

Klaus F X Mayer

List of Publications by Year in descending order

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206
papers

54,666
citations

5569

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h-index

2238

201
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233
docs citations

233
times ranked

36006
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 796-815.	13.7	8,336
2	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	2,860
3	The <i>Sorghum bicolor</i> genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	13.7	2,642
4	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	6.0	2,424
5	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. <i>Science</i> , 2008, 319, 64-69.	6.0	1,712
6	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	13.7	1,685
7	The Stem Cell Population of <i>Arabidopsis</i> Shoot Meristems Is Maintained by a Regulatory Loop between the <i>CLAVATA</i> and <i>WUSCHEL</i> Genes. <i>Cell</i> , 2000, 100, 635-644.	13.5	1,521
8	Role of <i>WUSCHEL</i> in Regulating Stem Cell Fate in the <i>Arabidopsis</i> Shoot Meristem. <i>Cell</i> , 1998, 95, 805-815.	13.5	1,487
9	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014, 345, 1251788.	6.0	1,479
10	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	13.7	1,416
11	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
12	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012, 492, 423-427.	13.7	1,204
13	The <i>Medicago</i> genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	13.7	1,166
14	Analysis of the bread wheat genome using whole-genome shotgun sequencing. <i>Nature</i> , 2012, 491, 705-710.	13.7	983
15	Comparative Analysis of the Receptor-Like Kinase Family in <i>Arabidopsis</i> and Rice [W]. <i>Plant Cell</i> , 2004, 16, 1220-1234.	3.1	980
16	The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , 2011, 43, 476-481.	9.4	814
17	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. <i>Science</i> , 2017, 357, 93-97.	6.0	781
18	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	6.0	768

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19	<i>Aegilops tauschii</i> draft genome sequence reveals a gene repertoire for wheat adaptation. <i>Nature</i> , 2013, 496, 91-95.	13.7	714
20	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	6.0	629
21	Green Evolution and Dynamic Adaptations Revealed by Genomes of the Marine Picoeukaryotes <i>Micromonas</i> . <i>Science</i> , 2009, 324, 268-272.	6.0	591
22	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019, 51, 885-895.	9.4	576
23	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	13.7	563
24	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014, 345, 1249721.	6.0	542
25	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	13.7	513
26	Unlocking the Barley Genome by Chromosomal and Comparative Genomics. <i>Plant Cell</i> , 2011, 23, 1249-1263.	3.1	448
27	Sequence and analysis of chromosome 4 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 1999, 402, 769-777.	13.7	413
28	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018, 93, 515-533.	2.8	406
29	An improved genome release (version Mt4.0) for the model legume <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2014, 15, 312.	1.2	381
30	Convergent Targeting of a Common Host Protein-Network by Pathogen Effectors from Three Kingdoms of Life. <i>Cell Host and Microbe</i> , 2014, 16, 364-375.	5.1	367
31	MIPS: analysis and annotation of proteins from whole genomes in 2005. <i>Nucleic Acids Research</i> , 2006, 34, D169-D172.	6.5	348
32	The genome sequence of African rice (<i>Oryza glaberrima</i>) and evidence for independent domestication. <i>Nature Genetics</i> , 2014, 46, 982-988.	9.4	342
33	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , 2018, 361, .	6.0	339
34	Gene selection from microarray data for cancer classification—a machine learning approach. <i>Computational Biology and Chemistry</i> , 2005, 29, 37-46.	1.1	336
35	Mass-spectrometry-based draft of the <i>Arabidopsis</i> proteome. <i>Nature</i> , 2020, 579, 409-414.	13.7	328
36	Genome interplay in the grain transcriptome of hexaploid bread wheat. <i>Science</i> , 2014, 345, 1250091.	6.0	318

