

Masaaki Kobayashi

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.

34
papers

834
citations

11
h-index

28
g-index

38
ext. papers

991
ext. citations

4.2
avg, IF

3.04
L-index

#	Paper	IF	Citations
34	RAD-seq-Based High-Density Linkage Map Construction and QTL Mapping of Biomass-Related Traits in Sorghum using the Japanese Landrace Takakibi NOG. <i>Plant and Cell Physiology</i> , 2020 , 61, 1262-1272	4.9	10
33	Evolution and Diversity of the Wild Rice <i>Oryza officinalis</i> Complex, across Continents, Genome Types, and Ploidy Levels. <i>Genome Biology and Evolution</i> , 2020 , 12, 413-428	3.9	6
32	Plant Omics Data Center and CATchUP: web databases for effective gene mining utilizing public RNA-Seq-based transcriptome data 2020 , 1137-1146		
31	Complete chloroplast genome sequence and phylogenetic analysis of wasabi (<i>Eutrema japonicum</i>) and its relatives. <i>Scientific Reports</i> , 2019 , 9, 14377	4.9	6
30	Expression of Genes from Paternal Alleles in Rice Zygotes and Involvement of OsASGR-BBML1 in Initiation of Zygotic Development. <i>Plant and Cell Physiology</i> , 2019 , 60, 725-737	4.9	19
29	Comparison of shape quantification methods for genomic prediction, and genome-wide association study of sorghum seed morphology. <i>PLoS ONE</i> , 2019 , 14, e0224695	3.7	6
28	TRANSNAP: a web database providing comprehensive information on Japanese pear transcriptome. <i>Scientific Reports</i> , 2019 , 9, 18922	4.9	5
27	Comparison of shape quantification methods for genomic prediction, and genome-wide association study of sorghum seed morphology 2019 , 14, e0224695		
26	Comparison of shape quantification methods for genomic prediction, and genome-wide association study of sorghum seed morphology 2019 , 14, e0224695		
25	Comparison of shape quantification methods for genomic prediction, and genome-wide association study of sorghum seed morphology 2019 , 14, e0224695		
24	Comparison of shape quantification methods for genomic prediction, and genome-wide association study of sorghum seed morphology 2019 , 14, e0224695		
23	TodoFirGene: Developing Transcriptome Resources for Genetic Analysis of <i>Abies sachalinensis</i> . <i>Plant and Cell Physiology</i> , 2018 , 59, 1276-1284	4.9	12
22	Repeated inversions within a pannier intron drive diversification of intraspecific colour patterns of ladybird beetles. <i>Nature Communications</i> , 2018 , 9, 3843	17.4	34
21	Differentiation capacities of PS-clusters, adult pituitary stem/progenitor cell clusters located in the parenchymal-niche, of the rat anterior lobe. <i>PLoS ONE</i> , 2018 , 13, e0196029	3.7	3
20	Heap: a highly sensitive and accurate SNP detection tool for low-coverage high-throughput sequencing data. <i>DNA Research</i> , 2017 , 24, 397-405	4.5	11
19	Development of simple sequence repeat markers in the halophytic turf grass <i>Sporobolus virginicus</i> and transferable genotyping across multiple grass genera/species/genotypes. <i>Euphytica</i> , 2017 , 213, 1	2.1	2
18	TOMATOMICS: A Web Database for Integrated Omics Information in Tomato. <i>Plant and Cell Physiology</i> , 2017 , 58, e8	4.9	19

17	Practical Utilization of OryzaExpress and Plant Omics Data Center Databases to Explore Gene Expression Networks in Oryza Sativa and Other Plant Species. <i>Methods in Molecular Biology</i> , 2017 , 1533, 229-240	1.4	1
16	High-Throughput Phenotyping of Sorghum Plant Height Using an Unmanned Aerial Vehicle and Its Application to Genomic Prediction Modeling. <i>Frontiers in Plant Science</i> , 2017 , 8, 421	6.2	144
15	Comparative analysis of microRNA profiles of rice anthers between cool-sensitive and cool-tolerant cultivars under cool-temperature stress. <i>Genes and Genetic Systems</i> , 2016 , 91, 97-109	1.4	7
14	Pleurochrysome: A Web Database of Pleurochrysis Transcripts and Orthologs Among Heterogeneous Algae. <i>Plant and Cell Physiology</i> , 2016 , 57, e6	4.9	2
13	Databases for Solanaceae and Cucurbitaceae Research. <i>Biotechnology in Agriculture and Forestry</i> , 2016 , 31-42		1
12	Be happy with your Perl scripts. <i>Ikushugaku Kenkyu</i> , 2016 , 18, 27-33	0.1	
11	Plant Omics Data Center: an integrated web repository for interspecies gene expression networks with NLP-based curation. <i>Plant and Cell Physiology</i> , 2015 , 56, e9	4.9	45
10	Omics Analysis and Databases for Plant Science 2015 , 150-159		2
9	Expression Analysis and Genome Annotations with RNA Sequencing 2015 , 1-12		
8	De novo transcriptome assembly of a fern, <i>Lygodium japonicum</i> , and a web resource database, Ljtrans DB. <i>Plant and Cell Physiology</i> , 2015 , 56, e5	4.9	28
7	Introduction of NIG supercomputer with command line-based NGS analysis. <i>Ikushugaku Kenkyu</i> , 2015 , 17, 88-93	0.1	
6	A-WINGS: an integrated genome database for <i>Pleurocybella porrigens</i> (Angel's wing oyster mushroom, Sugihiratake). <i>BMC Research Notes</i> , 2014 , 7, 866	2.3	4
5	Genome-wide analysis of intraspecific DNA polymorphism in Micro-Tom μ a model cultivar of tomato (<i>Solanum lycopersicum</i>). <i>Plant and Cell Physiology</i> , 2014 , 55, 445-54	4.9	49
4	Introduction to large-scale omics data analysis for plant breeding. <i>Ikushugaku Kenkyu</i> , 2014 , 16, 93-99	0.1	
3	Spatial and temporal expression of two transcriptional isoforms of Lhx3, a LIM class homeobox gene, during embryogenesis of two phylogenetically remote ascidians, <i>Halocynthia roretzi</i> and <i>Ciona intestinalis</i> . <i>Gene Expression Patterns</i> , 2010 , 10, 98-104	1.5	7
2	Evolutionary origins of blastoporal expression and organizer activity of the vertebrate gastrula organizer gene <i>lhx1</i> and its ancient metazoan paralog <i>lhx3</i> . <i>Development (Cambridge)</i> , 2009 , 136, 2005-14	6.6	22
1	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. <i>Genome Research</i> , 2008 , 18, 1100-11	9.7	387