

Ming-Cheng Luo

List of Publications by Year in descending order

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151
papers

22,169
citations

18482

62
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9589

142
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157
all docs

157
docs citations

157
times ranked

15483
citing authors

#	ARTICLE	IF	CITATIONS
1	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	12.6	2,424
2	Characterization of polyploid wheat genomic diversity using a high-density 90,000 single nucleotide polymorphism array. <i>Plant Biotechnology Journal</i> , 2014, 12, 787-796.	8.3	1,828
3	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	27.8	1,685
4	Draft genome sequence of chickpea (<i>Cicer arietinum</i>) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013, 31, 240-246.	17.5	1,049
5	Analysis of the bread wheat genome using whole-genome shotgun sequencing. <i>Nature</i> , 2012, 491, 705-710.	27.8	983
6	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
7	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	12.6	768
8	BatchPrimer3: A high throughput web application for PCR and sequencing primer design. <i>BMC Bioinformatics</i> , 2008, 9, 253.	2.6	707
9	Draft genome of the wheat A-genome progenitor <i>Triticum urartu</i> . <i>Nature</i> , 2013, 496, 87-90.	27.8	700
10	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	27.8	563
11	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
12	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
13	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.	12.6	370
14	The genome of cowpea (<i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019, 98, 767-782.	5.7	264
15	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
16	<i>Aegilops tauschii</i> single nucleotide polymorphisms shed light on the origins of wheat D-genome genetic diversity and pinpoint the geographic origin of hexaploid wheat. <i>New Phytologist</i> , 2013, 198, 925-937.	7.3	243
17	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
18	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

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19	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
20	Cassava genome from a wild ancestor to cultivated varieties. <i>Nature Communications</i> , 2014, 5, 5110.	12.8	230
21	Mapping of the K ⁺ /Na ⁺ discrimination locus Kna1 in wheat. <i>Theoretical and Applied Genetics</i> , 1996, 92-92, 448-454.	3.6	225
22	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.	7.1	214
23	The wheat Sr50 gene reveals rich diversity at a cereal disease resistance locus. <i>Nature Plants</i> , 2015, 1, 15186.	9.3	209
24	Genome resources for climate-resilient cowpea, an essential crop for food security. <i>Plant Journal</i> , 2017, 89, 1042-1054.	5.7	199
25	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
26	Nucleotide diversity maps reveal variation in diversity among wheat genomes and chromosomes. <i>BMC Genomics</i> , 2010, 11, 702.	2.8	189
27	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
28	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
29	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
30	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.	2.5	167
31	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
32	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
33	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.	2.5	146
34	Sequence Polymorphism in Polyploid Wheat and Their D-Genome Diploid Ancestor. <i>Genetics</i> , 2004, 167, 941-947.	2.9	140
35	Differentiation between homoeologous chromosomes 1A of wheat and 1Am of <i>Triticum monococcum</i> and its recognition by the wheat Ph1 locus.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 6645-6649.	7.1	134
36	The Origin of Spelt and Free-Threshing Hexaploid Wheat. <i>Journal of Heredity</i> , 2012, 103, 426-441.	2.4	133

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37	Chromosome-scale pseudomolecules refined by optical, physical and genetic maps in flax. <i>Plant Journal</i> , 2018, 95, 371-384.	5.7	119
38	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
39	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.	4.8	113
40	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.	4.1	111
41	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
42	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
43	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
44	Wheat Ms2 encodes for an orphan protein that confers male sterility in grass species. <i>Nature Communications</i> , 2017, 8, 15121.	12.8	97
45	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
46	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
47	A CNL protein in wild emmer wheat confers powdery mildew resistance. <i>New Phytologist</i> , 2020, 228, 1027-1037.	7.3	89
48	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
49	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
50	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
51	Syntenic 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
52	A physical map of the papaya genome with integrated genetic map and genome sequence. <i>BMC Genomics</i> , 2009, 10, 371.	2.8	81
53	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.	3.6	79
54	Recognition of Homeology by the Wheat <i>Ph1</i> Locus. <i>Genetics</i> , 1996, 144, 1195-1203.	2.9	74

