

Klaus F X Mayer

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

213
papers

40,834
citations

77
h-index

202
g-index

233
ext. papers

50,066
ext. citations

14.8
avg, IF

7.72
L-index

#	Paper	IF	Citations
213	The Barley and Wheat Pan-Genomes.. <i>Methods in Molecular Biology</i> , 2022 , 2443, 147-159	1.4	
212	Genome sequences of three Aegilops species of the section Sitopsis reveal phylogenetic relationships and provide resources for wheat improvement.. <i>Plant Journal</i> , 2022 ,	6.9	3
211	The mosaic oat genome gives insights into a uniquely healthy cereal crop.. <i>Nature</i> , 2022 ,	50.4	6
210	The Gene and Repetitive Element Landscape of the Rye Genome. <i>Compendium of Plant Genomes</i> , 2021 , 117-133	0.8	
209	Population genomic analysis of Aegilops tauschii identifies targets for bread wheat improvement. <i>Nature Biotechnology</i> , 2021 ,	44.5	10
208	High molecular weight glutenin gene diversity in Aegilops tauschii demonstrates unique origin of superior wheat quality. <i>Communications Biology</i> , 2021 , 4, 1242	6.7	3
207	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021 , 53, 564-573	36.3	35
206	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021 , 33, 1888-1906	11.6	26
205	Protein expression plasticity contributes to heat and drought tolerance of date palm. <i>Oecologia</i> , 2021 , 197, 903-919	2.9	2
204	Fusarium head blight resistance in European winter wheat: insights from genome-wide transcriptome analysis. <i>BMC Genomics</i> , 2021 , 22, 470	4.5	5
203	PYL8 ABA receptors of Phoenix dactylifera play a crucial role in response to abiotic stress and are stabilized by ABA. <i>Journal of Experimental Botany</i> , 2021 , 72, 757-774	7	3
202	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	4.9	8
201	Merging Genomics and Transcriptomics for Predicting Fusarium Head Blight Resistance in Wheat. <i>Genes</i> , 2021 , 12,	4.2	2
200	Aegilops tauschii genome assembly Aet v5.0 features greater sequence contiguity and improved annotation. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	1
199	Mass-spectrometry-based draft of the Arabidopsis proteome. <i>Nature</i> , 2020 , 579, 409-414	50.4	144
198	Extensive signal integration by the phytohormone protein network. <i>Nature</i> , 2020 , 583, 271-276	50.4	30
197	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020 , 588, 284-289	50.4	97

196	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020 , 588, 277-283	50.4	180
195	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,	4.5	9
194	Current status of the multinational Arabidopsis community. <i>Plant Direct</i> , 2020 , 4, e00248	3.3	4
193	European maize genomes highlight intraspecies variation in repeat and gene content. <i>Nature Genetics</i> , 2020 , 52, 950-957	36.3	34
192	Proteomic and transcriptomic profiling of aerial organ development in Arabidopsis. <i>Scientific Data</i> , 2020 , 7, 334	8.2	7
191	Tracing the ancestry of modern bread wheats. <i>Nature Genetics</i> , 2019 , 51, 905-911	36.3	99
190	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019 , 51, 885-895	36.3	289
189	The Systems Architecture of Molecular Memory in Poplar after Abiotic Stress. <i>Plant Cell</i> , 2019 , 31, 346-367.6	17	
188	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019 , 20, 284	18.3	89
187	Computational aspects underlying genome to phenome analysis in plants. <i>Plant Journal</i> , 2019 , 97, 182-188	33	
186	Footprints of parasitism in the genome of the parasitic flowering plant <i>Cuscuta campestris</i> . <i>Nature Communications</i> , 2018 , 9, 2515	17.4	79
185	Genome mapping of seed-borne allergens and immunoresponsive proteins in wheat. <i>Science Advances</i> , 2018 , 4, eaar8602	14.3	80
184	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018 , 361,	33.3	368
183	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018 , 361,	33.3	1296
182	Impact of transposable elements on genome structure and evolution in bread wheat. <i>Genome Biology</i> , 2018 , 19, 103	18.3	119
181	Hidden variation in polyploid wheat drives local adaptation. <i>Genome Research</i> , 2018 , 28, 1319-1332	9.7	27
180	Chromosome-scale comparative sequence analysis unravels molecular mechanisms of genome dynamics between two wheat cultivars. <i>Genome Biology</i> , 2018 , 19, 104	18.3	30
179	The pseudogenes of barley. <i>Plant Journal</i> , 2018 , 93, 502-514	6.9	8

