

Klaus F X Mayer

List of Publications by Year in descending order

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206
papers

54,666
citations

5574

82
h-index

2243

201
g-index

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.	17.5	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.	5.7	46
3	The Barley and Wheat Pan-Genomes. <i>Methods in Molecular Biology</i> , 2022, 2443, 147-159.	0.9	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.	7.3	8
5	The mosaic oat genome gives insights into a uniquely healthy cereal crop. <i>Nature</i> , 2022, 606, 113-119.	27.8	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.	4.8	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.	3.1	16
8	Merging Genomics and Transcriptomics for Predicting Fusarium Head Blight Resistance in Wheat. <i>Genes</i> , 2021, 12, 114.	2.4	10
9	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	21.4	138
10	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	6.6	180
11	Protein expression plasticity contributes to heat and drought tolerance of date palm. <i>Oecologia</i> , 2021, 197, 903-919.	2.0	17
12	Fusarium head blight resistance in European winter wheat: insights from genome-wide transcriptome analysis. <i>BMC Genomics</i> , 2021, 22, 470.	2.8	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, .	1.8	19
14	The Gene and Repetitive Element Landscape of the Rye Genome. <i>Compendium of Plant Genomes</i> , 2021, , 117-133.	0.5	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.	4.4	14
16	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	27.8	314
17	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	27.8	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, .	3.4	35

