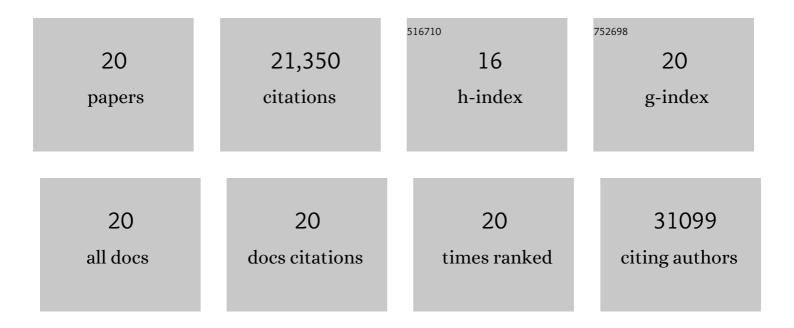
Zehua Chen

List of Publications by Year in descending order

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ZEHLIA CHEN

#	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, Microbotryum lychnidis-dioicae. Microbiology (United Kingdom), 2017, 163, 410-420.	1.8	10
3	Genome analysis of three Pneumocystis 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 Blastomyces and Close Relative Emmonsia. 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 Microbotryum lychnidis-dioicae, 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 Salpingoeca rosetta. Genome Biology, 2013, 14, R15.	9.6	219
9	The Capsaspora 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 Vibrio cholerae. 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 Colletotrichum fungi deciphered by genome and transcriptome analyses. Nature Genetics, 2012, 44, 1060-1065.	21.4	840
13	Genomic Analysis of the Necrotrophic Fungal Pathogens Sclerotinia sclerotiorum and Botrytis cinerea. 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 Escherichia coli Ï f 70 promoters. Nucleic Acids Research, 2007, 35, 771-788.	14.5	209
17	Discovery of Fur binding site clusters in Escherichia coli 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.

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