

Klaus F X Mayer

List of Publications by Year in descending order

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206
papers

54,666
citations

5569

82
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2238

201
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233
all docs

233
docs citations

233
times ranked

36006
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	Genome sequences of three <i>Aegilops</i> species of the section <i>Sitopsis</i> reveal phylogenetic relationships and provide resources for wheat improvement. <i>Plant Journal</i> , 2022, 110, 179-192.	2.8	46
3	The Barley and Wheat Pan-Genomes. <i>Methods in Molecular Biology</i> , 2022, 2443, 147-159.	0.4	2
4	Stalk cell polar ion transport provide for bladder-based salinity tolerance in <i>Chenopodium quinoa</i> . <i>New Phytologist</i> , 2022, 235, 1822-1835.	3.5	8
5	The mosaic oat genome gives insights into a uniquely healthy cereal crop. <i>Nature</i> , 2022, 606, 113-119.	13.7	70
6	PYL8 ABA receptors of <i>Phoenix dactylifera</i> play a crucial role in response to abiotic stress and are stabilized by ABA. <i>Journal of Experimental Botany</i> , 2021, 72, 757-774.	2.4	10
7	De Novo Genome Assembly of the Japanese Wheat Cultivar Norin 61 Highlights Functional Variation in Flowering Time and Fusarium-Resistant Genes in East Asian Genotypes. <i>Plant and Cell Physiology</i> , 2021, 62, 8-27.	1.5	16
8	Merging Genomics and Transcriptomics for Predicting Fusarium Head Blight Resistance in Wheat. <i>Genes</i> , 2021, 12, 114.	1.0	10
9	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	9.4	138
10	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	3.1	180
11	Protein expression plasticity contributes to heat and drought tolerance of date palm. <i>Oecologia</i> , 2021, 197, 903-919.	0.9	17
12	Fusarium head blight resistance in European winter wheat: insights from genome-wide transcriptome analysis. <i>BMC Genomics</i> , 2021, 22, 470.	1.2	20
13	<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
14	The Gene and Repetitive Element Landscape of the Rye Genome. <i>Compendium of Plant Genomes</i> , 2021, , 117-133.	0.3	0
15	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
16	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	13.7	314
17	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	13.7	513
18	Insights into the evolution of symbiosis gene copy number and distribution from a chromosome-scale <i>Lotus japonicus</i> Gifu genome sequence. <i>DNA Research</i> , 2020, 27, .	1.5	35

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19	Current status of the multinational Arabidopsis community. <i>Plant Direct</i> , 2020, 4, e00248.	0.8	13
20	European maize genomes highlight intraspecies variation in repeat and gene content. <i>Nature Genetics</i> , 2020, 52, 950-957.	9.4	84
21	Proteomic and transcriptomic profiling of aerial organ development in Arabidopsis. <i>Scientific Data</i> , 2020, 7, 334.	2.4	20
22	Mass-spectrometry-based draft of the Arabidopsis proteome. <i>Nature</i> , 2020, 579, 409-414.	13.7	328
23	Extensive signal integration by the phytohormone protein network. <i>Nature</i> , 2020, 583, 271-276.	13.7	104
24	Tracing the ancestry of modern bread wheats. <i>Nature Genetics</i> , 2019, 51, 905-911.	9.4	230
25	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019, 51, 885-895.	9.4	576
26	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019, 20, 284.	3.8	179
27	Computational aspects underlying genome to phenome analysis in plants. <i>Plant Journal</i> , 2019, 97, 182-198.	2.8	50
28	The Systems Architecture of Molecular Memory in Poplar after Abiotic Stress. <i>Plant Cell</i> , 2019, 31, 346-367.	3.1	29
29	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
30	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
31	Analysis of Stress Resistance Using Next Generation Techniques. <i>Agronomy</i> , 2018, 8, 130.	1.3	12
32	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , 2018, 361, .	6.0	339
33	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
34	Genome mapping of seed-borne allergens and immunoresponsive proteins in wheat. <i>Science Advances</i> , 2018, 4, eaar8602.	4.7	130
35	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	6.0	768
36	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	6.0	2,424

