Kentaro K Shimizu

List of Publications by Year
in descending order

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95 papers	5,227 citations	101543 36 h-index	106344 65 g-index
113 all docs	113 docs citations	113 times ranked	6882 citing authors

#	Article	IF	Citations
1	Multiple wheat genomes reveal global variation in modern breeding. Nature, 2020, 588, 277-283.	27.8	513
2	The wheat powdery mildew genome shows the unique evolution of an obligate biotroph. Nature Genetics, 2013, 45, 1092-1096.	21.4	236
3	Estimating genomic diversity and population differentiation â€“ an empirical comparison of microsatellite and SNP variation in Arabidopsis halleri. BMC Genomics, 2017, 18, 69.	2.8	216
4	Sequencing of the genus Arabidopsis identifies a complex history of nonbifurcating speciation and abundant trans-specific polymorphism. Nature Genetics, 2016, 48, 1077-1082.	21.4	198
5	Hybridization of powdery mildew strains gives rise to pathogens on novel agricultural crop species. Nature Genetics, 2016, 48, 201-205.	21.4	192
6	Robust control of the seasonal expression of the Arabidopsis FLC gene in a fluctuating environment. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11632-11637.	7.1	162
7	Diversity at theMlaPowdery Mildew Resistance Locus from Cultivated Barley Reveals Sites of Positive Selection. Molecular Plant-Microbe Interactions, 2010, 23, 497-509.	2.6	160
8	Evolution of Selfing: Recurrent Patterns in Molecular Adaptation. Annual Review of Ecology, Evolution, and Systematics, 2015, 46, 593-622.	8.3	132
9	Evolution of self-compatibility in Arabidopsis by a mutation in the male specificity gene. Nature, 2010, 464, 1342-1346.	27.8	131
10	Molecular basis of flowering under natural long-day conditions in Arabidopsis. Nature Plants, 2018, 4, 824-835.	9.3	115
11	Population genomic footprints of selection and associations with climate in natural populations of Arabidopsis halleri from the Alps. Molecular Ecology, 2013, 22, 5594-5607.	3.9	113
12	Evolution and Control of Imprinted FWA Genes in the Genus Arabidopsis. PLoS Genetics, 2008, 4, e1000048.	3.5	111
13	Gene duplication and genetic exchange drive the evolution of S-RNase-based self-incompatibility in Petunia. Nature Plants, 2015, 1, 14005.	9.3	111
14	Using knockout mutants to reveal the growth costs of defensive traits. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 2598-2603.	2.6	110
15	The allopolyploidArabidopsis kamchaticaoriginated from multiple individuals ofArabidopsis lyrataandArabidopsis halleri. Molecular Ecology, 2009, 18, 4024-4048.	3.9	109
16	Genome-wide quantification of homeolog expression ratio revealed nonstochastic gene regulation in synthetic allopolyploid Arabidopsis. Nucleic Acids Research, 2014, 42, e46-e46.	14.5	108
17	Genome assembly and annotation of Arabidopsis halleri, a model for heavy metal hyperaccumulation and evolutionary ecology. Molecular Ecology Resources, 2017, 17, 1025-1036.	4.8	98
18	Darwinian Selection on a Selfing Locus. Science, 2004, 306, 2081-2084.	12.6	91

