

Ming-Cheng Luo

List of Publications by Year in descending order

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#	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.	17.5	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.	7.3	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.	6.3	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.	5.7	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, .	1.8	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.	4.4	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.	8.3	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.	3.5	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.	3.3	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, .	6.4	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.	7.3	92
12	A CNL protein in wild emmer wheat confers powdery mildew resistance. <i>New Phytologist</i> , 2020, 228, 1027-1037.	7.3	89
13	Introgression of perennial growth habit from <i>Lophopyrum elongatum</i> into wheat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2545-2554.	3.6	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.	3.6	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.	12.8	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.	12.8	84
17	Recombination between homoeologous chromosomes induced in durum wheat by the <i>Aegilops speltoides</i> Su1-Ph1 suppressor. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3265-3276.	3.6	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.	1.8	1

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19	Rapid evolution of α -gliadin gene family revealed by analyzing Gli-2 locus regions of wild emmer wheat. <i>Functional and Integrative Genomics</i> , 2019, 19, 993-1005.	3.5	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.	1.9	10
21	The genome of cowpea (<i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019, 98, 767-782.	5.7	264
22	Sequencing a <i>Juglans regia</i> × <i>J. microcarpa</i> hybrid yields high-quality genome assemblies of parental species. <i>Horticulture Research</i> , 2019, 6, 55.	6.3	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.	1.8	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.	4.4	9
25	Chromosome-scale pseudomolecules refined by optical, physical and genetic maps in flax. <i>Plant Journal</i> , 2018, 95, 371-384.	5.7	119
26	Dynamic Evolution of α -Gliadin Prolamin Gene Family in Homeologous Genomes of Hexaploid Wheat. <i>Scientific Reports</i> , 2018, 8, 5181.	3.3	68
27	Uncovering the dispersion history, adaptive evolution and selection of wheat in China. <i>Plant Biotechnology Journal</i> , 2018, 16, 280-291.	8.3	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.	3.5	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.	5.7	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.	3.6	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.	8.8	41
32	Reassessment of the evolution of wheat chromosomes 4A, 5A, and 7B. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2451-2462.	3.6	66
33	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	12.6	768
34	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	12.6	2,424
35	Analysis of <i>Brachypodium</i> genomes with genome-wide optical maps. <i>Genome</i> , 2018, 61, 559-565.	2.0	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.	5.5	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.	12.8	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.	5.7	29
39	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	27.8	563
40	Genome resources for climateâ€resilient cowpea, an essential crop for food security. <i>Plant Journal</i> , 2017, 89, 1042-1054.	5.7	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.	3.9	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.	3.6	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.	3.6	33
44	Introgression of the <i>Aegilops speltoides</i> Su1-Ph1 Suppressor into Wheat. <i>Frontiers in Plant Science</i> , 2017, 8, 2163.	3.6	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.	2.5	12
46	A wholeâ€genome, radiation hybrid mapping resource of hexaploid wheat. <i>Plant Journal</i> , 2016, 86, 195-207.	5.7	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.	5.7	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.	8.3	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.	3.6	33
50	Optical Nano-mapping and Analysis of Plant Genomes. <i>Methods in Molecular Biology</i> , 2016, 1429, 103-117.	0.9	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.	1.2	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.	7.1	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.	2.8	31
54	Synten analysis in Rosids with a walnut physical map reveals slow genome evolution in long-lived woody perennials. <i>BMC Genomics</i> , 2015, 16, 707.	2.8	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	2.5	41
56	Dynamic evolution of resistance gene analogs in the orthologous genomic regions of powdery mildew resistance gene <i>MLW170</i> in <i>Triticum dicoccoides</i> and <i>Aegilops tauschii</i> . Theoretical and Applied Genetics, 2015, 128, 1617-1629.	3.6	21
57	Development of Microsatellite Markers in Tung Tree (<i>Vernicia fordii</i>) Using Cassava Genomic Sequences. Plant Molecular Biology Reporter, 2015, 33, 893-904.	1.8	4
58	High-Density Genetic Linkage Map Construction and QTL Mapping of Grain Shape and Size in the Wheat Population Yanda1817 Å— Beinong6. PLoS ONE, 2015, 10, e0118144.	2.5	167
59	Development of a D genome specific marker resource for diploid and hexaploid wheat. BMC Genomics, 2015, 16, 646.	2.8	6
60	The wheat <i>Sr50</i> gene reveals rich diversity at a cereal disease resistance locus. Nature Plants, 2015, 1, 15186.	9.3	209
61	Chromosomal genomics facilitates fine mapping of a Russian wheat aphid resistance gene. Theoretical and Applied Genetics, 2015, 128, 1373-1383.	3.6	7
62	Sequencing of 15Å22 geneâ€bearing BAC s clarifies the geneâ€dense regions of the barley genome. Plant Journal, 2015, 84, 216-227.	5.7	36
63	Genetic and physical mapping of powdery mildew resistance gene <i>MLHLT</i> in Chinese wheat landrace Hulutou. Theoretical and Applied Genetics, 2015, 128, 365-373.	3.6	48
64	Fine Physical and Genetic Mapping of Powdery Mildew Resistance Gene <i>MLW172</i> Originating from Wild Emmer (<i>Triticum dicoccoides</i>). PLoS ONE, 2014, 9, e100160.	2.5	36
65	Characterization of polyploid wheat genomic diversity using a highâ€density 90Å000 single nucleotide polymorphism array. Plant Biotechnology Journal, 2014, 12, 787-796.	8.3	1,828
66	Identification of a robust molecular marker for the detection of the stem rust resistance gene <i>Sr45</i> in common wheat. Theoretical and Applied Genetics, 2014, 127, 947-955.	3.6	62
67	Cassava genome from a wild ancestor to cultivated varieties. Nature Communications, 2014, 5, 5110.	12.8	230
68	Integrated physical, genetic and genome map of chickpea (<i>Cicer arietinum</i> L.). Functional and Integrative Genomics, 2014, 14, 59-73.	3.5	49
69	Recent emergence of the wheat <i>Lr34</i> multi-pathogen resistance: insights from haplotype analysis in wheat, rice, sorghum and <i>Aegilops tauschii</i> . Theoretical and Applied Genetics, 2013, 126, 663-672.	3.6	79
70	Draft genome sequence of chickpea (<i>Cicer arietinum</i>) provides a resource for trait improvement. Nature Biotechnology, 2013, 31, 240-246.	17.5	1,049
71	Draft genome of the wheat A-genome progenitor <i>Triticum urartu</i> . Nature, 2013, 496, 87-90.	27.8	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. New Phytologist, 2013, 198, 925-937.	7.3	243

