Klaus F X Mayer

List of Publications by Year
in descending order

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	Analysis of the genome sequence of the flowering plant Arabidopsis thaliana. Nature, 2000, 408, 796-815.	27.8	8,336
2	The tomato genome sequence provides insights into fleshy fruit evolution. Nature, 2012, 485, 635-641.	27.8	2,860
3	The Sorghum bicolor genome and the diversification of grasses. Nature, 2009, 457, 551-556.	27.8	2,642
4	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	2,424
5	The Physcomitrella Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. Science, 2008, 319, 64-69.	12.6	1,712
6	Genome sequencing and analysis of the model grass Brachypodium distachyon. Nature, 2010, 463, 763-768.	27.8	1,685
7	The Stem Cell Population of Arabidopsis Shoot Meristems Is Maintained by a Regulatory Loop between the CLAVATA and WUSCHEL Genes. Cell, 2000, 100, 635-644.	28.9	1,521
8	Role of WUSCHEL in Regulating Stem Cell Fate in the Arabidopsis Shoot Meristem. Cell, 1998, 95, 805-815.	28.9	1,487
9	A chromosome-based draft sequence of the hexaploid bread wheat (Triticum aestivum) genome. Science, 2014, 345, 1251788.	12.6	1,479
10	A physical, genetic and functional sequence assembly of the barley genome. Nature, 2012, 491, 711-716.	27.8	1,416
11	A chromosome conformation capture ordered sequence of the barley genome. Nature, 2017, 544, 427-433.	27.8	1,365
12	Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibres. Nature, 2012, 492, 423-427.	27.8	1,204
13	The Medicago genome provides insight into the evolution of rhizobial symbioses. Nature, 2011, 480, 520-524.	27.8	1,166
14	Analysis of the bread wheat genome using whole-genome shotgun sequencing. Nature, 2012, 491, 705-710.	27.8	983
15	Comparative Analysis of the Receptor-Like Kinase Family in Arabidopsis and Rice[W]. Plant Cell, 2004, 16, 1220-1234.	6.6	980
16	The Arabidopsis lyrata genome sequence and the basis of rapid genome size change. Nature Genetics, 2011, 43, 476-481.	21.4	814
17	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. Science, 2017, 357, 93-97.	12.6	781
18	The transcriptional landscape of polyploid wheat. Science, 2018, 361, .	12.6	768

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19	Aegilops tauschii draft genome sequence reveals a gene repertoire for wheat adaptation. Nature, 2013, 496, 91-95.	27.8	714
20	Ancient hybridizations among the ancestral genomes of bread wheat. Science, 2014, 345, 1250092.	12.6	629
21	Green Evolution and Dynamic Adaptations Revealed by Genomes of the Marine Picoeukaryotes Micromonas. Science, 2009, 324, 268-272.	12.6	591
22	Durum wheat genome highlights past domestication signatures and future improvement targets. Nature Genetics, 2019, 51, 885-895.	21.4	576
23	Genome sequence of the progenitor of the wheat D genome Aegilops tauschii. Nature, 2017, 551, 498-502.	27.8	563
24	Structural and functional partitioning of bread wheat chromosome 3B. Science, 2014, 345, 1249721.	12.6	542
25	Multiple wheat genomes reveal global variation in modern breeding. Nature, 2020, 588, 277-283.	27.8	513
26	Unlocking the Barley Genome by Chromosomal and Comparative Genomics Â. Plant Cell, 2011, 23, 1249-1263.	6.6	448
27	Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. Nature, 1999, 402, 769-777.	27.8	413
28	The Physcomitrella patens chromosomeâ€scale assembly reveals moss genome structure and evolution. Plant Journal, 2018, 93, 515-533.	5.7	406
29	An improved genome release (version Mt4.0) for the model legume Medicago truncatula. BMC Genomics, 2014, 15, 312.	2.8	381
30	Convergent Targeting of a Common Host Protein-Network by Pathogen Effectors from Three Kingdoms of Life. Cell Host and Microbe, 2014, 16, 364-375.	11.0	367
31	MIPS: analysis and annotation of proteins from whole genomes in 2005. Nucleic Acids Research, 2006, 34, D169-D172.	14.5	348
