

Hong Yu

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

59
papers

3,854
citations

29
h-index

62
g-index

65
ext. papers

5,774
ext. citations

15.4
avg, IF

5.1
L-index

#	Paper	IF	Citations
59	Rootstock-Scion Interactions Affect Fruit Flavor in Grafted Tomato. <i>Horticultural Plant Journal</i> , 2022 ,	4.3	1
58	Chromosome-level genome assembly of the diploid blueberry <i>Vaccinium darrowii</i> provides insights into its subtropical adaptation and cuticle synthesis. <i>Plant Communications</i> , 2022 , 100307	9	0
57	Breeding future crops to feed the world through de novo domestication.. <i>Nature Communications</i> , 2022 , 13, 1171	17.4	0
56	Targeting a gene regulatory element enhances rice grain yield by decoupling panicle number and size.. <i>Nature Biotechnology</i> , 2022 ,	44.5	2
55	Extensive sequence divergence between the reference genomes of <i>Taraxacum kok-saghyz</i> and <i>Taraxacum mongolicum</i> .. <i>Science China Life Sciences</i> , 2021 , 65, 515	8.5	3
54	High-efficiency prime editing with optimized, paired pegRNAs in plants. <i>Nature Biotechnology</i> , 2021 , 39, 923-927	44.5	61
53	A route to de novo domestication of wild allotetraploid rice. <i>Cell</i> , 2021 , 184, 1156-1170.e14	56.2	81
52	FED: a web tool for foreign element detection of genome-edited organism. <i>Science China Life Sciences</i> , 2021 , 64, 167-170	8.5	3
51	Short- and long-term challenges in crop breeding. <i>National Science Review</i> , 2021 , 8, nwab002	10.8	4
50	Expanding the scope of genome editing with SpG and SpRY variants in rice. <i>Science China Life Sciences</i> , 2021 , 64, 1784-1787	8.5	5
49	Immunopurification of Mitochondria from Arabidopsis. <i>Current Protocols</i> , 2021 , 1, e34		
48	RNA demethylation increases the yield and biomass of rice and potato plants in field trials. <i>Nature Biotechnology</i> , 2021 ,	44.5	20
47	Strigolactone and Karrikin Signaling Pathways Elicit Ubiquitination and Proteolysis of SMXL2 to Regulate Hypocotyl Elongation in Arabidopsis. <i>Plant Cell</i> , 2020 , 32, 2251-2270	11.6	38
46	Transcriptional regulation of strigolactone signalling in Arabidopsis. <i>Nature</i> , 2020 , 583, 277-281	50.4	68
45	Malate Circulation: Linking Chloroplast Metabolism to Mitochondrial ROS. <i>Trends in Plant Science</i> , 2020 , 25, 446-454	13.1	38
44	ScCas9 recognizes NNG protospacer adjacent motif in genome editing of rice. <i>Science China Life Sciences</i> , 2020 , 63, 450-452	8.5	7
43	Rapid and specific isolation of intact mitochondria from Arabidopsis leaves. <i>Journal of Genetics and Genomics</i> , 2020 , 47, 65-68	4	5

42	A Strigolactone Biosynthesis Gene Contributed to the Green Revolution in Rice. <i>Molecular Plant</i> , 2020 , 13, 923-932	14.4	35
41	Variations in Both FTL1 and SP5G, Two Tomato FT Paralogs, Control Day-Neutral Flowering. <i>Molecular Plant</i> , 2020 , 13, 939-942	14.4	10
40	FIS1 encodes a GA2-oxidase that regulates fruit firmness in tomato. <i>Nature Communications</i> , 2020 , 11, 5844	17.4	16
39	Arabidopsis-like C model system. <i>Nature Plants</i> , 2020 , 6, 1076-1077	11.5	1
38	Improving the efficiency of the CRISPR-Cas12a system with tRNA-crRNA arrays. <i>Crop Journal</i> , 2020 , 8, 403-407	4.6	9
37	Towards a deeper haplotype mining of complex traits in rice with RFGB v2.0. <i>Plant Biotechnology Journal</i> , 2020 , 18, 14-16	11.6	29
36	SLR1 inhibits MOC1 degradation to coordinate tiller number and plant height in rice. <i>Nature Communications</i> , 2019 , 10, 2738	17.4	44
35	Strigolactone promotes cytokinin degradation through transcriptional activation of in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 14319-14324	11.5	46
34	Tiller Bud Formation Regulators MOC1 and MOC3 Cooperatively Promote Tiller Bud Outgrowth by Activating FON1 Expression in Rice. <i>Molecular Plant</i> , 2019 , 12, 1090-1102	14.4	36
33	Regulation of mitochondrial NAD pool via NAD transporter 2 is essential for matrix NADH homeostasis and ROS production in Arabidopsis. <i>Science China Life Sciences</i> , 2019 , 62, 991-1002	8.5	17
32	xCas9 expands the scope of genome editing with reduced efficiency in rice. <i>Plant Biotechnology Journal</i> , 2019 , 17, 709-711	11.6	65
31	Genetic variations in ARE1 mediate grain yield by modulating nitrogen utilization in rice. <i>Nature Communications</i> , 2018 , 9, 735	17.4	45
30	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018 , 557, 43-49	50.4	582
29	Malate transported from chloroplast to mitochondrion triggers production of ROS and PCD in Arabidopsis thaliana. <i>Cell Research</i> , 2018 , 28, 448-461	24.7	71
28	Genome analysis of Taraxacum kok-saghyz Rodin provides new insights into rubber biosynthesis. <i>National Science Review</i> , 2018 , 5, 78-87	10.8	47
27	Genome-wide identification of transcription factors that are critical to non-small cell lung cancer. <i>Cancer Letters</i> , 2018 , 434, 132-143	9.9	31
26	Detection of major loci associated with the variation of 18 important agronomic traits between Solanum pimpinellifolium and cultivated tomatoes. <i>Plant Journal</i> , 2018 , 95, 312-323	6.9	16
25	A Core Regulatory Pathway Controlling Rice Tiller Angle Mediated by the -Dependent Asymmetric Distribution of Auxin. <i>Plant Cell</i> , 2018 , 30, 1461-1475	11.6	55