178	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018 , 93, 515-533	6.9	176
177	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	6.3	57
176	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , 2018 , 361,	33.3	167
175	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017 , 544, 427-433.	33.4	822
174	From plant genomes to phenotypes. <i>Journal of Biotechnology</i> , 2017 , 261, 46-52	3.7	22
173	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	11.6	11
172	PGSB/MIPS PlantsDB Database Framework for the Integration and Analysis of Plant Genome Data. <i>Methods in Molecular Biology</i> , 2017 , 1533, 33-44	1.4	5
171	Light and Plastid Signals Regulate Different Sets of Genes in the Albino Mutant <i>Pap7-1</i> . <i>Plant Physiology</i> , 2017 , 175, 1203-1219	6.6	13
170	The repetitive landscape of the 5100 Mbp barley genome. <i>Mobile DNA</i> , 2017 , 8, 22	4.4	33
169	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. <i>Science</i> , 2017 , 357, 93-97	33.3	474
168	The desert plant <i>Phoenix dactylifera</i> closes stomata via nitrate-regulated SLAC1 anion channel. <i>New Phytologist</i> , 2017 , 216, 150-162	9.8	44
167	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017 , 551, 498-502.	32.4	337
166	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	3.7	8
165	Towards a whole-genome sequence for rye (<i>Secale cereale</i> L.). <i>Plant Journal</i> , 2017 , 89, 853-869	6.9	136
164	Natural haplotypes of non-coding sequences fine-tune flowering time in ambient spring temperatures in <i>Arabidopsis</i> . <i>ELife</i> , 2017 , 6,	8.9	36
163	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	11.5	111
162	DNA transposon activity is associated with increased mutation rates in genes of rice and other grasses. <i>Nature Communications</i> , 2016 , 7, 12790	17.4	39
161	The <i>Cardamine hirsuta</i> genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , 2016 , 2, 16167	11.5	56

160	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, 1607-23	6	69
159	PGSB PlantsDB: updates to the database framework for comparative plant genome research. <i>Nucleic Acids Research</i> , 2016 , 44, D1141-7	20.1	64
158	The big five of the monocot genomes. <i>Current Opinion in Plant Biology</i> , 2016 , 30, 33-40	9.9	8
157	PGSB/MIPS Plant Genome Information Resources and Concepts for the Analysis of Complex Grass Genomes. <i>Methods in Molecular Biology</i> , 2016 , 1374, 165-86	1.4	2
156	transPLANT Resources for Triticeae Genomic Data. <i>Plant Genome</i> , 2016 , 9, plantgenome2015.06.0038	4.4	5
155	A comprehensive study of the genomic differentiation between temperate Dent and Flint maize. <i>Genome Biology</i> , 2016 , 17, 137	18.3	34
154	Examining the Transcriptional Response in Wheat Near-Isogenic Lines to Infection and Deoxynivalenol Treatment. <i>Plant Genome</i> , 2016 , 9, plantgenome2015.05.0032	4.4	27
153	Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016 , 14, 1511-22	11.6	18
152	Ribosome quality control is a central protection mechanism for yeast exposed to deoxynivalenol and trichothecins. <i>BMC Genomics</i> , 2016 , 17, 417	4.5	8
151	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	2.8	79
150	Barley: From Brittle to Stable Harvest. <i>Cell</i> , 2015 , 162, 469-71	56.2	7
149	Experimental constraints on phreatic eruption processes at Whakaari (White Island volcano). <i>Journal of Volcanology and Geothermal Research</i> , 2015 , 302, 150-162	2.8	43
148	Comparative transcriptome analysis within the Lolium/Festuca species complex reveals high sequence conservation. <i>BMC Genomics</i> , 2015 , 16, 249	4.5	16
147	Brassinosteroids Are Master Regulators of Gibberellin Biosynthesis in Arabidopsis. <i>Plant Cell</i> , 2015 , 27, 2261-72	11.6	131
146	Identification of Early Nuclear Target Genes of Plastidial Redox Signals that Trigger the Long-Term Response of Arabidopsis to Light Quality Shifts. <i>Molecular Plant</i> , 2015 , 8, 1237-52	14.4	26
145	New insights into the wheat chromosome 4D structure and virtual gene order, revealed by survey pyrosequencing. <i>Plant Science</i> , 2015 , 233, 200-212	5.3	15
144	Genes on B chromosomes: old questions revisited with new tools. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2015 , 1849, 64-70	6	58
143	Chloroplast phylogeny of Triticum/Aegilops 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	9.8	16

