

Hee-Jong Koh

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4482207/publications.pdf>

Version: 2024-02-01

106
papers

4,392
citations

147566

31
h-index

118652

62
g-index

111
all docs

111
docs citations

111
times ranked

4392
citing authors

#	ARTICLE	IF	CITATIONS
1	The Senescence-Induced Staygreen Protein Regulates Chlorophyll Degradation. <i>Plant Cell</i> , 2007, 19, 1649-1664.	3.1	475
2	Rice Chlorina-1 and Chlorina-9 encode ChlD and ChlI subunits of Mg-chelatase, a key enzyme for chlorophyll synthesis and chloroplast development. <i>Plant Molecular Biology</i> , 2006, 62, 325-337.	2.0	246
3	Rice <i>Virescent3</i> and <i>Stripe1</i> Encoding the Large and Small Subunits of Ribonucleotide Reductase Are Required for Chloroplast Biogenesis during Early Leaf Development. <i>Plant Physiology</i> , 2009, 150, 388-401.	2.3	201
4	Antioxidative activities of bran extracts from twenty one pigmented rice cultivars. <i>Food Chemistry</i> , 2006, 94, 613-620.	4.2	195
5	The rice <i>narrow leaf2</i> and <i>narrow leaf3</i> loci encode <i>WUSCHEL</i> -related homeobox 3 (<i>WOX3</i>) and function in leaf, spikelet, tiller and lateral root development. <i>New Phytologist</i> , 2013, 198, 1071-1084.	3.5	174
6	Complete chloroplast and ribosomal sequences for 30 accessions elucidate evolution of <i>Oryza</i> AA genome species. <i>Scientific Reports</i> , 2015, 5, 15655.	1.6	169
7	<i>SPL28</i> encodes a clathrin-associated adaptor protein complex 1, medium subunit 1 (AP1M1) and is responsible for spotted leaf and early senescence in rice (<i>Oryza sativa</i>). <i>New Phytologist</i> , 2010, 185, 258-274.	3.5	162
8	The rice <i>faded green leaf</i> locus encodes protochlorophyllide oxidoreductase and is essential for chlorophyll synthesis under high light conditions. <i>Plant Journal</i> , 2013, 74, 122-133.	2.8	153
9	High-resolution mapping of two rice brown planthopper resistance genes, <i>Bph20(t)</i> and <i>Bph21(t)</i> , originating from <i>Oryza minuta</i> . <i>Theoretical and Applied Genetics</i> , 2009, 119, 1237-1246.	1.8	147
10	The <i>BEL</i> type homeobox gene <i>SH5</i> induces seed shattering by enhancing abscission zone development and inhibiting lignin biosynthesis. <i>Plant Journal</i> , 2014, 79, 717-728.	2.8	127
11	Fine mapping and candidate gene analysis of dense and erect panicle 3, <i>DEP3</i> , which confers high grain yield in rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2011, 122, 1439-1449.	1.8	112
12	Characterization and Mapping of a Shattering Mutant in Rice That Corresponds to a Block of Domestication Genes. <i>Genetics</i> , 2006, 173, 995-1005.	1.2	108
13	Inactivation of the <i>UGPase1</i> gene causes genic male sterility and endosperm chalkiness in rice (<i>Oryza sativa</i> L.). <i>Plant Journal</i> , 2008, 54, 190-204.	2.8	98
14	KNOX Protein OSH15 Induces Grain Shattering by Repressing Lignin Biosynthesis Genes. <i>Plant Physiology</i> , 2017, 174, 312-325.	2.3	93
15	Inactivation of the CTD phosphatase-like gene <i>OsCPL1</i> enhances the development of the abscission layer and seed shattering in rice. <i>Plant Journal</i> , 2010, 61, 96-106.	2.8	89
16	The rice <i>zebra3</i> (<i>z3</i>) mutation disrupts citrate distribution and produces transverse dark-green/green variegation in mature leaves. <i>Rice</i> , 2018, 11, 1.	1.7	87
17	Map-based cloning of the ERECT PANICLE 3 gene in rice. <i>Theoretical and Applied Genetics</i> , 2009, 119, 1497-1506.	1.8	81
18	Mutation of <i>SPOTTED LEAF3</i> (<i>SPL3</i>) impairs abscisic acid-responsive signalling and delays leaf senescence in rice. <i>Journal of Experimental Botany</i> , 2015, 66, 7045-7059.	2.4	70