32	The genome sequence of African rice (Oryza glaberrima) and evidence for independent domestication. Nature Genetics, 2014, 46, 982-988.	21.4	342
33	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. Science, 2018, 361, .	12.6	339
34	Gene selection from microarray data for cancer classificationâ€”a machine learning approach. Computational Biology and Chemistry, 2005, 29, 37-46.	2.3	336
35	Mass-spectrometry-based draft of the Arabidopsis proteome. Nature, 2020, 579, 409-414.	27.8	328
36	Genome interplay in the grain transcriptome of hexaploid bread wheat. Science, 2014, 345, 1250091.	12.6	318

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37	The barley pan-genome reveals the hidden legacy of mutation breeding. Nature, 2020, 588, 284-289.	27.8	314
38	Sequence composition and genome organization of maize. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14349-14354.	7.1	290
39	Legume genome evolution viewed through the Medicago truncatula and Lotus japonicus genomes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14959-14964.	7.1	286
40	Deep-sequencing of plant viral small RNAs reveals effective and widespread targeting of viral genomes. Virology, 2009, 392, 203-214.	2.4	274
41	Anchoring and ordering <scp>NGS</scp> contig assemblies by population sequencing (<scp>POPSEQ</scp>). Plant Journal, 2013, 76, 718-727.	5.7	264
42	The Spirodela polyrhiza genome reveals insights into its neotenous reduction fast growth and aquatic lifestyle. Nature Communications, 2014, 5, 3311.	12.8	262
43	Barley whole exome capture: a tool for genomic research in the genus Hordeum and beyond. Plant Journal, 2013, 76, 494-505.	5.7	260
44	A powerful tool for genome analysis in maize: development and evaluation of the high density 600 k SNP genotyping array. BMC Genomics, 2014, 15, 823.	2.8	242
45	Towards a wholeâ€genome sequence for rye (Secale cereale L.). Plant Journal, 2017, 89, 853-869.	5.7	238
46	START lipid/sterol-binding domains are amplified in plants and are predominantly associated with homeodomain transcription factors. Genome Biology, 2004, 5, R41.	9.6	233
47	Tracing the ancestry of modern bread wheats. Nature Genetics, 2019, 51, 905-911.	21.4	230
48	Impact of transposable elements on genome structure and evolution in bread wheat. Genome Biology, 2018, 19, 103.	8.8	226
49	A 4-gigabase physical map unlocks the structure and evolution of the complex genome of Aegilops tauschii, the wheat D-genome progenitor. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7940-7945.	7.1	214
50	MIPS: a database for genomes and protein sequences. Nucleic Acids Research, 1999, 27, 44-48.	14.5	197
51	Reticulate Evolution of the Rye Genome. Plant Cell, 2013, 25, 3685-3698.	6.6	194
52	Frequent Gene Movement and Pseudogene Evolution Is Common to the Large and Complex Genomes of Wheat, Barley, and Their Relatives Â. Plant Cell, 2011, 23, 1706-1718.	6.6	190
53	Brassinosteroids Are Master Regulators of Gibberellin Biosynthesis in Arabidopsis. Plant Cell, 2015, 27, 2261-2272.	6.6	190
54	Sequence and analysis of chromosome 3 of the plant Arabidopsis thaliana. Nature, 2000, 408, 820-823.	27.8	188

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55	Long-read sequence assembly: a technical evaluation in barley. Plant Cell, 2021, 33, 1888-1906.	6.6	180
56	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. Genome Biology, 2019, 20, 284.	8.8	179
57	Sequence and analysis of chromosome 5 of the plant Arabidopsis thaliana. Nature, 2000, 408, 823-826.	27.8	175
58	Selfish supernumerary chromosome reveals its origin as a mosaic of host genome and organellar sequences. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13343-13346.	7.1	173
59	A syntenyâ€based draft genome sequence of the forage grass Lolium perenne. Plant Journal, 2015, 84, 816-826.	5.7	166
