

Yeisoo Yu

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

17,228
citations

87723

38
h-index

138251

58
g-index

60
all docs

60
docs citations

60
times ranked

15682
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	13.7	3,854
2	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
3	A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. japonica). <i>Science</i> , 2002, 296, 92-100.	6.0	2,866
4	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014, 46, 707-713.	9.4	1,159
5	Genome sequence of the hot pepper provides insights into the evolution of pungency in <i>Capsicum</i> species. <i>Nature Genetics</i> , 2014, 46, 270-278.	9.4	867
6	An Integrated Physical and Genetic Map of the Rice Genome. <i>Plant Cell</i> , 2002, 14, 537-545.	3.1	422
7	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	9.4	413
8	The genome sequence of African rice (<i>Oryza glaberrima</i>) and evidence for independent domestication. <i>Nature Genetics</i> , 2014, 46, 982-988.	9.4	342
9	Sequence composition and genome organization of maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14349-14354.	3.3	290
10	Curated genome annotation of <i>Oryza sativa</i> ssp. japonica and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	2.4	218
11	Extensive sequence divergence between the reference genomes of two elite <i>indica</i> rice varieties Zhenshan 97 and Minghui 63. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5163-71.	3.3	211
12	The <i>Oryza</i> bacterial artificial chromosome library resource: Construction and analysis of 12 deep-coverage large-insert BAC libraries that represent the 10 genome types of the genus <i>Oryza</i> . <i>Genome Research</i> , 2005, 16, 140-147.	2.4	197
13	Rice Transposable Elements: A Survey of 73,000 Sequence-Tagged-Connectors. <i>Genome Research</i> , 2000, 10, 982-990.	2.4	187
14	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
15	Sequencing, Mapping, and Analysis of 27,455 Maize Full-Length cDNAs. <i>PLoS Genetics</i> , 2009, 5, e1000740.	1.5	145
16	The <i>Oryza</i> Map Alignment Project: The Golden Path to Unlocking the Genetic Potential of Wild Rice Species. <i>Plant Molecular Biology</i> , 2005, 59, 53-62.	2.0	143
17	Genome and evolution of the shade-requiring medicinal herb <i>Panax ginseng</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1904-1917.	4.1	136
18	Dynamic Evolution of <i>Oryza</i> Genomes Is Revealed by Comparative Genomic Analysis of a Genus-Wide Vertical Data Set. <i>Plant Cell</i> , 2009, 20, 3191-3209.	3.1	128

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19	Rapid evolution of protein diversity by de novo origination in <i>Oryza</i> . <i>Nature Ecology and Evolution</i> , 2019, 3, 679-690.	3.4	121
20	Transposable element distribution, abundance and role in genome size variation in the genus <i>Oryza</i> . <i>BMC Evolutionary Biology</i> , 2007, 7, 152.	3.2	115
21	Evolutionary dynamics of an ancient retrotransposon family provides insights into evolution of genome size in the genus <i>Oryza</i> . <i>Plant Journal</i> , 2007, 52, 342-351.	2.8	99
22	Large-Scale Identification of Expressed Sequence Tags Involved in Rice and Rice Blast Fungus Interaction. <i>Plant Physiology</i> , 2005, 138, 105-115.	2.3	96
23	Genotyping-by-sequencing map permits identification of clubroot resistance QTLs and revision of the reference genome assembly in cabbage (<i>Brassica oleracea</i> L.). <i>DNA Research</i> , 2016, 23, dsv034.	1.5	94
24	Construction, alignment and analysis of 12 framework physical maps that represent the 10 genome types of the genus <i>Oryza</i> . <i>Genome Biology</i> , 2008, 9, R45.	13.9	82
25	Sequence, annotation, and analysis of synteny between rice chromosome 3 and diverged grass species. <i>Genome Research</i> , 2005, 15, 1284-1291.	2.4	73
26	BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean (<i>Phaseolus vulgaris</i> L.) Genome. <i>Tropical Plant Biology</i> , 2008, 1, 40-48.	1.0	70
27	Genome-wide SNP identification and QTL mapping for black rot resistance in cabbage. <i>BMC Plant Biology</i> , 2015, 15, 32.	1.6	63
28	De Novo Next Generation Sequencing of Plant Genomes. <i>Rice</i> , 2009, 2, 35-43.	1.7	59
29	A Phylogenetic Analysis of Indel Dynamics in the Cotton Genus. <i>Molecular Biology and Evolution</i> , 2008, 25, 1415-1428.	3.5	57
30	Genome-enabled discovery of anthraquinone biosynthesis in <i>Senna tora</i> . <i>Nature Communications</i> , 2020, 11, 5875.	5.8	57
31	Fifteen Million Years of Evolution in the <i>Oryza</i> Genus Shows Extensive Gene Family Expansion. <i>Molecular Plant</i> , 2014, 7, 642-656.	3.9	54
32	In-depth sequence analysis of the tomato chromosome 12 centromeric region: identification of a large CAA block and characterization of pericentromere retrotransposons. <i>Chromosoma</i> , 2005, 114, 103-117.	1.0	52
33	DNA transposon activity is associated with increased mutation rates in genes of rice and other grasses. <i>Nature Communications</i> , 2016, 7, 12790.	5.8	51
34	Genome and Comparative Transcriptomics of African Wild Rice <i>Oryza longistaminata</i> Provide Insights into Molecular Mechanism of Rhizomatousness and Self-Incompatibility. <i>Molecular Plant</i> , 2015, 8, 1683-1686.	3.9	49
35	A draft physical map of a D-genome cotton species (<i>Gossypium raimondii</i>). <i>BMC Genomics</i> , 2010, 11, 395.	1.2	48
36	Spatio-temporal patterns of genome evolution in allotetraploid species of the genus <i>Oryza</i> . <i>Plant Journal</i> , 2010, 63, 430-442.	2.8	48

