

Kousuke Hanada

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

6,714
citations

117625

34
h-index

138484

58
g-index

60
all docs

60
docs citations

60
times ranked

9880
citing authors

#	ARTICLE	IF	CITATIONS
1	Enhanced growth rate under elevated CO ₂ conditions was observed for transgenic lines of genes identified by intraspecific variation analyses in <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology</i> , 2022, 110, 333-345.	3.9	4
2	Degree of Functional Divergence in Duplicates Is Associated with Distinct Roles in Plant Evolution. <i>Molecular Biology and Evolution</i> , 2021, 38, 1447-1459.	8.9	17
3	Positive selective sweeps of epigenetic mutations regulating specialized metabolites in plants. <i>Genome Research</i> , 2021, 31, 1060-1068.	5.5	9
4	Identification of endogenous small peptides involved in rice immunity through transcriptomics and proteomics-based screening. <i>Plant Biotechnology Journal</i> , 2020, 18, 415-428.	8.3	33
5	Effect of small coding genes on the circadian rhythms under elevated CO ₂ conditions in plants. <i>Plant Molecular Biology</i> , 2020, 104, 55-65.	3.9	2
6	Dephosphorylation of clustered phosphoserine residues in human Grb14 by protein phosphatase 1 and its effect on insulin receptor complex formation. <i>Journal of Peptide Science</i> , 2019, 25, e3207.	1.4	1
7	Hormone-like peptides and small coding genes in plant stress signaling and development. <i>Current Opinion in Plant Biology</i> , 2019, 51, 88-95.	7.1	76
8	Tuning water-use efficiency and drought tolerance in wheat using abscisic acid receptors. <i>Nature Plants</i> , 2019, 5, 153-159.	9.3	203
9	Contribution of Functional Divergence Through Copy Number Variations to the Inter-Species and Intra-Species Diversity in Specialized Metabolites. <i>Frontiers in Plant Science</i> , 2019, 10, 1567.	3.6	7
10	Functional divergence of duplicate genes several million years after gene duplication in <i>Arabidopsis</i> . <i>DNA Research</i> , 2018, 25, 327-339.	3.4	9
11	AtPep3 is a hormone-like peptide that plays a role in the salinity stress tolerance of plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5810-5815.	7.1	89
12	A Highly Specific Genome-Wide Association Study Integrated with Transcriptome Data Reveals the Contribution of Copy Number Variations to Specialized Metabolites in <i>Arabidopsis thaliana</i> Accessions. <i>Molecular Biology and Evolution</i> , 2017, 34, 3111-3122.	8.9	14
13	Light Controls Protein Localization through Phytochrome-Mediated Alternative Promoter Selection. <i>Cell</i> , 2017, 171, 1316-1325.e12.	28.9	99
14	Mutant selection in the self-incompatible plant radish (<i>Raphanus sativus</i> L.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222 14	1.9	14
15	Drought stress differentially regulates the expression of small open reading frames (sORFs) in <i>Arabidopsis</i> roots and shoots. <i>Plant Signaling and Behavior</i> , 2016, 11, e1215792.	2.4	13
16	Molecular Evolution and Functional Characterization of a Bifunctional Decarboxylase Involved in Lycopodium Alkaloid Biosynthesis. <i>Plant Physiology</i> , 2016, 171, 2432-2444.	4.8	50
17	Which plant trait explains the variations in relative growth rate and its response to elevated carbon dioxide concentration among <i>Arabidopsis thaliana</i> ecotypes derived from a variety of habitats?. <i>Oecologia</i> , 2016, 180, 865-876.	2.0	13
18	Distinct Characteristics of Indole-3-Acetic Acid and Phenylacetic Acid, Two Common Auxins in Plants. <i>Plant and Cell Physiology</i> , 2015, 56, 1641-1654.	3.1	142

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19	A Genome Scan for Genes Underlying Microgeographic-Scale Local Adaptation in a Wild Arabidopsis Species. <i>PLoS Genetics</i> , 2015, 11, e1005361.	3.5	63
20	Substantial expression of novel small open reading frames in <i>Oryza sativa</i> . <i>Plant Signaling and Behavior</i> , 2014, 9, e27848.	2.4	9
21	Transcriptomic analysis of rice in response to iron deficiency and excess. <i>Rice</i> , 2014, 7, 18.	4.0	74
22	Phytochrome controls alternative splicing to mediate light responses in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18781-18786.	7.1	182
23	Small open reading frames associated with morphogenesis are hidden in plant genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2395-2400.	7.1	178
24	The RNA-binding protein FPA regulates flg22-triggered defense responses and transcription factor activity by alternative polyadenylation. <i>Scientific Reports</i> , 2013, 3, 2866.	3.3	58
25	Positional correlation analysis improves reconstruction of full-length transcripts and alternative isoforms from noisy array signals or short reads. <i>Bioinformatics</i> , 2012, 28, 929-937.	4.1	6
26	Tissue-Specific Transcriptome Analysis Reveals Cell Wall Metabolism, Flavonol Biosynthesis and Defense Responses are Activated in the Endosperm of Germinating <i>Arabidopsis thaliana</i> Seeds. <i>Plant and Cell Physiology</i> , 2012, 53, 16-27.	3.1	58
27	Two glycosyltransferases involved in anthocyanin modification delineated by transcriptome independent component analysis in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2012, 69, 154-167.	5.7	164
28	An evolutionary view of functional diversity in family 1 glycosyltransferases. <i>Plant Journal</i> , 2011, 66, 182-193.	5.7	335
29	Origin and evolution of genes related to ABA metabolism and its signaling pathways. <i>Journal of Plant Research</i> , 2011, 124, 455-465.	2.4	39
30	ARTADE2DB: Improved Statistical Inferences for Arabidopsis Gene Functions and Structure Predictions by Dynamic Structure-Based Dynamic Expression (DSDE) Analyses. <i>Plant and Cell Physiology</i> , 2011, 52, 254-264.	3.1	15
31	Functional Compensation of Primary and Secondary Metabolites by Duplicate Genes in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2011, 28, 377-382.	8.9	76
32	Toward genome-wide metabolotyping and elucidation of metabolic system: metabolic profiling of large-scale bioresources. <i>Journal of Plant Research</i> , 2010, 123, 291-298.	2.4	13
33	sORF finder: a program package to identify small open reading frames with high coding potential. <i>Bioinformatics</i> , 2010, 26, 399-400.	4.1	185
34	Evolutionary History and Stress Regulation of Plant Receptor-Like Kinase/Pelle Genes. <i>Plant Physiology</i> , 2009, 150, 12-26.	4.8	340
35	Genome-wide suppression of aberrant mRNA-like noncoding RNAs by NMD in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2453-2458.	7.1	165
36	PosMed-plus: An Intelligent Search Engine that Inferentially Integrates Cross-Species Information Resources for Molecular Breeding of Plants. <i>Plant and Cell Physiology</i> , 2009, 50, 1249-1259.	3.1	17

