

Klaus F X Mayer

List of Publications by Citations

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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	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000 , 408, 796-815	50.4	7262
212	The <i>Sorghum bicolor</i> genome and the diversification of grasses. <i>Nature</i> , 2009 , 457, 551-6	50.4	2200
211	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012 , 485, 635-41	50.4	2138
210	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
209	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010 , 463, 763-85	50.4	1399
208	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018 , 361,	33.3	1296
207	Role of WUSCHEL in regulating stem cell fate in the <i>Arabidopsis</i> shoot meristem. <i>Cell</i> , 1998 , 95, 805-15	56.2	1276
206	The stem cell population of <i>Arabidopsis</i> shoot meristems is maintained by a regulatory loop between the CLAVATA and WUSCHEL genes. <i>Cell</i> , 2000 , 100, 635-44	56.2	1242
205	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014 , 345, 1251788	33.3	1129
204	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012 , 491, 711-6	50.4	1124
203	The <i>Medicago</i> genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011 , 480, 520-4	50.4	936
202	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012 , 492, 423-7	50.4	839
201	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017 , 544, 427-433	50.4	822
200	Analysis of the bread wheat genome using whole-genome shotgun sequencing. <i>Nature</i> , 2012 , 491, 705-10	50.4	821
199	Comparative analysis of the receptor-like kinase family in <i>Arabidopsis</i> and rice. <i>Plant Cell</i> , 2004 , 16, 1220-34	33.4	772
198	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
197	<i>Aegilops tauschii</i> draft genome sequence reveals a gene repertoire for wheat adaptation. <i>Nature</i> , 2013 , 496, 91-5	50.4	601

196	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
195	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. <i>Science</i> , 2017 , 357, 93-97	33.3	474
194	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014 , 345, 1250092	33.3	419
193	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014 , 345, 1249721	33.3	397
192	Unlocking the barley genome by chromosomal and comparative genomics. <i>Plant Cell</i> , 2011 , 23, 1249-63	11.6	390
191	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018 , 361,	33.3	368
190	Sequence and analysis of chromosome 4 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 1999 , 402, 769-77	50.4	342
189	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017 , 551, 498-502	50.4	337
188	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019 , 51, 885-895	36.3	289
187	MIPS: analysis and annotation of proteins from whole genomes in 2005. <i>Nucleic Acids Research</i> , 2006 , 34, D169-72	20.1	278
186	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
185	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
184	Legume genome evolution viewed through the <i>Medicago truncatula</i> and <i>Lotus japonicus</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 14959-64	11.5	256
183	Gene selection from microarray data for cancer classification--a machine learning approach. <i>Computational Biology and Chemistry</i> , 2005 , 29, 37-46	3.6	254
182	Sequence composition and genome organization of maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 14349-54	11.5	247
181	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
180	Genome interplay in the grain transcriptome of hexaploid bread wheat. <i>Science</i> , 2014 , 345, 1250091	33.3	225
179	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

178	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <i>Plant Journal</i> , 2013 , 76, 718-27	6.9	219
177	START lipid/sterol-binding domains are amplified in plants and are predominantly associated with homeodomain transcription factors. <i>Genome Biology</i> , 2004 , 5, R41	18.3	201
176	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
175	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
174	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020 , 588, 277-283	50.4	180
173	MIPS: a database for genomes and protein sequences. <i>Nucleic Acids Research</i> , 1999 , 27, 44-8	20.1	177
172	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
171	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
170	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
169	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
168	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , 2018 , 361,	33.3	167
167	Sequence and analysis of chromosome 3 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000 , 408, 820-2	50.4	153
166	Mass-spectrometry-based draft of the <i>Arabidopsis</i> proteome. <i>Nature</i> , 2020 , 579, 409-414	50.4	144
165	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
164	MIPS <i>Arabidopsis thaliana</i> Database (MAtdB): an integrated biological knowledge resource based on the first complete plant genome. <i>Nucleic Acids Research</i> , 2002 , 30, 91-3	20.1	141
163	Reticulate evolution of the rye genome. <i>Plant Cell</i> , 2013 , 25, 3685-98	11.6	140
162	Transcriptional similarities, dissimilarities, and conservation of cis-elements in duplicated genes of <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2004 , 136, 3009-22	6.6	137
161	Sequence and analysis of chromosome 5 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000 , 408, 823-6	50.4	137

