, 925-937.	3.5	243

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73	Wheat Zapper: a flexible online tool for colinearity studies in grass genomes. <i>Functional and Integrative Genomics</i> , 2013, 13, 11-17.	1.4	9
74	A radiation hybrid map of chromosome 1D reveals synteny conservation at a wheat speciation locus. <i>Functional and Integrative Genomics</i> , 2013, 13, 19-32.	1.4	19
75	The Gene <i>Sr33</i> , an Ortholog of Barley <i>Mla</i> Genes, Encodes Resistance to Wheat Stem Rust Race Ug99. <i>Science</i> , 2013, 341, 786-788.	6.0	370
76	SNP-revealed genetic diversity in wild emmer wheat correlates with ecological factors. <i>BMC Evolutionary Biology</i> , 2013, 13, 169.	3.2	36
77	Genetic Diversity Revealed by Single Nucleotide Polymorphism Markers in a Worldwide Germplasm Collection of Durum Wheat. <i>International Journal of Molecular Sciences</i> , 2013, 14, 7061-7088.	1.8	111
78	Combinatorial Pooling Enables Selective Sequencing of the Barley Gene Space. <i>PLoS Computational Biology</i> , 2013, 9, e1003010.	1.5	20
79	A 4-gigabase physical map unlocks the structure and evolution of the complex genome of <i>Aegilops tauschii</i> , the wheat D-genome progenitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7940-7945.	3.3	214
80	PIECE: a database for plant gene structure comparison and evolution. <i>Nucleic Acids Research</i> , 2013, 41, D1159-D1166.	6.5	50
81	Insular Organization of Gene Space in Grass Genomes. <i>PLoS ONE</i> , 2013, 8, e54101.	1.1	16
82	Rapid Genome Mapping in Nanochannel Arrays for Highly Complete and Accurate De Novo Sequence Assembly of the Complex <i>Aegilops tauschii</i> Genome. <i>PLoS ONE</i> , 2013, 8, e55864.	1.1	146
83	Comparative Analysis of Syntenic Genes in Grass Genomes Reveals Accelerated Rates of Gene Structure and Coding Sequence Evolution in Polyploid Wheat. <i>Plant Physiology</i> , 2012, 161, 252-265.	2.3	113
84	Development of chromosome-specific microsatellite markers in <i>Triticum aestivum</i> (Poaceae) using NGS technology. <i>American Journal of Botany</i> , 2012, 99, e369-71.	0.8	25
85	PAPP2C Interacts with the Atypical Disease Resistance Protein RPW8.2 and Negatively Regulates Salicylic Acid-Dependent Defense Responses in Arabidopsis. <i>Molecular Plant</i> , 2012, 5, 1125-1137.	3.9	25
86	Analysis of the bread wheat genome using whole-genome shotgun sequencing. <i>Nature</i> , 2012, 491, 705-710.	13.7	983
87	Genome-wide SNP discovery in walnut with an AGSNP pipeline updated for SNP discovery in allogamous organisms. <i>BMC Genomics</i> , 2012, 13, 354.	1.2	47
88	Physical mapping resources for large plant genomes: radiation hybrids for wheat D-genome progenitor <i>Aegilops tauschii</i> . <i>BMC Genomics</i> , 2012, 13, 597.	1.2	33
89	Exploring the diploid wheat ancestral A genome through sequence comparison at the high-molecular-weight glutenin locus region. <i>Molecular Genetics and Genomics</i> , 2012, 287, 855-866.	1.0	7
90	The Origin of Spelt and Free-Threshing Hexaploid Wheat. <i>Journal of Heredity</i> , 2012, 103, 426-441.	1.0	133

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91	A Second Generation Integrated Map of the Rainbow Trout ( <i>Oncorhynchus mykiss</i> ) Genome: Analysis of Conserved Synteny with Model Fish Genomes. <i>Marine Biotechnology</i> , 2012, 14, 343-357.	1.1	45