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37	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	13.7	314
38	Sequence composition and genome organization of maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14349-14354.	3.3	290
39	Legume genome evolution viewed through the <i>Medicago truncatula</i> and <i>Lotus japonicus</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14959-14964.	3.3	286
40	Deep-sequencing of plant viral small RNAs reveals effective and widespread targeting of viral genomes. <i>Virology</i> , 2009, 392, 203-214.	1.1	274
41	Anchoring and ordering <sc>NGS</sc> contig assemblies by population sequencing (<sc>POPSEQ</sc>). <i>Plant Journal</i> , 2013, 76, 718-727.	2.8	264
42	The <i>Spirodela polyrhiza</i> genome reveals insights into its neotenus reduction fast growth and aquatic lifestyle. <i>Nature Communications</i> , 2014, 5, 3311.	5.8	262
43	Barley whole exome capture: a tool for genomic research in the genus <i>Hordeum</i> and beyond. <i>Plant Journal</i> , 2013, 76, 494-505.	2.8	260
44	A powerful tool for genome analysis in maize: development and evaluation of the high density 600 k SNP genotyping array. <i>BMC Genomics</i> , 2014, 15, 823.	1.2	242
45	Towards a whole-genome sequence for rye (<i>Secale cereale</i> L.). <i>Plant Journal</i> , 2017, 89, 853-869.	2.8	238
46	START lipid/sterol-binding domains are amplified in plants and are predominantly associated with homeodomain transcription factors. <i>Genome Biology</i> , 2004, 5, R41.	13.9	233
47	Tracing the ancestry of modern bread wheats. <i>Nature Genetics</i> , 2019, 51, 905-911.	9.4	230
48	Impact of transposable elements on genome structure and evolution in bread wheat. <i>Genome Biology</i> , 2018, 19, 103.	3.8	226
49	A 4-gigabase physical map unlocks the structure and evolution of the complex genome of <i>Aegilops tauschii</i>, <i>the wheat D-genome progenitor. Proceedings of the National Academy of Sciences of the United States of America</i>, 2013, 110, 7940-7945.	3.3	214
50	MIPS: a database for genomes and protein sequences. <i>Nucleic Acids Research</i> , 1999, 27, 44-48.	6.5	197
51	Reticulate Evolution of the Rye Genome. <i>Plant Cell</i> , 2013, 25, 3685-3698.	3.1	194
52	Frequent Gene Movement and Pseudogene Evolution Is Common to the Large and Complex Genomes of Wheat, Barley, and Their Relatives. <i>Plant Cell</i> , 2011, 23, 1706-1718.	3.1	190
53	Brassinosteroids Are Master Regulators of Gibberellin Biosynthesis in Arabidopsis. <i>Plant Cell</i> , 2015, 27, 2261-2272.	3.1	190
54	Sequence and analysis of chromosome 3 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 820-823.	13.7	188

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55	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	3.1	180
56	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019, 20, 284.	3.8	179
57	Sequence and analysis of chromosome 5 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 823-826.	13.7	175
58	Selfish supernumerary chromosome reveals its origin as a mosaic of host genome and organellar sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13343-13346.	3.3	173
59	A synteny-based draft genome sequence of the forage grass <i>Lolium perenne</i> . <i>Plant Journal</i> , 2015, 84, 816-826.	2.8	166
60	Plant genome sequencing – applications for crop improvement. <i>Current Opinion in Biotechnology</i> , 2014, 26, 31-37.	3.3	164
61	Brassinosteroids participate in the control of basal and acquired freezing tolerance of plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5982-E5991.	3.3	162
62	MIPS Arabidopsisthaliana Database (MAtdB): an integrated biological knowledge resource based on the first complete plant genome. <i>Nucleic Acids Research</i> , 2002, 30, 91-93.	6.5	159
63	Structure and Architecture of the Maize Genome. <i>Plant Physiology</i> , 2005, 139, 1612-1624.	2.3	159
64	Transcriptional Similarities, Dissimilarities, and Conservation of cis-Elements in Duplicated Genes of <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2004, 136, 3009-3022.	2.3	158
65	MIPS: analysis and annotation of genome information in 2007. <i>Nucleic Acids Research</i> , 2007, 36, D196-D201.	6.5	156
66	Footprints of parasitism in the genome of the parasitic flowering plant <i>Cuscuta campestris</i> . <i>Nature Communications</i> , 2018, 9, 2515.	5.8	141
67	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	9.4	138
68	Next-generation sequencing and syntenic integration of flow-sorted arms of wheat chromosome 4A exposes the chromosome structure and gene content. <i>Plant Journal</i> , 2012, 69, 377-386.	2.8	137
69	Impact of natural genetic variation on the transcriptome of autotetraploid <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17809-17814.	3.3	136
70	Red clover (<i>Trifolium pratense</i> L.) draft genome provides a platform for trait improvement. <i>Scientific Reports</i> , 2015, 5, 17394.	1.6	136
71	Gene Content and Virtual Gene Order of Barley Chromosome 1H. <i>Plant Physiology</i> , 2009, 151, 496-505.	2.3	135
72	Genome mapping of seed-borne allergens and immunoresponsive proteins in wheat. <i>Science Advances</i> , 2018, 4, eaar8602.	4.7	130