#	ARTICLE	IF	CITATIONS
19	ZEBRA-NECROSIS, a thylakoid-bound protein, is critical for the photoprotection of developing chloroplasts during early leaf development. <i>Plant Journal</i> , 2010, 62, 713-725.	2.8	67
20	Molecular Aspect of Good Eating Quality Formation in Japonica Rice. <i>PLoS ONE</i> , 2011, 6, e18385.	1.1	62
21	Teosinte Branched 1 modulates tillering in rice plants. <i>Plant Cell Reports</i> , 2012, 31, 57-65.	2.8	61
22	The rice (<i>Oryza sativa</i>) Blast Lesion Mimic Mutant, <i>blm</i> , may confer resistance to blast pathogens by triggering multiple defense-associated signaling pathways. <i>Plant Physiology and Biochemistry</i> , 2005, 43, 397-406.	2.8	60
23	Proteomics Analysis of Rice Lesion Mimic Mutant (<i>blm1</i>) Reveals Tightly Localized Probenazole-Induced Protein (PBZ1) in Cells Undergoing Programmed Cell Death. <i>Journal of Proteome Research</i> , 2008, 7, 1750-1760.	1.8	55
24	PCR Marker-Based Evaluation of the Eating Quality of Japonica Rice (<i>Oryza sativa</i> L.). <i>Journal of Agricultural and Food Chemistry</i> , 2009, 57, 2754-2762.	2.4	51
25	Antiallergic Activities of Pigmented Rice Bran Extracts in Cell Assays. <i>Journal of Food Science</i> , 2007, 72, S719-S726.	1.5	48
26	Identification of QTLs for Seed Germination Capability after Various Storage Periods Using Two RIL Populations in Rice. <i>Molecules and Cells</i> , 2011, 31, 385-392.	1.0	48
27	Leaf Variegation in the Rice <i>zebra2</i> Mutant Is Caused by Photoperiodic Accumulation of Tetra-Cis-Lycopene and Singlet Oxygen. <i>Molecules and Cells</i> , 2012, 33, 87-98.	1.0	43
28	Identification of Active Transposon <i>dTok</i> , a Member of the hAT Family, in Rice. <i>Plant and Cell Physiology</i> , 2006, 47, 1473-1483.	1.5	42
29	Identification and quantification of flavonoids in yellow grain mutant of rice (<i>Oryza sativa</i> L.). <i>Food Chemistry</i> , 2018, 241, 154-162.	4.2	38
30	Pyrophosphate-fructose 6-phosphate phosphotransferase (<i>PFP1</i>) regulates starch biosynthesis and seed development via heterotetramer formation in rice (<i>Oryza sativa</i> L.). <i>Plant Biotechnology Journal</i> , 2020, 18, 83-95.	4.1	38
31	Differential Expression of Defense/Stress-Related Marker Proteins in Leaves of a Unique Rice Blast Lesion Mimic Mutant (<i>blm</i>). <i>Journal of Proteome Research</i> , 2006, 5, 2586-2598.	1.8	37
32	Molecular mapping of quantitative trait loci for zinc toxicity tolerance in rice seedling (<i>Oryza sativa</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.3	32
33	New Genetic Loci Associated with Preharvest Sprouting and Its Evaluation Based on the Model Equation in Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 1393.	1.7	32
34	Genome-wide analyses of late pollen-preferred genes conserved in various rice cultivars and functional identification of a gene involved in the key processes of late pollen development. <i>Rice</i> , 2018, 11, 28.	1.7	32
35	Identification of Quantitative Trait Loci Associated with Rice Eating Quality Traits Using a Population of Recombinant Inbred Lines Derived from a Cross between Two Temperate japonica Cultivars. <i>Molecules and Cells</i> , 2011, 31, 437-446.	1.0	31
36	Quantitative Trait Loci for Cold Tolerance of Rice Recombinant Inbred Lines in Low Temperature Environments. <i>Molecules and Cells</i> , 2011, 32, 579-588.	1.0	27

