Yongbiao Xue

List of Publications by Year in descending order

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71651 81839 6,301 89 39 76 citations g-index h-index papers 110 110 110 7064 times ranked docs citations citing authors all docs

#	Article	IF	CITATIONS
1	Genomic analyses provide insights into the history of tomato breeding. Nature Genetics, 2014, 46, 1220-1226.	9.4	801
2	Sequence and analysis of rice chromosome 4. Nature, 2002, 420, 316-320.	13.7	471
3	An F-box gene linked to the self-incompatibility (S) locus of Antirrhinum is expressed specifically in pollen and tapetum. Plant Molecular Biology, 2002, 50, 29-41.	2.0	318
4	A Novel Nuclear-Localized CCCH-Type Zinc Finger Protein, OsDOS, Is Involved in Delaying Leaf Senescence in Rice. Plant Physiology, 2006, 141, 1376-1388.	2.3	241
5	The F-Box Protein AhSLF-S2 Controls the Pollen Function of S-RNase–Based Self-Incompatibility. Plant Cell, 2004, 16, 2307-2322.	3.1	217
6	The F-Box Protein AhSLF-S2 Physically Interacts with S-RNases That May Be Inhibited by the Ubiquitin/26S Proteasome Pathway of Protein Degradation during Compatible Pollination in Antirrhinum. Plant Cell, 2004, 16, 582-595.	3.1	190
7	Evolution in Action: Following Function in Duplicated Floral Homeotic Genes. Current Biology, 2005, 15, 1508-1512.	1.8	165
8	Proteomic analyses of Oryza sativa mature pollen reveal novel proteins associated with pollen germination and tube growth. Proteomics, 2006, 6, 2504-2529.	1.3	165
9	Database Resources of the National Genomics Data Center in 2020. Nucleic Acids Research, 2020, 48, D24-D33.	6. 5	165
10	F-Box Protein DOR Functions As a Novel Inhibitory Factor for Abscisic Acid-Induced Stomatal Closure under Drought Stress in Arabidopsis Â. Plant Physiology, 2008, 148, 2121-2133.	2.3	163
11	The R2R3 MYB Transcription Factor GhMYB109 Is Required for Cotton Fiber Development. Genetics, 2008, 180, 811-820.	1.2	156
12	Genome-scale analysis and comparison of gene expression profiles in developing and germinated pollen in Oryza sativa. BMC Genomics, 2010, 11, 338.	1.2	149
13	Proteomics Identification of Differentially Expressed Proteins Associated with Pollen Germination and Tube Growth Reveals Characteristics of Germinated Oryza sativa Pollen. Molecular and Cellular Proteomics, 2007, 6, 207-230.	2.5	133
14	The U-Box E3 Ubiquitin Ligase TUD1 Functions with a Heterotrimeric G α Subunit to Regulate Brassinosteroid-Mediated Growth in Rice. PLoS Genetics, 2013, 9, e1003391.	1.5	117
15	Calcineurin B-like interacting protein kinase OsCIPK23 functions in pollination and drought stress responses in rice (Oryza sativa L.). Journal of Genetics and Genomics, 2008, 35, 531-S2.	1.7	114
16	Towards molecular breeding and improvement of rice in China. Trends in Plant Science, 2005, 10, 610-614.	4.3	108
17	Genome-Wide Gene Expression Profiling Reveals Conserved and Novel Molecular Functions of the Stigma in Rice. Plant Physiology, 2007, 144, 1797-1812.	2.3	108
18	Genome-wide intraspecific DNA-sequence variations in rice. Current Opinion in Plant Biology, 2003, 6, 134-138.	3.5	99