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19	Independent origins of selfâ€compatibility in Arabidopsis thaliana. Molecular Ecology, 2008, 17, 704-714.	3.9	90
20	The Cardamine hirsuta genome offers insight into the evolution of morphological diversity. Nature Plants, 2016, 2, 16167.	9.3	90
21	The More the Merrier: Recent Hybridization and Polyploidy in Cardamine. Plant Cell, 2013, 25, 3280-3295.	6.6	88
22	Nitrogen as a key regulator of flowering in Fagus crenata: understanding the physiological mechanism of masting by gene expression analysis. Ecology Letters, 2014, 17, 1299-1309.	6.4	86
23	Reference-guided de novo assembly approach improves genome reconstruction for related species. BMC Bioinformatics, 2017, 18, 474.	2.6	85
24	Multiple hybrid de novo genome assembly of finger millet, an orphan allotetraploid crop. DNA Research, 2018, 25, 39-47.	3.4	85
25	Allopolyploid origin of Cardamine asarifolia (Brassicaceae): Incongruence between plastid and nuclear ribosomal DNA sequences solved by a single-copy nuclear gene. Molecular Phylogenetics and Evolution, 2006, 39, 759-786.	2.7	78
26	Plant adaptive radiation mediated by polyploid plasticity in transcriptomes. Molecular Ecology, 2017, 26, 193-207.	3.9	76
27	Recent Loss of Self-Incompatibility by Degradation of the Male Component in Allotetraploid Arabidopsis kamchatica. PLoS Genetics, 2012, 8, e1002838.	3.5	72
28	Plant sexual reproduction during climate change: gene function in natura studied by ecological and evolutionary systems biology. Annals of Botany, 2011, 108, 777-787.	2.9	71
29	Mass flowering of the tropical tree <scp>S</scp>horea beccariana was preceded by expression changes in flowering and droughtâ€responsive genes. Molecular Ecology, 2013, 22, 4767-4782.	3.9	71
30	MAA3 (MAGATAMA3) Helicase Gene is Required for Female Gametophyte Development and Pollen Tube Guidance in Arabidopsis thaliana. Plant and Cell Physiology, 2008, 49, 1478-1483.	3.1	61
31	The Current Genomic Landscape of Western South America: Andes, Amazonia, and Pacific Coast. Molecular Biology and Evolution, 2019, 36, 2698-2713.	8.9	59
32	Evolutionary and Ecological Genomics of Arabidopsis. Plant Physiology, 2005, 138, 578-584.	4.8	58
33	Patterns of polymorphism and selection in the subgenomes of the allopolyploid Arabidopsis kamchatica. Nature Communications, 2018, 9, 3909.	12.8	52
34	The predominantly selfing plant Arabidopsis thaliana experienced a recent reduction in transposable element abundance compared to its outcrossing relative Arabidopsis lyrata. Mobile DNA, 2012, 3, 2.	3.6	50
35	Multiple hybridization events in Cardamine (Brassicaceae) during the last 150 years: revisiting a textbook example of neoallopolyploidy. Annals of Botany, 2014, 113, 817-830.	2.9	46
36	Local adaptation (mostly) remains local: reassessing environmental associations of climate-related candidate SNPs in Arabidopsis halleri. Heredity, 2017, 118, 193-201.	2.6	43

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37	Genomics meets remote sensing in global change studies: monitoring and predicting phenology, evolution and biodiversity. Current Opinion in Environmental Sustainability, 2017, 29, 177-186.	6.3	42
38	Genome structure analysis of molluscs revealed whole genome duplication and lineage specific repeat variation. Gene, 2011, 483, 63-71.	2.2	41
39	Selection Is No More Efficient in Haploid than in Diploid Life Stages of an Angiosperm and a Moss. Molecular Biology and Evolution, 2013, 30, 1929-1939.	8.9	41
40	Conserved but Attenuated Parental Gene Expression in Allopolyploids: Constitutive Zinc Hyperaccumulation in the AllotetraploidArabidopsis kamchatica. Molecular Biology and Evolution, 2016, 33, 2781-2800.	8.9	40
41	Efficient Purging of Deleterious Mutations in Plants with Haploid Selfing. Genome Biology and Evolution, 2014, 6, 1238-1252.	2.5	38
42	Cell Type-Specific Transcriptome of Brassicaceae Stigmatic Papilla Cells From a Combination of Laser Microdissection and RNA Sequencing. Plant and Cell Physiology, 2013, 54, 1894-1906.	3.1	37
43	Evolution of the Selfing Syndrome in Arabis alpina (Brassicaceae). PLoS ONE, 2015, 10, e0126618.	2.5	37
44	A stigmatic gene confers interspecies incompatibility in the Brassicaceae. Nature Plants, 2019, 5, 731-741.	9.3	37
45	The Nagoya Protocol could backfire on the Global South. Nature Ecology and Evolution, 2018, 2, 917-919.	7.8	31
46	Coexistence of Trichome Variation in a Natural Plant Population: A Combined Study Using Ecological and Candidate Gene Approaches. PLoS ONE, 2011, 6, e22184.	2.5	30
47	In Situ Enzyme Activity in the Dissolved and Particulate Fraction of the Fluid from Four Pitcher Plant Species of the Genus Nepenthes. PLoS ONE, 2011, 6, e25144.	2.5	30
48	Homeolog expression quantification methods for allopolyploids. Briefings in Bioinformatics, 2020, 21, 395-407.	6.5	29
49	Plant trichomes and a single gene GLABRA1 contribute to insect community composition on field-grown Arabidopsis thaliana. BMC Plant Biology, 2019, 19, 163.	3.6	28
50	Loss of the six3/6 controlling pathways might have resulted in pinhole-eye evolution in Nautilus. Scientific Reports, 2013, 3, 1432.	3.3	27
51	Bacterial diversity and composition in the fluid of pitcher plants of the genus Nepenthes. Systematic and Applied Microbiology, 2015, 38, 330-339.	2.8	27
52	Adaptive reduction of male gamete number in the selfing plant Arabidopsis thaliana. Nature Communications, 2020, 11, 2885.	12.8	27
53	Ultralong Oxford Nanopore Reads Enable the Development of a Reference-Grade Perennial Ryegrass Genome Assembly. Genome Biology and Evolution, 2021, 13, .	2.5	26
54	Duplicated pollenâ€“pistil recognition loci control intraspecific unilateral incompatibility in Brassica rapa. Nature Plants, 2017, 3, 17096.	9.3	25

