

Christina A Cuomo

List of Publications by Year in descending order

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155
papers

30,717
citations

20036

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docs citations

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times ranked

36774
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#	ARTICLE	IF	CITATIONS
1	Chromosome-Level Genome Assembly of a Human Fungal Pathogen Reveals Synteny among Geographically Distinct Species. <i>MBio</i> , 2022, 13, e0257421.	1.8	7
2	2021 Acknowledgment of <i>Microbiology Spectrum</i> Reviewers. <i>Microbiology Spectrum</i> , 2022, 10, e0248721.	1.2	0
3	Population genetics and microevolution of clinical <i>Candida glabrata</i> reveals recombinant sequence types and hyper-variation within mitochondrial genomes, virulence genes, and drug targets. <i>Genetics</i> , 2022, 221, .	1.2	11
4	Inter-species geographic signatures for tracing horizontal gene transfer and long-term persistence of carbapenem resistance. <i>Genome Medicine</i> , 2022, 14, 37.	3.6	15
5	InÂvivo emergence of high-level resistance during treatment reveals the first identified mechanism of amphotericin B resistance in <i>Candida auris</i> . <i>Clinical Microbiology and Infection</i> , 2022, 28, 838-843.	2.8	31
6	MycosNP: A Portable Workflow for Performing Whole-Genome Sequencing Analysis of <i>Candida auris</i> . <i>Methods in Molecular Biology</i> , 2022, , 215-228.	0.4	13
7	Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic<i>Fusarium</i>that Includes the<i>Fusarium solani</i>Species Complex. <i>Phytopathology</i> , 2021, 111, 1064-1079.	1.1	107
8	Blastomycosis in Africa and the Middle East: A Comprehensive Review of Reported Cases and Reanalysis of Historical Isolates Based on Molecular Data. <i>Clinical Infectious Diseases</i> , 2021, 73, e1560-e1569.	2.9	19
9	Comparative genomics of white and opaque cell states supports an epigenetic mechanism of phenotypic switching in <i>Candida albicans</i>. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	10
10	Clade-specific chromosomal rearrangements and loss of subtelomeric adhesins in <i>Candida auris</i>. <i>Genetics</i> , 2021, 218, .	1.2	54
11	Genomic insights into the host specific adaptation of the <i>Pneumocystis</i> genus. <i>Communications Biology</i> , 2021, 4, 305.	2.0	23
12	Genomic epidemiology of a <i>Cryptococcus neoformans</i> case cluster in Glasgow, Scotland, 2018. <i>Microbial Genomics</i> , 2021, 7, .	1.0	6
13	Editorial: Genomic Characterization of Emerging Human Fungal Pathogens. <i>Frontiers in Genetics</i> , 2021, 12, 674765.	1.1	1
14	Amoeba Predation of <i>Cryptococcus neoformans</i> Results in Pleiotropic Changes to Traits Associated with Virulence. <i>MBio</i> , 2021, 12, .	1.8	27
15	Genome-Wide Analysis of Experimentally Evolved <i>Candida auris</i> Reveals Multiple Novel Mechanisms of Multidrug Resistance. <i>MBio</i> , 2021, 12, .	1.8	75
16	Best practices on the differential expression analysis of multi-species RNA-seq. <i>Genome Biology</i> , 2021, 22, 121.	3.8	51
17	Whole-genome sequencing of multiple isolates of <i>Puccinia triticina</i> reveals asexual lineages evolving by recurrent mutations. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	13
18	The Relaunch of <i>Microbiology Spectrum</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0039621.	1.2	2

