

# Shiguo Zhou

## List of Publications by Year in descending order

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49  
papers

18,699  
citations

87888

38  
h-index

197818

49  
g-index

50  
all docs

50  
docs citations

50  
times ranked

23250  
citing authors

#	ARTICLE	IF	CITATIONS
1	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	12.6	3,612
2	The Genome of the Diatom <i>Thalassiosira Pseudonana</i> : Ecology, Evolution, and Metabolism. <i>Science</i> , 2004, 306, 79-86.	12.6	1,862
3	Improvement of the <i>Oryza sativa</i> Nipponbare reference genome using next generation sequence and optical map data. <i>Rice</i> , 2013, 6, 4.	4.0	1,777
4	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	27.8	1,442
5	Genome sequence and analysis of the Irish potato famine pathogen <i>Phytophthora infestans</i> . <i>Nature</i> , 2009, 461, 393-398.	27.8	1,405
6	The Genome of the Kinetoplastid Parasite, <i>Leishmania major</i> . <i>Science</i> , 2005, 309, 436-442.	12.6	1,237
7	The <i>Medicago</i> genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	27.8	1,166
8	Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. <i>Nature Genetics</i> , 2012, 44, 1060-1065.	21.4	840
9	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	6.4	582
10	Genome Sequence of <i>Yersinia pestis</i> KIM. <i>Journal of Bacteriology</i> , 2002, 184, 4601-4611.	2.2	534
11	Genome sequence of the model medicinal mushroom <i>Ganoderma lucidum</i> . <i>Nature Communications</i> , 2012, 3, 913.	12.8	458
12	Lineage-Specific Biology Revealed by a Finished Genome Assembly of the Mouse. <i>PLoS Biology</i> , 2009, 7, e1000112.	5.6	419
13	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. <i>PLoS Genetics</i> , 2009, 5, e1000618.	3.5	402
14	An improved genome release (version Mt4.0) for the model legume <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2014, 15, 312.	2.8	381
15	A gapless genome sequence of the fungus <i>Botrytis cinerea</i> . <i>Molecular Plant Pathology</i> , 2017, 18, 75-89.	4.2	265
16	Comparative Genomics of a Plant-Pathogenic Fungus, <i>Pyrenophora tritici-repentis</i> , Reveals Transduplication and the Impact of Repeat Elements on Pathogenicity and Population Divergence. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 41-63.	1.8	167
17	An algorithm for assembly of ordered restriction maps from single DNA molecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15770-15775.	7.1	164
18	High-resolution human genome structure by single-molecule analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10848-10853.	7.1	161

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19	Primers for amplification of mt SSU rDNA, and a phylogenetic study of Botryosphaeria and associated anamorphic fungi. Mycological Research, 2001, 105, 1033-1044.	2.5	128
20	A Single Molecule Scaffold for the Maize Genome. PLoS Genetics, 2009, 5, e1000711.	3.5	122
21	Validation of rice genome sequence by optical mapping. BMC Genomics, 2007, 8, 278.	2.8	111
22	Gapless genome assembly of Colletotrichum higginsianum reveals chromosome structure and association of transposable elements with secondary metabolite gene clusters. BMC Genomics, 2017, 18, 667.	2.8	111
23	The Physical and Genetic Framework of the Maize B73 Genome. PLoS Genetics, 2009, 5, e1000715.	3.5	95
24	Relationships among Botryosphaeria Species and Associated Anamorphic Fungi Inferred from the Analyses of ITS and 5.8S rDNA Sequences. Mycologia, 2001, 93, 516.	1.9	80
25	Differentiation of Botryosphaeria species and related anamorphic fungi using Inter Simple or Short Sequence Repeat (ISSR) fingerprinting. Mycological Research, 2001, 105, 919-926.	2.5	79
26	Chromosome-level genome map provides insights into diverse defense mechanisms in the medicinal fungus Ganoderma sinense. Scientific Reports, 2015, 5, 11087.	3.3	76
27	Relationships among <i>Botryosphaeria</i> species and associated anamorphic fungi inferred from the analyses of ITS and 5.8S rDNA sequences. Mycologia, 2001, 93, 516-527.	1.9	75
28	High-coverage sequencing and annotated assemblies of the budgerigar genome. GigaScience, 2014, 3, 11.	6.4	75
29	A Whole-Genome Shotgun Optical Map of Yersinia pestis Strain KIM. Applied and Environmental Microbiology, 2002, 68, 6321-6331.	3.1	65
30	Single-Molecule Approach to Bacterial Genomic Comparisons via Optical Mapping. Journal of Bacteriology, 2004, 186, 7773-7782.	2.2	63
31	Whole-Genome Shotgun Optical Mapping of Rhodospirillum rubrum. Applied and Environmental Microbiology, 2005, 71, 5511-5522.	3.1	62
32	The sequence and analysis of Trypanosoma brucei chromosome II. Nucleic Acids Research, 2003, 31, 4856-4863.	14.5	59
33	The genome of opportunistic fungal pathogen Fusarium oxysporum carries a unique set of lineage-specific chromosomes. Communications Biology, 2020, 3, 50.	4.4	55
34	Genome sequencing of ovine isolates of Mycobacterium avium subspecies paratuberculosis offers insights into host association. BMC Genomics, 2012, 13, 89.	2.8	54
35	Whole-Genome Shotgun Optical Mapping of Rhodobacter sphaeroides strain 2.4.1 and Its Use for Whole-Genome Shotgun Sequence Assembly. Genome Research, 2003, 13, 2142-2151.	5.5	49
36	Single-molecule analysis reveals widespread structural variation in multiple myeloma. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7689-7694.	7.1	43

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37	AGORA: Assembly Guided by Optical Restriction Alignment. BMC Bioinformatics, 2012, 13, 189.	2.6	42
38	Shotgun optical mapping of the entire Leishmania major Friedlin genome. Molecular and Biochemical Parasitology, 2004, 138, 97-106.	1.1	41
39	Genome Sequence and Annotation of <i>Colletotrichum higginsianum</i> , a Causal Agent of Crucifer Anthracnose Disease. Genome Announcements, 2016, 4, .	0.8	41
40	Allele-Specific Quantification of Structural Variations in Cancer Genomes. Cell Systems, 2016, 3, 21-34.	6.2	41
41	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. PLoS Genetics, 2009, 5, e1000728.	3.5	39
42	Optical mapping discerns genome wide DNA methylation profiles. BMC Molecular Biology, 2008, 9, 68.	3.0	35
43	Optical mapping of the Mycobacterium avium subspecies paratuberculosis genome. BMC Genomics, 2009, 10, 25.	2.8	35
44	Improving mammalian genome scaffolding using large insert mate-pair next-generation sequencing. BMC Genomics, 2013, 14, 257.	2.8	35
45	Discovery of structural alterations in solid tumor oligodendroglioma by single molecule analysis. BMC Genomics, 2013, 14, 505.	2.8	30
46	Comparative Genomics of <i>Cryptosporidium</i> . International Journal of Genomics, 2013, 2013, 1-8.	1.6	28
47	Electrostatic confinement and manipulation of DNA molecules for genome analysis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 13400-13405.	7.1	25
48	Chapter 9 A Single Molecule System for Whole Genome Analysis. Perspectives in Bioanalysis, 2007, , 265-300.	0.3	18
49	A clone-free, single molecule map of the domestic cow ( <i>Bos taurus</i> ) genome. BMC Genomics, 2015, 16, 644.	2.8	12