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19	Nucleolar DEAD-Box RNA Helicase TOGR1 Regulates Thermotolerant Growth as a Pre-rRNA Chaperone in Rice. PLoS Genetics, 2016, 12, e1005844.	1.5	95
20	The Skp1-like protein SSK1 is required for cross-pollen compatibility in <i>S</i> -RNase-based self-incompatibility. Plant Journal, 2010, 62, 52-63.	2.8	91
21	The bread wheat epigenomic map reveals distinct chromatin architectural and evolutionary features of functional genetic elements. Genome Biology, 2019, 20, 139.	3.8	90
22	The Global Landscape of SARS-CoV-2 Genomes, Variants, and Haplotypes in 2019nCoVR. Genomics, Proteomics and Bioinformatics, 2020, 18, 749-759.	3.0	88
23	Genome structure and evolution of Antirrhinum majus L. Nature Plants, 2019, 5, 174-183.	4.7	85
24	AhSSK1, a novel SKP1-like protein that interacts with the S-locus F-box protein SLF. Plant Journal, 2006, 46, 780-793.	2.8	83
25	A putative lipase gene <i>EXTRA GLUME1</i> regulates both emptyâ€glume fate and spikelet development in rice. Plant Journal, 2009, 57, 593-605.	2.8	81
26	Roles of Proteolysis in Plant Self-Incompatibility. Annual Review of Plant Biology, 2009, 60, 21-42.	8.6	80
27	A Snapshot of the Emerging Tomato Genome Sequence. Plant Genome, 2009, 2, .	1.6	73
28	Structural and transcriptional analysis of S -locus F-box genes in Antirrhinum. Sexual Plant Reproduction, 2003, 16, 165-177.	2.2	70
29	Selection and gene flow shape genomic islands that control floral guides. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11006-11011.	3.3	67
30	Monitoring of Gene Expression Profiles and Isolation of Candidate Genes Involved in Pollination and Fertilization in Rice (Oryza Sativa L.) with a 10K cDNA Microarray. Plant Molecular Biology, 2004, 54, 471-487.	2.0	66
31	A Fine Physical Map of the Rice Chromosome 4. Genome Research, 2002, 12, 817-823.	2.4	64
32	Microarray Analysis Reveals Similarities and Variations in Genetic Programs Controlling Pollination/Fertilization and Stress Responses in Rice (Oryza sativa L.). Plant Molecular Biology, 2005, 59, 151-164.	2.0	61
33	Microarray Analysis of Gene Expression Involved in Anther Development in rice (Oryza sativa L.). Plant Molecular Biology, 2005, 58, 721-737.	2.0	61
34	Genome-wide analysis of S-Locus F-box-like genes in Arabidopsis thaliana. Plant Molecular Biology, 2004, 56, 929-945.	2.0	60
35	Organizational Innovation of Apical Actin Filaments Drives Rapid Pollen Tube Growth and Turning. Molecular Plant, 2017, 10, 930-947.	3.9	57
36	A PECTIN METHYLESTERASE gene at the maize Ga1 locus confers male function in unilateral cross-incompatibility. Nature Communications, 2018, 9, 3678.	5.8	54

