

Kentaro Yoshida

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.

40
papers

3,704
citations

21
h-index

41
g-index

41
ext. papers

5,066
ext. citations

8.3
avg, IF

4.71
L-index

#	Paper	IF	Citations
40	RNA-Seq-based DNA marker analysis of the genetics and molecular evolution of Triticeae species. <i>Functional and Integrative Genomics</i> , 2021 , 21, 535-542	3.8	0
39	GRAS-Di system facilitates high-density genetic map construction and QTL identification in recombinant inbred lines of the wheat progenitor <i>Aegilops tauschii</i> . <i>Scientific Reports</i> , 2020 , 10, 21455	4.9	7
38	Production and phenotypic characterization of nascent synthetic decaploids derived from interspecific crosses between a durum wheat cultivar and hexaploid <i>Aegilops</i> species. <i>Genetic Resources and Crop Evolution</i> , 2020 , 67, 1905-1917	2	2
37	Diploid genome differentiation conferred by RNA sequencing-based survey of genome-wide polymorphisms throughout homoeologous loci in <i>Triticum</i> and <i>Aegilops</i> . <i>BMC Genomics</i> , 2020 , 21, 246	4.5	3
36	Introgression of chromosomal segments conferring early heading date from wheat diploid progenitor, <i>Aegilops tauschii</i> Coss., into Japanese elite wheat cultivars. <i>PLoS ONE</i> , 2020 , 15, e0228397	3.7	5
35	Identification of a hard kernel texture line of synthetic allohexaploid wheat reducing the puroindoline accumulation on the D genome from <i>Aegilops tauschii</i> . <i>Journal of Cereal Science</i> , 2020 , 93, 102964	3.8	2
34	Phenotypic effects of the U-genome variation in nascent synthetic hexaploids derived from interspecific crosses between durum wheat and its diploid relative <i>Aegilops umbellulata</i> . <i>PLoS ONE</i> , 2020 , 15, e0231129	3.7	3
33	Origin of wheat B-genome chromosomes inferred from RNA sequencing analysis of leaf transcripts from section <i>Sitopsis</i> species of <i>Aegilops</i> . <i>DNA Research</i> , 2019 , 26, 171-182	4.5	24
32	Genome-wide polymorphisms from RNA sequencing assembly of leaf transcripts facilitate phylogenetic analysis and molecular marker development in wild einkorn wheat. <i>Molecular Genetics and Genomics</i> , 2019 , 294, 1327-1341	3.1	9
31	The ash dieback invasion of Europe was founded by two genetically divergent individuals. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1000-1008	12.3	49
30	Core microbiomes for sustainable agroecosystems. <i>Nature Plants</i> , 2018 , 4, 247-257	11.5	328
29	Effect of the U genome on grain hardness in nascent synthetic hexaploids derived from interspecific hybrids between durum wheat and <i>Aegilops umbellulata</i> . <i>Journal of Cereal Science</i> , 2018 , 83, 153-161	3.8	7
28	RNA-seq analysis reveals considerable genetic diversity and provides genetic markers saturating all chromosomes in the diploid wild wheat relative <i>Aegilops umbellulata</i> . <i>BMC Plant Biology</i> , 2018 , 18, 271	5.3	16
27	RNA Sequencing-Based Bulk Segregant Analysis Facilitates Efficient D-genome Marker Development for a Specific Chromosomal Region of Synthetic Hexaploid Wheat. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	7
26	<i>Lentinula edodes</i> Genome Survey and Postharvest Transcriptome Analysis. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	35
25	Hybrid incompatibilities in interspecific crosses between tetraploid wheat and its wild diploid relative <i>Aegilops umbellulata</i> . <i>Plant Molecular Biology</i> , 2017 , 95, 625-645	4.6	13
24	Evolution of the wheat blast fungus through functional losses in a host specificity determinant. <i>Science</i> , 2017 , 357, 80-83	33.3	150