24	Towards molecular design of rice plant architecture and grain quality. <i>Chinese Science Bulletin</i> , 2018 , 63, 1275-1289	2.9	2
23	Retrospective and perspective of rice breeding in China. <i>Journal of Genetics and Genomics</i> , 2018 , 45, 603-612	25	
22	A single transcription factor promotes both yield and immunity in rice. <i>Science</i> , 2018 , 361, 1026-1028	33.3	138
21	Construction of a Genome-Wide Mutant Library in Rice Using CRISPR/Cas9. <i>Molecular Plant</i> , 2017 , 10, 1238-1241	14.4	127
20	A D53 repression motif induces oligomerization of TOPLESS corepressors and promotes assembly of a corepressor-nucleosome complex. <i>Science Advances</i> , 2017 , 3, e1601217	14.3	40
19	Tissue-Specific Ubiquitination by IPA1 INTERACTING PROTEIN1 Modulates IPA1 Protein Levels to Regulate Plant Architecture in Rice. <i>Plant Cell</i> , 2017 , 29, 697-707	11.6	58
18	A natural tandem array alleviates epigenetic repression of IPA1 and leads to superior yielding rice. <i>Nature Communications</i> , 2017 , 8, 14789	17.4	85
17	Genome-wide association studies dissect the genetic networks underlying agronomical traits in soybean. <i>Genome Biology</i> , 2017 , 18, 161	18.3	190
16	IPA1 functions as a downstream transcription factor repressed by D53 in strigolactone signaling in rice. <i>Cell Research</i> , 2017 , 27, 1128-1141	24.7	115
15	DWARF14, A Receptor Covalently Linked with the Active Form of Strigolactones, Undergoes Strigolactone-Dependent Degradation in Rice. <i>Frontiers in Plant Science</i> , 2017 , 8, 1935	6.2	24
14	Critical roles of soluble starch synthase SSIIIa and granule-bound starch synthase Waxy in synthesizing resistant starch in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 12844-12849	11.5	100
13	Guest Editorial for Special Section on Big Data Computing and Processing in Computational Biology and Bioinformatics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016 , 13, 810-811	1	1
12	Identification of Regulatory DNA Elements Using Genome-wide Mapping of DNase I Hypersensitive Sites during Tomato Fruit Development. <i>Molecular Plant</i> , 2016 , 9, 1168-1182	14.4	16
11	Copy number variation at the GL7 locus contributes to grain size diversity in rice. <i>Nature Genetics</i> , 2015 , 47, 944-8	36.3	317
10	Rice functional genomics and breeding database (RFGB)-3K-rice SNP and InDel sub-database. <i>Chinese Science Bulletin</i> , 2015 , 60, 367-371	2.9	27
9	Deficient plastidic fatty acid synthesis triggers cell death by modulating mitochondrial reactive oxygen species. <i>Cell Research</i> , 2015 , 25, 621-33	24.7	57
8	Heterogeneous Cloud Framework for Big Data Genome Sequencing. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015 , 12, 166-78	3	22
7	Genome-wide binding analysis of the transcription activator ideal plant architecture1 reveals a complex network regulating rice plant architecture. <i>Plant Cell</i> , 2013 , 25, 3743-59	11.6	417

6	DWARF 53 acts as a repressor of strigolactone signalling in rice. <i>Nature</i> , 2013 , 504, 401-5	50.4	475
5	Network Analysis to Interpret Complex Phenotypes 2011 , 1-12		1
4	eResponseNet: a package prioritizing candidate disease genes through cellular pathways. <i>Bioinformatics</i> , 2011 , 27, 2319-20	7.2	8
3	Evaluating diabetes and hypertension disease causality using mouse phenotypes. <i>BMC Systems Biology</i> , 2010 , 4, 97	3.5	3
2	Improving the thermostability of N-carbamyl-D-amino acid amidohydrolase by error-prone PCR. <i>Applied Microbiology and Biotechnology</i> , 2009 , 82, 279-85	5.7	12
1	Inferring causal relationships among different histone modifications and gene expression. <i>Genome Research</i> , 2008 , 18, 1314-24	9.7	97