

Shohei Takuno

List of Publications by Year in descending order

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34
papers

3,217
citations

331670

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377865

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37
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37
docs citations

37
times ranked

5129
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptional regulation of genes bearing intronic heterochromatin in the rice genome. <i>PLoS Genetics</i> , 2020, 16, e1008637.	3.5	23
2	Single-cell expression noise and gene-body methylation in <i>Arabidopsis thaliana</i> . <i>Heredity</i> , 2019, 123, 81-91.	2.6	30
3	Coalescent framework for prokaryotes undergoing interspecific homologous recombination. <i>Heredity</i> , 2018, 120, 474-484.	2.6	6
4	Genome-wide characterization of DNA methylation, small RNA expression, and histone H3 lysine nine di-methylation in <i>Brassica rapa</i> L.. <i>DNA Research</i> , 2018, 25, 511-520.	3.4	25
5	The Evolutionary Dynamics of Orthologs That Shift in Gene Body Methylation between <i>Arabidopsis</i> Species. <i>Molecular Biology and Evolution</i> , 2017, 34, 1479-1491.	8.9	29
6	Evolutionary patterns of genic DNA methylation vary across land plants. <i>Nature Plants</i> , 2016, 2, 15222.	9.3	178
7	A role for palindromic structures in the <i>cis</i> -region of maize Sirevirus LTRs in transposable element evolution and host epigenetic response. <i>Genome Research</i> , 2016, 26, 226-237.	5.5	22
8	CG Methylation Covaries with Differential Gene Expression between Leaf and Floral Bud Tissues of <i>Brachypodium distachyon</i> . <i>PLoS ONE</i> , 2016, 11, e0150002.	2.5	25
9	Epigenetic regulation of intragenic transposable elements impacts gene transcription in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2015, 43, 3911-3921.	14.5	86
10	Independent Molecular Basis of Convergent Highland Adaptation in Maize. <i>Genetics</i> , 2015, 200, 1297-1312.	2.9	67
11	Population Genomics of the Fission Yeast <i>Schizosaccharomyces pombe</i> . <i>PLoS ONE</i> , 2014, 9, e104241.	2.5	44
12	Identical sets of methylated and nonmethylated genes in <i>Ciona intestinalis</i> sperm and muscle cells. <i>Epigenetics and Chromatin</i> , 2013, 6, 38.	3.9	29
13	Gene body methylation is conserved between plant orthologs and is of evolutionary consequence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1797-1802.	7.1	206
14	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, 174-183.	5.7	1,065
15	The <i>Capsella rubella</i> genome and the genomic consequences of rapid mating system evolution. <i>Nature Genetics</i> , 2013, 45, 831-835.	21.4	374
16	Comparative Analyses Identify the Contributions of Exotic Donors to Disease Resistance in a Barley Experimental Population. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1945-1953.	1.8	11
17	From Many, One: Genetic Control of Prolificacy during Maize Domestication. <i>PLoS Genetics</i> , 2013, 9, e1003604.	3.5	111
18	QTL Map Meets Population Genomics: An Application to Rice. <i>PLoS ONE</i> , 2013, 8, e83720.	2.5	9

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19	Population Genomics in Bacteria: A Case Study of <i>Staphylococcus aureus</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 797-809.	8.9	37
20	Recent Retrotransposon Insertions Are Methylated and Phylogenetically Clustered in Japonica Rice (<i>Oryza sativa</i> spp. japonica). <i>Molecular Biology and Evolution</i> , 2012, 29, 3193-3203.	8.9	22
21	Body-Methylated Genes in <i>Arabidopsis thaliana</i> Are Functionally Important and Evolve Slowly. <i>Molecular Biology and Evolution</i> , 2012, 29, 219-227.	8.9	222
22	Modeling evolutionary growth of a microRNA-mediated regulation system. <i>Journal of Theoretical Biology</i> , 2012, 311, 54-65.	1.7	2
23	The Power of QTL Mapping with RILs. <i>PLoS ONE</i> , 2012, 7, e46545.	2.5	33
24	The Patterns and Causes of Variation in Plant Nucleotide Substitution Rates. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2011, 42, 245-266.	8.3	136
25	Artificial selection for a green revolution gene during japonica rice domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11034-11039.	7.1	179
26	Simple and efficient methods for S genotyping and S screening in genus Brassica by dot-blot analysis. <i>Molecular Breeding</i> , 2011, 28, 1-12.	2.1	19
27	Selection Fine-Tunes the Expression of MicroRNA Target Genes in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2011, 28, 2429-2434.	8.9	11
28	Lowly Expressed Genes in <i>Arabidopsis thaliana</i> Bear the Signature of Possible Pseudogenization by Promoter Degradation. <i>Molecular Biology and Evolution</i> , 2011, 28, 1193-1203.	8.9	59
29	Selection to Maintain Paralogous Amino Acid Differences Under the Pressure of Gene Conversion in the Heat-Shock Protein Genes in Yeast. <i>Molecular Biology and Evolution</i> , 2009, 26, 2655-2659.	8.9	9
30	Evolution of complexity in miRNA-mediated gene regulation systems. <i>Trends in Genetics</i> , 2008, 24, 56-59.	6.7	14
31	Preservation of a Pseudogene by Gene Conversion and Diversifying Selection. <i>Genetics</i> , 2008, 180, 517-531.	2.9	34
32	The pattern of amplification and differentiation of Ty1-copia and Ty3-gypsy retrotransposons in Brassicaceae species. <i>Genes and Genetic Systems</i> , 2008, 83, 13-22.	0.7	8
33	Effects of Recombination on Hitchhiking Diversity in the Brassica Self-incompatibility Locus Complex. <i>Genetics</i> , 2007, 177, 949-958.	2.9	42
34	Phylogenetic relationships among cultivated types of <i>Brassica rapa</i> L. em. Metzg. as revealed by AFLP analysis. <i>Genetic Resources and Crop Evolution</i> , 2007, 54, 279-285.	1.6	45