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37	Impact of transposable elements on genome structure and evolution in bread wheat. <i>Genome Biology</i> , 2018, 19, 103.	3.8	226
38	Hidden variation in polyploid wheat drives local adaptation. <i>Genome Research</i> , 2018, 28, 1319-1332.	2.4	41
39	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
40	The pseudogenes of barley. <i>Plant Journal</i> , 2018, 93, 502-514.	2.8	14
41	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
42	From plant genomes to phenotypes. <i>Journal of Biotechnology</i> , 2017, 261, 46-52.	1.9	29
43	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
44	PGSB/MIPS PlantsDB Database Framework for the Integration and Analysis of Plant Genome Data. <i>Methods in Molecular Biology</i> , 2017, 1533, 33-44.	0.4	8
45	Light and Plastid Signals Regulate Different Sets of Genes in the Albino Mutant Pap7-1. <i>Plant Physiology</i> , 2017, 175, 1203-1219.	2.3	29
46	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. <i>Science</i> , 2017, 357, 93-97.	6.0	781
47	The desert plant <i>Phoenix dactylifera</i> closes stomata via nitrate-regulated <i>SLAC1</i> anion channel. <i>New Phytologist</i> , 2017, 216, 150-162.	3.5	62
48	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	13.7	563
49	Bioinformatics in the plant genomic and phenomic domain: The German contribution to resources, services and perspectives. <i>Journal of Biotechnology</i> , 2017, 261, 37-45.	1.9	12
50	Towards a whole-genome sequence for rye (<i>Secale cereale</i> L.). <i>Plant Journal</i> , 2017, 89, 853-869.	2.8	238
51	The repetitive landscape of the 5100 Mbp barley genome. <i>Mobile DNA</i> , 2017, 8, 22.	1.3	49
52	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
53	transPLANT Resources for Triticeae Genomic Data. <i>Plant Genome</i> , 2016, 9, plantgenome2015.06.0038.	1.6	8
54	Identification and Characterization of Carboxylesterases from <i>Brachypodium distachyon</i> Deacetylating Trichothecene Mycotoxins. <i>Toxins</i> , 2016, 8, 6.	1.5	17

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55	A comprehensive study of the genomic differentiation between temperate Dent and Flint maize. <i>Genome Biology</i> , 2016, 17, 137.	3.8	51
56	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
57	Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016, 14, 1511-1522.	4.1	20
58	Ribosome quality control is a central protection mechanism for yeast exposed to deoxynivalenol and trichothecin. <i>BMC Genomics</i> , 2016, 17, 417.	1.2	23
59	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
60	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
61	The <i>Cardamine hirsuta</i> genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , 2016, 2, 16167.	4.7	90
62	Suppressed recombination and unique candidate genes in the divergent haplotype encoding <i>Fhb1</i> , a major <i>Fusarium</i> head blight resistance locus in wheat. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1607-1623.	1.8	103
63	PGSB PlantsDB: updates to the database framework for comparative plant genome research. <i>Nucleic Acids Research</i> , 2016, 44, D1141-D1147.	6.5	79
64	The big five of the monocot genomes. <i>Current Opinion in Plant Biology</i> , 2016, 30, 33-40.	3.5	10
65	PGSB/MIPS Plant Genome Information Resources and Concepts for the Analysis of Complex Grass Genomes. <i>Methods in Molecular Biology</i> , 2016, 1374, 165-186.	0.4	2
66	Chloroplast phylogeny of <i>Triticum/Aegilops</i> species is not incongruent with an ancient homoploid hybrid origin of the ancestor of the bread wheat D genome. <i>New Phytologist</i> , 2015, 208, 9-10.	3.5	28
67	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
68	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
69	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
70	Assessing the Barley Genome Zipper and Genomic Resources for Breeding Purposes. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.06.0045.	1.6	10
71	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
72	High-throughput physical map anchoring via BAC-pool sequencing. <i>BMC Plant Biology</i> , 2015, 15, 99.	1.6	8