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73	Wheat Zapper: a flexible online tool for colinearity studies in grass genomes. Functional and Integrative Genomics, 2013, 13, 11-17.	3.5	9
74	A radiation hybrid map of chromosome 1D reveals synteny conservation at a wheat speciation locus. Functional and Integrative Genomics, 2013, 13, 19-32.	3.5	19
75	The Gene <i>Sr33</i> , an Ortholog of Barley <i>Mla</i> Genes, Encodes Resistance to Wheat Stem Rust Race Ug99. Science, 2013, 341, 786-788.	12.6	370
76	SNP-revealed genetic diversity in wild emmer wheat correlates with ecological factors. BMC Evolutionary Biology, 2013, 13, 169.	3.2	36
77	Genetic Diversity Revealed by Single Nucleotide Polymorphism Markers in a Worldwide Germplasm Collection of Durum Wheat. International Journal of Molecular Sciences, 2013, 14, 7061-7088.	4.1	111
78	Combinatorial Pooling Enables Selective Sequencing of the Barley Gene Space. PLoS Computational Biology, 2013, 9, e1003010.	3.2	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. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7940-7945.	7.1	214
80	PIECE: a database for plant gene structure comparison and evolution. Nucleic Acids Research, 2013, 41, D1159-D1166.	14.5	50
81	Insular Organization of Gene Space in Grass Genomes. PLoS ONE, 2013, 8, e54101.	2.5	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. PLoS ONE, 2013, 8, e55864.	2.5	146
83	Comparative Analysis of Syntenic Genes in Grass Genomes Reveals Accelerated Rates of Gene Structure and Coding Sequence Evolution in Polyploid Wheat. Plant Physiology, 2012, 161, 252-265.	4.8	113
84	Development of chromosome-specific microsatellite markers in <i>Triticum aestivum</i> (Poaceae) using NGS technology. American Journal of Botany, 2012, 99, e369-71.	1.7	25
85	PAPP2C Interacts with the Atypical Disease Resistance Protein RPW8.2 and Negatively Regulates Salicylic Acid-Dependent Defense Responses in Arabidopsis. Molecular Plant, 2012, 5, 1125-1137.	8.3	25
86	Analysis of the bread wheat genome using whole-genome shotgun sequencing. Nature, 2012, 491, 705-710.	27.8	983
87	Genome-wide SNP discovery in walnut with an AGSNP pipeline updated for SNP discovery in allogamous organisms. BMC Genomics, 2012, 13, 354.	2.8	47
88	Physical mapping resources for large plant genomes: radiation hybrids for wheat D-genome progenitor <i>Aegilops tauschii</i> . BMC Genomics, 2012, 13, 597.	2.8	33
89	Exploring the diploid wheat ancestral A genome through sequence comparison at the high-molecular-weight glutenin locus region. Molecular Genetics and Genomics, 2012, 287, 855-866.	2.1	7
90	The Origin of Spelt and Free-Threshing Hexaploid Wheat. Journal of Heredity, 2012, 103, 426-441.	2.4	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.	2.4	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.	3.6	20
93	Characterizing the walnut genome through analyses of BAC end sequences. <i>Plant Molecular Biology</i> , 2012, 78, 95-107.	3.9	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.	2.5	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.	0.8	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.	8.9	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.	8.5	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.	2.8	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.	3.6	70
100	A first generation integrated map of the rainbow trout genome. <i>BMC Genomics</i> , 2011, 12, 180.	2.8	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.	4.8	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.	2.8	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.	2.8	12
105	A new implementation of high-throughput five-dimensional clone pooling strategy for BAC library screening. <i>BMC Genomics</i> , 2010, 11, 692.	2.8	10
106	Nucleotide diversity maps reveal variation in diversity among wheat genomes and chromosomes. <i>BMC Genomics</i> , 2010, 11, 702.	2.8	189
107	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	27.8	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.	14.5	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.	2.8	234
110	A physical map of the papaya genome with integrated genetic map and genome sequence. <i>BMC Genomics</i> , 2009, 10, 371.	2.8	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.	2.8	19