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37	Gene Expression Profiles Deciphering Rice Phenotypic Variation between Nipponbare (Japonica) and 93-11 (Indica) during Oxidative Stress. PLoS ONE, 2010, 5, e8632.	1.1	52
38	Evolution of flower color pattern through selection on regulatory small RNAs. Science, 2017, 358, 925-928.	6.0	48
39	An atlas of wheat epigenetic regulatory elements reveals subgenome divergence in the regulation of development and stress responses. Plant Cell, 2021, 33, 865-881.	3.1	48
40	An Auxin-Inducible F-Box Protein CEGENDUO Negatively Regulates Auxin-Mediated Lateral Root Formation in Arabidopsis. Plant Molecular Biology, 2006, 60, 599-615.	2.0	47
41	Population Genetics of SARS-CoV-2: Disentangling Effects of Sampling Bias and Infection Clusters. Genomics, Proteomics and Bioinformatics, 2020, 18, 640-647.	3.0	44
42	Molecular Cytogenetic Characterization of the Antirrhinum majus GenomeSequence data from this article have been deposited with the EMBL/GenBank Data Libraries under the accession nos. AY630561 (for BAC 5E10) and AY6305612 (for BAC 36D21) Genetics, 2005, 169, 325-335.	1.2	42
43	Analysis of genetic architecture and favorable allele usage of agronomic traits in a large collection of Chinese rice accessions. Science China Life Sciences, 2020, 63, 1688-1702.	2.3	41
44	SCFSLF-mediated cytosolic degradation of S-RNase is required for cross-pollen compatibility in S-RNase-based self-incompatibility in Petunia hybrida. Frontiers in Genetics, 2014, 5, 228.	1.1	40
45	AhSL28, a senescence- and phosphate starvation-induced S-like RNase gene in Antirrhinum. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2002, 1579, 64-71.	2.4	39
46	<i>Dwarf and deformed flower</i> â€f <i>1,</i> encoding an Fâ€box protein, is critical for vegetative and floral development in rice (<i>Oryza sativa</i> L.). Plant Journal, 2012, 72, 829-842.	2.8	39
47	Identification of a canonical SCFSLF complex involved in S-RNase-based self-incompatibility of Pyrus (Rosaceae). Plant Molecular Biology, 2013, 81, 245-257.	2.0	38
48	Recent highlights of the China Rice Functional Genomics Program. Trends in Genetics, 2003, 19, 390-394.	2.9	37
49	'A life or death decision' for pollen tubes in S-RNase-based self-incompatibility. Journal of Experimental Botany, 2010, 61, 2027-2037.	2.4	37
50	Transcriptome Phase Distribution Analysis Reveals Diurnal Regulated Biological Processes and Key Pathways in Rice Flag Leaves and Seedling Leaves. PLoS ONE, 2011, 6, e17613.	1.1	37
51	Tracing the Evolution of the Floral Homeotic B- and C-Function Genes through Genome Synteny. Molecular Biology and Evolution, 2010, 27, 2651-2664.	3.5	36
52	Isolation and characterization of male-germ-cell transcripts in Nicotiana tabacum. Sexual Plant Reproduction, 2002, 14, 339-346.	2.2	35
53	A High Temperature-Dependent Mitochondrial Lipase EXTRA GLUME1 Promotes Floral Phenotypic Robustness against Temperature Fluctuation in Rice (Oryza sativa L.). PLoS Genetics, 2016, 12, e1006152.	1.5	33
54	Heterochromatic and genetic features are consistent with recombination suppression of the self-incompatibility locus in Antirrhinum. Plant Journal, 2007, 51, 140-151.	2.8	30

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55	Genetic features of a pollen-part mutation suggest an inhibitory role for the Antirrhinum pollen self-incompatibility determinant. Plant Molecular Biology, 2009, 70, 499-509.	2.0	30
56	Origin, loss, and regain of self-incompatibility in angiosperms. Plant Cell, 2022, 34, 579-596.	3.1	30
57	Rice functional genomics research in China. Philosophical Transactions of the Royal Society B: Biological Sciences, 2007, 362, 1009-1021.	1.8	28
58	Characterization of Osmads6-5, a null allele, reveals that OsMADS6 is a critical regulator for early flower development in rice (Oryza sativa L.). Plant Molecular Biology, 2012, 80, 429-442.	2.0	28
59	Electrostatic potentials of the <i>S</i> â€locus Fâ€box proteins contribute to the pollen <i>S</i> specificity in selfâ€incompatibility in <i>Petunia hybrida</i> . Plant Journal, 2017, 89, 45-57.	2.8	28
60	Tracing the origins of SARS-CoV-2: lessons learned from the past. Cell Research, 2021, 31, 1139-1141.	5.7	25
61	The twin-beginnings of COVID-19 in Asia and Europe—one prevails quickly. National Science Review, 2022, 9, nwab223.	4.6	22
62	On the origin of SARS-CoV-2â€"The blind watchmaker argument. Science China Life Sciences, 2021, 64, 1560-1563.	2.3	18
63	PcTGD, a highly expressed gene in stem, is related to water stress in reed (Phragmites communis Trin.). Science Bulletin, 2001, 46, 850-854.	1.7	14
64	The Protein Arginine Methylase 5 (PRMT5/SKB1) Gene Is Required for the Maintenance of Root Stem Cells in Response to DNA Damage. Journal of Genetics and Genomics, 2016, 43, 187-197.	1.7	13
65	Ectopic expression of nucleolar DEAD-Box RNA helicase OsTOGR1 confers improved heat stress tolerance in transgenic Chinese cabbage. Plant Cell Reports, 2020, 39, 1803-1814.	2.8	13
66	Identification of a Ubiquitin-Binding Structure in the S-Locus F-Box Protein Controlling S-RNase-Based Self-Incompatibility. Journal of Genetics and Genomics, 2012, 39, 93-102.	1.7	12
67	Identification and evolutionary analysis of a relic S-RNase in Antirrhinum. Sexual Plant Reproduction, 2003, 16, 17-22.	2.2	11
68	<i>RETINOBLASTOMA-RELATED</i> Genes Specifically Control Inner Floral Organ Morphogenesis and Pollen Development in Rice. Plant Physiology, 2019, 181, 1600-1614.	2.3	10
69	Villin Controls the Formation and Enlargement of Punctate Actin Foci in Pollen Tubes. Journal of Cell Science, 2020, 133, .	1.2	10
70	Primary restriction of Sâ€RNase cytotoxicity by a stepwise ubiquitination and degradation pathway in <i>Petuniahybrida</i> . New Phytologist, 2021, 231, 1249-1264.	3.5	10
71	Fine Mapping of the Maize Crossâ€Incompatibility Locus <i>Gametophytic Factor 1</i> (<i>ga1</i>) Using a Homogeneous Population. Crop Science, 2014, 54, 873-881.	0.8	9
72	Ongoing Positive Selection Drives the Evolution of SARS-CoV-2 Genomes. Genomics, Proteomics and Bioinformatics, 2022, 20, 1214-1223.	3.0	9