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73	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
74	Parallel Selection Revealed by Population Sequencing in Chicken. <i>Genome Biology and Evolution</i> , 2015, 7, 3299-3306.	1.1	25
75	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
76	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
77	Barley: From Brittle to Stable Harvest. <i>Cell</i> , 2015, 162, 469-471.	13.5	10
78	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
79	Comparative transcriptome analysis within the <i>Lolium/Festuca</i> species complex reveals high sequence conservation. <i>BMC Genomics</i> , 2015, 16, 249.	1.2	24
80	Brassinosteroids Are Master Regulators of Gibberellin Biosynthesis in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2015, 27, 2261-2272.	3.1	190
81	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
82	New insights into the wheat chromosome 4D structure and virtual gene order, revealed by survey pyrosequencing. <i>Plant Science</i> , 2015, 233, 200-212.	1.7	20
83	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
84	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
85	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
86	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
87	chromoWIZ: a web tool to query and visualize chromosome-anchored genes from cereal and model genomes. <i>BMC Plant Biology</i> , 2014, 14, 348.	1.6	7
88	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
89	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
90	Plant genome sequencing – applications for crop improvement. <i>Current Opinion in Biotechnology</i> , 2014, 26, 31-37.	3.3	164

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91	High-resolution mapping of the barley Ryd3 locus controlling tolerance to BYDV. <i>Molecular Breeding</i> , 2014, 33, 477-488.	1.0	13
92	RNASeqExpressionBrowser—a web interface to browse and visualize high-throughput expression data. <i>Bioinformatics</i> , 2014, 30, 2519-2520.	1.8	23
93	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
94	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
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	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
97	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
98	Slicing the wheat genome. <i>Science</i> , 2014, 345, 285-287.	6.0	40
99	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
100	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
101	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014, 345, 1249721.	6.0	542
102	Genome interplay in the grain transcriptome of hexaploid bread wheat. <i>Science</i> , 2014, 345, 1250091.	6.0	318
103	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	6.0	629
104	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
105	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
106	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
107	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
108	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	3.8	125

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109	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
110	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
111	Analysing complex Triticeae genomes – concepts and strategies. <i>Plant Methods</i> , 2013, 9, 35.	1.9	19
112	Conserved synteny-based anchoring of the barley genome physical map. <i>Functional and Integrative Genomics</i> , 2013, 13, 339-350.	1.4	10
113	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <i>Plant Journal</i> , 2013, 76, 718-727.	2.8	264
114	<i>Aegilops tauschii</i> draft genome sequence reveals a gene repertoire for wheat adaptation. <i>Nature</i> , 2013, 496, 91-95.	13.7	714
115	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
116	Genomics-based high-resolution mapping of the BaMMV/BaYMV resistance gene <i>rym11</i> in barley (<i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 1201-1212.	1.8	28
117	GABI – DUPLO: a collection of double mutants to overcome genetic redundancy in <i>A. rabidopsis thaliana</i> . <i>Plant Journal</i> , 2013, 75, 157-171.	2.8	48
118	Flow Sorting and Sequencing Meadow Fescue Chromosome 4F. <i>Plant Physiology</i> , 2013, 163, 1323-1337.	2.3	27
119	Reticulate Evolution of the Rye Genome. <i>Plant Cell</i> , 2013, 25, 3685-3698.	3.1	194
120	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
121	The Perennial Ryegrass GenomeZipper: Targeted Use of Genome Resources for Comparative Grass Genomics. <i>Plant Physiology</i> , 2013, 161, 571-582.	2.3	75
122	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
123	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
124	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
125	Evidence for a Contribution of ALA Synthesis to Plastid-To-Nucleus Signaling. <i>Frontiers in Plant Science</i> , 2012, 3, 236.	1.7	41
126	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