142	Red clover (<i>Trifolium pratense</i> L.) draft genome provides a platform for trait improvement. <i>Scientific Reports</i> , 2015 , 5, 17394	4.9	85
141	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	5	46
140	A synteny-based draft genome sequence of the forage grass <i>Lolium perenne</i> . <i>Plant Journal</i> , 2015 , 84, 816-26	6.9	115
139	Assessing the Barley Genome Zipper and Genomic Resources for Breeding Purposes. <i>Plant Genome</i> , 2015 , 8, eplantgenome2015.06.0045	4.4	10
138	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	6	61
137	High-throughput physical map anchoring via BAC-pool sequencing. <i>BMC Plant Biology</i> , 2015 , 15, 99	5.3	7
136	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, 1429-38	3.2	39
135	Parallel Selection Revealed by Population Sequencing in Chicken. <i>Genome Biology and Evolution</i> , 2015 , 7, 3299-306	3.9	13
134	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, 2579-92	3.2	25
133	Identification and Characterization of Carboxylesterases from <i>Brachypodium distachyon</i> Deacetylating Trichothecene Mycotoxins. <i>Toxins</i> , 2015 , 8,	4.9	9
132	High-resolution mapping of the barley <i>Ryd3</i> locus controlling tolerance to BYDV. <i>Molecular Breeding</i> , 2014 , 33, 477-488	3.4	6
131	RNASeqExpressionBrowser—a web interface to browse and visualize high-throughput expression data. <i>Bioinformatics</i> , 2014 , 30, 2519-20	7.2	20
130	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, 1167-90	14.4	47
129	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, 334-47	6.9	34
128	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, 2133-51	6.6	45
127	Extensive and biased intergenomic nonreciprocal DNA exchanges shaped a nascent polyploid genome, <i>Gossypium</i> (cotton). <i>Genetics</i> , 2014 , 197, 1153-63	4	36
126	The genome sequence of African rice (<i>Oryza glaberrima</i>) and evidence for independent domestication. <i>Nature Genetics</i> , 2014 , 46, 982-8	36.3	259
125	Slicing the wheat genome. Introduction. <i>Science</i> , 2014 , 345, 285-7	33.3	35

124	Convergent targeting of a common host protein-network by pathogen effectors from three kingdoms of life. <i>Cell Host and Microbe</i> , 2014 , 16, 364-75	23.4	242
123	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014 , 345, 1251788	33.3	1129
122	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014 , 345, 1249721	33.3	397
121	Genome interplay in the grain transcriptome of hexaploid bread wheat. <i>Science</i> , 2014 , 345, 1250091	33.3	225
120	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014 , 345, 1250092	33.3	419
119	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	4.5	68
118	An improved genome release (version Mt4.0) for the model legume <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2014 , 15, 312	4.5	258
117	A sequence-ready physical map of barley anchored genetically by two million single-nucleotide polymorphisms. <i>Plant Physiology</i> , 2014 , 164, 412-23	6.6	70
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	4.9	32
115	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	4.5	168
114	Genetic analysis of DEFECTIVE KERNEL1 loop function in three-dimensional body patterning in <i>Physcomitrella patens</i> . <i>Plant Physiology</i> , 2014 , 166, 903-19	6.6	28
113	The <i>Spirodela polyrhiza</i> genome reveals insights into its neotenus reduction fast growth and aquatic lifestyle. <i>Nature Communications</i> , 2014 , 5, 3311	17.4	180
112	chromoWIZ: a web tool to query and visualize chromosome-anchored genes from cereal and model genomes. <i>BMC Plant Biology</i> , 2014 , 14, 348	5.3	6
111	Functional diversification within the family of B-GATA transcription factors through the leucine-leucine-methionine domain. <i>Plant Physiology</i> , 2014 , 166, 293-305	6.6	30
110	Fifteen million years of evolution in the <i>Oryza</i> genus shows extensive gene family expansion. <i>Molecular Plant</i> , 2014 , 7, 642-56	14.4	32
109	Plant genome sequencing - applications for crop improvement. <i>Current Opinion in Biotechnology</i> , 2014 , 26, 31-7	11.4	128
108	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013 , 14, R58	18.3	81
107	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	18.3	39