92	Fine genetic mapping of greenbug aphid-resistance gene Gb3 in <i>Aegilops tauschii</i> . <i>Theoretical and Applied Genetics</i> , 2012, 124, 555-564.	1.8	20
93	Characterizing the walnut genome through analyses of BAC end sequences. <i>Plant Molecular Biology</i> , 2012, 78, 95-107.	2.0	27
94	Fine Mapping of the Bsr1 Barley Stripe Mosaic Virus Resistance Gene in the Model Grass <i>Brachypodium distachyon</i> . <i>PLoS ONE</i> , 2012, 7, e38333.	1.1	67
95	N.I. Vavilov's theory of centres of diversity in the light of current understanding of wheat diversity, domestication and evolution. <i>Czech Journal of Genetics and Plant Breeding</i> , 2011, 47, S20-S27.	0.4	41
96	Gene Space Dynamics During the Evolution of <i>Aegilops tauschii</i> , <i>Brachypodium distachyon</i> , <i>Oryza sativa</i> , and <i>Sorghum bicolor</i> Genomes. <i>Molecular Biology and Evolution</i> , 2011, 28, 2537-2547.	3.5	46
97	Transferability of Microsatellite Markers from <i>Brachypodium distachyon</i> to <i>Miscanthus sinensis</i> , a Potential Biomass Crop F. <i>Journal of Integrative Plant Biology</i> , 2011, 53, 232-245.	4.1	34
98	Annotation-based genome-wide SNP discovery in the large and complex <i>Aegilops tauschii</i> genome using next-generation sequencing without a reference genome sequence. <i>BMC Genomics</i> , 2011, 12, 59.	1.2	146
99	Comparison of a high-density genetic linkage map to genome features in the model grass <i>Brachypodium distachyon</i> . <i>Theoretical and Applied Genetics</i> , 2011, 123, 455-464.	1.8	70
100	A first generation integrated map of the rainbow trout genome. <i>BMC Genomics</i> , 2011, 12, 180.	1.2	51
101	Identification and utilization of a sow thistle powdery mildew as a poorly adapted pathogen to dissect post-invasion non-host resistance mechanisms in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2011, 62, 2117-2129.	2.4	39
102	BAC Libraries from Wheat Chromosome 7D: Efficient Tool for Positional Cloning of Aphid Resistance Genes. <i>Journal of Biomedicine and Biotechnology</i> , 2011, 2011, 1-11.	3.0	33
103	Feasibility of physical map construction from fingerprinted bacterial artificial chromosome libraries of polyploid plant species. <i>BMC Genomics</i> , 2010, 11, 122.	1.2	22
104	Physical mapping of a large plant genome using global high-information-content-fingerprinting: the distal region of the wheat ancestor <i>Aegilops tauschii</i> chromosome 3DS. <i>BMC Genomics</i> , 2010, 11, 382.	1.2	12
105	A new implementation of high-throughput five-dimensional clone pooling strategy for BAC library screening. <i>BMC Genomics</i> , 2010, 11, 692.	1.2	10
106	Nucleotide diversity maps reveal variation in diversity among wheat genomes and chromosomes. <i>BMC Genomics</i> , 2010, 11, 702.	1.2	189
107	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	13.7	1,685
108	RJPrimers: unique transposable element insertion junction discovery and PCR primer design for marker development. <i>Nucleic Acids Research</i> , 2010, 38, W313-W320.	6.5	34

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109	Population- and genome-specific patterns of linkage disequilibrium and SNP variation in spring and winter wheat ( <i>Triticum aestivum</i> L.). <i>BMC Genomics</i> , 2010, 11, 727.	1.2	234
110	A physical map of the papaya genome with integrated genetic map and genome sequence. <i>BMC Genomics</i> , 2009, 10, 371.	1.2	81
