

# Huihui Yu

## List of Publications by Year in descending order

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Version: 2024-02-01

28  
papers

2,087  
citations

394421

19  
h-index

526287

27  
g-index

29  
all docs

29  
docs citations

29  
times ranked

2812  
citing authors

#	ARTICLE	IF	CITATIONS
1	Pervasive misannotation of microexons that are evolutionarily conserved and crucial for gene function in plants. <i>Nature Communications</i> , 2022, 13, 820.	12.8	4
2	Genome-wide discovery of natural variation in pre-mRNA splicing and prioritising causal alternative splicing to salt stress response in rice. <i>New Phytologist</i> , 2021, 230, 1273-1287.	7.3	20
3	Serrate-Associated Protein 1, a splicing-related protein, promotes miRNA biogenesis in Arabidopsis. <i>New Phytologist</i> , 2021, 232, 1959-1973.	7.3	18
4	Artificial Selection in Domestication and Breeding Prevents Speciation in Rice. <i>Molecular Plant</i> , 2020, 13, 650-657.	8.3	12
5	<i>MADS78</i> and <i>MADS79</i> Are Essential Regulators of Early Seed Development in Rice. <i>Plant Physiology</i> , 2020, 182, 933-948.	4.8	49
6	Network-based feature selection reveals substructures of gene modules responding to salt stress in rice. <i>Plant Direct</i> , 2019, 3, e00154.	1.9	14
7	Stacking <i>S5-n</i> and <i>f5-n</i> to overcome sterility in indica-japonica hybrid rice. <i>Theoretical and Applied Genetics</i> , 2016, 129, 563-575.	3.6	37
8	Genome-wide Association Study (GWAS) of mesocotyl elongation based on re-sequencing approach in rice. <i>BMC Plant Biology</i> , 2015, 15, 218.	3.6	116
9	Molecular breeding of thermo-sensitive genic male sterile (TGMS) lines of rice for blast resistance using <i>Pi2</i> gene. <i>Rice</i> , 2015, 8, 11.	4.0	39
10	Identification of quantitative trait loci for phosphorus use efficiency traits in rice using a high density SNP map. <i>BMC Genetics</i> , 2014, 15, 155.	2.7	26
11	A whole-genome SNP array ( <i>RICE6K</i> ) for genomic breeding in rice. <i>Plant Biotechnology Journal</i> , 2014, 12, 28-37.	8.3	163
12	An expression quantitative trait loci-guided co-expression analysis for constructing regulatory network using a rice recombinant inbred line population. <i>Journal of Experimental Botany</i> , 2014, 65, 1069-1079.	4.8	74
13	A High-Density SNP Genotyping Array for Rice Biology and Molecular Breeding. <i>Molecular Plant</i> , 2014, 7, 541-553.	8.3	251
14	Development of genomics-based genotyping platforms and their applications in rice breeding. <i>Current Opinion in Plant Biology</i> , 2013, 16, 247-254.	7.1	46
15	QTL Scanning for Rice Yield Using a Whole Genome SNP Array. <i>Journal of Genetics and Genomics</i> , 2013, 40, 629-638.	3.9	21
16	Expression patterns of photoperiod and temperature regulated heading date genes in <i>Oryza sativa</i> . <i>Computational Biology and Chemistry</i> , 2013, 45, 36-41.	2.3	5
17	Identification of quantitative trait loci for grain size and the contributions of major grain-size QTLs to grain weight in rice. <i>Molecular Breeding</i> , 2013, 31, 451-461.	2.1	20
18	Genomics-Based Breeding Technology. , 2013, , 329-348.		3

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19	Rice functional genomics research: Progress and implications for crop genetic improvement. <i>Biotechnology Advances</i> , 2012, 30, 1059-1070.	11.7	100
20	Manipulating Broad-Spectrum Disease Resistance by Suppressing Pathogen-Induced Auxin Accumulation in Rice. <i>Plant Physiology</i> , 2011, 155, 589-602.	4.8	220
21	Two complementary recessive genes in duplicated segments control etiolation in rice. <i>Theoretical and Applied Genetics</i> , 2011, 122, 373-383.	3.6	20
22	Fine mapping a major QTL for flag leaf size and yield-related traits in rice. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1319-1330.	3.6	81
23	Rice <i>GH3</i> gene family. <i>Plant Signaling and Behavior</i> , 2011, 6, 570-574.	2.4	56
24	Gains in QTL Detection Using an Ultra-High Density SNP Map Based on Population Sequencing Relative to Traditional RFLP/SSR Markers. <i>PLoS ONE</i> , 2011, 6, e17595.	2.5	228
25	Genomic survey, characterization and expression profile analysis of the peptide transporter family in rice ( <i>Oryza sativa</i> L.). <i>BMC Plant Biology</i> , 2010, 10, 92.	3.6	46
26	A global analysis of QTLs for expression variations in rice shoots at the early seedling stage. <i>Plant Journal</i> , 2010, 63, 1063-1074.	5.7	69
27	Parent-independent genotyping for constructing an ultrahigh-density linkage map based on population sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10578-10583.	7.1	299
28	The ankyrin repeat gene family in rice: genome-wide identification, classification and expression profiling. <i>Plant Molecular Biology</i> , 2009, 71, 207-226.	3.9	47