60	Plant genome sequencing â€" applications for crop improvement. Current Opinion in Biotechnology, 2014, 26, 31-37.	6.6	164
61	Brassinosteroids participate in the control of basal and acquired freezing tolerance of plants. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5982-E5991.	7.1	162
62	MIPS Arabidopsisthaliana Database (MAtDB): an integrated biological knowledge resource based on the first complete plant genome. Nucleic Acids Research, 2002, 30, 91-93.	14.5	159
63	Structure and Architecture of the Maize Genome. Plant Physiology, 2005, 139, 1612-1624.	4.8	159
64	Transcriptional Similarities, Dissimilarities, and Conservation of cis-Elements in Duplicated Genes of Arabidopsis. Plant Physiology, 2004, 136, 3009-3022.	4.8	158
65	MIPS: analysis and annotation of genome information in 2007. Nucleic Acids Research, 2007, 36, D196-D201.	14.5	156
66	Footprints of parasitism in the genome of the parasitic flowering plant Cuscuta campestris. Nature Communications, 2018, 9, 2515.	12.8	141
67	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. Nature Genetics, 2021, 53, 564-573.	21.4	138
68	Nextâ€generation sequencing and syntenic integration of flowâ€sorted arms of wheat chromosomeâ€ƒ4A exposes the chromosome structure and gene content. Plant Journal, 2012, 69, 377-386.	5.7	137
69	Impact of natural genetic variation on the transcriptome of autotetraploid Arabidopsis thaliana. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17809-17814.	7.1	136
70	Red clover (Trifolium pratense L.) draft genome provides a platform for trait improvement. Scientific Reports, 2015, 5, 17394.	3.3	136
71	Gene Content and Virtual Gene Order of Barley Chromosome 1H Â Â Â. Plant Physiology, 2009, 151, 496-505.	4.8	135
72	Genome mapping of seed-borne allergens and immunoresponsive proteins in wheat. Science Advances, 2018, 4, eaar8602.	10.3	130

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73	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. Genome Biology, 2013, 14, R58.	8.8	125
74	Snipping polymorphisms from large EST collections in barley (Hordeum vulgare L.). Molecular Genetics and Genomics, 2003, 270, 24-33.	2.1	116
75	Crosstalk and differential response to abiotic and biotic stressors reflected at the transcriptional level of effector genes from secondary metabolism. Plant Molecular Biology, 2004, 54, 817-835.	3.9	111
76	From RNA-seq to large-scale genotyping - genomics resources for rye (Secale cereale L.). BMC Plant Biology, 2011, 11, 131.	3.6	109
77	Uneven chromosome contraction and expansion in the maize genome. Genome Research, 2006, 16, 1241-1251.	5.5	105
78	Quantitative trait loci-dependent analysis of a gene co-expression network associated with Fusarium head blight resistance in bread wheat (Triticum aestivumL.). BMC Genomics, 2013, 14, 728.	2.8	105
79	Extensive signal integration by the phytohormone protein network. Nature, 2020, 583, 271-276.	27.8	104
80	Modulation of Ambient Temperature-Dependent Flowering in Arabidopsis thaliana by Natural Variation of FLOWERING LOCUS M. PLoS Genetics, 2015, 11, e1005588.	3.5	103
81	Suppressed recombination and unique candidate genes in the divergent haplotype encoding Fhb1, a major Fusarium head blight resistance locus in wheat. Theoretical and Applied Genetics, 2016, 129, 1607-1623.	3.6	103
82	Population genomic analysis of Aegilops tauschii identifies targets for bread wheat improvement. Nature Biotechnology, 2022, 40, 422-431.	17.5	102
83	Mechanical behaviour and failure modes in the Whakaari (White Island volcano) hydrothermal system, New Zealand. Journal of Volcanology and Geothermal Research, 2015, 295, 26-42.	2.1	101
84	Understanding the Molecular Basis of Salt Sequestration in Epidermal Bladder Cells of Chenopodium quinoa. Current Biology, 2018, 28, 3075-3085.e7.	3.9	98
