

# Qiandong Zeng

## List of Publications by Year in descending order

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87  
papers

51,511  
citations

39113

52  
h-index

54771

88  
g-index

92  
all docs

92  
docs citations

92  
times ranked

71822  
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	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012, 486, 207-214.	13.7	9,614
3	Pilon: An Integrated Tool for Comprehensive Microbial Variant Detection and Genome Assembly Improvement. <i>PLoS ONE</i> , 2014, 9, e112963.	1.1	6,781
4	A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.	13.7	2,249
5	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	13.7	1,442
6	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	6.0	1,025
7	Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes. <i>Nature</i> , 2009, 459, 657-662.	13.7	963
8	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
9	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
10	Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium <i>Clostridium acetobutylicum</i> . <i>Journal of Bacteriology</i> , 2001, 183, 4823-4838.	1.0	725
11	A Catalog of Reference Genomes from the Human Microbiome. <i>Science</i> , 2010, 328, 994-999.	6.0	621
12	Comparative Genomics Yields Insights into Niche Adaptation of Plant Vascular Wilt Pathogens. <i>PLoS Pathogens</i> , 2011, 7, e1002137.	2.1	477
13	Comparative Functional Genomics of the Fission Yeasts. <i>Science</i> , 2011, 332, 930-936.	6.0	458
14	Genomic insights into the <i>Ixodes scapularis</i> tick vector of Lyme disease. <i>Nature Communications</i> , 2016, 7, 10507.	5.8	450
15	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.	3.3	389
16	Emergence of Epidemic Multidrug-Resistant <i>Enterococcus faecium</i> from Animal and Commensal Strains. <i>MBio</i> , 2013, 4, .	1.8	336
17	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.	1.5	336
18	Genomic Analysis of the Basal Lineage Fungus <i>Rhizopus oryzae</i> Reveals a Whole-Genome Duplication. <i>PLoS Genetics</i> , 2009, 5, e1000549.	1.5	332

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19	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.	2.1	306
20	Genetic and phenotypic intra-species variation in <i>Candida albicans</i> . <i>Genome Research</i> , 2015, 25, 413-425.	2.4	305
21	Comparative genomic analyses of the human fungal pathogens <i>Coccidioides</i> and their relatives. <i>Genome Research</i> , 2009, 19, 1722-1731.	2.4	295
22	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.	3.3	262
23	The malaria parasite <i>Plasmodium vivax</i> exhibits greater genetic diversity than <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2012, 44, 1046-1050.	9.4	256
24	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.	3.9	236
25	Microsporidian genome analysis reveals evolutionary strategies for obligate intracellular growth. <i>Genome Research</i> , 2012, 22, 2478-2488.	2.4	235
26	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.	1.5	221
27	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
28	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
29	Genomics of <i>Loa loa</i> , a <i>Wolbachia</i> -free filarial parasite of humans. <i>Nature Genetics</i> , 2013, 45, 495-500.	9.4	173
30	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.	0.8	167
31	Population genomic sequencing of <i>Coccidioides</i> fungi reveals recent hybridization and transposon control. <i>Genome Research</i> , 2010, 20, 938-946.	2.4	166
32	Comparative Genomic Analysis of Human Fungal Pathogens Causing Paracoccidioidomycosis. <i>PLoS Genetics</i> , 2011, 7, e1002345.	1.5	164
33	Multi-institute analysis of carbapenem resistance reveals remarkable diversity, unexplained mechanisms, and limited clonal outbreaks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1135-1140.	3.3	158
34	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
35	Exploring the genomic diversity of black yeasts and relatives ( <i>Chaetothyriales</i> , <i>Ascomycota</i> ). <i>Studies in Mycology</i> , 2017, 86, 1-28.	4.5	144
36	Structure of the germline genome of <i>Tetrahymena thermophila</i> and relationship to the massively rearranged somatic genome. <i>ELife</i> , 2016, 5, .	2.8	130

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37	The N-terminal domain of TFIIIB from <i>Pyrococcus furiosus</i> forms a zinc ribbon. <i>Nature Structural Biology</i> , 1996, 3, 122-124.	9.7	128
38	Comparative Analysis Highlights Variable Genome Content of Wheat Rusts and Divergence of the Mating Loci. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 361-376.	0.8	127
39	DNA sequence and analysis of human chromosome 8. <i>Nature</i> , 2006, 439, 331-335.	13.7	115
40	Comparative Genomic Characterization of <i>Francisella tularensis</i> Strains Belonging to Low and High Virulence Subspecies. <i>PLoS Pathogens</i> , 2009, 5, e1000459.	2.1	112
41	Comparative and Functional Genomics of <i>Rhodococcus opacus</i> PD630 for Biofuels Development. <i>PLoS Genetics</i> , 2011, 7, e1002219.	1.5	109
42	Approaches to Fungal Genome Annotation. <i>Mycology</i> , 2011, 2, 118-141.	2.0	109
43	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.	1.0	106
44	Genome Evolution and Innovation across the Four Major Lineages of <i>Cryptococcus gattii</i> . <i>MBio</i> , 2015, 6, e00868-15.	1.8	101
45	Genomes of marine cyanopodoviruses reveal multiple origins of diversity. <i>Environmental Microbiology</i> , 2013, 15, 1356-1376.	1.8	99
46	Contrasting host-pathogen interactions and genome evolution in two generalist and specialist microsporidian pathogens of mosquitoes. <i>Nature Communications</i> , 2015, 6, 7121.	5.8	90
47	Evolution of Invasion in a Diverse Set of <i>Fusobacterium</i> Species. <i>MBio</i> , 2014, 5, e01864.	1.8	82
48	High-Quality Draft Genome Sequences of 28 <i>Enterococcus</i> sp. Isolates. <i>Journal of Bacteriology</i> , 2010, 192, 2469-2470.	1.0	80
49	Analysis of High-Throughput Sequencing and Annotation Strategies for Phage Genomes. <i>PLoS ONE</i> , 2010, 5, e9083.	1.1	76
50	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.	1.8	68
51	Evolutionary Dynamics of the Accessory Genome of <i>Listeria monocytogenes</i> . <i>PLoS ONE</i> , 2013, 8, e67511.	1.1	63
52	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
53	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
54	Phylogenetic footprinting and genome scanning identify vertebrate BMP response elements and new target genes. <i>Developmental Biology</i> , 2005, 281, 210-226.	0.9	57

