## Kousuke Hanada

List of Publications by Year in descending order

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117625 138484 6,714 57 34 58 citations g-index h-index papers 60 60 60 9880 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	The $\langle i \rangle$ Physcomitrella $\langle  i \rangle$ Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. Science, 2008, 319, 64-69.	12.6	1,712
2	Importance of Lineage-Specific Expansion of Plant Tandem Duplicates in the Adaptive Response to Environmental Stimuli Â. Plant Physiology, 2008, 148, 993-1003.	4.8	415
3	Evolutionary History and Stress Regulation of Plant Receptor-Like Kinase/Pelle Genes  Â. Plant Physiology, 2009, 150, 12-26.	4.8	340
4	An evolutionary view of functional diversity in family 1 glycosyltransferases. Plant Journal, 2011, 66, 182-193.	5.7	335
5	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
6	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. PLoS Biology, 2004, 2, e162.	5.6	290
7	Tuning water-use efficiency and drought tolerance in wheat using abscisic acid receptors. Nature Plants, 2019, 5, 153-159.	9.3	203
8	A Large Variation in the Rates of Synonymous Substitution for RNA Viruses and Its Relationship to a Diversity of Viral Infection and Transmission Modes. Molecular Biology and Evolution, 2004, 21, 1074-1080.	8.9	192
9	sORF finder: a program package to identify small open reading frames with high coding potential. Bioinformatics, 2010, 26, 399-400.	4.1	185
10	Phytochrome controls alternative splicing to mediate light responses in <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18781-18786.	7.1	182
11	Small open reading frames associated with morphogenesis are hidden in plant genomes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2395-2400.	7.1	178
12	Genome-wide suppression of aberrant mRNA-like noncoding RNAs by NMD in <i>Arabidopsis</i> Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2453-2458.	7.1	165
13	Two glycosyltransferases involved in anthocyanin modification delineated by transcriptome independent component analysis in <i>Arabidopsis thaliana</i> . Plant Journal, 2012, 69, 154-167.	5.7	164
14	A large number of novel coding small open reading frames in the intergenic regions of the Arabidopsis thaliana genome are transcribed and/or under purifying selection. Genome Research, 2007, 17, 632-640.	5.5	157
15	The Origin and Evolution of Porcine Reproductive and Respiratory Syndrome Viruses. Molecular Biology and Evolution, 2005, 22, 1024-1031.	8.9	151
16	Distinct Characteristics of Indole-3-Acetic Acid and Phenylacetic Acid, Two Common Auxins in Plants. Plant and Cell Physiology, 2015, 56, 1641-1654.	3.1	142
17	Light Controls Protein Localization through Phytochrome-Mediated Alternative Promoter Selection. Cell, 2017, 171, 1316-1325.e12.	28.9	99
18	Large-Scale, Lineage-Specific Expansion of a Bric-a-Brac/Tramtrack/Broad Complex Ubiquitin-Ligase Gene Family in Rice. Plant Cell, 2007, 19, 2329-2348.	6.6	96

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19	The Functional Role of Pack-MULEs in Rice Inferred from Purifying Selection and Expression Profile. Plant Cell, 2009, 21, 25-38.	6.6	91
20	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
21	AtPep3 is a hormone-like peptide that plays a role in the salinity stress tolerance of plants. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 5810-5815.	7.1	89
22	Evolutionary Persistence of Functional Compensation by Duplicate Genes in Arabidopsis. Genome Biology and Evolution, 2009, 1, 409-414.	2.5	81
23	The Nonsynonymous/Synonymous Substitution Rate Ratio versus the Radical/Conservative Replacement Rate Ratio in the Evolution of Mammalian Genes. Molecular Biology and Evolution, 2007, 24, 2235-2241.	8.9	77
24	Functional Compensation of Primary and Secondary Metabolites by Duplicate Genes in Arabidopsis thaliana. Molecular Biology and Evolution, 2011, 28, 377-382.	8.9	76
25	Hormone-like peptides and small coding genes in plant stress signaling and development. Current Opinion in Plant Biology, 2019, 51, 88-95.	7.1	76
26	Transcriptomic analysis of rice in response to iron deficiency and excess. Rice, 2014, 7, 18.	4.0	74
27	A Genome Scan for Genes Underlying Microgeographic-Scale Local Adaptation in a Wild Arabidopsis Species. PLoS Genetics, 2015, 11, e1005361.	3.5	63
28	Tissue-Specific Transcriptome Analysis Reveals Cell Wall Metabolism, Flavonol Biosynthesis and Defense Responses are Activated in the Endosperm of Germinating Arabidopsis thaliana Seeds. Plant and Cell Physiology, 2012, 53, 16-27.	3.1	58
29	The RNA-binding protein FPA regulates flg22-triggered defense responses and transcription factor activity by alternative polyadenylation. Scientific Reports, 2013, 3, 2866.	3.3	58
30	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. Nucleic Acids Research, 2007, 36, D793-D799.	14.5	57
31	Molecular evolutionary analyses implicate injection treatment for schistosomiasis in the initial hepatitis C epidemics in Japan. Journal of Hepatology, 2005, 42, 47-53.	3.7	53
32	Increased Expression and Protein Divergence in Duplicate Genes Is Associated with Morphological Diversification. PLoS Genetics, 2009, 5, e1000781.	3.5	50
33	Molecular Evolution and Functional Characterization of a Bifunctional Decarboxylase Involved in Lycopodium Alkaloid Biosynthesis. Plant Physiology, 2016, 171, 2432-2444.	4.8	50
34	Origin and evolution of genes related to ABA metabolism and its signaling pathways. Journal of Plant Research, 2011, 124, 455-465.	2.4	39
35	Evola: Ortholog database of all human genes in H-InvDB with manual curation of phylogenetic trees. Nucleic Acids Research, 2007, 36, D787-D792.	14.5	33
36	Identification of endogenous small peptides involved in rice immunity through transcriptomics―and proteomicsâ€based screening. Plant Biotechnology Journal, 2020, 18, 415-428.	8.3	33