85	The Cardamine hirsuta genome offers insight into the evolution of morphological diversity. Nature Plants, 2016, 2, 16167.	9.3	90
86	The complete nucleotide sequences of the five genetically distinct plastid genomes of Oenothera , subsection Oenothera : I. Sequence evaluation and plastome evolution â€. Nucleic Acids Research, 2008, 36, 2366-2378.	14.5	88
87	Functional Characterization of Two Clusters of Brachypodium distachyon UDP-Glycosyltransferases Encoding Putative Deoxynivalenol Detoxification Genes. Molecular Plant-Microbe Interactions, 2013, 26, 781-792.	2.6	85
88	European maize genomes highlight intraspecies variation in repeat and gene content. Nature Genetics, 2020, 52, 950-957.	21.4	84
89	A first genetic map of date palm (Phoenix dactylifera) reveals long-range genome structure conservation in the palms. BMC Genomics, 2014, 15, 285.	2.8	83
90	MIPS Arabidopsis thaliana Database (MAtDB): an integrated biological knowledge resource for plant genomics. Nucleic Acids Research, 2004, 32, 373D-376.	14.5	82

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91	Characterization of the Maize Endosperm Transcriptome and Its Comparison to the Rice Genome. Genome Research, 2004, 14, 1932-1937.	5.5	80
92	PGSB PlantsDB: updates to the database framework for comparative plant genome research. Nucleic Acids Research, 2016, 44, D1141-D1147.	14.5	79
93	MIPS: curated databases and comprehensive secondary data resources in 2010. Nucleic Acids Research, 2011, 39, D220-D224.	14.5	77
94	A Sequence-Ready Physical Map of Barley Anchored Genetically by Two Million Single-Nucleotide Polymorphisms Â Â. Plant Physiology, 2014, 164, 412-423.	4.8	77
95	Bacteria-Triggered Systemic Immunity in Barley Is Associated with WRKY and ETHYLENE RESPONSIVE FACTORs But Not with Salicylic Acid. Plant Physiology, 2014, 166, 2133-2151.	4.8	76
96	The Perennial Ryegrass GenomeZipper: Targeted Use of Genome Resources for Comparative Grass Genomics Â Â. Plant Physiology, 2013, 161, 571-582.	4.8	75
97	Expressed sequence tag analysis in Cycas, the most primitive living seed plant. Genome Biology, 2003, 4, R78.	9.6	74
98	TriAnnot: A Versatile and High Performance Pipeline for the Automated Annotation of Plant Genomes. Frontiers in Plant Science, 2012, 3, 5.	3.6	73
99	The mosaic oat genome gives insights into a uniquely healthy cereal crop. Nature, 2022, 606, 113-119.	27.8	70
100	De novo 454 sequencing of barcoded BAC pools for comprehensive gene survey and genome analysis in the complex genome of barley. BMC Genomics, 2009, 10, 547.	2.8	69
101	Meta-Analysis of Retrograde Signaling in Arabidopsis thaliana Reveals a Core Module of Genes Embedded in Complex Cellular Signaling Networks. Molecular Plant, 2014, 7, 1167-1190.	8.3	69
102	Genes on B chromosomes: Old questions revisited with new tools. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2015, 1849, 64-70.	1.9	68
103	Sequence and analysis of the Arabidopsis genome. Current Opinion in Plant Biology, 2001, 4, 105-110.	7.1	66
104	Molecular characterisation of the STRUBBELIG-RECEPTOR FAMILY of genes encoding putative leucine-rich repeat receptor-like kinases in Arabidopsis thaliana. BMC Plant Biology, 2007, 7, 16.	3.6	64
105	Conservation of Microstructure between a Sequenced Region of the Genome of Rice and Multiple Segments of the Genome of Arabidopsis thaliana. Genome Research, 2001, 11, 1167-1174.	5.5	64
106	Sequence-Based Analysis of Translocations and Inversions in Bread Wheat (Triticum aestivum L.). PLoS ONE, 2013, 8, e79329.	2.5	62
107	DroughtDB: an expert-curated compilation of plant drought stress genes and their homologs in nine species. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav046.	3.0	62