#	ARTICLE	IF	CITATIONS
37	Single Nucleotide Polymorphisms and Haplotype Diversity in Rice Sucrose Synthase 3. <i>Journal of Heredity</i> , 2011, 102, 735-746.	1.0	25
38	Chromatin interacting factor OsVIL2 increases biomass and rice grain yield. <i>Plant Biotechnology Journal</i> , 2019, 17, 178-187.	4.1	25
39	Tiller formation in rice is altered by overexpression of OsIAGLU gene encoding an IAA-conjugating enzyme or exogenous treatment of free IAA. <i>Journal of Plant Biology</i> , 2012, 55, 429-435.	0.9	24
40	Key DNA Markers for Predicting Heterosis in F1 Hybrids of japonica Rice. <i>Breeding Science</i> , 2004, 54, 389-397.	0.9	23
41	Fine Mapping and Candidate Gene Analysis of the Floury Endosperm Gene, FLO(a), in Rice. <i>Molecules and Cells</i> , 2010, 29, 167-174.	1.0	23
42	Influence of Multi-Gene Allele Combinations on Grain Size of Rice and Development of a Regression Equation Model to Predict Grain Parameters. <i>Rice</i> , 2015, 8, 33.	1.7	23
43	Fine mapping and candidate gene analysis of hwh1 and hwh2, a set of complementary genes controlling hybrid breakdown in rice. <i>Theoretical and Applied Genetics</i> , 2008, 116, 1117-1127.	1.8	22
44	Development of SNP-based CAPS and dCAPS markers in eight different genes involved in starch biosynthesis in rice. <i>Molecular Breeding</i> , 2009, 24, 93-101.	1.0	22
45	Development and application of indica-japonica SNP assays using the Fluidigm platform for rice genetic analysis and molecular breeding. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	22
46	Molecular characterization and physico-chemical analysis of a new giant embryo mutant allele (ge t) in rice (<i>Oryza sativa</i> L.). <i>Genes and Genomics</i> , 2009, 31, 277-282.	0.5	20
47	The rice bright green leaf (bgl) locus encodes OsRopGEF10, which activates the development of small cuticular papillae on leaf surfaces. <i>Plant Molecular Biology</i> , 2011, 77, 631-641.	2.0	20
48	Identification of nucleosome assembly protein 1 (NAP1) as an interacting partner of plant ribosomal protein S6 (RPS6) and a positive regulator of rDNA transcription. <i>Biochemical and Biophysical Research Communications</i> , 2015, 465, 200-205.	1.0	20
49	Identification of a Spotted Leaf Sheath Gene Involved in Early Senescence and Defense Response in Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 1274.	1.7	20
50	The Rice Rolled Fine Striped (RFS) CHD3/Mi-2 Chromatin Remodeling Factor Epigenetically Regulates Genes Involved in Oxidative Stress Responses During Leaf Development. <i>Frontiers in Plant Science</i> , 2018, 9, 364.	1.7	20
51	Isolation and Characterization of a Dominant Dwarf Gene, D-h, in Rice. <i>PLoS ONE</i> , 2014, 9, e86210.	1.1	20
52	Sugary Endosperm is Modulated by Starch Branching Enzyme IIa in Rice (<i>Oryza sativa</i> L.). <i>Rice</i> , 2017, 10, 33.	1.7	19
53	The Rice SPOTTED LEAF4 (SPL4) Encodes a Plant Spastin That Inhibits ROS Accumulation in Leaf Development and Functions in Leaf Senescence. <i>Frontiers in Plant Science</i> , 2018, 9, 1925.	1.7	19
54	Novel allelic variant of Lpa1 gene associated with a significant reduction in seed phytic acid content in rice (<i>Oryza sativa</i> L.). <i>PLoS ONE</i> , 2019, 14, e0209636.	1.1	19