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19	Current status of the multinational Arabidopsis community. Plant Direct, 2020, 4, e00248.	1.9	13
20	European maize genomes highlight intraspecies variation in repeat and gene content. Nature Genetics, 2020, 52, 950-957.	21.4	84
21	Proteomic and transcriptomic profiling of aerial organ development in Arabidopsis. Scientific Data, 2020, 7, 334.	5.3	20
22	Mass-spectrometry-based draft of the Arabidopsis proteome. Nature, 2020, 579, 409-414.	27.8	328
23	Extensive signal integration by the phytohormone protein network. Nature, 2020, 583, 271-276.	27.8	104
24	Tracing the ancestry of modern bread wheats. Nature Genetics, 2019, 51, 905-911.	21.4	230
25	Durum wheat genome highlights past domestication signatures and future improvement targets. Nature Genetics, 2019, 51, 885-895.	21.4	576
26	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. Genome Biology, 2019, 20, 284.	8.8	179
27	Computational aspects underlying genome to phenome analysis in plants. Plant Journal, 2019, 97, 182-198.	5.7	50
28	The Systems Architecture of Molecular Memory in Poplar after Abiotic Stress. Plant Cell, 2019, 31, 346-367.	6.6	29
29	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. Plant Journal, 2018, 93, 515-533.	5.7	406
30	Understanding the Molecular Basis of Salt Sequestration in Epidermal Bladder Cells of Chenopodium quinoa. Current Biology, 2018, 28, 3075-3085.e7.	3.9	98
31	Analysis of Stress Resistance Using Next Generation Techniques. Agronomy, 2018, 8, 130.	3.0	12
32	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. Science, 2018, 361, .	12.6	339
33	Footprints of parasitism in the genome of the parasitic flowering plant Cuscuta campestris. Nature Communications, 2018, 9, 2515.	12.8	141
34	Genome mapping of seed-borne allergens and immunoresponsive proteins in wheat. Science Advances, 2018, 4, eaar8602.	10.3	130
35	The transcriptional landscape of polyploid wheat. Science, 2018, 361, .	12.6	768
36	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	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.	8.8	226
38	Hidden variation in polyploid wheat drives local adaptation. <i>Genome Research</i> , 2018, 28, 1319-1332.	5.5	41
39	Chromosome-scale comparative sequence analysis unravels molecular mechanisms of genome dynamics between two wheat cultivars. <i>Genome Biology</i> , 2018, 19, 104.	8.8	54
40	The pseudogenes of barley. <i>Plant Journal</i> , 2018, 93, 502-514.	5.7	14
41	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	27.8	1,365
42	From plant genomes to phenotypes. <i>Journal of Biotechnology</i> , 2017, 261, 46-52.	3.8	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.	8.3	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.	0.9	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.	4.8	29
46	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. <i>Science</i> , 2017, 357, 93-97.	12.6	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.	7.3	62
48	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	27.8	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.	3.8	12
50	Towards a whole-genome sequence for rye (<i>Secale cereale</i> L.). <i>Plant Journal</i> , 2017, 89, 853-869.	5.7	238
51	The repetitive landscape of the 5100 Mbp barley genome. <i>Mobile DNA</i> , 2017, 8, 22.	3.6	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, .	6.0	48
53	transPLANT Resources for Triticeae Genomic Data. <i>Plant Genome</i> , 2016, 9, plantgenome2015.06.0038.	2.8	8
54	Identification and Characterization of Carboxylesterases from <i>Brachypodium distachyon</i> Deacetylating Trichothecene Mycotoxins. <i>Toxins</i> , 2016, 8, 6.	3.4	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.	8.8	51
56	Examining the Transcriptional Response in Wheat <i><i>Fhb1</i></i> Near-Isogenic Lines to <i><i>Fusarium graminearum</i></i> Infection and Deoxynivalenol Treatment. <i>Plant Genome</i> , 2016, 9, plantgenome2015.05.0032.	2.8	44
57	Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016, 14, 1511-1522.	8.3	20
58	Ribosome quality control is a central protection mechanism for yeast exposed to deoxynivalenol and trichothecin. <i>BMC Genomics</i> , 2016, 17, 417.	2.8	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.	7.1	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.	12.8	51
61	The <i>Cardamine hirsuta</i> genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , 2016, 2, 16167.	9.3	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.	3.6	103
63	PGSB PlantsDB: updates to the database framework for comparative plant genome research. <i>Nucleic Acids Research</i> , 2016, 44, D1141-D1147.	14.5	79
64	The big five of the monocot genomes. <i>Current Opinion in Plant Biology</i> , 2016, 30, 33-40.	7.1	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.	0.9	2
66	Chloroplast phylogeny of <i><i>Triticum/Aegilops</i></i> species is not incongruent with an ancient homoploid hybrid origin of the ancestor of the bread wheat <i>D</i> -genome. <i>New Phytologist</i> , 2015, 208, 9-10.	7.3	28
67	Red clover (<i>Trifolium pratense</i> L.) draft genome provides a platform for trait improvement. <i>Scientific Reports</i> , 2015, 5, 17394.	3.3	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.	3.0	62
69	A synteny-based draft genome sequence of the forage grass <i><i>Lolium perenne</i></i> . <i>Plant Journal</i> , 2015, 84, 816-826.	5.7	166
70	Assessing the Barley Genome Zipper and Genomic Resources for Breeding Purposes. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.06.0045.	2.8	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.	3.5	103
72	High-throughput physical map anchoring via BAC-pool sequencing. <i>BMC Plant Biology</i> , 2015, 15, 99.	3.6	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.	1.8	58
74	Parallel Selection Revealed by Population Sequencing in Chicken. <i>Genome Biology and Evolution</i> , 2015, 7, 3299-3306.	2.5	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.	1.8	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.	2.1	101
77	Barley: From Brittle to Stable Harvest. <i>Cell</i> , 2015, 162, 469-471.	28.9	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.	2.1	47
79	Comparative transcriptome analysis within the <i>Lolium/Festuca</i> species complex reveals high sequence conservation. <i>BMC Genomics</i> , 2015, 16, 249.	2.8	24
80	Brassinosteroids Are Master Regulators of Gibberellin Biosynthesis in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2015, 27, 2261-2272.	6.6	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.	8.3	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.	3.6	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.	1.9	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.	2.8	242
85	Genetic Analysis of <i>DEFFECTIVE KERNEL1</i> Loop Function in Three-Dimensional Body Patterning in <i>Physcomitrella patens</i> . <i>Plant Physiology</i> , 2014, 166, 903-919.	4.8	40
86	The <i>Spirodela polyrhiza</i> genome reveals insights into its neotenuous reduction fast growth and aquatic lifestyle. <i>Nature Communications</i> , 2014, 5, 3311.	12.8	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.	3.6	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.	4.8	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.	8.3	54
90	Plant genome sequencing – applications for crop improvement. <i>Current Opinion in Biotechnology</i> , 2014, 26, 31-37.	6.6	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.	2.1	13
92	RNASeqExpressionBrowser—a web interface to browse and visualize high-throughput expression data. <i>Bioinformatics</i> , 2014, 30, 2519-2520.	4.1	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.	8.3	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.	5.7	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.	4.8	76
96	Extensive and Biased Inter-genomic Nonreciprocal DNA Exchanges Shaped a Nascent Polyploid Genome, <i>Gossypium</i> (Cotton). <i>Genetics</i> , 2014, 197, 1153-1163.	2.9	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.	21.4	342
98	Slicing the wheat genome. <i>Science</i> , 2014, 345, 285-287.	12.6	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.	11.0	367
100	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014, 345, 1251788.	12.6	1,479
101	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014, 345, 1249721.	12.6	542
102	Genome interplay in the grain transcriptome of hexaploid bread wheat. <i>Science</i> , 2014, 345, 1250091.	12.6	318
103	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	12.6	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.	2.8	83
105	An improved genome release (version Mt4.0) for the model legume <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2014, 15, 312.	2.8	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.	4.8	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.	3.3	51
108	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	8.8	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.	8.8	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.	5.7	260
111	Analysing complex Triticeae genomes – concepts and strategies. <i>Plant Methods</i> , 2013, 9, 35.	4.3	19
112	Conserved synteny-based anchoring of the barley genome physical map. <i>Functional and Integrative Genomics</i> , 2013, 13, 339-350.	3.5	10
113	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <i>Plant Journal</i> , 2013, 76, 718-727.	5.7	264
114	<i>Aegilops tauschii</i> draft genome sequence reveals a gene repertoire for wheat adaptation. <i>Nature</i> , 2013, 496, 91-95.	27.8	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.	2.6	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.	3.6	28
117	GABI – DUPLO: a collection of double mutants to overcome genetic redundancy in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2013, 75, 157-171.	5.7	48
118	Flow Sorting and Sequencing Meadow Fescue Chromosome 4F. <i>Plant Physiology</i> , 2013, 163, 1323-1337.	4.8	27
119	Reticulate Evolution of the Rye Genome. <i>Plant Cell</i> , 2013, 25, 3685-3698.	6.6	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.	7.1	214
121	The Perennial Ryegrass GenomeZipper: Targeted Use of Genome Resources for Comparative Grass Genomics. <i>Plant Physiology</i> , 2013, 161, 571-582.	4.8	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.	2.8	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.	2.5	58
124	Sequence-Based Analysis of Translocations and Inversions in Bread Wheat (<i>Triticum aestivum</i> L.). <i>PLoS ONE</i> , 2013, 8, e79329.	2.5	62
125	Evidence for a Contribution of ALA Synthesis to Plastid-To-Nucleus Signaling. <i>Frontiers in Plant Science</i> , 2012, 3, 236.	3.6	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.	7.1	173