108	The desert plant Phoenix dactylifera closes stomata via nitrateâ€regulated <scp>SLAC</scp>1 anion channel. New Phytologist, 2017, 216, 150-162.	7.3	62

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109	Mercury-induced genes in Arabidopsis thaliana : identification of induced genes upon long-term mercuric ion exposure. Plant, Cell and Environment, 2001, 24, 1227-1234.	5.7	58
110	Molecular and Immunological Characterization of Ragweed (Ambrosia artemisiifolia L.) Pollen after Exposure of the Plants to Elevated Ozone over a Whole Growing Season. PLoS ONE, 2013, 8, e61518.	2.5	58
111	A Genome-Wide Survey of Date Palm Cultivars Supports Two Major Subpopulations inPhoenix dactylifera. G3: Genes, Genomes, Genetics, 2015, 5, 1429-1438.	1.8	58
112	Fifteen Million Years of Evolution in the Oryza Genus Shows Extensive Gene Family Expansion. Molecular Plant, 2014, 7, 642-656.	8.3	54
113	Chromosome-scale comparative sequence analysis unravels molecular mechanisms of genome dynamics between two wheat cultivars. Genome Biology, 2018, 19, 104.	8.8	54
114	Exon discovery by genomic sequence alignment. Bioinformatics, 2002, 18, 777-787.	4.1	51
115	Extensive and Biased Intergenomic Nonreciprocal DNA Exchanges Shaped a Nascent Polyploid Genome, Gossypium (Cotton). Genetics, 2014, 197, 1153-1163.	2.9	51
116	Separating the wheat from the chaff â€“ a strategy to utilize plant genetic resources from ex situ genebanks. Scientific Reports, 2014, 4, 5231.	3.3	51
117	A comprehensive study of the genomic differentiation between temperate Dent and Flint maize. Genome Biology, 2016, 17, 137.	8.8	51
118	DNA transposon activity is associated with increased mutation rates in genes of rice and other grasses. Nature Communications, 2016, 7, 12790.	12.8	51
119	Large-Scale cis-Element Detection by Analysis of Correlated Expression and Sequence Conservation between Arabidopsis and Brassica oleracea Â. Plant Physiology, 2006, 142, 1589-1602.	4.8	50
120	Computational aspects underlying genome to phenome analysis in plants. Plant Journal, 2019, 97, 182-198.	5.7	50
121	MicroRNAs coordinately regulate protein complexes. BMC Systems Biology, 2011, 5, 136.	3.0	49
122	The repetitive landscape of the 5100 Mbp barley genome. Mobile DNA, 2017, 8, 22.	3.6	49
123	<scp>GABI</scp>â€<scp>DUPLO</scp>: a collection of double mutants to overcome genetic redundancy in <scp>A</scp>rabidopsis thaliana. Plant Journal, 2013, 75, 157-171.	5.7	48
124	Natural haplotypes of FLM non-coding sequences fine-tune flowering time in ambient spring temperatures in Arabidopsis. ELife, 2017, 6, .	6.0	48
125	MIPSPlantsDB--plant database resource for integrative and comparative plant genome research. Nucleic Acids Research, 2007, 35, D834-D840.	14.5	47
126	Experimental constraints on phreatic eruption processes at Whakaari (White Island volcano). Journal of Volcanology and Geothermal Research, 2015, 302, 150-162.	2.1	47

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127	Genome sequences of three Aegilops species of the section Sitopsis reveal phylogenetic relationships and provide resources for wheat improvement. Plant Journal, 2022, 110, 179-192.	5.7	46
128	The Complete Nucleotide Sequences of the 5 Genetically Distinct Plastid Genomes of Oenothera, Subsection Oenothera: II. A Microevolutionary View Using Bioinformatics and Formal Genetic Data. Molecular Biology and Evolution, 2008, 25, 2019-2030.	8.9	45
129	A high density physical map of chromosome 1BL supports evolutionary studies, map-based cloning and sequencing in wheat. Genome Biology, 2013, 14, R64.	8.8	45
130	Wholeâ€genome profiling and shotgun sequencing delivers an anchored, geneâ€decorated, physical map assembly of bread wheat chromosome 6A. Plant Journal, 2014, 79, 334-347.	5.7	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 toFusarium graminearum. G3: Genes, Genomes, Genetics, 2015, 5, 2579-2592.	1.8	45