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73	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	3.8	125
74	Snipping polymorphisms from large EST collections in barley (<i>Hordeum vulgare</i> L.). <i>Molecular Genetics and Genomics</i> , 2003, 270, 24-33.	1.0	116
75	Crosstalk and differential response to abiotic and biotic stressors reflected at the transcriptional level of effector genes from secondary metabolism. <i>Plant Molecular Biology</i> , 2004, 54, 817-835.	2.0	111
76	From RNA-seq to large-scale genotyping - genomics resources for rye (<i>Secale cereale</i> L.). <i>BMC Plant Biology</i> , 2011, 11, 131.	1.6	109
77	Uneven chromosome contraction and expansion in the maize genome. <i>Genome Research</i> , 2006, 16, 1241-1251.	2.4	105
78	Quantitative trait loci-dependent analysis of a gene co-expression network associated with Fusarium head blight resistance in bread wheat (<i>Triticum aestivum</i> L.). <i>BMC Genomics</i> , 2013, 14, 728.	1.2	105
79	Extensive signal integration by the phytohormone protein network. <i>Nature</i> , 2020, 583, 271-276.	13.7	104
80	Modulation of Ambient Temperature-Dependent Flowering in <i>Arabidopsis thaliana</i> by Natural Variation of FLOWERING LOCUS M. <i>PLoS Genetics</i> , 2015, 11, e1005588.	1.5	103
81	Suppressed recombination and unique candidate genes in the divergent haplotype encoding Fhb1, a major Fusarium head blight resistance locus in wheat. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1607-1623.	1.8	103
82	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
83	Mechanical behaviour and failure modes in the Whakaari (White Island volcano) hydrothermal system, New Zealand. <i>Journal of Volcanology and Geothermal Research</i> , 2015, 295, 26-42.	0.8	101
84	Understanding the Molecular Basis of Salt Sequestration in Epidermal Bladder Cells of <i>Chenopodium quinoa</i> . <i>Current Biology</i> , 2018, 28, 3075-3085.e7.	1.8	98
85	The <i>Cardamine hirsuta</i> genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , 2016, 2, 16167.	4.7	90
86	The complete nucleotide sequences of the five genetically distinct plastid genomes of <i>Oenothera</i> , subsection <i>Oenothera</i> : I. Sequence evaluation and plastome evolution. <i>Nucleic Acids Research</i> , 2008, 36, 2366-2378.	6.5	88
87	Functional Characterization of Two Clusters of <i>Brachypodium distachyon</i> UDP-Glycosyltransferases Encoding Putative Deoxynivalenol Detoxification Genes. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 781-792.	1.4	85
88	European maize genomes highlight intraspecies variation in repeat and gene content. <i>Nature Genetics</i> , 2020, 52, 950-957.	9.4	84
89	A first genetic map of date palm (<i>Phoenix dactylifera</i>) reveals long-range genome structure conservation in the palms. <i>BMC Genomics</i> , 2014, 15, 285.	1.2	83
90	MIPS <i>Arabidopsis thaliana</i> Database (MATDB): an integrated biological knowledge resource for plant genomics. <i>Nucleic Acids Research</i> , 2004, 32, 373D-376.	6.5	82