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55	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
56	Systematic Discovery of New Genes in the <i>Saccharomyces cerevisiae</i> Genome. <i>Genome Research</i> , 2003, 13, 264-271.	2.4	56
57	A diploid assembly-based benchmark for variants in the major histocompatibility complex. <i>Nature Communications</i> , 2020, 11, 4794.	5.8	56
58	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.	2.0	55
59	DNA sequence and analysis of human chromosome 18. <i>Nature</i> , 2005, 437, 551-555.	13.7	53
60	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.	1.2	51
61	Whole-Genome Analysis Illustrates Global Clonal Population Structure of the Ubiquitous Dermatophyte Pathogen <i>Trichophyton rubrum</i> . <i>Genetics</i> , 2018, 208, 1657-1669.	1.2	48
62	The Core Metal-Recognition Domain of MerR. <i>Biochemistry</i> , 1998, 37, 15885-15895.	1.2	46
63	Kinannotate, a computer program to identify and classify members of the eukaryotic protein kinase superfamily. <i>Bioinformatics</i> , 2013, 29, 2387-2394.	1.8	43
64	Genome Update of the Dimorphic Human Pathogenic Fungi Causing Paracoccidioidomycosis. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3348.	1.3	38
65	Genome Sequences of Three Phytopathogenic Species of the Magnaporthaceae Family of Fungi. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2539-2545.	0.8	33
66	Genome Sequence of the Pathogenic Fungus <i>Sporothrix schenckii</i> (ATCC 58251). <i>Genome Announcements</i> , 2014, 2, .	0.8	30
67	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
68	Towards Viral Genome Annotation Standards, Report from the 2010 NCBI Annotation Workshop. <i>Viruses</i> , 2010, 2, 2258-2268.	1.5	27
69	CandidaDB: a multi-genome database for <i>Candida</i> species and related <i>Saccharomycotina</i> . <i>Nucleic Acids Research</i> , 2007, 36, D557-D561.	6.5	26
70	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.	1.0	26
71	Fungi and humans: closer than you think. <i>Trends in Genetics</i> , 2001, 17, 682-684.	2.9	23
72	Mitochondrial genome sequences reveal evolutionary relationships of the <i>Phytophthora</i> 1c clade species. <i>Current Genetics</i> , 2015, 61, 567-577.	0.8	23

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73	Genome Sequence of <i>Spizellomyces punctatus</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	20
74	Evaluation of a 27-gene inherited cancer panel across 630 consecutive patients referred for testing in a clinical diagnostic laboratory. <i>Hereditary Cancer in Clinical Practice</i> , 2018, 16, 1.	0.6	17
75	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.	0.9	14
76	Thermal stability of the [Fe(SCys) <sub>4</sub> ] 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.	1.1	14
77	A strategy for building and using a human reference pangenome. <i>F1000Research</i> , 2019, 8, 1751.	0.8	14
78	Genome Sequence for <i>Candida albicans</i> Clinical Oral Isolate 529L. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	13
79	Near-Zero Background Cloning of PCR Products. <i>BioTechniques</i> , 1997, 23, 412-418.	0.8	10
80	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
81	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
82	A strategy for building and using a human reference pangenome. <i>F1000Research</i> , 2019, 8, 1751.	0.8	5
83	A transcription factor IIB homolog from the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> binds Zn or Fe in an N-terminal Cys <sub>4</sub> motif. <i>Journal of Biological Inorganic Chemistry</i> , 1996, 1, 162-168.	1.1	4
84	A customized scaffolds approach for the detection and phasing of complex variants by next-generation sequencing. <i>Scientific Reports</i> , 2020, 10, 15060.	1.6	3
85	An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. <i>F1000Research</i> , 2021, 10, 246.	0.8	3
86	A glutamate uptake regulatory protein (Grp) in <i>Escherichia coli</i> ?. <i>Molecular Microbiology</i> , 1997, 24, 231-2.	1.2	3
87	An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. <i>F1000Research</i> , 2021, 10, 246.	0.8	2