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55	Effects of pollen availability and the mutation bias on the fixation of mutations disabling the male specificity of selfâ€incompatibility. Journal of Evolutionary Biology, 2013, 26, 2221-2232.	1.7	24
56	Multiple factors contribute to outcrossing in a tropical emergent Dipterocarpus tempehes, including a new pollenâ€tube guidance mechanism for selfâ€incompatibility. American Journal of Botany, 2002, 89, 60-66.	1.7	23
57	The population genomic signature of environmental association and gene flow in an ecologically divergent tree species Metrosideros polymorpha (Myrtaceae). Molecular Ecology, 2017, 26, 1515-1532.	3.9	22
58	Exploring correlations in genetic and cultural variation across language families in northeast Asia. Science Advances, 2021, 7, .	10.3	22
59	Female sterility associated with increased clonal propagation suggests a unique combination of androdioecy and asexual reproduction in populations of Cardamine amara (Brassicaceae). Annals of Botany, 2015, 115, 763-776.	2.9	19
60	Genetic diversity of two tropical tree species of the Dipterocarpaceae following logging and restoration in Borneo: high genetic diversity in plots with high species diversity. Plant Ecology and Diversity, 2016, 9, 459-469.	2.4	18
61	Genome sequencing of Metrosideros polymorpha (Myrtaceae), a dominant species in various habitats in the Hawaiian Islands with remarkable phenotypic variations. Journal of Plant Research, 2016, 129, 727-736.	2.4	18
62	Fineâ€scale empirical data on niche divergence and homeolog expression patterns in an allopolyploid and its diploid progenitor species. New Phytologist, 2021, 229, 3587-3601.	7.3	18
63	Genomic signatures of convergent adaptation to Alpine environments in three Brassicaceae species. Molecular Ecology, 2020, 29, 4350-4365.	3.9	17
64	Transcriptional Characteristics and Differences in Arabidopsis Stigmatic Papilla Cells Pre- and Post-Pollination. Plant and Cell Physiology, 2015, 56, 663-673.	3.1	16
65	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. Plant and Cell Physiology, 2021, 62, 8-27.	3.1	16
66	Agrobacterium-mediated floral dip transformation of the model polyploid species Arabidopsis kamchatica. Journal of Plant Research, 2018, 131, 349-358.	2.4	14
67	Using a two-stage convolutional neural network to rapidly identify tiny herbivorous beetles in the field. Ecological Informatics, 2021, 66, 101466.	5.2	14
68	Current status of the multinational Arabidopsis community. Plant Direct, 2020, 4, e00248.	1.9	13
69	The genome of Shorea leprosula (Dipterocarpaceae) highlights the ecological relevance of drought in aseasonal tropical rainforests. Communications Biology, 2021, 4, 1166.	4.4	13
70	Positional bias in variant calls against draft reference assemblies. BMC Genomics, 2017, 18, 263.	2.8	11
71	A Recently Formed Triploid Cardamine insueta Inherits Leaf Vivipary and Submergence Tolerance Traits of Parents. Frontiers in Genetics, 2020, 11, 567262.	2.3	11
72	Challenges in studies on flowering time: interfaces between phenological research and the molecular network of flowering genes. Ecological Research, 2013, 28, 161-172.	1.5	10

