

Qiandong Zeng

List of Publications by Year in descending order

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87
papers

51,511
citations

34105

52
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48315

88
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92
docs citations

92
times ranked

65486
citing authors

#	ARTICLE	IF	CITATIONS
1	An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. F1000Research, 2021, 10, 246.	1.6	3
2	An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. F1000Research, 2021, 10, 246.	1.6	2
3	A customized scaffolds approach for the detection and phasing of complex variants by next-generation sequencing. Scientific Reports, 2020, 10, 15060.	3.3	3
4	A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794.	12.8	56
5	The genome of opportunistic fungal pathogen <i>Fusarium oxysporum</i> carries a unique set of lineage-specific chromosomes. Communications Biology, 2020, 3, 50.	4.4	55
6	Genome Sequence for <i>Candida albicans</i> Clinical Oral Isolate 529L. Microbiology Resource Announcements, 2019, 8, .	0.6	13
7	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	5
8	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	14
9	Whole-Genome Analysis Illustrates Global Clonal Population Structure of the Ubiquitous Dermatophyte Pathogen <i>Trichophyton rubrum</i> . Genetics, 2018, 208, 1657-1669.	2.9	48
10	Evaluation of a 27-gene inherited cancer panel across 630 consecutive patients referred for testing in a clinical diagnostic laboratory. Hereditary Cancer in Clinical Practice, 2018, 16, 1.	1.5	17
11	Multi-institute analysis of carbapenem resistance reveals remarkable diversity, unexplained mechanisms, and limited clonal outbreaks. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1135-1140.	7.1	158
12	Comparative Analysis Highlights Variable Genome Content of Wheat Rusts and Divergence of the Mating Loci. G3: Genes, Genomes, Genetics, 2017, 7, 361-376.	1.8	127
13	Exploring the genomic diversity of black yeasts and relatives (<i>Chaetothyriales</i> , <i>Ascomycota</i>). Studies in Mycology, 2017, 86, 1-28.	7.2	144
14	Genome Sequence of <i>Spizellomyces punctatus</i> . Genome Announcements, 2016, 4, .	0.8	20
15	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
16	Genomic insights into the <i>Ixodes scapularis</i> tick vector of Lyme disease. Nature Communications, 2016, 7, 10507.	12.8	450
17	Structure of the germline genome of <i>Tetrahymena thermophila</i> and relationship to the massively rearranged somatic genome. ELife, 2016, 5, .	6.0	130
18	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

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19	Mitochondrial genome sequences reveal evolutionary relationships of the Phytophthora 1c clade species. <i>Current Genetics</i> , 2015, 61, 567-577.	1.7	23
20	Genome Sequences of Three Phytopathogenic Species of the Magnaporthaceae Family of Fungi. G3: Genes, Genomes, Genetics, 2015, 5, 2539-2545.	1.8	33
21	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.	2.8	58
22	Contrasting host-pathogen interactions and genome evolution in two generalist and specialist microsporidian pathogens of mosquitoes. <i>Nature Communications</i> , 2015, 6, 7121.	12.8	90
23	Genome Evolution and Innovation across the Four Major Lineages of <i>Cryptococcus gattii</i> . <i>MBio</i> , 2015, 6, e00868-15.	4.1	101
24	Genetic and phenotypic intra-species variation in <i>Candida albicans</i> . <i>Genome Research</i> , 2015, 25, 413-425.	5.5	305
25	Evolution of Extensively Drug-Resistant Tuberculosis over Four Decades: Whole Genome Sequencing and Dating Analysis of <i>Mycobacterium tuberculosis</i> Isolates from KwaZulu-Natal. <i>PLoS Medicine</i> , 2015, 12, e1001880.	8.4	236
26	Genome Update of the Dimorphic Human Pathogenic Fungi Causing Paracoccidioidomycosis. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3348.	3.0	38
27	Analysis of the Genome and Transcriptome of <i>Cryptococcus neoformans</i> var. <i>grubii</i> Reveals Complex RNA Expression and Microevolution Leading to Virulence Attenuation. <i>PLoS Genetics</i> , 2014, 10, e1004261.	3.5	336
28	Evolution of Invasion in a Diverse Set of <i>Fusobacterium</i> Species. <i>MBio</i> , 2014, 5, e01864.	4.1	82
29	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.	1.8	58
30	Genome Sequence of the Pathogenic Fungus <i>Sporothrix schenckii</i> (ATCC 58251). <i>Genome Announcements</i> , 2014, 2, .	0.8	30
31	Genome Sequence of <i>Fusarium oxysporum</i> f. sp. <i>melonis</i> Strain NRRL 26406, a Fungus Causing Wilt Disease on Melon. <i>Genome Announcements</i> , 2014, 2, .	0.8	28
32	Pilon: An Integrated Tool for Comprehensive Microbial Variant Detection and Genome Assembly Improvement. <i>PLoS ONE</i> , 2014, 9, e112963.	2.5	6,781
33	Premetazoan genome evolution and the regulation of cell differentiation in the choanoflagellate <i>Salpingoeca rosetta</i> . <i>Genome Biology</i> , 2013, 14, R15.	9.6	219
34	Genomes of marine cyanopodoviruses reveal multiple origins of diversity. <i>Environmental Microbiology</i> , 2013, 15, 1356-1376.	3.8	99
35	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
36	High-Quality Draft Genome Sequence of <i>Vagococcus lutrae</i> Strain LBD1, Isolated from the Largemouth Bass <i>Micropterus salmoides</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	8