132	Sputnik: a database platform for comparative plant genomics. Nucleic Acids Research, 2003, 31, 128-132.	14.5	44
133	Examining the Transcriptional Response in Wheat Fhb1 Nearâ€Isogenic Lines to Fusarium graminearum Infection and Deoxynivalenol Treatment. Plant Genome, 2016, 9, plantgenome2015.05.0032.	2.8	44
134	Evidence for a Contribution of ALA Synthesis to Plastid-To-Nucleus Signaling. Frontiers in Plant Science, 2012, 3, 236.	3.6	41
135	Hidden variation in polyploid wheat drives local adaptation. Genome Research, 2018, 28, 1319-1332.	5.5	41
136	Genome-Wide in Silico Mapping of Scaffold/Matrix Attachment Regions in Arabidopsis Suggests Correlation of Intragenic Scaffold/Matrix Attachment Regions with Gene Expression. Plant Physiology, 2004, 135, 715-722.	4.8	40
137	PlantMarkers--a database of predicted molecular markers from plants. Nucleic Acids Research, 2004, 33, D628-D632.	14.5	40
138	Intracompartmental and Intercompartmental Transcriptional Networks Coordinate the Expression of Genes for Organellar Functions Â. Plant Physiology, 2011, 157, 386-404.	4.8	40
139	Genetic Analysis of DEFECTIVE KERNEL1 Loop Function in Three-Dimensional Body Patterning in Physcomitrella patens Â Â Â Â. Plant Physiology, 2014, 166, 903-919.	4.8	40
140	Functional Diversification within the Family of B-GATA Transcription Factors through the Leucine-Leucine-Methionine Domain Â Â Â. Plant Physiology, 2014, 166, 293-305.	4.8	40
141	Slicing the wheat genome. Science, 2014, 345, 285-287.	12.6	40
142	Integrating cereal genomics to support innovation in the Triticeae. Functional and Integrative Genomics, 2012, 12, 573-583.	3.5	39
143	Identification of Early Nuclear Target Genes of Plastidial Redox Signals that Trigger the Long-Term Response of Arabidopsis to Light Quality Shifts. Molecular Plant, 2015, 8, 1237-1252.	8.3	38
144	Genetic and genomic analysis of legume flowers and seeds. Current Opinion in Plant Biology, 2006, 9, 133-141.	7.1	35

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145	Insights into the evolution of symbiosis gene copy number and distribution from a chromosome-scaleLotus japonicusGifu genome sequence. DNA Research, 2020, 27, .	3.4	35
146	How can we deliver the large plant genomes? Strategies and perspectives. Current Opinion in Plant Biology, 2002, 5, 173-177.	7.1	34
147	Characterization of Reflector Types by Phase-Sensitive Ultrasonic Data Processing and Imaging. Journal of Nondestructive Evaluation, 2008, 27, 35-45.	2.4	34
148	Evidence for an ancient chromosomal duplication inArabidopsis thalianaby sequencing and analyzing a 400-kb contig at theAPETALA2locus on chromosome 41. FEBS Letters, 1999, 445, 237-245.	2.8	33
149	Timeâ€course expression QTLâ€atlas of the global transcriptional response of wheat to Fusarium graminearum. Plant Biotechnology Journal, 2017, 15, 1453-1464.	8.3	32
150	Spatiotemporal Expression Control Correlates with Intragenic Scaffold Matrix Attachment Regions (S/MARs) in Arabidopsis thaliana. PLoS Computational Biology, 2006, 2, e21.	3.2	29
151	From plant genomes to phenotypes. Journal of Biotechnology, 2017, 261, 46-52.	3.8	29
152	Light and Plastid Signals Regulate Different Sets of Genes in the Albino Mutant Pap7-1. Plant Physiology, 2017, 175, 1203-1219.	4.8	29
153	The Systems Architecture of Molecular Memory in Poplar after Abiotic Stress. Plant Cell, 2019, 31, 346-367.	6.6	29
154	Genomics-based high-resolution mapping of the BaMMV/BaYMV resistance gene rym11 in barley (Hordeum vulgare L.). Theoretical and Applied Genetics, 2013, 126, 1201-1212.	3.6	28
155	Chloroplast phylogeny of Triticum/Aegilops species is not incongruent with an ancient homoploid hybrid origin of the ancestor of the bread wheat Dâ€genome. New Phytologist, 2015, 208, 9-10.	7.3	28