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19	Diagnostic Allele-Specific PCR for the Identification of <i>Candida auris</i> Clades. <i>Journal of Fungi (Basel)</i> , 2021, 11, .	1.5	14
20	Application of an optimized annotation pipeline to the <i>Cryptococcus deuterogattii</i> genome reveals dynamic primary metabolic gene clusters and genomic impact of RNAi loss. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	16
21	Gene Expression of Diverse <i>Cryptococcus</i> Isolates during Infection of the Human Central Nervous System. <i>MBio</i> , 2021, 12, e0231321.	1.8	23
22	Diversity, multifaceted evolution, and facultative saprotrophism in the European <i>Batrachomyces salamandrivorans</i> epidemic. <i>Nature Communications</i> , 2021, 12, 6688.	5.8	11
23	Phenotypic Characterization and Comparative Genomics of the Melanin-Producing Yeast <i>Exophiala lecanii-corni</i> Reveals a Distinct Stress Tolerance Profile and Reduced Ribosomal Genetic Content. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 1078.	1.5	9
24	Human Blastomycosis in South Africa Caused by <i>Blastomyces persicus</i> and <i>Blastomyces emzantsi</i> sp. nov., 1967 to 2014. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	35
25	Experimental Evolution Identifies Adaptive Aneuploidy as a Mechanism of Fluconazole Resistance in <i>Candida auris</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 65, .	1.4	46
26	An oxindole efflux inhibitor potentiates azoles and impairs virulence in the fungal pathogen <i>Candida auris</i> . <i>Nature Communications</i> , 2020, 11, 6429.	5.8	49
27	Threats Posed by the Fungal Kingdom to Humans, Wildlife, and Agriculture. <i>MBio</i> , 2020, 11, .	1.8	275
28	Mutations in <i>TAC1B</i> : a Novel Genetic Determinant of Clinical Fluconazole Resistance in <i>Candida auris</i> . <i>MBio</i> , 2020, 11, .	1.8	101
29	Understanding the Emergence of Multidrug-Resistant <i>Candida</i> : Using Whole-Genome Sequencing to Describe the Population Structure of <i>Candida haemulonii</i> Species Complex. <i>Frontiers in Genetics</i> , 2020, 11, 554.	1.1	24
30	Evolutionary Persistence of DNA Methylation for Millions of Years after Ancient Loss of a De Novo Methyltransferase. <i>Cell</i> , 2020, 180, 263-277.e20.	13.5	87
31	Tracing the Evolutionary History and Global Expansion of <i>Candida auris</i> Using Population Genomic Analyses. <i>MBio</i> , 2020, 11, .	1.8	224
32	Complete Genome Sequences for Two <i>Talaromyces marneffeii</i> Clinical Isolates from Northern and Southern Vietnam. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	7
33	Genomic diversity of the human pathogen <i>Paracoccidioides</i> across the South American continent. <i>Fungal Genetics and Biology</i> , 2020, 140, 103395.	0.9	33
34	Diversity and Complexity of the Large Surface Protein Family in the Compacted Genomes of Multiple <i>Pneumocystis</i> Species. <i>MBio</i> , 2020, 11, .	1.8	11
35	Landscape of gene expression variation of natural isolates of <i>Cryptococcus neoformans</i> in response to biologically relevant stresses. <i>Microbial Genomics</i> , 2020, 6, .	1.0	24
36	Tracking a Global Threat: a New Genotyping Method for <i>Candida auris</i> . <i>MBio</i> , 2020, 11, .	1.8	9

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37	738. A Novel Molecular Diagnostic Assay for Identification of Fungal Pathogens. Open Forum Infectious Diseases, 2020, 7, S418-S419.	0.4	1
38	Identification of <i>Candida auris</i> by Use of the Updated Vitek 2 Yeast Identification System, Version 8.01: a Multilaboratory Evaluation Study. Journal of Clinical Microbiology, 2019, 57, .	1.8	47
39	<i>Emergomyces</i> : The global rise of new dimorphic fungal pathogens. PLoS Pathogens, 2019, 15, e1007977.	2.1	54
40	Genome Sequence of the Black Yeast <i>Exophiala lecanii-corni</i> . Microbiology Resource Announcements, 2019, 8, .	0.3	7
41	Genetic Analysis of <i>Candida auris</i> Implicates Hsp90 in Morphogenesis and Azole Tolerance and Cdr1 in Azole Resistance. MBio, 2019, 10, .	1.8	77
42	Genetic and Genomic Analyses Reveal Boundaries between Species Closely Related to <i>Cryptococcus</i> Pathogens. MBio, 2019, 10, .	1.8	37
43	Genome Sequence for <i>Candida albicans</i> Clinical Oral Isolate 529L. Microbiology Resource Announcements, 2019, 8, .	0.3	13
44	Coordinated host-pathogen transcriptional dynamics revealed using sorted subpopulations and single macrophages infected with <i>Candida albicans</i> . Nature Communications, 2019, 10, 1607.	5.8	65
45	A New Lineage of <i>Cryptococcus gattii</i> (VGV) Discovered in the Central Zambezi Miombo Woodlands. MBio, 2019, 10, .	1.8	66
46	<i>Cryptococcus neoformans</i> Recovered From Olive Trees (<i>Olea europaea</i>) in Turkey Reveal Allopatry With African and South American Lineages. Frontiers in Cellular and Infection Microbiology, 2019, 9, 384.	1.8	12
47	Antagonistic paralogs control a switch between growth and pathogen resistance in <i>C. elegans</i> . PLoS Pathogens, 2019, 15, e1007528.	2.1	72
48	Future-Proofing Your <i>Microbiology Resource Announcements</i> Genome Assembly for Reproducibility and Clarity. Microbiology Resource Announcements, 2019, 8, .	0.3	2
49	RNAi is a critical determinant of centromere evolution in closely related fungi. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3108-3113.	3.3	112
50	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
51	Genomic epidemiology of the UK outbreak of the emerging human fungal pathogen <i>Candida auris</i> . Emerging Microbes and Infections, 2018, 7, 1-12.	3.0	169
52	Genome analysis reveals evolutionary mechanisms of adaptation in systemic dimorphic fungi. Scientific Reports, 2018, 8, 4473.	1.6	28
53	Genomic Understanding of an Infectious Brain Disease from the Desert. G3: Genes, Genomes, Genetics, 2018, 8, 909-922.	0.8	39
54	<i>Pas de deux</i> : An Intricate Dance of Anther Smut and Its Host. G3: Genes, Genomes, Genetics, 2018, 8, 505-518.	0.8	6