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37	Comparative Genomics of Recent Shiga Toxin-Producing <i>Escherichia coli</i> O104:H4: Short-Term Evolution of an Emerging Pathogen. <i>MBio</i> , 2013, 4, e00452-12.	4.1	68
38	Kinannoter, a computer program to identify and classify members of the eukaryotic protein kinase superfamily. <i>Bioinformatics</i> , 2013, 29, 2387-2394.	4.1	43
39	Distinctive Expansion of Potential Virulence Genes in the Genome of the Oomycete Fish Pathogen <i>Saprolegnia parasitica</i> . <i>PLoS Genetics</i> , 2013, 9, e1003272.	3.5	221
40	Emergence of Epidemic Multidrug-Resistant <i>Enterococcus faecium</i> from Animal and Commensal Strains. <i>MBio</i> , 2013, 4, .	4.1	336
41	Genomics of <i>Loa loa</i> , a <i>Wolbachia</i> -free filarial parasite of humans. <i>Nature Genetics</i> , 2013, 45, 495-500.	21.4	173
42	Evolutionary Dynamics of the Accessory Genome of <i>Listeria monocytogenes</i> . <i>PLoS ONE</i> , 2013, 8, e67511.	2.5	63
43	Whole Genome Deep Sequencing of HIV-1 Reveals the Impact of Early Minor Variants Upon Immune Recognition During Acute Infection. <i>PLoS Pathogens</i> , 2012, 8, e1002529.	4.7	306
44	Genomic epidemiology of the <i>Escherichia coli</i> O104:H4 outbreaks in Europe, 2011. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3065-3070.	7.1	262
45	Comparative Genome Analysis of <i>Trichophyton rubrum</i> and Related Dermatophytes Reveals Candidate Genes Involved in Infection. <i>MBio</i> , 2012, 3, e00259-12.	4.1	211
46	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012, 486, 207-214.	27.8	9,614
47	A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.	27.8	2,249
48	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
49	Microsporidian genome analysis reveals evolutionary strategies for obligate intracellular growth. <i>Genome Research</i> , 2012, 22, 2478-2488.	5.5	235
50	The malaria parasite <i>Plasmodium vivax</i> exhibits greater genetic diversity than <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2012, 44, 1046-1050.	21.4	256
51	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011, 7, e1002230.	3.5	902
52	Comparative Functional Genomics of the Fission Yeasts. <i>Science</i> , 2011, 332, 930-936.	12.6	458
53	High quality draft genome sequence of <i>Segniliparus rugosus</i> CDC 945T= (ATCC BAA-974T). <i>Standards in Genomic Sciences</i> , 2011, 5, 389-397.	1.5	6
54	Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011, 29, 644-652.	17.5	17,264