106	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	6.9	191
105	Analysing complex Triticeae genomes - concepts and strategies. <i>Plant Methods</i> , 2013 , 9, 35	5.8	17
104	Conserved synteny-based anchoring of the barley genome physical map. <i>Functional and Integrative Genomics</i> , 2013 , 13, 339-50	3.8	10
103	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <i>Plant Journal</i> , 2013 , 76, 718-27	6.9	219
102	<i>Aegilops tauschii</i> draft genome sequence reveals a gene repertoire for wheat adaptation. <i>Nature</i> , 2013 , 496, 91-5	50.4	601
101	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, 781-92	3.6	52
100	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, 1201-12	6	21
99	GABI-DUPLO: a collection of double mutants to overcome genetic redundancy in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2013 , 75, 157-171	6.9	40
98	Flow sorting and sequencing meadow fescue chromosome 4F. <i>Plant Physiology</i> , 2013 , 163, 1323-37	6.6	22
97	Reticulate evolution of the rye genome. <i>Plant Cell</i> , 2013 , 25, 3685-98	11.6	140
96	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, 7940-5	11.5	173
95	The perennial ryegrass GenomeZipper: targeted use of genome resources for comparative grass genomics. <i>Plant Physiology</i> , 2013 , 161, 571-82	6.6	63
94	Quantitative trait loci-dependent analysis of a gene co-expression network associated with <i>Fusarium</i> head blight resistance in bread wheat (<i>Triticum aestivum</i> L.). <i>BMC Genomics</i> , 2013 , 14, 728	4.5	67
93	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	3.7	48
92	Sequence-based analysis of translocations and inversions in bread wheat (<i>Triticum aestivum</i> L.). <i>PLoS ONE</i> , 2013 , 8, e79329	3.7	45
91	Analysis of the bread wheat genome using whole-genome shotgun sequencing. <i>Nature</i> , 2012 , 491, 705-10	50.4	821
90	Integrating cereal genomics to support innovation in the Triticeae. <i>Functional and Integrative Genomics</i> , 2012 , 12, 573-83	3.8	35
89	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012 , 491, 711-6	50.4	1124

88	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012 , 492, 423-7	50.4	839
87	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012 , 485, 635-41	50.4	2138
86	TriAnnot: A Versatile and High Performance Pipeline for the Automated Annotation of Plant Genomes. <i>Frontiers in Plant Science</i> , 2012 , 3, 5	6.2	54
85	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, 377-86	6.9	122
84	Evidence for a Contribution of ALA Synthesis to Plastid-To-Nucleus Signaling. <i>Frontiers in Plant Science</i> , 2012 , 3, 236	6.2	34
83	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, 13343-6	11.5	144
82	The Medicago genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011 , 480, 520-4	50.4	936
81	Unlocking the barley genome by chromosomal and comparative genomics. <i>Plant Cell</i> , 2011 , 23, 1249-63	11.6	390
80	Exploring the genomes: from Arabidopsis to crops. <i>Journal of Plant Physiology</i> , 2011 , 168, 3-8	3.6	14
79	The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , 2011 , 43, 476-81	36.3	638
78	Intracompartmental and intercompartmental transcriptional networks coordinate the expression of genes for organellar functions. <i>Plant Physiology</i> , 2011 , 157, 386-404	6.6	37
77	Comparative sequence analysis of VRN1 alleles of <i>Lolium perenne</i> with the co-linear regions in barley, wheat, and rice. <i>Molecular Genetics and Genomics</i> , 2011 , 286, 433-47	3.1	23
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	5.3	86
75	MicroRNAs coordinately regulate protein complexes. <i>BMC Systems Biology</i> , 2011 , 5, 136	3.5	48
74	Sequencing of BAC pools by different next generation sequencing platforms and strategies. <i>BMC Research Notes</i> , 2011 , 4, 411	2.3	11
73	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, 1706-18	11.6	172
72	MIPS: curated databases and comprehensive secondary data resources in 2010. <i>Nucleic Acids Research</i> , 2011 , 39, D220-4	20.1	65
71	The Non-coding Landscape of the Genome of <i>Arabidopsis thaliana</i> 2011 , 67-121		

