

# Sihai Yang

## List of Publications by Year in descending order

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Version: 2024-02-01

43  
papers

2,629  
citations

257450

24  
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243625

44  
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44  
all docs

44  
docs citations

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times ranked

3955  
citing authors

#	ARTICLE	IF	CITATIONS
1	In rice splice variants that restore the reading frame after frameshifting indel introduction are common, often induced by the indels and sometimes lead to organism-level rescue. <i>PLoS Genetics</i> , 2022, 18, e1010071.	3.5	2
2	Mitotic gene conversion can be as important as meiotic conversion in driving genetic variability in plants and other species without early germline segregation. <i>PLoS Biology</i> , 2021, 19, e3001164.	5.6	5
3	Ancient rapid functional differentiation and fixation of the duplicated members in rice <i>&lt;i&gt;Dof&lt;/i&gt;</i> genes after whole genome duplication. <i>Plant Journal</i> , 2021, 108, 1365-1381.	5.7	5
4	Somatic mutation analysis in <i>Salix suchowensis</i> reveals early segregated cell lineages. <i>Molecular Biology and Evolution</i> , 2021, 38, 5292-5308.	8.9	10
5	CRISPR-based assessment of genomic structure in the conserved <i>SQUAMOSA</i> promoter-binding-like gene clusters in rice. <i>Plant Journal</i> , 2020, 104, 1301-1314.	5.7	14
6	Repeat-induced point mutation in <i>Neurospora crassa</i> causes the highest known mutation rate and mutational burden of any cellular life. <i>Genome Biology</i> , 2020, 21, 142.	8.8	24
7	Pleiotropic changes revealed by in situ recovery of the semi-dwarf gene <i>sd1</i> in rice. <i>Journal of Plant Physiology</i> , 2020, 248, 153141.	3.5	11
8	Large-scale identification and functional analysis of <i>&lt;i&gt;NLR&lt;/i&gt;</i> genes in blast resistance in the Tetep rice genome sequence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18479-18487.	7.1	63
9	CRISPR-Based Assessment of Gene Specialization in the Gibberellin Metabolic Pathway in Rice. <i>Plant Physiology</i> , 2019, 180, 2091-2105.	4.8	24
10	Different knockout genotypes of <i>OslAA23</i> in rice using CRISPR/Cas9 generating different phenotypes. <i>Plant Molecular Biology</i> , 2019, 100, 467-479.	3.9	18
11	The architecture of intra-organism mutation rate variation in plants. <i>PLoS Biology</i> , 2019, 17, e3000191.	5.6	89
12	<i>Liriodendron</i> genome sheds light on angiosperm phylogeny and species-pair differentiation. <i>Nature Plants</i> , 2019, 5, 18-25.	9.3	163
13	High-resolution insight into recombination events at the <i>&lt;sc&gt;SD&lt;/sc&gt;1&lt;/i&gt; locus in rice. <i>Plant Journal</i>, 2019, 97, 683-692.</i>	5.7	8
14	Tetrad analysis in plants and fungi finds large differences in gene conversion rates but no GC bias. <i>Nature Ecology and Evolution</i> , 2018, 2, 164-173.	7.8	65
15	Phylogenetic and CRISPR/Cas9 Studies in Deciphering the Evolutionary Trajectory and Phenotypic Impacts of Rice <i>ERECTA</i> Genes. <i>Frontiers in Plant Science</i> , 2018, 9, 473.	3.6	33
16	Identifying a large number of high-yield genes in rice by pedigree analysis, whole-genome sequencing, and CRISPR-Cas9 gene knockout. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7559-E7567.	7.1	50
17	Direct Determination of the Mutation Rate in the Bumblebee Reveals Evidence for Weak Recombination-Associated Mutation and an Approximate Rate Constancy in Insects. <i>Molecular Biology and Evolution</i> , 2017, 34, 119-130.	8.9	93
18	Selective sweep with significant positive selection serves as the driving force for the differentiation of japonica and indica rice cultivars. <i>BMC Genomics</i> , 2017, 18, 307.	2.8	25