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127	Analysis of the bread wheat genome using whole-genome shotgun sequencing. <i>Nature</i> , 2012, 491, 705-710.	13.7	983
128	Integrating cereal genomics to support innovation in the Triticeae. <i>Functional and Integrative Genomics</i> , 2012, 12, 573-583.	1.4	39
129	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	13.7	1,416
130	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
131	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	2,860
132	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
133	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
134	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
135	The <i>Medicago</i> genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	13.7	1,166
136	Unlocking the Barley Genome by Chromosomal and Comparative Genomics. <i>Plant Cell</i> , 2011, 23, 1249-1263.	3.1	448
137	Exploring the genomes: From <i>Arabidopsis</i> to crops. <i>Journal of Plant Physiology</i> , 2011, 168, 3-8.	1.6	15
138	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
139	Intracompartamental and Intercompartmental Transcriptional Networks Coordinate the Expression of Genes for Organellar Functions. <i>Plant Physiology</i> , 2011, 157, 386-404.	2.3	40
140	Comparative sequence analysis of <i>VRN1</i> alleles of <i>Lolium perenne</i> with the co-linear regions in barley, wheat, and rice. <i>Molecular Genetics and Genomics</i> , 2011, 286, 433-447.	1.0	25
141	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
142	MicroRNAs coordinately regulate protein complexes. <i>BMC Systems Biology</i> , 2011, 5, 136.	3.0	49
143	Sequencing of BAC pools by different next generation sequencing platforms and strategies. <i>BMC Research Notes</i> , 2011, 4, 411.	0.6	13
144	MIPS: curated databases and comprehensive secondary data resources in 2010. <i>Nucleic Acids Research</i> , 2011, 39, D220-D224.	6.5	77

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145	The Non-coding Landscape of the Genome of <i>Arabidopsis thaliana</i> . , 2011, , 67-121.		0
146	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	13.7	1,685
147	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
148	Gene Content and Virtual Gene Order of Barley Chromosome 1H. <i>Plant Physiology</i> , 2009, 151, 496-505.	2.3	135
149	Discovery of cis-elements between sorghum and rice using co-expression and evolutionary conservation. <i>BMC Genomics</i> , 2009, 10, 284.	1.2	26
150	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
151	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
152	The <i>Sorghum bicolor</i> genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	13.7	2,642
153	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
154	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
155	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
156	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
157	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
158	MIPSPplantsDB—plant database resource for integrative and comparative plant genome research. <i>Nucleic Acids Research</i> , 2007, 35, D834-D840.	6.5	47
159	MIPS: analysis and annotation of genome information in 2007. <i>Nucleic Acids Research</i> , 2007, 36, D196-D201.	6.5	156
160	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
161	Apollo2Go: a web service adapter for the Apollo genome viewer to enable distributed genome annotation. <i>BMC Bioinformatics</i> , 2007, 8, 320.	1.2	5
162	MIPS Plant Genome Information Resources. , 2007, 406, 137-159.		6