112	A first generation BAC-based physical map of the rainbow trout genome. <i>BMC Genomics</i> , 2009, 10, 462.	2.8	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.	2.8	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.	2.1	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.	3.9	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.	3.6	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.	7.1	190
118	Rapid development of PCR-based genome-specific repetitive DNA junction markers in wheat. <i>Genome</i> , 2009, 52, 576-587.	2.0	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.	3.5	83
120	BatchPrimer3: A high throughput web application for PCR and sequencing primer design. <i>BMC Bioinformatics</i> , 2008, 9, 253.	2.6	707
121	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
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.	2.0	50
123	GenoProfiler: batch processing of high-throughput capillary fingerprinting data. <i>Bioinformatics</i> , 2007, 23, 240-242.	4.1	58
124	Efficacy of clone fingerprinting methodologies. <i>Genomics</i> , 2007, 89, 160-165.	2.9	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.	3.6	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.	2.0	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.	8.9	187
128	Discovery and Mapping of Wheat <i>Ph1</i> Suppressors. <i>Genetics</i> , 2006, 174, 17-27.	2.9	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.	5.7	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.	3.6	37
131	Deletion Polymorphism in Wheat Chromosome Regions With Contrasting Recombination Rates. <i>Genetics</i> , 2004, 168, 1665-1675.	2.9	54
132	Sequence Polymorphism in Polyploid Wheat and Their D-Genome Diploid Ancestor. <i>Genetics</i> , 2004, 167, 941-947.	2.9	140
133	Genomic organization of the complex α -gliadin gene loci in wheat. <i>Theoretical and Applied Genetics</i> , 2004, 109, 648-657.	3.6	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.	2.9	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.	2.9	51
136	The structure of the <i>Aegilops tauschii</i> genepool and the evolution of hexaploid wheat. <i>Theoretical and Applied Genetics</i> , 1998, 97, 657-670.	3.6	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.	2.9	177
138	Position Effects of Ribosomal RNA Multigene Loci on Meiotic Recombination in Wheat. <i>Genetics</i> , 1998, 149, 1105-1113.	2.9	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.	3.6	66
140	Genetic analysis and physiology of a trait for enhanced K ⁺ /Na ⁺ discrimination in wheat. <i>New Phytologist</i> , 1997, 137, 109-116.	7.3	106
141	Molecular mapping of an aluminum tolerance locus on chromosome 4D of Chinese Spring wheat. <i>Euphytica</i> , 1996, 91, 31-35.	1.2	73
142	Mapping of the K ⁺ /Na ⁺ discrimination locus <i>Kna1</i> in wheat. <i>Theoretical and Applied Genetics</i> , 1996, 92-92, 448-454.	3.6	225
143	Engineering of interstitial foreign chromosome segments containing the K ⁺ /Na ⁺ selectivity gene <i>Kna1</i> by sequential homoeologous recombination in durum wheat. <i>Theoretical and Applied Genetics</i> , 1996, 93, 1180-1184.	3.6	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.	2.9	250

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145	Recognition of Homeology by the Wheat <i>Ph1</i> Locus. Genetics, 1996, 144, 1195-1203.	2.9	74
146	Differentiation between homoeologous chromosomes 1A of wheat and 1Am of Triticum monococcum and its recognition by the wheat <i>Ph1</i> locus.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 6645-6649.	7.1	134
147	Linkage relationships among stress-induced genes in wheat. Theoretical and Applied Genetics, 1995, 91, 795-801.	3.6	44
148	Differentiation between wheat chromosomes 4B and 4D. Genome, 1995, 38, 1139-1147.	2.0	20
149	Crossability percentages of bread wheat landraces from Shaanxi and Henan provinces, China with rye. Euphytica, 1993, 67, 1-8.	1.2	13
150	Crossability percentages of bread wheat collections from Tibet, China with rye. Euphytica, 1993, 70, 127-129.	1.2	4
151	Crossability percentages of bread wheat landraces from Sichuan Province, China with rye. Euphytica, 1992, 61, 1-7.	1.2	18