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37	Rice structural variation: a comparative analysis of structural variation between rice and three of its closest relatives in the genus <i>Oryza</i> . <i>Plant Journal</i> , 2010, 63, 990-1003.	2.8	47
38	An Integrated Physical, Genetic and Cytogenetic Map of <i>Brachypodium distachyon</i> , a Model System for Grass Research. <i>PLoS ONE</i> , 2010, 5, e13461.	1.1	45
39	A lineage-specific centromere retrotransposon in <i>Oryza brachyantha</i> . <i>Plant Journal</i> , 2009, 60, 820-831.	2.8	41
40	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000728.	1.5	39
41	Random sheared fosmid library as a new genomic tool to accelerate complete finishing of rice (<i>Oryza</i>) euchromatic portions of the genome. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1596-1607.	1.8	36
42	The Subtelomere of <i>Oryza sativa</i> Chromosome 3 Short Arm as a Hot Bed of New Gene Origination in Rice. <i>Molecular Plant</i> , 2008, 1, 839-850.	3.9	36
43	The <i>Oryza</i> BAC resource: a genus-wide and genome scale tool for exploring rice genome evolution and leveraging useful genetic diversity from wild relatives. <i>Breeding Science</i> , 2010, 60, 536-543.	0.9	34
44	Building two indica rice reference genomes with PacBio long-read and Illumina paired-end sequencing data. <i>Scientific Data</i> , 2016, 3, 160076.	2.4	34
45	Orthologous Comparisons of the Hd1 Region across Genera Reveal Hd1 Gene Lability within Diploid <i>Oryza</i> Species and Disruptions to Microsynteny in <i>Sorghum</i> . <i>Molecular Biology and Evolution</i> , 2010, 27, 2487-2506.	3.5	31
46	A physical map for the <i>Amborella trichopoda</i> genome sheds light on the evolution of angiosperm genome structure. <i>Genome Biology</i> , 2011, 12, R48.	13.9	28
47	Utilization of a zebra finch BAC library to determine the structure of an avian androgen receptor genomic region. <i>Genomics</i> , 2006, 87, 181-190.	1.3	25
48	Genomic structure and evolution of the Pi2/9 locus in wild rice species. <i>Theoretical and Applied Genetics</i> , 2010, 121, 295-309.	1.8	25
49	The 19 Genomes of <i>Drosophila</i> : A BAC Library Resource for Genus-Wide and Genome-Scale Comparative Evolutionary Research. <i>Genetics</i> , 2011, 187, 1023-1030.	1.2	22
50	Genome puzzle master (GPM): an integrated pipeline for building and editing pseudomolecules from fragmented sequences. <i>Bioinformatics</i> , 2016, 32, 3058-3064.	1.8	22
51	Toward closing rice telomere gaps: mapping and sequence characterization of rice subtelomere regions. <i>Theoretical and Applied Genetics</i> , 2005, 111, 467-478.	1.8	21
52	The Future of Rice Genomics: Sequencing the Collective <i>Oryza</i> Genome. <i>Rice</i> , 2010, 3, 89-97.	1.7	21
53	Construction and utility of 10-kb libraries for efficient clone-gap closure for rice genome sequencing. <i>Theoretical and Applied Genetics</i> , 2003, 107, 652-660.	1.8	18
54	Comparative sequence analysis of the SALT OVERLY SENSITIVE1 orthologous region in <i>Thellungiella halophila</i> and <i>Arabidopsis thaliana</i> . <i>Genomics</i> , 2009, 94, 196-203.	1.3	17

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55	Exceptional lability of a genomic complex in rice and its close relatives revealed by interspecific and intraspecific comparison and population analysis. <i>BMC Genomics</i> , 2011, 12, 142.	1.2	14
56	The Oryza Map Alignment Project (OMAP): A New Resource for Comparative Genome Studies within <i>Oryza</i> . , 2007, , 395-409.		9
57	Integration of the Draft Sequence and Physical Map as a Framework for Genomic Research in Soybean (<i>Glycine max</i> (L.) Merr.) and Wild Soybean (<i>Glycine soja</i> Sieb. and Zucc.). <i>C3: Genes, Genomes, Genetics</i> , 2012, 2, 321-329.	0.8	9
58	Assessing the Extent of Substitution Rate Variation of Retrotransposon Long Terminal Repeat Sequences in <i>Oryza sativa</i> and <i>Oryza glaberrima</i> . <i>Rice</i> , 2010, 3, 242-250.	1.7	5
59	A Framework for Sequencing the Rice Genome. <i>Novartis Foundation Symposium</i> , 2001, 236, 13-27.	1.2	2
60	Whole Genome Sequencing: Methodology and Progress in Cereals. , 2004, , 385-423.		0