156	MOsDB: an integrated information resource for rice genomics. Nucleic Acids Research, 2003, 31, 190-192.	14.5	27
157	Significant sequence similarities in promoters and precursors of Arabidopsis thaliana non-conserved microRNAs. Bioinformatics, 2006, 22, 2585-2589.	4.1	27
158	Flow Sorting and Sequencing Meadow Fescue Chromosome 4F. Plant Physiology, 2013, 163, 1323-1337.	4.8	27
159	Discovery of cis-elements between sorghum and rice using co-expression and evolutionary conservation. BMC Genomics, 2009, 10, 284.	2.8	26
160	Comparative sequence analysis of VRN1 alleles of Lolium perenne with the co-linear regions in barley, wheat, and rice. Molecular Genetics and Genomics, 2011, 286, 433-447.	2.1	25
161	Parallel Selection Revealed by Population Sequencing in Chicken. Genome Biology and Evolution, 2015, 7, 3299-3306.	2.5	25
162	Comparative transcriptome analysis within the Lolium/Festuca species complex reveals high sequence conservation. BMC Genomics, 2015, 16, 249.	2.8	24

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163	RNASeqExpressionBrowserâ€"a web interface to browse and visualize high-throughput expression data. Bioinformatics, 2014, 30, 2519-2520.	4.1	23
164	Ribosome quality control is a central protection mechanism for yeast exposed to deoxynivalenol and trichothecin. BMC Genomics, 2016, 17, 417.	2.8	23
165	New insights into the wheat chromosome 4D structure and virtual gene order, revealed by survey pyrosequencing. Plant Science, 2015, 233, 200-212.	3.6	20
166	Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. Plant Biotechnology Journal, 2016, 14, 1511-1522.	8.3	20
167	Proteomic and transcriptomic profiling of aerial organ development in Arabidopsis. Scientific Data, 2020, 7, 334.	5.3	20
168	Fusarium head blight resistance in European winter wheat: insights from genome-wide transcriptome analysis. BMC Genomics, 2021, 22, 470.	2.8	20
169	Cell fate regulation in the shoot meristem. Seminars in Cell and Developmental Biology, 1998, 9, 195-200.	5.0	19
170	Analysing complex Triticeae genomes â€" concepts and strategies. Plant Methods, 2013, 9, 35.	4.3	19
171	Aegilops tauschii genome assembly Aet v5.0 features greater sequence contiguity and improved annotation. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	19
172	Identification and Characterization of Carboxylesterases from Brachypodium distachyon Deacetylating Trichothecene Mycotoxins. Toxins, 2016, 8, 6.	3.4	17
173	Protein expression plasticity contributes to heat and drought tolerance of date palm. Oecologia, 2021, 197, 903-919.	2.0	17
174	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. Plant and Cell Physiology, 2021, 62, 8-27.	3.1	16
175	Exploring the genomes: From Arabidopsis to crops. Journal of Plant Physiology, 2011, 168, 3-8.	3.5	15
176	The pseudogenes of barley. Plant Journal, 2018, 93, 502-514.	5.7	14
177	High molecular weight glutenin gene diversity in Aegilops tauschii demonstrates unique origin of superior wheat quality. Communications Biology, 2021, 4, 1242.	4.4	14
178	Munich Information Center for Protein Sequences Plant Genome Resources. A Framework for Integrative and Comparative Analyses. Plant Physiology, 2005, 138, 1301-1309.	4.8	13
179	Sequencing of BAC pools by different next generation sequencing platforms and strategies. BMC Research Notes, 2011, 4, 411.	1.4	13
180	High-resolution mapping of the barley Ryd3 locus controlling tolerance to BYDV. Molecular Breeding, 2014, 33, 477-488.	2.1	13

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181	Current status of the multinational Arabidopsis community. Plant Direct, 2020, 4, e00248.	1.9	13
182	Bioinformatics in the plant genomic and phenomic domain: The German contribution to resources, services and perspectives. Journal of Biotechnology, 2017, 261, 37-45.	3.8	12
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