#	ARTICLE	IF	CITATIONS
163	Significant sequence similarities in promoters and precursors of Arabidopsis thaliana non-conserved microRNAs. <i>Bioinformatics</i> , 2006, 22, 2585-2589.	1.8	27
164	Genetic and genomic analysis of legume flowers and seeds. <i>Current Opinion in Plant Biology</i> , 2006, 9, 133-141.	3.5	35
165	MIPS: analysis and annotation of proteins from whole genomes in 2005. <i>Nucleic Acids Research</i> , 2006, 34, D169-D172.	6.5	348
166	Spatiotemporal Expression Control Correlates with Intragenic Scaffold Matrix Attachment Regions (S/MARs) in Arabidopsis thaliana. <i>PLoS Computational Biology</i> , 2006, 2, e21.	1.5	29
167	Uneven chromosome contraction and expansion in the maize genome. <i>Genome Research</i> , 2006, 16, 1241-1251.	2.4	105
168	Large-Scale cis-Element Detection by Analysis of Correlated Expression and Sequence Conservation between Arabidopsis and Brassica oleracea. <i>Plant Physiology</i> , 2006, 142, 1589-1602.	2.3	50
169	Legume genome evolution viewed through the Medicago truncatula and Lotus japonicus genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14959-14964.	3.3	286
170	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
171	cDNA array analysis of mercury- and ozone-induced genes in Arabidopsis thaliana. <i>Acta Physiologiae Plantarum</i> , 2005, 27, 45-51.	1.0	6
172	CREDO: a web-based tool for computational detection of conserved sequence motifs in noncoding sequences. <i>Bioinformatics</i> , 2005, 21, 4304-4306.	1.8	4
173	Munich Information Center for Protein Sequences Plant Genome Resources. A Framework for Integrative and Comparative Analyses. <i>Plant Physiology</i> , 2005, 138, 1301-1309.	2.3	13
174	Structure and Architecture of the Maize Genome. <i>Plant Physiology</i> , 2005, 139, 1612-1624.	2.3	159
175	Genome-Wide in Silico Mapping of Scaffold/Matrix Attachment Regions in Arabidopsis Suggests Correlation of Intragenic Scaffold/Matrix Attachment Regions with Gene Expression. <i>Plant Physiology</i> , 2004, 135, 715-722.	2.3	40
176	Comparative Analysis of the Receptor-Like Kinase Family in Arabidopsis and Rice [W]. <i>Plant Cell</i> , 2004, 16, 1220-1234.	3.1	980
177	PlantMarkers—a database of predicted molecular markers from plants. <i>Nucleic Acids Research</i> , 2004, 33, D628-D632.	6.5	40
178	Transcriptional Similarities, Dissimilarities, and Conservation of cis-Elements in Duplicated Genes of Arabidopsis. <i>Plant Physiology</i> , 2004, 136, 3009-3022.	2.3	158
179	Characterization of the Maize Endosperm Transcriptome and Its Comparison to the Rice Genome. <i>Genome Research</i> , 2004, 14, 1932-1937.	2.4	80
180	MIPS Arabidopsis thaliana Database (MATDB): an integrated biological knowledge resource for plant genomics. <i>Nucleic Acids Research</i> , 2004, 32, 373D-376.	6.5	82

#	ARTICLE	IF	CITATIONS
181	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
182	The PlaNet Consortium: A Network of European Plant Databases Connecting Plant Genome Data in an Integrated Biological Knowledge Resource. <i>Comparative and Functional Genomics</i> , 2004, 5, 184-189.	2.0	6
183	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
184	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
185	The Arabidopsis Genome and Its Use in Cereal Genomics. , 2004, , 515-534.		0
186	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
187	Expressed sequence tag analysis in <i>Cycas</i> , the most primitive living seed plant. <i>Genome Biology</i> , 2003, 4, R78.	13.9	74
188	Sputnik: a database platform for comparative plant genomics. <i>Nucleic Acids Research</i> , 2003, 31, 128-132.	6.5	44
189	MOsDB: an integrated information resource for rice genomics. <i>Nucleic Acids Research</i> , 2003, 31, 190-192.	6.5	27
190	Exon discovery by genomic sequence alignment. <i>Bioinformatics</i> , 2002, 18, 777-787.	1.8	51
191	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
192	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
193	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
194	Sequence and analysis of the Arabidopsis genome. <i>Current Opinion in Plant Biology</i> , 2001, 4, 105-110.	3.5	66
195	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
196	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	8
197	Sequence and analysis of chromosome 5 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 823-826.	13.7	175
198	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 796-815.	13.7	8,336

#	ARTICLE	IF	CITATIONS
199	Sequence and analysis of chromosome 3 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 820-823.	13.7	188
200	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
201	MIPS: a database for genomes and protein sequences. <i>Nucleic Acids Research</i> , 1999, 27, 44-48.	6.5	197
202	Sequence and analysis of chromosome 4 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 1999, 402, 769-777.	13.7	413
203	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
204	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
205	Cell fate regulation in the shoot meristem. <i>Seminars in Cell and Developmental Biology</i> , 1998, 9, 195-200.	2.3	19
206	Differential and complementary selection of heterotic groups. <i>Nature Plants</i> , 0, , .	4.7	0