

# Zehua Chen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12067813/publications.pdf>

Version: 2024-02-01

20  
papers

21,350  
citations

516710

16  
h-index

752698

20  
g-index

20  
all docs

20  
docs citations

20  
times ranked

31099  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Pas de deux</i> : An Intricate Dance of Anther Smut and Its Host. G3: Genes, Genomes, Genetics, 2018, 8, 505-518.	1.8	6
2	Transcriptional analysis of mating and pre-infection stages of the anther smut, <i>Microbotryum lychnidis-dioicae</i> . Microbiology (United Kingdom), 2017, 163, 410-420.	1.8	10
3	Genome analysis of three <i>Pneumocystis</i> species reveals adaptation mechanisms to life exclusively in mammalian hosts. Nature Communications, 2016, 7, 10740.	12.8	153
4	The Dynamic Genome and Transcriptome of the Human Fungal Pathogen <i>Blastomyces</i> and Close Relative <i>Emmonsia</i> . PLoS Genetics, 2015, 11, e1005493.	3.5	57
5	Degeneration of the Nonrecombining Regions in the Mating-Type Chromosomes of the Anther-Smut Fungi. Molecular Biology and Evolution, 2015, 32, 928-943.	8.9	49
6	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus. BMC Genomics, 2015, 16, 461.	2.8	58
7	Comparative Genomic and Transcriptomic Analysis of <i>Wangiella dermatitidis</i> , A Major Cause of Phaeohyphomycosis and a Model Black Yeast Human Pathogen. G3: Genes, Genomes, Genetics, 2014, 4, 561-578.	1.8	58
8	Premetazoan genome evolution and the regulation of cell differentiation in the choanoflagellate <i>Salpingoeca rosetta</i> . Genome Biology, 2013, 14, R15.	9.6	219
9	The <i>Capsaspora</i> genome reveals a complex unicellular prehistory of animals. Nature Communications, 2013, 4, 2325.	12.8	244
10	The genome of VP3, a T7-like phage used for the typing of <i>Vibrio cholerae</i> . Archives of Virology, 2013, 158, 1865-1876.	2.1	7
11	Comparative Genome Analysis of <i>Trichophyton rubrum</i> and Related Dermatophytes Reveals Candidate Genes Involved in Infection. MBio, 2012, 3, e00259-12.	4.1	211
12	Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. Nature Genetics, 2012, 44, 1060-1065.	21.4	840
13	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . PLoS Genetics, 2011, 7, e1002230.	3.5	902
14	Comparative Functional Genomics of the Fission Yeasts. Science, 2011, 332, 930-936.	12.6	458
15	Full-length transcriptome assembly from RNA-Seq data without a reference genome. Nature Biotechnology, 2011, 29, 644-652.	17.5	17,264
16	Anatomy of <i>Escherichia coli</i> 70 promoters. Nucleic Acids Research, 2007, 35, 771-788.	14.5	209
17	Discovery of Fur binding site clusters in <i>Escherichia coli</i> by information theory models. Nucleic Acids Research, 2007, 35, 6762-6777.	14.5	79
18	Comparative analysis of tandem T7-like promoter containing regions in enterobacterial genomes reveals a novel group of genetic islands. Nucleic Acids Research, 2006, 34, 1133-1147.	14.5	10

#	ARTICLE	IF	CITATIONS
19	Information theory based T7-like promoter models: classification of bacteriophages and differential evolution of promoters and their polymerases. Nucleic Acids Research, 2005, 33, 6172-6187.	14.5	45
20	Sequence and analysis of rice chromosome 4. Nature, 2002, 420, 316-320.	27.8	471