160	Towards a whole-genome sequence for rye (<i>Secale cereale</i> L.). <i>Plant Journal</i> , 2017 , 89, 853-869	6.9	136
159	Brassinosteroids Are Master Regulators of Gibberellin Biosynthesis in Arabidopsis. <i>Plant Cell</i> , 2015 , 27, 2261-72	11.6	131
158	Structure and architecture of the maize genome. <i>Plant Physiology</i> , 2005 , 139, 1612-24	6.6	130
157	Plant genome sequencing - applications for crop improvement. <i>Current Opinion in Biotechnology</i> , 2014 , 26, 31-7	11.4	128
156	Gene content and virtual gene order of barley chromosome 1H. <i>Plant Physiology</i> , 2009 , 151, 496-505	6.6	126
155	MIPS: analysis and annotation of genome information in 2007. <i>Nucleic Acids Research</i> , 2008 , 36, D196-2010.1	10.1	123
154	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
153	Impact of transposable elements on genome structure and evolution in bread wheat. <i>Genome Biology</i> , 2018 , 19, 103	18.3	119
152	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
151	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
150	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
149	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, 817-35	4.6	104
148	Snipping polymorphisms from large EST collections in barley (<i>Hordeum vulgare</i> L.). <i>Molecular Genetics and Genomics</i> , 2003 , 270, 24-33	3.1	100
147	Tracing the ancestry of modern bread wheats. <i>Nature Genetics</i> , 2019 , 51, 905-911	36.3	99
146	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020 , 588, 284-289	50.4	97
145	Uneven chromosome contraction and expansion in the maize genome. <i>Genome Research</i> , 2006 , 16, 1241-51	5.1	95
144	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019 , 20, 284	18.3	89
143	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

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	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013 , 14, R58	18.3	81
140	Genome mapping of seed-borne allergens and immunoresponsive proteins in wheat. <i>Science Advances</i> , 2018 , 4, eaar8602	14.3	80
139	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
138	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
137	MIPS Arabidopsis thaliana Database (MAtdB): an integrated biological knowledge resource for plant genomics. <i>Nucleic Acids Research</i> , 2004 , 32, D373-6	20.1	74
136	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
135	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
134	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	6.23	69
133	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
132	Characterization of the maize endosperm transcriptome and its comparison to the rice genome. <i>Genome Research</i> , 2004 , 14, 1932-7	9.7	68
131	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	4.5	67
130	MIPS: curated databases and comprehensive secondary data resources in 2010. <i>Nucleic Acids Research</i> , 2011 , 39, D220-4	20.1	65
129	PGSB PlantsDB: updates to the database framework for comparative plant genome research. <i>Nucleic Acids Research</i> , 2016 , 44, D1141-7	20.1	64
128	The perennial ryegrass GenomeZipper: targeted use of genome resources for comparative grass genomics. <i>Plant Physiology</i> , 2013 , 161, 571-82	6.6	63
127	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
126	Sequence and analysis of the Arabidopsis genome. <i>Current Opinion in Plant Biology</i> , 2001 , 4, 105-10	9.9	62
125	Modulation of Ambient Temperature-Dependent Flowering in Arabidopsis thaliana by Natural Variation of FLOWERING LOCUS M. <i>PLoS Genetics</i> , 2015 , 11, e1005588	6	61

124	Expressed sequence tag analysis in Cycas, the most primitive living seed plant. <i>Genome Biology</i> , 2003 , 4, R78	18.3	61
123	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
122	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, 1167-74	9.7	59
121	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
120	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
119	The <i>Cardamine hirsuta</i> genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , 2016 , 2, 16167	11.5	56
118	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
117	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
116	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	8.4	51
115	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
114	MicroRNAs coordinately regulate protein complexes. <i>BMC Systems Biology</i> , 2011 , 5, 136	3.5	48
113	Exon discovery by genomic sequence alignment. <i>Bioinformatics</i> , 2002 , 18, 777-87	7.2	48
112	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
111	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
110	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
109	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
108	Large-scale cis-element detection by analysis of correlated expression and sequence conservation between <i>Arabidopsis</i> and <i>Brassica oleracea</i> . <i>Plant Physiology</i> , 2006 , 142, 1589-602	6.6	45
107	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