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73	Genomic Epidemiology of SARS-CoV-2 in Pakistan. Genomics, Proteomics and Bioinformatics, 2021, 19, 727-740.	3.0	8
74	Case study for identification of potentially indel-caused alternative expression isoforms in the rice subspecies japonica and indica by integrative genome analysis. Genomics, 2008, 91, 186-194.	1.3	6
75	Expressional profiling of genes related to pollination and fertilization in rice. Comptes Rendus De L'Académie Des Sciences Série 3, Sciences De La Vie, 2001, 324, 1111-1116.	0.8	5
76	cDNA-AFLP analysis reveals that maize resistance toBipolaris maydis is associated with the induction of multiple defense-related genes. Science Bulletin, 2001, 46, 1454-1458.	1.7	4
77	An Introduction to the China Rice Functional Genomics Program. Comparative and Functional Genomics, 2002, 3, 161-163.	2.0	4
78	Identification, Expression and Functional Analysis of a Receptor-like Cytoplasmic Kinase, OsRLCK1, in Rice. Journal of Integrative Plant Biology, 2007, 49, 898-907.	4.1	4
79	DOR. Plant Signaling and Behavior, 2009, 4, 470-471.	1.2	4
80	Isolation of candidateR disease resistance genes from rice. Science Bulletin, 1998, 43, 497-500.	1.7	2
81	The pathogenic site of the C-toxin derived fromBipolaris maydis race C in maize (Zea mays). Science Bulletin, 2000, 45, 1787-1791.	1.7	2
82	Genetic analysis and gene mapping ofleafy head (lhd), a mutant blocking the differentiation of rachis branches in rice (Oryza sativa L.). Science Bulletin, 2003, 48, 2201-2205.	1.7	2
83	Title is missing!. Plant Cell, Tissue and Organ Culture, 2004, 76, 61-65.	1.2	1
84	Highlights of genetics research over the past four decades in China. Journal of Genetics and Genomics, 2018, 45, 561-562.	1.7	1
85	Molecular Control of S-RNase-based Self-Incompatibility. , 2007, , 63-73.		1
86	Pinpointing the animal origins of SARS-CoV-2: a genomic approach. Journal of Genetics and Genomics, 2022, 49, 900-902.	1.7	1
87	Expression of self-incompatibility ribonucleases of Antirrhinum inEscherichia coli. Science Bulletin, 2000, 45, 512-515.	1.7	0
88	S RNASES AND SELF AND NON-SELF POLLEN RECOGNITION IN FLOWERING PLANTS. , 2001, , 149-155.		0
89	Metagenomic evidence for the co-existence of SARS and H1N1 in patients from 2007-2012 flu seasons in France. Biosafety and Health, 2021, 3, 307-307.	1.2	0