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55	Complete Genome Sequence of <i>Algoriphagus</i> sp. PR1, Bacterial Prey of a Colony-Forming Choanoflagellate. <i>Journal of Bacteriology</i> , 2011, 193, 1485-1486.	2.2	26
56	Comparative Genomic Analysis of Human Fungal Pathogens Causing Paracoccidioidomycosis. <i>PLoS Genetics</i> , 2011, 7, e1002345.	3.5	164
57	Comparative Genomics Yields Insights into Niche Adaptation of Plant Vascular Wilt Pathogens. <i>PLoS Pathogens</i> , 2011, 7, e1002137.	4.7	477
58	Comparative and Functional Genomics of <i>Rhodococcus opacus</i> PD630 for Biofuels Development. <i>PLoS Genetics</i> , 2011, 7, e1002219.	3.5	109
59	Approaches to Fungal Genome Annotation. <i>Mycology</i> , 2011, 2, 118-141.	4.4	109
60	Elucidation of \hat{I}^2 -Oxidation Pathways in <i>Ralstonia eutropha</i> H16 by Examination of Global Gene Expression. <i>Journal of Bacteriology</i> , 2010, 192, 5454-5464.	2.2	106
61	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	27.8	1,442
62	Analysis of High-Throughput Sequencing and Annotation Strategies for Phage Genomes. <i>PLoS ONE</i> , 2010, 5, e9083.	2.5	76
63	High-Quality Draft Genome Sequences of 28 <i>Enterococcus</i> sp. Isolates. <i>Journal of Bacteriology</i> , 2010, 192, 2469-2470.	2.2	80
64	Towards Viral Genome Annotation Standards, Report from the 2010 NCBI Annotation Workshop. <i>Viruses</i> , 2010, 2, 2258-2268.	3.3	27
65	Insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom <i>Coprinopsis cinerea</i> (<i>Coprinus cinereus</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 11889-11894.	7.1	389
66	A Catalog of Reference Genomes from the Human Microbiome. <i>Science</i> , 2010, 328, 994-999.	12.6	621
67	Population genomic sequencing of <i>Coccidioides</i> fungi reveals recent hybridization and transposon control. <i>Genome Research</i> , 2010, 20, 938-946.	5.5	166
68	Comparative genomic analyses of the human fungal pathogens <i>Coccidioides</i> and their relatives. <i>Genome Research</i> , 2009, 19, 1722-1731.	5.5	295
69	Comparative Genomic Characterization of <i>Francisella tularensis</i> Strains Belonging to Low and High Virulence Subspecies. <i>PLoS Pathogens</i> , 2009, 5, e1000459.	4.7	112
70	Genomic Analysis of the Basal Lineage Fungus <i>Rhizopus oryzae</i> Reveals a Whole-Genome Duplication. <i>PLoS Genetics</i> , 2009, 5, e1000549.	3.5	332
71	Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes. <i>Nature</i> , 2009, 459, 657-662.	27.8	963
72	<i>CandidaDB</i> : a multi-genome database for <i>Candida</i> species and related Saccharomycotina. <i>Nucleic Acids Research</i> , 2007, 36, D557-D561.	14.5	26

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73	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	12.6	1,025
74	DNA sequence and analysis of human chromosome 8. <i>Nature</i> , 2006, 439, 331-335.	27.8	115
75	DNA sequence and analysis of human chromosome 18. <i>Nature</i> , 2005, 437, 551-555.	27.8	53
76	Phylogenetic footprinting and genome scanning identify vertebrate BMP response elements and new target genes. <i>Developmental Biology</i> , 2005, 281, 210-226.	2.0	57
77	Systematic Discovery of New Genes in the <i>Saccharomyces cerevisiae</i> Genome. <i>Genome Research</i> , 2003, 13, 264-271.	5.5	56
78	The use of direct cDNA selection to rapidly and effectively identify genes in the fungus <i>Aspergillus fumigatus</i> . <i>Fungal Genetics and Biology</i> , 2002, 36, 59-70.	2.1	14
79	Thermal stability of the [Fe(SCys) ₄] site in <i>Clostridium pasteurianum</i> rubredoxin: contributions of the local environment and Cys ligand protonation. <i>Journal of Biological Inorganic Chemistry</i> , 2002, 7, 427-436.	2.6	14
80	Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium <i>Clostridium acetobutylicum</i> . <i>Journal of Bacteriology</i> , 2001, 183, 4823-4838.	2.2	725
81	Fungi and humans: closer than you think. <i>Trends in Genetics</i> , 2001, 17, 682-684.	6.7	23
82	The Core Metal-Recognition Domain of MerR. <i>Biochemistry</i> , 1998, 37, 15885-15895.	2.5	46
83	Near-Zero Background Cloning of PCR Products. <i>BioTechniques</i> , 1997, 23, 412-418.	1.8	10
84	A glutamate uptake regulatory protein (Grp) in <i>Escherichia coli</i> ?. <i>Molecular Microbiology</i> , 1997, 24, 231-2.	2.5	3
85	A transcription factor IIB homolog from the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> binds Zn or Fe in an N-terminal Cys ₄ motif. <i>Journal of Biological Inorganic Chemistry</i> , 1996, 1, 162-168.	2.6	4
86	Protein determinants of metal site reduction potentials: site-directed mutagenesis studies of <i>Clostridium pasteurianum</i> rubredoxin. <i>Inorganica Chimica Acta</i> , 1996, 242, 245-251.	2.4	51
87	The N-terminal domain of TFIIB from <i>Pyrococcus furiosus</i> forms a zinc ribbon. <i>Nature Structural Biology</i> , 1996, 3, 122-124.	9.7	128