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55	Molecular mapping of an aluminum tolerance locus on chromosome 4D of Chinese Spring wheat. <i>Euphytica</i> , 1996, 91, 31-35.	1.2	73
56	Structural characterization of Brachypodium genome and its syntenic relationship with rice and wheat. <i>Plant Molecular Biology</i> , 2009, 70, 47-61.	3.9	71
57	Comparison of a high-density genetic linkage map to genome features in the model grass Brachypodium distachyon. <i>Theoretical and Applied Genetics</i> , 2011, 123, 455-464.	3.6	70
58	Dynamic Evolution of α -Gliadin Prolamin Gene Family in Homeologous Genomes of Hexaploid Wheat. <i>Scientific Reports</i> , 2018, 8, 5181.	3.3	68
59	Discovery and Mapping of Wheat <i>Ph1</i> Suppressors. <i>Genetics</i> , 2006, 174, 17-27.	2.9	67
60	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
61	Fine Mapping of the Bsr1 Barley Stripe Mosaic Virus Resistance Gene in the Model Grass Brachypodium distachyon. <i>PLoS ONE</i> , 2012, 7, e38333.	2.5	67
62	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
63	Reassessment of the evolution of wheat chromosomes 4A, 5A, and 7B. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2451-2462.	3.6	66
64	Construction and characterization of two BAC libraries from Brachypodium distachyon, a new model for grass genomics. <i>Genome</i> , 2006, 49, 1099-1108.	2.0	64
65	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
66	Genomic organization of the complex α -gliadin gene loci in wheat. <i>Theoretical and Applied Genetics</i> , 2004, 109, 648-657.	3.6	62
67	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.	3.6	62
68	Uncovering the dispersion history, adaptive evolution and selection of wheat in China. <i>Plant Biotechnology Journal</i> , 2018, 16, 280-291.	8.3	62
69	GenoProfiler: batch processing of high-throughput capillary fingerprinting data. <i>Bioinformatics</i> , 2007, 23, 240-242.	4.1	58
70	Rapid development of PCR-based genome-specific repetitive DNA junction markers in wheat. <i>Genome</i> , 2009, 52, 576-587.	2.0	56
71	Deletion Polymorphism in Wheat Chromosome Regions With Contrasting Recombination Rates. <i>Genetics</i> , 2004, 168, 1665-1675.	2.9	54
72	<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

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73	A first generation integrated map of the rainbow trout genome. BMC Genomics, 2011, 12, 180.	2.8	51
74	Recombination of Chromosomes 3Am and 5Am of Triticum monococcum With Homeologous Chromosomes 3A and 5A of Wheat: The Distribution of Recombination Across Chromosomes. Genetics, 2000, 154, 1301-1308.	2.9	51
75	Microsatellite discovery from BAC end sequences and genetic mapping to anchor the soybean physical and genetic maps. Genome, 2008, 51, 294-302.	2.0	50
76	PIECE: a database for plant gene structure comparison and evolution. Nucleic Acids Research, 2013, 41, D1159-D1166.	14.5	50
77	Analysis of tandem gene copies in maize chromosomal regions reconstructed from long sequence reads. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7949-7956.	7.1	50
78	Integrated physical, genetic and genome map of chickpea (<i>Cicer arietinum</i> L.). Functional and Integrative Genomics, 2014, 14, 59-73.	3.5	49
79	Engineering of interstitial foreign chromosome segments containing the K ⁺ /Na ⁺ selectivity gene Kna1 by sequential homoeologous recombination in durum wheat. Theoretical and Applied Genetics, 1996, 93, 1180-1184.	3.6	48
80	Genetic and physical mapping of powdery mildew resistance gene MHLT in Chinese wheat landrace Hulutou. Theoretical and Applied Genetics, 2015, 128, 365-373.	3.6	48
81	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
82	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. Molecular Biology and Evolution, 2011, 28, 2537-2547.	8.9	46
83	A Second Generation Integrated Map of the Rainbow Trout (<i>Oncorhynchus mykiss</i>) Genome: Analysis of Conserved Synteny with Model Fish Genomes. Marine Biotechnology, 2012, 14, 343-357.	2.4	45
84	Introgression of the <i>Aegilops speltoides</i> Su1-Ph1 Suppressor into Wheat. Frontiers in Plant Science, 2017, 8, 2163.	3.6	45
85	Linkage relationships among stress-induced genes in wheat. Theoretical and Applied Genetics, 1995, 91, 795-801.	3.6	44
86	A BAC-based physical map of <i>Brachypodium distachyon</i> and its comparative analysis with rice and wheat. BMC Genomics, 2009, 10, 496.	2.8	42
87	A first generation BAC-based physical map of the rainbow trout genome. BMC Genomics, 2009, 10, 462.	2.8	41
88	N.I. Vavilov's theory of centres of diversity in the light of current understanding of wheat diversity, domestication and evolution. Czech Journal of Genetics and Plant Breeding, 2011, 47, S20-S27.	0.8	41
89	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
90	Optical and physical mapping with local finishing enables megabase-scale resolution of agronomically important regions in the wheat genome. Genome Biology, 2018, 19, 112.	8.8	41

