

# Qiandong Zeng

## List of Publications by Year in descending order

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Version: 2024-02-01

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  | An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. F1000Research, 2021, 10, 246.  | 0.8 | 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.  | 0.8 | 2         |
| 3  | A customized scaffolds approach for the detection and phasing of complex variants by next-generation sequencing. Scientific Reports, 2020, 10, 15060.  | 1.6 | 3         |
| 4  | A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794.  | 5.8 | 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.   | 2.0 | 55        |
| 6  | Genome Sequence for <i>Candida albicans</i> Clinical Oral Isolate 529L. Microbiology Resource Announcements, 2019, 8, .  | 0.3 | 13        |
| 7  | A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.   | 0.8 | 5         |
| 8  | A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.   | 0.8 | 14        |
| 9  | Whole-Genome Analysis Illustrates Global Clonal Population Structure of the Ubiquitous Dermatophyte Pathogen <i>Trichophyton rubrum</i> . Genetics, 2018, 208, 1657-1669.  | 1.2 | 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.  | 0.6 | 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. | 3.3 | 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.  | 0.8 | 127       |
| 13 | Exploring the genomic diversity of black yeasts and relatives ( <i>Chaetothyriales</i> , <i>Ascomycota</i> ). Studies in Mycology, 2017, 86, 1-28.   | 4.5 | 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.  | 5.8 | 153       |
| 16 | Genomic insights into the <i>Ixodes scapularis</i> tick vector of Lyme disease. Nature Communications, 2016, 7, 10507.   | 5.8 | 450       |
| 17 | Structure of the germline genome of <i>Tetrahymena thermophila</i> and relationship to the massively rearranged somatic genome. ELife, 2016, 5, .  | 2.8 | 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.   | 1.5 | 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.   | 0.8  | 23        |
| 20 | Genome Sequences of Three Phytopathogenic Species of the Magnaporthaceae Family of Fungi. G3: Genes, Genomes, Genetics, 2015, 5, 2539-2545.   | 0.8  | 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.  | 1.2  | 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.  | 5.8  | 90        |
| 23 | Genome Evolution and Innovation across the Four Major Lineages of <i>Cryptococcus gattii</i> . <i>MBio</i> , 2015, 6, e00868-15.  | 1.8  | 101       |
| 24 | Genetic and phenotypic intra-species variation in <i>Candida albicans</i> . <i>Genome Research</i> , 2015, 25, 413-425.   | 2.4  | 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.                      | 3.9  | 236       |
| 26 | Genome Update of the Dimorphic Human Pathogenic Fungi Causing Paracoccidioidomycosis. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3348.   | 1.3  | 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.                          | 1.5  | 336       |
| 28 | Evolution of Invasion in a Diverse Set of <i>Fusobacterium</i> Species. <i>MBio</i> , 2014, 5, e01864.  | 1.8  | 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.                                 | 0.8  | 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.  | 1.1  | 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.   | 13.9 | 219       |
| 34 | Genomes of marine cyanopodoviruses reveal multiple origins of diversity. <i>Environmental Microbiology</i> , 2013, 15, 1356-1376.   | 1.8  | 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. | 0.8  | 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.                                 | 1.8  | 68        |
| 38 | Kinannoter, a computer program to identify and classify members of the eukaryotic protein kinase superfamily. <i>Bioinformatics</i> , 2013, 29, 2387-2394.  | 1.8  | 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.                              | 1.5  | 221       |
| 40 | Emergence of Epidemic Multidrug-Resistant <i>Enterococcus faecium</i> from Animal and Commensal Strains. <i>MBio</i> , 2013, 4, .   | 1.8  | 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.  | 9.4  | 173       |
| 42 | Evolutionary Dynamics of the Accessory Genome of <i>Listeria monocytogenes</i> . <i>PLoS ONE</i> , 2013, 8, e67511.   | 1.1  | 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.                           | 2.1  | 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. | 3.3  | 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.                                  | 1.8  | 211       |
| 46 | Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012, 486, 207-214.  | 13.7 | 9,614     |
| 47 | A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.  | 13.7 | 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.                                  | 9.4  | 840       |
| 49 | Microsporidian genome analysis reveals evolutionary strategies for obligate intracellular growth. <i>Genome Research</i> , 2012, 22, 2478-2488.   | 2.4  | 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.                                     | 9.4  | 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.   | 1.5  | 902       |
| 52 | Comparative Functional Genomics of the Fission Yeasts. <i>Science</i> , 2011, 332, 930-936.   | 6.0  | 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.   | 9.4  | 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.  | 1.0  | 26        |
| 56 | Comparative Genomic Analysis of Human Fungal Pathogens Causing Paracoccidioidomycosis. <i>PLoS Genetics</i> , 2011, 7, e1002345.  | 1.5  | 164       |
| 57 | Comparative Genomics Yields Insights into Niche Adaptation of Plant Vascular Wilt Pathogens. <i>PLoS Pathogens</i> , 2011, 7, e1002137.   | 2.1  | 477       |
| 58 | Comparative and Functional Genomics of <i>Rhodococcus opacus</i> PD630 for Biofuels Development. <i>PLoS Genetics</i> , 2011, 7, e1002219.  | 1.5  | 109       |
| 59 | Approaches to Fungal Genome Annotation. <i>Mycology</i> , 2011, 2, 118-141.   | 2.0  | 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.  | 1.0  | 106       |
| 61 | Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.  | 13.7 | 1,442     |
| 62 | Analysis of High-Throughput Sequencing and Annotation Strategies for Phage Genomes. <i>PLoS ONE</i> , 2010, 5, e9083.   | 1.1  | 76        |
| 63 | High-Quality Draft Genome Sequences of 28 <i>Enterococcus</i> sp. Isolates. <i>Journal of Bacteriology</i> , 2010, 192, 2469-2470.  | 1.0  | 80        |
| 64 | Towards Viral Genome Annotation Standards, Report from the 2010 NCBI Annotation Workshop. <i>Viruses</i> , 2010, 2, 2258-2268.  | 1.5  | 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. | 3.3  | 389       |
| 66 | A Catalog of Reference Genomes from the Human Microbiome. <i>Science</i> , 2010, 328, 994-999.  | 6.0  | 621       |
| 67 | 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       |
| 68 | 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       |
| 69 | 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       |
| 70 | 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       |
| 71 | Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes. <i>Nature</i> , 2009, 459, 657-662.   | 13.7 | 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.  | 6.5  | 26        |