#	ARTICLE	IF	CITATIONS
55	Evaluating Genotype × Environment Interactions of Yield Traits and Adaptability in Rice Cultivars Grown under Temperate, Subtropical and Tropical Environments. <i>Agriculture (Switzerland)</i> , 2021, 11, 558.	1.4	19
56	Shotgun proteomic analysis for detecting differentially expressed proteins in the reduced culm number rice. <i>Proteomics</i> , 2011, 11, 455-468.	1.3	18
57	Genotypic Variation among Okra (<i>Abelmoschus esculentus</i> (L.) Moench) Germplasms in South India. <i>Plant Breeding and Biotechnology</i> , 2016, 4, 234-241.	0.3	18
58	Molecular mapping of a gene <i>ld(t)</i> ™ controlling cleistogamy in rice. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1429-1433.	1.8	17
59	Development of New CAPS/dCAPS and SNAP Markers for Rice Eating Quality. <i>HAYATI Journal of Biosciences</i> , 2013, 20, 15-23.	0.1	17
60	Genetic mapping and QTL analysis for yield and agronomic traits with an F2:3 population derived from a waxy corn × Sweet corn cross. <i>Genes and Genomics</i> , 2014, 36, 179-189.	0.5	17
61	QTL Analysis for Fe and Zn Concentrations in Rice Grains Using a Doubled Haploid Population Derived from a Cross Between Rice (<i>Oryza sativa</i>) Cultivar 93-11 and Milyang 352. <i>Plant Breeding and Biotechnology</i> , 2020, 8, 69-76.	0.3	17
62	Genotype × environment interactions for chilling tolerance of rice recombinant inbred lines under different low temperature environments. <i>Field Crops Research</i> , 2010, 117, 226-236.	2.3	16
63	Identification of QTLs for hybrid fertility in inter-subspecific crosses of rice (<i>Oryza sativa</i> L.). <i>Genes and Genomics</i> , 2011, 33, 39-48.	0.5	16
64	Identification and Characterization of LARGE EMBRYO, a New Gene Controlling Embryo Size in Rice (<i>Oryza sativa</i> L.). <i>Rice</i> , 2019, 12, 22.	1.7	16
65	Evaluation of Whole-Genome Sequence, Genetic Diversity, and Agronomic Traits of Basmati Rice (<i>Oryza</i>) Tj ETQq1 1.0.784314 rgBT /Ov	1.1	14
66	Expression of hpa1 Gene Encoding a Bacterial Harpin Protein in <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Enhances Disease Resistance to Both Fungal and Bacterial Pathogens in Rice and Arabidopsis. <i>Plant Pathology Journal</i> , 2012, 28, 364-372.	0.7	14
67	Identification of Heterosis QTLs for Yield and Yield-Related Traits in Indica-Japonica Recombinant Inbred Lines of Rice (<i>Oryza sativa</i> L.). <i>Plant Breeding and Biotechnology</i> , 2017, 5, 371-389.	0.3	14
68	QTL analyses of heterosis for grain yield and yield-related traits in indica-japonica crosses of rice (<i>Oryza sativa</i> L.). <i>Genes and Genomics</i> , 2012, 34, 367-377.	0.5	12
69	Variation in pre-harvest sprouting resistance, seed germination and changes in abscisic acid levels during grain development in diverse rice genetic resources. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2018, 16, 18-27.	0.4	12
70	Fine mapping and candidate gene analysis of a new mutant gene for panicle apical abortion in rice. <i>Euphytica</i> , 2014, 197, 387-398.	0.6	11
71	Association between sequence variants in panicle development genes and the number of spikelets per panicle in rice. <i>BMC Genetics</i> , 2018, 19, 5.	2.7	11
72	OsCOP1 regulates embryo development and flavonoid biosynthesis in rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 2587-2601.	1.8	11

#	ARTICLE	IF	CITATIONS
73	Genetic Basis of Tiller Dynamics of Rice Revealed by Genome-Wide Association Studies. <i>Plants</i> , 2020, 9, 1695.	1.6	10
74	Identification of quantitative trait loci for panicle length and yield related traits under different water and P application conditions in tropical region in rice (<i>Oryza sativa</i> L.). <i>Euphytica</i> , 2017, 213, 1.	0.6	9
75	QTLs for hybrid fertility and their association with female and male sterility in rice. <i>Genes and Genomics</i> , 2012, 34, 355-365.	0.5	8
76	Analysis of evolutionary relationships provides new clues to the origins of weedy rice. <i>Ecology and Evolution</i> , 2020, 10, 891-900.	0.8	8
77	Genetic structure and isolation by altitude in rice landraces of Yunnan, China revealed by nucleotide and microsatellite marker polymorphisms. <i>PLoS ONE</i> , 2017, 12, e0175731.	1.1	8
78	DNA markers for eating quality of indica rice in Indonesia. <i>Plant Breeding</i> , 2015, 134, 40-48.	1.0	7
79	Characterization and mapping of d13, a dwarfing mutant gene, in rice. <i>Genes and Genomics</i> , 2015, 37, 893-903.	0.5	7
80	Characterization of indica-japonica subspecies-specific InDel loci in wild relatives of rice (<i>Oryza</i>). <i>Journal of Experimental Botany</i> , 2020, 71, 405-418.	0.8	7
81	The DROOPING LEAF (DR) gene encoding GDSL esterase is involved in silica deposition in rice (<i>Oryza</i>). <i>Journal of Experimental Botany</i> , 2021, 72, 1078-1084.	1.1	7
82	Early Vigor of a Pyramiding Line Containing Two Quantitative Trait Loci, Phosphorus Uptake 1 (Pup1) and Anaerobic Germination 1 (AG1) in Rice (<i>O. Sativa</i> L.). <i>Agriculture (Switzerland)</i> , 2020, 10, 453.	1.4	6
83	Identification of Yield and Yield-Related Quantitative Trait Loci for the Field High Temperature Condition in Backcross Populations of Rice (<i>Oryza sativa</i> L.). <i>Plant Breeding and Biotechnology</i> , 2019, 7, 415-426.	0.3	6
84	Transcriptional Changes in the Developing Rice Seeds Under Salt Stress Suggest Targets for Manipulating Seed Quality. <i>Frontiers in Plant Science</i> , 2021, 12, 748273.	1.7	6
85	Prediction of Physicochemical Properties of Indonesian Indica Rice Using Molecular Markers. <i>HAYATI Journal of Biosciences</i> , 2014, 21, 76-86.	0.1	5
86	Identification of a Candidate Gene for the Novel Cytoplasmic Male Sterility Derived from Inter-Subspecific Crosses in Rice (<i>Oryza sativa</i> L.). <i>Genes</i> , 2021, 12, 590.	1.0	5
87	<i>Arachis hypogaea</i> resveratrol synthase 3 alters the expression pattern of UDP-glycosyltransferase genes in developing rice seeds. <i>PLoS ONE</i> , 2021, 16, e0245446.	1.1	4
88	Evidence for evolution and selection of drought-resistant genes based on high-throughput resequencing in weedy rice. <i>Journal of Experimental Botany</i> , 2022, 73, 1949-1962.	2.4	4
89	Gene identification using rice genome sequences. <i>Genes and Genomics</i> , 2013, 35, 415-424.	0.5	3
90	Identification of a novel candidate gene for rolled leaf in rice. <i>Genes and Genomics</i> , 2016, 38, 1077-1084.	0.5	3