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73	Transcriptional Variation in Glucosinolate Biosynthetic Genes and Inducible Responses to Aphid Herbivory on Field-Grown Arabidopsis thaliana. Frontiers in Genetics, 2019, 10, 787.	2.3	10
74	Experimental and Field Data Support Range Expansion in an Allopolyploid Arabidopsis Owing to Parental Legacy of Heavy Metal Hyperaccumulation. Frontiers in Genetics, 2020, 11, 565854.	2.3	10
75	Fermentation Ability of Gut Microbiota of Wild Japanese Macaques in the Highland and Lowland Yakushima: In Vitro Fermentation Assay and Genetic Analyses. Microbial Ecology, 2020, 80, 459-474.	2.8	10
76	Neighbor GWAS: incorporating neighbor genotypic identity into genome-wide association studies of field herbivory. Heredity, 2021, 126, 597-614.	2.6	10
77	Genet assignment and population structure analysis in a clonal forest-floor herb, Cardamine leucantha, using RAD-seq. AoB PLANTS, 2020, 12, plz080.	2.3	9
78	Metal accumulation and its effect on leaf herbivory in an allopolyploid species Arabidopsis kamchatica inherited from a diploid hyperaccumulator A. halleri. Plant Species Biology, 2021, 36, 208-217.	1.0	9
79	Multiple Wheat Genomes Reveal Novel Gli-2 Sublocus Location and Variation of Celiac Disease Epitopes in Duplicated Î±-Gliadin Genes. Frontiers in Plant Science, 2021, 12, 715985.	3.6	7
80	PRIMA: a rapid and cost-effective genotyping method to detect single-nucleotide differences using probe-induced heteroduplexes. Scientific Reports, 2021, 11, 20741.	3.3	7
81	Integrative research efforts at the boundary of biodiversity and global change research. Current Opinion in Environmental Sustainability, 2017, 29, 215-222.	6.3	6
82	Double-Locking Mechanism of Self-Compatibility in Arabidopsis thaliana: The Synergistic Effect of Transcriptional Depression and Disruption of Coding Region in the Male Specificity Gene. Frontiers in Plant Science, 2020, 11, 576140.	3.6	6
83	Artificial selection reveals the role of transcriptional constraints in the maintenance of life history variation. Evolution Letters, 2020, 4, 200-211.	3.3	6
84	Efficient Detection of Novel Nuclear Markers for Brassicaceae by Transcriptome Sequencing. PLoS ONE, 2015, 10, e0128181.	2.5	5
85	Pollen Number and Ribosome Gene Expression Altered in a Genome-Editing Mutant of REDUCED POLLEN NUMBER1 Gene. Frontiers in Plant Science, 2021, 12, 768584.	3.6	5
86	Updated Genome Assembly and Annotation for Metrosideros polymorpha, an Emerging Model Tree Species of Ecological Divergence. G3: Genes, Genomes, Genetics, 2019, 9, 3513-3520.	1.8	4
87	ARPEGGIO: Automated Reproducible Polyploid EpiGenetic GuIdance workflOw. BMC Genomics, 2021, 22, 547.	2.8	4
88	KOMPEITO, an Atypical Arabidopsis Rhomboid-Related Gene, Is Required for Callose Accumulation and Pollen Wall Development. International Journal of Molecular Sciences, 2022, 23, 5959.	4.1	4
89	An Affordable Image-Analysis Platform to Accelerate Stomatal Phenotyping During Microscopic Observation. Frontiers in Plant Science, 2021, 12, 715309.	3.6	3
90	Pollen Grain Counting Using a Cell Counter. Methods in Molecular Biology, 2020, 2160, 1-11.	0.9	3

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91	Demography and selection analysis of the incipient adaptive radiation of a Hawaiian woody species. PLoS Genetics, 2022, 18, e1009987.	3.5	3
92	Whole-Genome Sequencing of a 900-Year-Old Human Skeleton Supports Two Past Migration Events from the Russian Far East to Northern Japan. Genome Biology and Evolution, 2021, 13, .	2.5	2
93	Cost-Effective Discovery of Nucleotide Polymorphisms in Populations of an Allopolyploid Species Using Pool-Seq. American Journal of Molecular Biology, 2017, 07, 1031-1046.	0.3	2
94	A Natural Low Phytic Acid Finger Millet Accession Significantly Improves Iron Bioavailability in Indian Women. Frontiers in Nutrition, 2021, 8, 791392.	3.7	2
95	Potential Application of Pollen Genotyping for Evolutionary Genetic and Genomic Studies: Linkage/Recombination Analysis and Haplotype Sequencing. Structure and Function of Mountain Ecosystems in Japan, 2011, , 111-123.	0.5	0