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|----|---|------|-----------|
| 73 | Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.  | 6.0  | 1,025     |
| 74 | DNA sequence and analysis of human chromosome 8. <i>Nature</i> , 2006, 439, 331-335.  | 13.7 | 115       |
| 75 | DNA sequence and analysis of human chromosome 18. <i>Nature</i> , 2005, 437, 551-555.   | 13.7 | 53        |
| 76 | 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        |
| 77 | Systematic Discovery of New Genes in the <i>Saccharomyces cerevisiae</i> Genome. <i>Genome Research</i> , 2003, 13, 264-271.  | 2.4  | 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.   | 0.9  | 14        |
| 79 | 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        |
| 80 | 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       |
| 81 | Fungi and humans: closer than you think. <i>Trends in Genetics</i> , 2001, 17, 682-684.   | 2.9  | 23        |
| 82 | The Core Metal-Recognition Domain of MerR. <i>Biochemistry</i> , 1998, 37, 15885-15895.   | 1.2  | 46        |
| 83 | Near-Zero Background Cloning of PCR Products. <i>BioTechniques</i> , 1997, 23, 412-418.   | 0.8  | 10        |
| 84 | A glutamate uptake regulatory protein (Grp) in <i>Escherichia coli</i> ?. <i>Molecular Microbiology</i> , 1997, 24, 231-2.  | 1.2  | 3         |
| 85 | 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         |
| 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.  | 1.2  | 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       |