#	ARTICLE	IF	CITATIONS
91	Identification of a novel SPLIT-HULL (SPH) gene associated with hull splitting in rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 1469-1480.	1.8	3
92	The Effect of Water Level in Rice Cropping System on Phosphorus Uptake Activity of Pup1 in a Pup1+Sub1 Breeding Line. <i>Plants</i> , 2021, 10, 1523.	1.6	3
93	Fine Mapping and Candidate Gene Analysis of Small Round Grain Mutant in Rice. <i>Plant Breeding and Biotechnology</i> , 2017, 5, 354-362.	0.3	3
94	Morphological and genetic characterization of off-type rice plants collected from farm fields in Korea. <i>Journal of Plant Biology</i> , 2013, 56, 160-167.	0.9	2
95	Genome-wide transcriptome comparison of flag leaves among japonica and indica varieties. <i>Journal of Plant Biology</i> , 2015, 58, 333-343.	0.9	2
96	Major QTLs, qARO1 and qARO9, Additively Regulate Adaxial Leaf Rolling in Rice. <i>Frontiers in Plant Science</i> , 2021, 12, 626523.	1.7	2
97	Characterization of the Common Japonica-Originated Genomic Regions in the High-Yielding Varieties Developed from Inter-Subspecific Crosses in Temperate Rice (<i>Oryza sativa</i> L.). <i>Genes</i> , 2020, 11, 562.	1.0	2
98	Characterization of Selected Rice Varieties Adapted in Africa. <i>Plant Breeding and Biotechnology</i> , 2016, 4, 297-305.	0.3	2
99	Identification of QTLs Associated with <i>indica</i> - <i>japonica</i> Differentiation-Related Traits in Rice (<i>Oryza sativa</i> L.). <i>Plant Breeding and Biotechnology</i> , 2018, 6, 193-205.	0.3	2
100	Evaluating Multiple Allelic Combination to Determine Tiller Angle Variation in Rice. <i>Agriculture (Switzerland)</i> , 2020, 10, 428.	1.4	1
101	Characterization and Genetic Mapping of White-Spotted Leaf (wspl) Mutant in Rice. <i>Plant Breeding and Biotechnology</i> , 2019, 7, 340-349.	0.3	1
102	Phenotypic Characterization and Genetic Mapping of An Open-hull Sterile Mutant in Rice. <i>Plant Breeding and Biotechnology</i> , 2013, 1, 24-32.	0.3	1
103	Identification of Quantitative Trait Loci for Agronomic Traits in Two Rice Populations Derived from a Cross with a Wide Compatibility Line. <i>Plant Breeding and Biotechnology</i> , 2014, 2, 231-246.	0.3	1
104	Identification of QTLs for cold tolerance at the booting and flowering stages in rice (<i>Oryza sativa</i> L.). <i>Euphytica</i> , 2021, 217, 1.	0.6	1
105	Comparison of Agronomic and Seed Traits of Common Bean (<i>Phaseolus vulgaris</i> L.) Germplasm from Korea, Bulgaria, and El Salvador. <i>Han'guk Yukchong Hakhoe Chi</i> , 2022, 54, 8-15.	0.2	1
106	Identification and characterization of the stunted sterile (ss) mutant in rice. <i>Genes and Genomics</i> , 2020, 42, 869-882.	0.5	0