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91	Characterization of the Maize Endosperm Transcriptome and Its Comparison to the Rice Genome. <i>Genome Research</i> , 2004, 14, 1932-1937.	2.4	80
92	PGSB PlantsDB: updates to the database framework for comparative plant genome research. <i>Nucleic Acids Research</i> , 2016, 44, D1141-D1147.	6.5	79
93	MIPS: curated databases and comprehensive secondary data resources in 2010. <i>Nucleic Acids Research</i> , 2011, 39, D220-D224.	6.5	77
94	A Sequence-Ready Physical Map of Barley Anchored Genetically by Two Million Single-Nucleotide Polymorphisms. <i>Plant Physiology</i> , 2014, 164, 412-423.	2.3	77
95	Bacteria-Triggered Systemic Immunity in Barley Is Associated with WRKY and ETHYLENE RESPONSIVE FACTORS But Not with Salicylic Acid. <i>Plant Physiology</i> , 2014, 166, 2133-2151.	2.3	76
96	The Perennial Ryegrass GenomeZipper: Targeted Use of Genome Resources for Comparative Grass Genomics. <i>Plant Physiology</i> , 2013, 161, 571-582.	2.3	75
97	Expressed sequence tag analysis in <i>Cycas</i> , the most primitive living seed plant. <i>Genome Biology</i> , 2003, 4, R78.	13.9	74
98	TriAnnot: A Versatile and High Performance Pipeline for the Automated Annotation of Plant Genomes. <i>Frontiers in Plant Science</i> , 2012, 3, 5.	1.7	73
99	The mosaic oat genome gives insights into a uniquely healthy cereal crop. <i>Nature</i> , 2022, 606, 113-119.	13.7	70
100	De novo 454 sequencing of barcoded BAC pools for comprehensive gene survey and genome analysis in the complex genome of barley. <i>BMC Genomics</i> , 2009, 10, 547.	1.2	69
101	Meta-Analysis of Retrograde Signaling in <i>Arabidopsis thaliana</i> Reveals a Core Module of Genes Embedded in Complex Cellular Signaling Networks. <i>Molecular Plant</i> , 2014, 7, 1167-1190.	3.9	69
102	Genes on B chromosomes: Old questions revisited with new tools. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2015, 1849, 64-70.	0.9	68
103	Sequence and analysis of the <i>Arabidopsis</i> genome. <i>Current Opinion in Plant Biology</i> , 2001, 4, 105-110.	3.5	66
104	Molecular characterisation of the STRUBBELIG-RECEPTOR FAMILY of genes encoding putative leucine-rich repeat receptor-like kinases in <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2007, 7, 16.	1.6	64
105	Conservation of Microstructure between a Sequenced Region of the Genome of Rice and Multiple Segments of the Genome of <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2001, 11, 1167-1174.	2.4	64
106	Sequence-Based Analysis of Translocations and Inversions in Bread Wheat (<i>Triticum aestivum</i> L.). <i>PLoS ONE</i> , 2013, 8, e79329.	1.1	62
107	DroughtDB: an expert-curated compilation of plant drought stress genes and their homologs in nine species. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav046.	1.4	62
108	The desert plant <i>Phoenix dactylifera</i> closes stomata via nitrate-regulated SLAC1 anion channel. <i>New Phytologist</i> , 2017, 216, 150-162.	3.5	62

