

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

586496

16
h-index

843174

20
g-index

20
all docs

20
docs citations

20
times ranked

34269
citing authors

#	ARTICLE	IF	CITATIONS
1	Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011, 29, 644-652.	9.4	17,264
2	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011, 7, e1002230.	1.5	902
3	Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. <i>Nature Genetics</i> , 2012, 44, 1060-1065.	9.4	840
4	Sequence and analysis of rice chromosome 4. <i>Nature</i> , 2002, 420, 316-320.	13.7	471
5	Comparative Functional Genomics of the Fission Yeasts. <i>Science</i> , 2011, 332, 930-936.	6.0	458
6	The <i>Capsaspora</i> genome reveals a complex unicellular prehistory of animals. <i>Nature Communications</i> , 2013, 4, 2325.	5.8	244
7	Premetazoan genome evolution and the regulation of cell differentiation in the choanoflagellate <i>Salpingoeca rosetta</i> . <i>Genome Biology</i> , 2013, 14, R15.	13.9	219
8	Comparative Genome Analysis of <i>Trichophyton rubrum</i> and Related Dermatophytes Reveals Candidate Genes Involved in Infection. <i>MBio</i> , 2012, 3, e00259-12.	1.8	211
9	Anatomy of <i>Escherichia coli</i> 70 promoters. <i>Nucleic Acids Research</i> , 2007, 35, 771-788.	6.5	209
10	Genome analysis of three <i>Pneumocystis</i> species reveals adaptation mechanisms to life exclusively in mammalian hosts. <i>Nature Communications</i> , 2016, 7, 10740.	5.8	153
11	Discovery of Fur binding site clusters in <i>Escherichia coli</i> by information theory models. <i>Nucleic Acids Research</i> , 2007, 35, 6762-6777.	6.5	79
12	Comparative Genomic and Transcriptomic Analysis of <i>Wangiella dermatitidis</i> , A Major Cause of Phaeohyphomycosis and a Model Black Yeast Human Pathogen. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 561-578.	0.8	58
13	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus. <i>BMC Genomics</i> , 2015, 16, 461.	1.2	58
14	The Dynamic Genome and Transcriptome of the Human Fungal Pathogen <i>Blastomyces</i> and Close Relative <i>Emmonsia</i> . <i>PLoS Genetics</i> , 2015, 11, e1005493.	1.5	57
15	Degeneration of the Nonrecombining Regions in the Mating-Type Chromosomes of the Anther-Smut Fungi. <i>Molecular Biology and Evolution</i> , 2015, 32, 928-943.	3.5	49
16	Information theory based T7-like promoter models: classification of bacteriophages and differential evolution of promoters and their polymerases. <i>Nucleic Acids Research</i> , 2005, 33, 6172-6187.	6.5	45
17	Comparative analysis of tandem T7-like promoter containing regions in enterobacterial genomes reveals a novel group of genetic islands. <i>Nucleic Acids Research</i> , 2006, 34, 1133-1147.	6.5	10
18	Transcriptional analysis of mating and pre-infection stages of the anther smut, <i>Microbotryum lychnidis-dioicae</i> . <i>Microbiology (United Kingdom)</i> , 2017, 163, 410-420.	0.7	10

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19	The genome of VP3, a T7-like phage used for the typing of <i>Vibrio cholerae</i> . <i>Archives of Virology</i> , 2013, 158, 1865-1876.	0.9	7
20	<i>Pas de deux</i> : An Intricate Dance of Anther Smut and Its Host. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 505-518.	0.8	6