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127	Analysis of the bread wheat genome using whole-genome shotgun sequencing. <i>Nature</i> , 2012, 491, 705-710.	27.8	983
128	Integrating cereal genomics to support innovation in the Triticeae. <i>Functional and Integrative Genomics</i> , 2012, 12, 573-583.	3.5	39
129	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	27.8	1,416
130	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012, 492, 423-427.	27.8	1,204
131	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	27.8	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.	3.6	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.	5.7	137
134	Frequent Gene Movement and Pseudogene Evolution Is Common to the Large and Complex Genomes of Wheat, Barley, and Their Relatives Å. <i>Plant Cell</i> , 2011, 23, 1706-1718.	6.6	190
135	The <i>Medicago</i> genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	27.8	1,166
136	Unlocking the Barley Genome by Chromosomal and Comparative Genomics Å. <i>Plant Cell</i> , 2011, 23, 1249-1263.	6.6	448
137	Exploring the genomes: From <i>Arabidopsis</i> to crops. <i>Journal of Plant Physiology</i> , 2011, 168, 3-8.	3.5	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.	21.4	814
139	Intracompartmental and Intercompartmental Transcriptional Networks Coordinate the Expression of Genes for Organellar Functions Å. <i>Plant Physiology</i> , 2011, 157, 386-404.	4.8	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.	2.1	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.	3.6	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.	1.4	13
144	MIPS: curated databases and comprehensive secondary data resources in 2010. <i>Nucleic Acids Research</i> , 2011, 39, D220-D224.	14.5	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.	27.8	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.	7.1	136
148	Gene Content and Virtual Gene Order of Barley Chromosome 1H. <i>Plant Physiology</i> , 2009, 151, 496-505.	4.8	135
149	Discovery of cis-elements between sorghum and rice using co-expression and evolutionary conservation. <i>BMC Genomics</i> , 2009, 10, 284.	2.8	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.	2.8	69
151	Deep-sequencing of plant viral small RNAs reveals effective and widespread targeting of viral genomes. <i>Virology</i> , 2009, 392, 203-214.	2.4	274
152	The <i>Sorghum bicolor</i> genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	27.8	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.	12.6	591
154	Characterization of Reflector Types by Phase-Sensitive Ultrasonic Data Processing and Imaging. <i>Journal of Nondestructive Evaluation</i> , 2008, 27, 35-45.	2.4	34
155	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. <i>Science</i> , 2008, 319, 64-69.	12.6	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.	14.5	88
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