

# 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 genome of opportunistic fungal pathogen <i>Fusarium oxysporum</i> carries a unique set of lineage-specific chromosomes. <i>Communications Biology</i> , 2020, 3, 50.	4.4	55
2	A gapless genome sequence of the fungus <i>Botrytis cinerea</i> . <i>Molecular Plant Pathology</i> , 2017, 18, 75-89.	4.2	265
3	Electrostatic confinement and manipulation of DNA molecules for genome analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13400-13405.	7.1	25
4	Gapless genome assembly of <i>Colletotrichum higginsianum</i> reveals chromosome structure and association of transposable elements with secondary metabolite gene clusters. <i>BMC Genomics</i> , 2017, 18, 667.	2.8	111
5	Genome Sequence and Annotation of <i>Colletotrichum higginsianum</i> , a Causal Agent of Crucifer Anthracnose Disease. <i>Genome Announcements</i> , 2016, 4, .	0.8	41
6	Allele-Specific Quantification of Structural Variations in Cancer Genomes. <i>Cell Systems</i> , 2016, 3, 21-34.	6.2	41
7	Chromosome-level genome map provides insights into diverse defense mechanisms in the medicinal fungus <i>Ganoderma sinense</i> . <i>Scientific Reports</i> , 2015, 5, 11087.	3.3	76
8	Single-molecule analysis reveals widespread structural variation in multiple myeloma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7689-7694.	7.1	43
9	A clone-free, single molecule map of the domestic cow ( <i>Bos taurus</i> ) genome. <i>BMC Genomics</i> , 2015, 16, 644.	2.8	12
10	High-coverage sequencing and annotated assemblies of the budgerigar genome. <i>GigaScience</i> , 2014, 3, 11.	6.4	75
11	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
12	Discovery of structural alterations in solid tumor oligodendroglioma by single molecule analysis. <i>BMC Genomics</i> , 2013, 14, 505.	2.8	30
13	Improving mammalian genome scaffolding using large insert mate-pair next-generation sequencing. <i>BMC Genomics</i> , 2013, 14, 257.	2.8	35
14	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
15	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	6.4	582
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	Comparative Genomics of <i>Cryptosporidium</i> . <i>International Journal of Genomics</i> , 2013, 2013, 1-8.	1.6	28
18	Genome sequence of the model medicinal mushroom <i>Ganoderma lucidum</i> . <i>Nature Communications</i> , 2012, 3, 913.	12.8	458

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19	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
20	AGORA: Assembly Guided by Optical Restriction Alignment. <i>BMC Bioinformatics</i> , 2012, 13, 189.	2.6	42
21	Genome sequencing of ovine isolates of <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> offers insights into host association. <i>BMC Genomics</i> , 2012, 13, 89.	2.8	54
22	The <i>Medicago</i> genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	27.8	1,166
23	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	27.8	1,442
24	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
25	The Physical and Genetic Framework of the Maize B73 Genome. <i>PLoS Genetics</i> , 2009, 5, e1000715.	3.5	95
26	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000728.	3.5	39
27	Lineage-Specific Biology Revealed by a Finished Genome Assembly of the Mouse. <i>PLoS Biology</i> , 2009, 7, e1000112.	5.6	419
28	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. <i>PLoS Genetics</i> , 2009, 5, e1000618.	3.5	402
29	Optical mapping of the <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> genome. <i>BMC Genomics</i> , 2009, 10, 25.	2.8	35
30	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
31	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	12.6	3,612
32	A Single Molecule Scaffold for the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000711.	3.5	122
33	Optical mapping discerns genome wide DNA methylation profiles. <i>BMC Molecular Biology</i> , 2008, 9, 68.	3.0	35
34	Chapter 9 A Single Molecule System for Whole Genome Analysis. <i>Perspectives in Bioanalysis</i> , 2007, , 265-300.	0.3	18
35	Validation of rice genome sequence by optical mapping. <i>BMC Genomics</i> , 2007, 8, 278.	2.8	111
36	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

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37	Whole-Genome Shotgun Optical Mapping of <i>Rhodospirillum rubrum</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 5511-5522.	3.1	62
38	The Genome of the Kinetoplastid Parasite, <i>Leishmania major</i> . <i>Science</i> , 2005, 309, 436-442.	12.6	1,237
39	Single-Molecule Approach to Bacterial Genomic Comparisons via Optical Mapping. <i>Journal of Bacteriology</i> , 2004, 186, 7773-7782.	2.2	63
40	Shotgun optical mapping of the entire <i>Leishmania major</i> Friedlin genome. <i>Molecular and Biochemical Parasitology</i> , 2004, 138, 97-106.	1.1	41
41	The Genome of the Diatom <i>Thalassiosira Pseudonana</i> : Ecology, Evolution, and Metabolism. <i>Science</i> , 2004, 306, 79-86.	12.6	1,862
42	The sequence and analysis of <i>Trypanosoma brucei</i> chromosome II. <i>Nucleic Acids Research</i> , 2003, 31, 4856-4863.	14.5	59
43	Whole-Genome Shotgun Optical Mapping of <i>Rhodobacter sphaeroides</i> strain 2.4.1 and Its Use for Whole-Genome Shotgun Sequence Assembly. <i>Genome Research</i> , 2003, 13, 2142-2151.	5.5	49
44	Genome Sequence of <i>Yersinia pestis</i> KIM. <i>Journal of Bacteriology</i> , 2002, 184, 4601-4611.	2.2	534
45	A Whole-Genome Shotgun Optical Map of <i>Yersinia pestis</i> Strain KIM. <i>Applied and Environmental Microbiology</i> , 2002, 68, 6321-6331.	3.1	65
46	Relationships among <i>Botryosphaeria</i> species and associated anamorphic fungi inferred from the analyses of ITS and 5.8S rDNA sequences. <i>Mycologia</i> , 2001, 93, 516-527.	1.9	75
47	Differentiation of <i>Botryosphaeria</i> species and related anamorphic fungi using Inter Simple or Short Sequence Repeat (ISSR) fingerprinting. <i>Mycological Research</i> , 2001, 105, 919-926.	2.5	79
48	Primers for amplification of mt SSU rDNA, and a phylogenetic study of <i>Botryosphaeria</i> and associated anamorphic fungi. <i>Mycological Research</i> , 2001, 105, 1033-1044.	2.5	128
49	Relationships among <i>Botryosphaeria</i> Species and Associated Anamorphic Fungi Inferred from the Analyses of ITS and 5.8S rDNA Sequences. <i>Mycologia</i> , 2001, 93, 516.	1.9	80