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109	Mercury-induced genes in <i>Arabidopsis thaliana</i> : identification of induced genes upon long-term mercuric ion exposure. <i>Plant, Cell and Environment</i> , 2001, 24, 1227-1234.	2.8	58
110	Molecular and Immunological Characterization of Ragweed (<i>Ambrosia artemisiifolia</i> L.) Pollen after Exposure of the Plants to Elevated Ozone over a Whole Growing Season. <i>PLoS ONE</i> , 2013, 8, e61518.	1.1	58
111	A Genome-Wide Survey of Date Palm Cultivars Supports Two Major Subpopulations in <i>Phoenix dactylifera</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1429-1438.	0.8	58
112	Fifteen Million Years of Evolution in the <i>Oryza</i> Genus Shows Extensive Gene Family Expansion. <i>Molecular Plant</i> , 2014, 7, 642-656.	3.9	54
113	Chromosome-scale comparative sequence analysis unravels molecular mechanisms of genome dynamics between two wheat cultivars. <i>Genome Biology</i> , 2018, 19, 104.	3.8	54
114	Exon discovery by genomic sequence alignment. <i>Bioinformatics</i> , 2002, 18, 777-787.	1.8	51
115	Extensive and Biased Intergenomic Nonreciprocal DNA Exchanges Shaped a Nascent Polyploid Genome, <i>Gossypium</i> (Cotton). <i>Genetics</i> , 2014, 197, 1153-1163.	1.2	51
116	Separating the wheat from the chaff – a strategy to utilize plant genetic resources from ex situ genebanks. <i>Scientific Reports</i> , 2014, 4, 5231.	1.6	51
117	A comprehensive study of the genomic differentiation between temperate Dent and Flint maize. <i>Genome Biology</i> , 2016, 17, 137.	3.8	51
118	DNA transposon activity is associated with increased mutation rates in genes of rice and other grasses. <i>Nature Communications</i> , 2016, 7, 12790.	5.8	51
119	Large-Scale cis-Element Detection by Analysis of Correlated Expression and Sequence Conservation between <i>Arabidopsis</i> and <i>Brassica oleracea</i> . <i>Plant Physiology</i> , 2006, 142, 1589-1602.	2.3	50
120	Computational aspects underlying genome to phenome analysis in plants. <i>Plant Journal</i> , 2019, 97, 182-198.	2.8	50
121	MicroRNAs coordinately regulate protein complexes. <i>BMC Systems Biology</i> , 2011, 5, 136.	3.0	49
122	The repetitive landscape of the 5100 Mbp barley genome. <i>Mobile DNA</i> , 2017, 8, 22.	1.3	49
123	<i>GABI</i> – <i>DUPLO</i> : a collection of double mutants to overcome genetic redundancy in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2013, 75, 157-171.	2.8	48
124	Natural haplotypes of FLM non-coding sequences fine-tune flowering time in ambient spring temperatures in <i>Arabidopsis</i> . <i>ELife</i> , 2017, 6, .	2.8	48
125	MIPSPplantsDB–plant database resource for integrative and comparative plant genome research. <i>Nucleic Acids Research</i> , 2007, 35, D834-D840.	6.5	47
126	Experimental constraints on phreatic eruption processes at Whakaari (White Island volcano). <i>Journal of Volcanology and Geothermal Research</i> , 2015, 302, 150-162.	0.8	47