70	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010 , 463, 763-850.4	1399
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, 17809-14	11.5 113
68	Gene content and virtual gene order of barley chromosome 1H. <i>Plant Physiology</i> , 2009 , 151, 496-505	6.6 126
67	Discovery of cis-elements between sorghum and rice using co-expression and evolutionary conservation. <i>BMC Genomics</i> , 2009 , 10, 284	4.5 24
66	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	4.5 62
65	Deep-sequencing of plant viral small RNAs reveals effective and widespread targeting of viral genomes. <i>Virology</i> , 2009 , 392, 203-14	3.6 224
64	The Sorghum bicolor genome and the diversification of grasses. <i>Nature</i> , 2009 , 457, 551-6	50.4 2200
63	Green evolution and dynamic adaptations revealed by genomes of the marine picoeukaryotes <i>Micromonas</i> . <i>Science</i> , 2009 , 324, 268-72	33.3 503
62	The <i>Physcomitrella</i> genome reveals evolutionary insights into the conquest of land by plants. <i>Science</i> , 2008 , 319, 64-9	33.3 1419
61	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, 2366-78	20.1 72
60	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, 2019-30	8.3 41
59	Characterization of Reflector Types by Phase-Sensitive Ultrasonic Data Processing and Imaging. <i>Journal of Nondestructive Evaluation</i> , 2008 , 27, 35-45	2.1 25
58	MIPS: analysis and annotation of genome information in 2007. <i>Nucleic Acids Research</i> , 2008 , 36, D196-2010.1	10.1 123
57	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	5.3 59
56	Apollo2Go: a web service adapter for the Apollo genome viewer to enable distributed genome annotation. <i>BMC Bioinformatics</i> , 2007 , 8, 320	3.6 4
55	MIPS plant genome information resources. <i>Methods in Molecular Biology</i> , 2007 , 406, 137-59	1.4 6
54	MIPSPplantsDB--plant database resource for integrative and comparative plant genome research. <i>Nucleic Acids Research</i> , 2007 , 35, D834-40	20.1 42
53	Genetic and genomic analysis of legume flowers and seeds. <i>Current Opinion in Plant Biology</i> , 2006 , 9, 133-41	9.9 31

52	MIPS: analysis and annotation of proteins from whole genomes in 2005. <i>Nucleic Acids Research</i> , 2006 , 34, D169-72	20.1	278
51	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	5	26
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8	Chromosome-scale comparative sequence analysis unravels molecular mechanisms of genome evolution between two wheat cultivars		1
7	The genome and metabolome of the tobacco tree, <i>Nicotiana glauca</i> : a potential renewable feedstock for the bioeconomy		3
6	Impact of transposable elements on genome structure and evolution in bread wheat		3
5	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools		7
4	European maize genomes unveil pan-genomic dynamics of repeats and genes		3
3	Evolution of the bread wheat D-subgenome and enriching it with diversity from <i>Aegilops tauschii</i>		2
2	Calpain DEK1 acts as a developmental switch gatekeeping cell fate transitions		1
1	Genome sequences of <i>Aegilops</i> species of section Sitopsis reveal phylogenetic relationships and provide resources for wheat improvement		2