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19	Insertions/Deletions-Associated Nucleotide Polymorphism in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1792.	3.6	4
20	Dissimilar manifestation of heterosis under nutrient-deficient and nutrient-sufficient condition. <i>Plant Physiology</i> , 2016, 172, pp.00579.2016.	4.8	4
21	Mutation rate analysis via parentâ€“progeny sequencing of the perennial peach. I. A low rate in woody perennials and a higher mutagenicity in hybrids. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161016.	2.6	64
22	Mutation rate analysis via parentâ€“progeny sequencing of the perennial peach. II. No evidence for recombination-associated mutation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161785.	2.6	17
23	Cloning of novel rice blast resistance genes from two rapidly evolving NBS-LRR gene families in rice. <i>Plant Molecular Biology</i> , 2016, 90, 95-105.	3.9	19
24	High genetic abundance of Rpi-blb2/Mi-1.2/Cami gene family in Solanaceae. <i>BMC Evolutionary Biology</i> , 2015, 15, 215.	3.2	1
25	A genome-wide survey reveals abundant rice blast <i>R</i> genes in resistant cultivars. <i>Plant Journal</i> , 2015, 84, 20-28.	5.7	42
26	Evolutionary analysis of RB/Rpi-blb1 locus in the Solanaceae family. <i>Molecular Genetics and Genomics</i> , 2015, 290, 2173-2186.	2.1	3
27	GC-Content of Synonymous Codons Profoundly Influences Amino Acid Usage. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2027-2036.	1.8	59
28	Relationship between amino acid usage and amino acid evolution in primates. <i>Gene</i> , 2015, 557, 182-187.	2.2	12
29	Parentâ€“progeny sequencing indicates higher mutation rates in heterozygotes. <i>Nature</i> , 2015, 523, 463-467.	27.8	157
30	Causes and consequences of crossing-over evidenced via a high-resolution recombinational landscape of the honey bee. <i>Genome Biology</i> , 2015, 16, 15.	8.8	67
31	Extreme expansion of NBS-encoding genes in Rosaceae. <i>BMC Genetics</i> , 2015, 16, 48.	2.7	84
32	Widely distributed hot and cold spots in meiotic recombination as shown by the sequencing of rice $F_2$ plants. <i>New Phytologist</i> , 2015, 206, 1491-1502.	7.3	86
33	Allele-mining of rice blast resistance genes at AC134922 locus. <i>Biochemical and Biophysical Research Communications</i> , 2014, 446, 1085-1090.	2.1	14
34	Rapidly evolving <i>R</i> genes in diverse grass species confer resistance to rice blast disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18572-18577.	7.1	120
35	Great majority of recombination events in <i>Arabidopsis</i> are gene conversion events. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20992-20997.	7.1	69
36	Tracing the origin and evolutionary history of plant nucleotide-binding siteâ€“leucine-rich repeat ( <i>NBS-LRR</i> ) genes. <i>New Phytologist</i> , 2012, 193, 1049-1063.	7.3	198

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37	Genome-wide investigation reveals high evolutionary rates in annual model plants. <i>BMC Plant Biology</i> , 2010, 10, 242.	3.6	42
38	Genetic variation of NBS-LRR class resistance genes in rice lines. <i>Theoretical and Applied Genetics</i> , 2008, 116, 165-177.	3.6	67
39	Recent duplications dominate NBS-encoding gene expansion in two woody species. <i>Molecular Genetics and Genomics</i> , 2008, 280, 187-198.	2.1	405
40	Single-nucleotide mutation rate increases close to insertions/deletions in eukaryotes. <i>Nature</i> , 2008, 455, 105-108.	27.8	226
41	A molecular isolation mechanism associated with high intra-specific diversity in rice. <i>Gene</i> , 2007, 394, 87-95.	2.2	12
42	Highly asymmetric rice genomes. <i>BMC Genomics</i> , 2007, 8, 154.	2.8	38
43	Genome-wide investigation on the genetic variations of rice disease resistance genes. <i>Plant Molecular Biology</i> , 2006, 62, 181-193.	3.9	105