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127	Genome sequences of three <i>Aegilops</i> species of the section Sitopsis reveal phylogenetic relationships and provide resources for wheat improvement. <i>Plant Journal</i> , 2022, 110, 179-192.	2.8	46
128	The Complete Nucleotide Sequences of the 5 Genetically Distinct Plastid Genomes of <i>Oenothera</i> , Subsection <i>Oenothera</i> : II. A Microevolutionary View Using Bioinformatics and Formal Genetic Data. <i>Molecular Biology and Evolution</i> , 2008, 25, 2019-2030.	3.5	45
129	A high density physical map of chromosome 1BL supports evolutionary studies, map-based cloning and sequencing in wheat. <i>Genome Biology</i> , 2013, 14, R64.	3.8	45
130	Whole-genome profiling and shotgun sequencing delivers an anchored, gene-decorated, physical map assembly of bread wheat chromosome 6A. <i>Plant Journal</i> , 2014, 79, 334-347.	2.8	45
131	Joint Transcriptomic and Metabolomic Analyses Reveal Changes in the Primary Metabolism and Imbalances in the Subgenome Orchestration in the Bread Wheat Molecular Response to <i>Fusarium graminearum</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2579-2592.	0.8	45
132	Sputnik: a database platform for comparative plant genomics. <i>Nucleic Acids Research</i> , 2003, 31, 128-132.	6.5	44
133	Examining the Transcriptional Response in Wheat <i>Fhb1</i> Near-Isogenic Lines to <i>Fusarium graminearum</i> Infection and Deoxynivalenol Treatment. <i>Plant Genome</i> , 2016, 9, plantgenome2015.05.0032.	1.6	44
134	Evidence for a Contribution of ALA Synthesis to Plastid-To-Nucleus Signaling. <i>Frontiers in Plant Science</i> , 2012, 3, 236.	1.7	41
135	Hidden variation in polyploid wheat drives local adaptation. <i>Genome Research</i> , 2018, 28, 1319-1332.	2.4	41
136	Genome-Wide in Silico Mapping of Scaffold/Matrix Attachment Regions in <i>Arabidopsis</i> Suggests Correlation of Intragenic Scaffold/Matrix Attachment Regions with Gene Expression. <i>Plant Physiology</i> , 2004, 135, 715-722.	2.3	40
137	PlantMarkers—a database of predicted molecular markers from plants. <i>Nucleic Acids Research</i> , 2004, 33, D628-D632.	6.5	40
138	Intracompartmental and Intercompartmental Transcriptional Networks Coordinate the Expression of Genes for Organellar Functions. <i>Plant Physiology</i> , 2011, 157, 386-404.	2.3	40
139	Genetic Analysis of <i>DEFECTIVE KERNEL1</i> Loop Function in Three-Dimensional Body Patterning in <i>Physcomitrella patens</i> . <i>Plant Physiology</i> , 2014, 166, 903-919.	2.3	40
140	Functional Diversification within the Family of B-GATA Transcription Factors through the Leucine-Leucine-Methionine Domain. <i>Plant Physiology</i> , 2014, 166, 293-305.	2.3	40
141	Slicing the wheat genome. <i>Science</i> , 2014, 345, 285-287.	6.0	40
142	Integrating cereal genomics to support innovation in the Triticeae. <i>Functional and Integrative Genomics</i> , 2012, 12, 573-583.	1.4	39
143	Identification of Early Nuclear Target Genes of Plastidial Redox Signals that Trigger the Long-Term Response of <i>Arabidopsis</i> to Light Quality Shifts. <i>Molecular Plant</i> , 2015, 8, 1237-1252.	3.9	38
144	Genetic and genomic analysis of legume flowers and seeds. <i>Current Opinion in Plant Biology</i> , 2006, 9, 133-141.	3.5	35

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145	Insights into the evolution of symbiosis gene copy number and distribution from a chromosome-scale <i>Lotus japonicus</i> Cifu genome sequence. <i>DNA Research</i> , 2020, 27, .	1.5	35
146	How can we deliver the large plant genomes? Strategies and perspectives. <i>Current Opinion in Plant Biology</i> , 2002, 5, 173-177.	3.5	34
147	Characterization of Reflector Types by Phase-Sensitive Ultrasonic Data Processing and Imaging. <i>Journal of Nondestructive Evaluation</i> , 2008, 27, 35-45.	1.1	34
148	Evidence for an ancient chromosomal duplication in <i>Arabidopsis thaliana</i> by sequencing and analyzing a 400-kb contig at the <i>APETALA2</i> locus on chromosome 41. <i>FEBS Letters</i> , 1999, 445, 237-245.	1.3	33
149	Time-course expression QTL atlas of the global transcriptional response of wheat to <i>Fusarium graminearum</i> . <i>Plant Biotechnology Journal</i> , 2017, 15, 1453-1464.	4.1	32
150	Spatiotemporal Expression Control Correlates with Intragenic Scaffold Matrix Attachment Regions (S/MARs) in <i>Arabidopsis thaliana</i> . <i>PLoS Computational Biology</i> , 2006, 2, e21.	1.5	29
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