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37	The Functional Role of Pack-MULEs in Rice Inferred from Purifying Selection and Expression Profile. <i>Plant Cell</i> , 2009, 21, 25-38.	6.6	91
38	Evolutionary Persistence of Functional Compensation by Duplicate Genes in Arabidopsis. <i>Genome Biology and Evolution</i> , 2009, 1, 409-414.	2.5	81
39	Increased Expression and Protein Divergence in Duplicate Genes Is Associated with Morphological Diversification. <i>PLoS Genetics</i> , 2009, 5, e1000781.	3.5	50
40	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. <i>Science</i> , 2008, 319, 64-69.	12.6	1,712
41	Importance of Lineage-Specific Expansion of Plant Tandem Duplicates in the Adaptive Response to Environmental Stimuli. <i>Plant Physiology</i> , 2008, 148, 993-1003.	4.8	415
42	Evola: Ortholog database of all human genes in H-InvDB with manual curation of phylogenetic trees. <i>Nucleic Acids Research</i> , 2007, 36, D787-D792.	14.5	33
43	The Nonsynonymous/Synonymous Substitution Rate Ratio versus the Radical/Conservative Replacement Rate Ratio in the Evolution of Mammalian Genes. <i>Molecular Biology and Evolution</i> , 2007, 24, 2235-2241.	8.9	77
44	Increasing genetic diversity of hepatitis C virus in haemophiliacs with human immunodeficiency virus coinfection. <i>Journal of General Virology</i> , 2007, 88, 2513-2519.	2.9	9
45	Large-Scale, Lineage-Specific Expansion of a Bric-a-Brac/Tramtrack/Broad Complex Ubiquitin-Ligase Gene Family in Rice. <i>Plant Cell</i> , 2007, 19, 2329-2348.	6.6	96
46	Genetic Stability of Human T Lymphotropic Virus Type I despite Antiviral Pressures by CTLs. <i>Journal of Immunology</i> , 2007, 178, 5966-5972.	0.8	24
47	A large number of novel coding small open reading frames in the intergenic regions of the <i>Arabidopsis thaliana</i> genome are transcribed and/or under purifying selection. <i>Genome Research</i> , 2007, 17, 632-640.	5.5	157
48	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , 2007, 36, D793-D799.	14.5	57
49	A reduction in selective immune pressure during the course of chronic hepatitis C correlates with diminished biochemical evidence of hepatic inflammation. <i>Virology</i> , 2007, 361, 27-33.	2.4	8
50	Radical amino acid change versus positive selection in the evolution of viral envelope proteins. <i>Gene</i> , 2006, 385, 83-88.	2.2	23
51	Genetic variation of the prevailing porcine respiratory and reproductive syndrome viruses occurring on a pig farm upon vaccination. <i>Archives of Virology</i> , 2006, 151, 2269-2276.	2.1	22
52	The Origin and Evolution of Porcine Reproductive and Respiratory Syndrome Viruses. <i>Molecular Biology and Evolution</i> , 2005, 22, 1024-1031.	8.9	151
53	Molecular evolutionary analyses implicate injection treatment for schistosomiasis in the initial hepatitis C epidemics in Japan. <i>Journal of Hepatology</i> , 2005, 42, 47-53.	3.7	53
54	A Large Variation in the Rates of Synonymous Substitution for RNA Viruses and Its Relationship to a Diversity of Viral Infection and Transmission Modes. <i>Molecular Biology and Evolution</i> , 2004, 21, 1074-1080.	8.9	192

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55	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. PLoS Biology, 2004, 2, e162.	5.6	290
56	Human cytomegalovirus glycoprotein N (gpUL73-gN) genomic variants: identification of a novel subgroup, geographical distribution and evidence of positive selective pressure. Journal of General Virology, 2003, 84, 647-655.	2.9	90
57	A comparison of the molecular clock of hepatitis C virus in the United States and Japan predicts that hepatocellular carcinoma incidence in the United States will increase over the next two decades. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15584-15589.	7.1	307