23	Comparative secretome analysis of <i>Rhizoctonia solani</i> isolates with different host ranges reveals unique secretomes and cell death inducing effectors. <i>Scientific Reports</i> , 2017 , 7, 10410	4.9	32
22	Global gene expression profiling related to temperature-sensitive growth abnormalities in interspecific crosses between tetraploid wheat and <i>Aegilops tauschii</i> . <i>PLoS ONE</i> , 2017 , 12, e0176497	3.7	3
21	Host specialization of the blast fungus <i>Magnaporthe oryzae</i> is associated with dynamic gain and loss of genes linked to transposable elements. <i>BMC Genomics</i> , 2016 , 17, 370	4.5	98
20	Genome-wide identification of novel genetic markers from RNA sequencing assembly of diverse <i>Aegilops tauschii</i> accessions. <i>Molecular Genetics and Genomics</i> , 2016 , 291, 1681-94	3.1	16
19	Grouping of multicopper oxidases in <i>Lentinula edodes</i> by sequence similarities and expression patterns. <i>AMB Express</i> , 2015 , 5, 63	4.1	13
18	Rice Exo70 interacts with a fungal effector, AVR-Pii, and is required for AVR-Pii-triggered immunity. <i>Plant Journal</i> , 2015 , 83, 875-87	6.9	72
17	Accelerated senescence and enhanced disease resistance in hybrid chlorosis lines derived from interspecific crosses between tetraploid wheat and <i>Aegilops tauschii</i> . <i>PLoS ONE</i> , 2015 , 10, e0121583	3.7	11
16	Computational analyses of ancient pathogen DNA from herbarium samples: challenges and prospects. <i>Frontiers in Plant Science</i> , 2015 , 6, 771	6.2	13
15	Effector specialization in a lineage of the Irish potato famine pathogen. <i>Science</i> , 2014 , 343, 552-5	33.3	143
14	MutMap-Gap: whole-genome resequencing of mutant F2 progeny bulk combined with de novo assembly of gap regions identifies the rice blast resistance gene Pii. <i>New Phytologist</i> , 2013 , 200, 276-283 ^{9.8}	9.8	149
13	From pathogen genomes to host plant processes: the power of plant parasitic oomycetes. <i>Genome Biology</i> , 2013 , 14, 211	18.3	53
12	QTL-seq: rapid mapping of quantitative trait loci in rice by whole genome resequencing of DNA from two bulked populations. <i>Plant Journal</i> , 2013 , 74, 174-83	6.9	619
11	Deployment of the <i>Burkholderia glumae</i> type III secretion system as an efficient tool for translocating pathogen effectors to monocot cells. <i>Plant Journal</i> , 2013 , 74, 701-12	6.9	35
10	Coval: improving alignment quality and variant calling accuracy for next-generation sequencing data. <i>PLoS ONE</i> , 2013 , 8, e75402	3.7	44
9	Arms race co-evolution of <i>Magnaporthe oryzae</i> AVR-Pik and rice Pik genes driven by their physical interactions. <i>Plant Journal</i> , 2012 , 72, 894-907	6.9	180
8	Genome sequencing reveals agronomically important loci in rice using MutMap. <i>Nature Biotechnology</i> , 2012 , 30, 174-8	44.5	73 ¹
7	Large-scale gene disruption in <i>Magnaporthe oryzae</i> identifies MC69, a secreted protein required for infection by monocot and dicot fungal pathogens. <i>PLoS Pathogens</i> , 2012 , 8, e1002711	7.6	110
6	A multifaceted genomics approach allows the isolation of the rice Pia-blast resistance gene consisting of two adjacent NBS-LRR protein genes. <i>Plant Journal</i> , 2011 , 66, 467-79	6.9	213

5	Multiple translocation of the AVR-Pita effector gene among chromosomes of the rice blast fungus <i>Magnaporthe oryzae</i> and related species. <i>PLoS Pathogens</i> , 2011 , 7, e1002147	7.6	169
4	Towards population genomics of effector-effector target interactions. <i>New Phytologist</i> , 2010 , 187, 929-398	398	25
3	Association genetics reveals three novel avirulence genes from the rice blast fungal pathogen <i>Magnaporthe oryzae</i> . <i>Plant Cell</i> , 2009 , 21, 1573-91	11.6	302
2	Crowdsourced analysis of ash and ash dieback through the Open Ash Dieback project: A year 1 report on datasets and analyses contributed by a self-organising community		5
1	Lessons in effector and NLR biology of plant-microbe systems		1