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91	Identification and utilization of a sow thistle powdery mildew as a poorly adapted pathogen to dissect post-invasion non-host resistance mechanisms in Arabidopsis. Journal of Experimental Botany, 2011, 62, 2117-2129.	4.8	39
92	Comparative genetic maps reveal extreme crossover localization in the Aegilops speltoides chromosomes. Theoretical and Applied Genetics, 2005, 111, 1098-1106.	3.6	37
93	Saturation and comparative mapping of the genomic region harboring Hessian fly resistance gene H26 in wheat. Theoretical and Applied Genetics, 2009, 118, 1589-1599.	3.6	37
94	SNP-revealed genetic diversity in wild emmer wheat correlates with ecological factors. BMC Evolutionary Biology, 2013, 13, 169.	3.2	36
95	Fine Physical and Genetic Mapping of Powdery Mildew Resistance Gene MlW172 Originating from Wild Emmer (Triticum dicoccoides). PLoS ONE, 2014, 9, e100160.	2.5	36
96	Sequencing of 15,622 genes bearing BACs clarifies the gene-dense regions of the barley genome. Plant Journal, 2015, 84, 216-227.	5.7	36
97	RJPrimers: unique transposable element insertion junction discovery and PCR primer design for marker development. Nucleic Acids Research, 2010, 38, W313-W320.	14.5	34
98	Transferability of Microsatellite Markers from <i>Brachypodium distachyon</i> to <i>Miscanthus sinensis</i> , a Potential Biomass Crop F. Journal of Integrative Plant Biology, 2011, 53, 232-245.	8.5	34
99	BAC Libraries from Wheat Chromosome 7D: Efficient Tool for Positional Cloning of Aphid Resistance Genes. Journal of Biomedicine and Biotechnology, 2011, 2011, 1-11.	3.0	33
100	Physical mapping resources for large plant genomes: radiation hybrids for wheat D-genome progenitor Aegilops tauschii. BMC Genomics, 2012, 13, 597.	2.8	33
101	Rapid evolutionary dynamics in a 2.8-Mb chromosomal region containing multiple prolamin and resistance gene families in <i>Aegilops tauschii</i> . Plant Journal, 2016, 87, 495-506.	5.7	33
102	Genetic mapping of SrCad and SNP marker development for marker-assisted selection of Ug99 stem rust resistance in wheat. Theoretical and Applied Genetics, 2016, 129, 1373-1382.	3.6	33
103	A High-Density Genetic Map of Wild Emmer Wheat from the Karaca Dağ Region Provides New Evidence on the Structure and Evolution of Wheat Chromosomes. Frontiers in Plant Science, 2017, 8, 1798.	3.6	33
104	Radiation hybrid maps of the D-genome of Aegilops tauschii and their application in sequence assembly of large and complex plant genomes. BMC Genomics, 2015, 16, 800.	2.8	31
105	Structural variation and rates of genome evolution in the grass family seen through comparison of sequences of genomes greatly differing in size. Plant Journal, 2018, 95, 487-503.	5.7	31
106	New insights into structural organization and gene duplication in a 1.75-Mb genomic region harboring the ω -gliadin gene family in Aegilops tauschii, the source of wheat D genome. Plant Journal, 2017, 92, 571-583.	5.7	29
107	Rapid evolution of ω -gliadin gene family revealed by analyzing Gli-2 locus regions of wild emmer wheat. Functional and Integrative Genomics, 2019, 19, 993-1005.	3.5	28
108	Characterizing the walnut genome through analyses of BAC end sequences. Plant Molecular Biology, 2012, 78, 95-107.	3.9	27