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37	Genetic Stability of Human T Lymphotropic Virus Type I despite Antiviral Pressures by CTLs. Journal of Immunology, 2007, 178, 5966-5972.	0.8	24
38	Radical amino acid change versus positive selection in the evolution of viral envelope proteins. Gene, 2006, 385, 83-88.	2.2	23
39	Genetic variation of the prevailing porcine respiratory and reproductive syndrome viruses occurring on a pig farm upon vaccination. Archives of Virology, 2006, 151, 2269-2276.	2.1	22
40	PosMed-plus: An Intelligent Search Engine that Inferentially Integrates Cross-Species Information Resources for Molecular Breeding of Plants. Plant and Cell Physiology, 2009, 50, 1249-1259.	3.1	17
41	Degree of Functional Divergence in Duplicates Is Associated with Distinct Roles in Plant Evolution. Molecular Biology and Evolution, 2021, 38, 1447-1459.	8.9	17
42	ARTADE2DB: Improved Statistical Inferences for Arabidopsis Gene Functions and Structure Predictions by Dynamic Structure-Based Dynamic Expression (DSDE) Analyses. Plant and Cell Physiology, 2011, 52, 254-264.	3.1	15
43	A Highly Specific Genome-Wide Association Study Integrated with Transcriptome Data Reveals the Contribution of Copy Number Variations to Specialized Metabolites in Arabidopsis thaliana Accessions. Molecular Biology and Evolution, 2017, 34, 3111-3122.	8.9	14
44	Mutant selection in the self-incompatible plant radish ( <i>Raphanus sativus</i> L.) Tj ETQq0 0 0 rgBT	/Overlock	10 <sub>1</sub> 7f 50 462
45	Toward genome-wide metabolotyping and elucidation of metabolic system: metabolic profiling of large-scale bioresources. Journal of Plant Research, 2010, 123, 291-298.	2.4	13
46	Drought stress differentially regulates the expression of small open reading frames (sORFs) in Arabidopsis roots and shoots. Plant Signaling and Behavior, 2016, 11, e1215792.	2.4	13
47	Which plant trait explains the variations in relative growth rate and its response to elevated carbon dioxide concentration among Arabidopsis thaliana ecotypes derived from a variety of habitats?. Oecologia, 2016, 180, 865-876.	2.0	13
48	Increasing genetic diversity of hepatitis C virus in haemophiliacs with human immunodeficiency virus coinfection. Journal of General Virology, 2007, 88, 2513-2519.	2.9	9
49	Substantial expression of novel small open reading frames in <i>Oryza sativa</i> . Plant Signaling and Behavior, 2014, 9, e27848.	2.4	9
50	Functional divergence of duplicate genes several million years after gene duplication in Arabidopsis. DNA Research, 2018, 25, 327-339.	3.4	9
51	Positive selective sweeps of epigenetic mutations regulating specialized metabolites in plants. Genome Research, 2021, 31, 1060-1068.	5.5	9
52	A reduction in selective immune pressure during the course of chronic hepatitis C correlates with diminished biochemical evidence of hepatic inflammation. Virology, 2007, 361, 27-33.	2.4	8
53	Contribution of Functional Divergence Through Copy Number Variations to the Inter-Species and Intra-Species Diversity in Specialized Metabolites. Frontiers in Plant Science, 2019, 10, 1567.	3.6	7
54	Positional correlation analysis improves reconstruction of full-length transcripts and alternative isoforms from noisy array signals or short reads. Bioinformatics, 2012, 28, 929-937.	4.1	6

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55	Enhanced growth rate under elevated CO2 conditions was observed for transgenic lines of genes identified by intraspecific variation analyses in Arabidopsis thaliana. Plant Molecular Biology, 2022, 110, 333-345.	3.9	4
56	Effect of small coding genes on the circadian rhythms under elevated CO2 conditions in plants. Plant Molecular Biology, 2020, 104, 55-65.	3.9	2
57	Dephosphorylation of clustered phosphoserine residues in human Grb14 by protein phosphatase 1 and its effect on insulin receptor complex formation. Journal of Peptide Science, 2019, 25, e3207.	1.4	1