111	A high-throughput strategy for screening of bacterial artificial chromosome libraries and anchoring of clones on a genetic map constructed with single nucleotide polymorphisms. <i>BMC Genomics</i> , 2009, 10, 28.	1.2	19
112	A first generation BAC-based physical map of the rainbow trout genome. <i>BMC Genomics</i> , 2009, 10, 462.	1.2	41
113	A BAC-based physical map of <i>Brachypodium distachyon</i> and its comparative analysis with rice and wheat. <i>BMC Genomics</i> , 2009, 10, 496.	1.2	42
114	Analysis of gene-derived SNP marker polymorphism in US wheat ( <i>Triticum aestivum</i> L.) cultivars. <i>Molecular Breeding</i> , 2009, 23, 23-33.	1.0	153
115	Structural characterization of <i>Brachypodium</i> genome and its syntenic relationship with rice and wheat. <i>Plant Molecular Biology</i> , 2009, 70, 47-61.	2.0	71
116	Saturation and comparative mapping of the genomic region harboring Hessian fly resistance gene H26 in wheat. <i>Theoretical and Applied Genetics</i> , 2009, 118, 1589-1599.	1.8	37
117	Genome comparisons reveal a dominant mechanism of chromosome number reduction in grasses and accelerated genome evolution in Triticeae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15780-15785.	3.3	190
118	Rapid development of PCR-based genome-specific repetitive DNA junction markers in wheat. <i>Genome</i> , 2009, 52, 576-587.	0.9	56
119	The nuclear genome of <i>Brachypodium distachyon</i> : analysis of BAC end sequences. <i>Functional and Integrative Genomics</i> , 2008, 8, 135-147.	1.4	83
120	BatchPrimer3: A high throughput web application for PCR and sequencing primer design. <i>BMC Bioinformatics</i> , 2008, 9, 253.	1.2	707
121	The draft genome of the transgenic tropical fruit tree papaya ( <i>Carica papaya</i> Linnaeus). <i>Nature</i> , 2008, 452, 991-996.	13.7	964
122	Microsatellite discovery from BAC end sequences and genetic mapping to anchor the soybean physical and genetic maps. <i>Genome</i> , 2008, 51, 294-302.	0.9	50
123	GenoProfiler: batch processing of high-throughput capillary fingerprinting data. <i>Bioinformatics</i> , 2007, 23, 240-242.	1.8	58
124	Efficacy of clone fingerprinting methodologies. <i>Genomics</i> , 2007, 89, 160-165.	1.3	21
125	The structure of wild and domesticated emmer wheat populations, gene flow between them, and the site of emmer domestication. <i>Theoretical and Applied Genetics</i> , 2007, 114, 947-959.	1.8	184
126	Construction and characterization of two BAC libraries from <i>Brachypodium distachyon</i> , a new model for grass genomics. <i>Genome</i> , 2006, 49, 1099-1108.	0.9	64



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127	Molecular Characterization of a Diagnostic DNA Marker for Domesticated Tetraploid Wheat Provides Evidence for Gene Flow from Wild Tetraploid Wheat to Hexaploid Wheat. <i>Molecular Biology and Evolution</i> , 2006, 23, 1386-1396.	3.5	187
128	Discovery and Mapping of Wheat Ph1 Suppressors. <i>Genetics</i> , 2006, 174, 17-27.	1.2	67
129	The R1 resistance gene cluster contains three groups of independently evolving, type I R1 homologues and shows substantial structural variation among haplotypes of <i>Solanum demissum</i> . <i>Plant Journal</i> , 2005, 44, 37-51.	2.8	94
130	Comparative genetic maps reveal extreme crossover localization in the <i>Aegilops speltoides</i> chromosomes. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1098-1106.	1.8	37