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109	Development of chromosomeâ€armâ€specific microsatellite markers in <i>Triticum aestivum</i> (Poaceae) using NGS technology. American Journal of Botany, 2012, 99, e369-71.	1.7	25
110	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
111	Sequencing and comparative analyses of <i>Aegilops tauschii</i> chromosome arm 3DS reveal rapid evolution of Triticeae genomes. Journal of Genetics and Genomics, 2017, 44, 51-61.	3.9	25
112	A wholeâ€genome, radiation hybrid mapping resource of hexaploid wheat. Plant Journal, 2016, 86, 195-207.	5.7	23
113	Reduced chromatin accessibility underlies gene expression differences in homologous chromosome arms of diploid <i>Aegilops tauschii</i> and hexaploid wheat. GigaScience, 2020, 9, .	6.4	23
114	Feasibility of physical map construction from fingerprinted bacterial artificial chromosome libraries of polyploid plant species. BMC Genomics, 2010, 11, 122.	2.8	22
115	Efficacy of clone fingerprinting methodologies. Genomics, 2007, 89, 160-165.	2.9	21
116	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> . Theoretical and Applied Genetics, 2015, 128, 1617-1629.	3.6	21
117	Differentiation between wheat chromosomes 4B and 4D. Genome, 1995, 38, 1139-1147.	2.0	20
118	Fine genetic mapping of greenbug aphid-resistance gene Gb3 in <i>Aegilops tauschii</i> . Theoretical and Applied Genetics, 2012, 124, 555-564.	3.6	20
119	Combinatorial Pooling Enables Selective Sequencing of the Barley Gene Space. PLoS Computational Biology, 2013, 9, e1003010.	3.2	20
120	A high-throughput strategy for screening of bacterial artificial chromosome libraries and anchoring of clones on a genetic map constructed with single nucleotide polymorphisms. BMC Genomics, 2009, 10, 28.	2.8	19
121	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
122	<i>Aegilops tauschii</i> genome assembly Aet v5.0 features greater sequence contiguity and improved annotation. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	19
123	Crossability percentages of bread wheat landraces from Sichuan Province, China with rye. Euphytica, 1992, 61, 1-7.	1.2	18
124	Position Effects of Ribosomal RNA Multigene Loci on Meiotic Recombination in Wheat. Genetics, 1998, 149, 1105-1113.	2.9	18
125	Insular Organization of Gene Space in Grass Genomes. PLoS ONE, 2013, 8, e54101.	2.5	16
126	High molecular weight glutenin gene diversity in <i>Aegilops tauschii</i> demonstrates unique origin of superior wheat quality. Communications Biology, 2021, 4, 1242.	4.4	14

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127	Crossability percentages of bread wheat landraces from Shaanxi and Henan provinces, China with rye. <i>Euphytica</i> , 1993, 67, 1-8.	1.2	13
128	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
129	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
130	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
131	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
132	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
133	Identification of candidate chromosome region of Sbwm1 for Soil-borne wheat mosaic virus resistance in wheat. <i>Scientific Reports</i> , 2020, 10, 8119.	3.3	10
134	Wheat Zapper: a flexible online tool for colinearity studies in grass genomes. <i>Functional and Integrative Genomics</i> , 2013, 13, 11-17.	3.5	9
135	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
136	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
137	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
138	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.	2.1	7
139	Chromosomal genomics facilitates fine mapping of a Russian wheat aphid resistance gene. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1373-1383.	3.6	7
140	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
141	Development of a D genome specific marker resource for diploid and hexaploid wheat. <i>BMC Genomics</i> , 2015, 16, 646.	2.8	6
142	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
143	Analysis of <i>Brachypodium</i> genomes with genome-wide optical maps. <i>Genome</i> , 2018, 61, 559-565.	2.0	6
144	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

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145	Crossability percentages of bread wheat collections from Tibet, China with rye. <i>Euphytica</i> , 1993, 70, 127-129.	1.2	4
146	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.	1.8	4
147	Optical Nano-mapping and Analysis of Plant Genomes. <i>Methods in Molecular Biology</i> , 2016, 1429, 103-117.	0.9	4
148	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
149	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> Å— <i>J. regia</i> hybrids. <i>Horticulture Research</i> , 2021, 8, 111.	6.3	4
150	<i>Aegilops tauschii</i> Genome Sequence: A Framework for Meta-analysis of Wheat QTLs. G3: Genes, Genomes, Genetics, 2019, 9, 841-853.	1.8	1
151	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