106	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
105	MIPSPPlantsDB--plant database resource for integrative and comparative plant genome research. <i>Nucleic Acids Research</i> , 2007 , 35, D834-40	20.1	42
104	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
103	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
102	Sputnik: a database platform for comparative plant genomics. <i>Nucleic Acids Research</i> , 2003 , 31, 128-32	20.1	40
101	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
100	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
99	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
98	Intracompartmental and intercompartmental transcriptional networks coordinate the expression of genes for organellar functions. <i>Plant Physiology</i> , 2011 , 157, 386-404	6.6	37
97	Genome-wide in silico mapping of scaffold/matrix attachment regions in <i>Arabidopsis</i> suggests correlation of intragenic scaffold/matrix attachment regions with gene expression. <i>Plant Physiology</i> , 2004 , 135, 715-22	6.6	37
96	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
95	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
94	Slicing the wheat genome. Introduction. <i>Science</i> , 2014 , 345, 285-7	33.3	35
93	Integrating cereal genomics to support innovation in the Triticeae. <i>Functional and Integrative Genomics</i> , 2012 , 12, 573-83	3.8	35
92	PlantMarkers--a database of predicted molecular markers from plants. <i>Nucleic Acids Research</i> , 2005 , 33, D628-32	20.1	35
91	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021 , 53, 564-573	36.3	35
90	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
89	Evidence for a Contribution of ALA Synthesis to Plastid-To-Nucleus Signaling. <i>Frontiers in Plant Science</i> , 2012 , 3, 236	6.2	34

88	European maize genomes highlight intraspecies variation in repeat and gene content. <i>Nature Genetics</i> , 2020 , 52, 950-957	36.3	34
87	A comprehensive study of the genomic differentiation between temperate Dent and Flint maize. <i>Genome Biology</i> , 2016 , 17, 137	18.3	34
86	The repetitive landscape of the 5100 Mbp barley genome. <i>Mobile DNA</i> , 2017 , 8, 22	4.4	33
85	Computational aspects underlying genome to phenome analysis in plants. <i>Plant Journal</i> , 2019 , 97, 182-188	10.8	33
84	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
83	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
82	How can we deliver the large plant genomes? Strategies and perspectives. <i>Current Opinion in Plant Biology</i> , 2002 , 5, 173-7	9.9	32
81	Genetic and genomic analysis of legume flowers and seeds. <i>Current Opinion in Plant Biology</i> , 2006 , 9, 133-41	9.9	31
80	Extensive signal integration by the phytohormone protein network. <i>Nature</i> , 2020 , 583, 271-276	50.4	30
79	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
78	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
77	Evidence for an ancient chromosomal duplication in <i>Arabidopsis thaliana</i> by sequencing and analyzing a 400-kb contig at the APETALA2 locus on chromosome 4. <i>FEBS Letters</i> , 1999 , 445, 237-45	3.8	30
76	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
75	Hidden variation in polyploid wheat drives local adaptation. <i>Genome Research</i> , 2018 , 28, 1319-1332	9.7	27
74	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
73	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, 1237-52	14.4	26
72	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
71	Significant sequence similarities in promoters and precursors of <i>Arabidopsis thaliana</i> non-conserved microRNAs. <i>Bioinformatics</i> , 2006 , 22, 2585-9	7.2	26

70	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021 , 33, 1888-1906	11.6	26
69	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
68	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
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	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
65	MOsDB: an integrated information resource for rice genomics. <i>Nucleic Acids Research</i> , 2003 , 31, 190-2	20.1	23
64	From plant genomes to phenotypes. <i>Journal of Biotechnology</i> , 2017 , 261, 46-52	3.7	22
63	Flow sorting and sequencing meadow fescue chromosome 4F. <i>Plant Physiology</i> , 2013 , 163, 1323-37	6.6	22
62	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
61	RNASeqExpressionBrowser--a web interface to browse and visualize high-throughput expression data. <i>Bioinformatics</i> , 2014 , 30, 2519-20	7.2	20
60	Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016 , 14, 1511-22	11.6	18
59	Analysing complex Triticeae genomes - concepts and strategies. <i>Plant Methods</i> , 2013 , 9, 35	5.8	17
58	The Systems Architecture of Molecular Memory in Poplar after Abiotic Stress. <i>Plant Cell</i> , 2019 , 31, 346-367	11.6	17
57	Comparative transcriptome analysis within the <i>Lolium/Festuca</i> species complex reveals high sequence conservation. <i>BMC Genomics</i> , 2015 , 16, 249	4.5	16
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8	Insights into the evolution of symbiosis gene copy number and distribution from a chromosome-scale <i>Lotus japonicus</i> Gifu genome sequence		1
7	Chromosome-scale comparative sequence analysis unravels molecular mechanisms of genome evolution between two wheat cultivars		1
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