131	Deletion Polymorphism in Wheat Chromosome Regions With Contrasting Recombination Rates. <i>Genetics</i> , 2004, 168, 1665-1675.	1.2	54
132	Sequence Polymorphism in Polyploid Wheat and Their D-Genome Diploid Ancestor. <i>Genetics</i> , 2004, 167, 941-947.	1.2	140
133	Genomic organization of the complex $\hat{\pm}$ -gliadin gene loci in wheat. <i>Theoretical and Applied Genetics</i> , 2004, 109, 648-657.	1.8	62
134	High-throughput fingerprinting of bacterial artificial chromosomes using the snapshot labeling kit and sizing of restriction fragments by capillary electrophoresis. <i>Genomics</i> , 2003, 82, 378-389.	1.3	242
135	Recombination of Chromosomes 3Am and 5Am of <i>Triticum monococcum</i> With Homeologous Chromosomes 3A and 5A of Wheat: The Distribution of Recombination Across Chromosomes. <i>Genetics</i> , 2000, 154, 1301-1308.	1.2	51
136	The structure of the <i>Aegilops tauschii</i> gene pool and the evolution of hexaploid wheat. <i>Theoretical and Applied Genetics</i> , 1998, 97, 657-670.	1.8	386
137	Restriction Fragment Length Polymorphism and Divergence in the Genomic Regions of High and Low Recombination in Self-Fertilizing and Cross-Fertilizing <i>Aegilops</i> Species. <i>Genetics</i> , 1998, 148, 423-434.	1.2	177
138	Position Effects of Ribosomal RNA Multigene Loci on Meiotic Recombination in Wheat. <i>Genetics</i> , 1998, 149, 1105-1113.	1.2	18
139	Seed-storage-protein loci in RFLP maps of diploid, tetraploid, and hexaploid wheat. <i>Theoretical and Applied Genetics</i> , 1997, 95, 1169-1180.	1.8	66
140	Genetic analysis and physiology of a trait for enhanced K <sup>+</sup> /Na <sup>+</sup> discrimination in wheat. <i>New Phytologist</i> , 1997, 137, 109-116.	3.5	106
141	Molecular mapping of an aluminum tolerance locus on chromosome 4D of Chinese Spring wheat. <i>Euphytica</i> , 1996, 91, 31-35.	0.6	73
142	Mapping of the K <sup>+</sup> /Na <sup>+</sup> discrimination locus Kna1 in wheat. <i>Theoretical and Applied Genetics</i> , 1996, 92-92, 448-454.	1.8	225
143	Engineering of interstitial foreign chromosome segments containing the K <sup>+</sup> /Na <sup>+</sup> selectivity gene Kna1 by sequential homoeologous recombination in durum wheat. <i>Theoretical and Applied Genetics</i> , 1996, 93, 1180-1184.	1.8	48
144	Genetic Map of Diploid Wheat, <i>Triticum monococcum</i> L., and Its Comparison With Maps of <i>Hordeum vulgare</i> L.. <i>Genetics</i> , 1996, 143, 983-999.	1.2	250

#	ARTICLE	IF	CITATIONS
145	Recognition of Homeology by the Wheat <i>Ph1</i> Locus. <i>Genetics</i> , 1996, 144, 1195-1203.	1.2	74
146	Differentiation between homoeologous chromosomes 1A of wheat and 1Am of <i>Triticum monococcum</i> and its recognition by the wheat <i>Ph1</i> locus.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 6645-6649.	3.3	134
147	Linkage relationships among stress-induced genes in wheat. <i>Theoretical and Applied Genetics</i> , 1995, 91, 795-801.	1.8	44
148	Differentiation between wheat chromosomes 4B and 4D. <i>Genome</i> , 1995, 38, 1139-1147.	0.9	20
149	Crossability percentages of bread wheat landraces from Shaanxi and Henan provinces, China with rye. <i>Euphytica</i> , 1993, 67, 1-8.	0.6	13
150	Crossability percentages of bread wheat collections from Tibet, China with rye. <i>Euphytica</i> , 1993, 70, 127-129.	0.6	4
151	Crossability percentages of bread wheat landraces from Sichuan Province, China with rye. <i>Euphytica</i> , 1992, 61, 1-7.	0.6	18