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55	Transcriptional Heterogeneity of <i>Cryptococcus gattii</i> VGII Compared with Non-VGII Lineages Underpins Key Pathogenicity Pathways. <i>MSphere</i> , 2018, 3, .	1.3	12
56	Genomic insights into multidrug-resistance, mating and virulence in <i>Candida auris</i> and related emerging species. <i>Nature Communications</i> , 2018, 9, 5346.	5.8	298
57	Pathways of Pathogenicity: Transcriptional Stages of Germination in the Fatal Fungal Pathogen <i>Rhizopus delemar</i> . <i>MSphere</i> , 2018, 3, .	1.3	19
58	Phenotypic Variability Correlates with Clinical Outcome in <i>Cryptococcus</i> Isolates Obtained from Botswanan HIV/AIDS Patients. <i>MBio</i> , 2018, 9, .	1.8	50
59	Global analysis of mutations driving microevolution of a heterozygous diploid fungal pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8688-E8697.	3.3	109
60	Genomic characterization of recurrent mold infections in thoracic transplant recipients. <i>Transplant Infectious Disease</i> , 2018, 20, e12935.	0.7	5
61	Titan cells formation in <i>Cryptococcus neoformans</i> is finely tuned by environmental conditions and modulated by positive and negative genetic regulators. <i>PLoS Pathogens</i> , 2018, 14, e1006982.	2.1	119
62	Comparative Population Genomics Analysis of the Mammalian Fungal Pathogen <i>Pneumocystis</i> . <i>MBio</i> , 2018, 9, .	1.8	23
63	Advances in <i>Cryptococcus</i> genomics: insights into the evolution of pathogenesis. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2018, 113, e170473.	0.8	33
64	<i>Paracoccidioides</i> spp. catalases and their role in antioxidant defense against host defense responses. <i>Fungal Genetics and Biology</i> , 2017, 100, 22-32.	0.9	16
65	The Case for Adopting the "Species Complex" Nomenclature for the Etiologic Agents of Cryptococcosis. <i>MSphere</i> , 2017, 2, .	1.3	274
66	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
67	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
68	Novel taxa of thermally dimorphic systemic pathogens in the <i>Ajellomycetaceae</i> (<i>Onygenales</i>). <i>Mycoses</i> , 2017, 60, 296-309.	1.8	111
69	Population genomics and the evolution of virulence in the fungal pathogen <i>Cryptococcus neoformans</i> . <i>Genome Research</i> , 2017, 27, 1207-1219.	2.4	134
70	Harnessing Whole Genome Sequencing in Medical Mycology. <i>Current Fungal Infection Reports</i> , 2017, 11, 52-59.	0.9	20
71	Genomic innovations linked to infection strategies across emerging pathogenic chytrid fungi. <i>Nature Communications</i> , 2017, 8, 14742.	5.8	96
72	Microevolution of Serial Clinical Isolates of <i>Cryptococcus neoformans</i> var. <i>grubii</i> and <i>C. gattii</i> . <i>MBio</i> , 2017, 8, .	1.8	69

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73	Zinc Cluster Transcription Factors Alter Virulence in <i>Candida albicans</i> . <i>Genetics</i> , 2017, 205, 559-576.	1.2	31
74	Whole Genome Sequence of the Heterozygous Clinical Isolate <i>Candida krusei</i> 81-B-5. G3: Genes, Genomes, <i>Genetics</i> , 2017, 7, 2883-2889.	0.8	31
75	Tracing Genetic Exchange and Biogeography of <i>Cryptococcus neoformans</i> var. <i>grubii</i> at the Global Population Level. <i>Genetics</i> , 2017, 207, 327-346.	1.2	105
76	Simultaneous Emergence of Multidrug-Resistant <i>Candida auris</i> on 3 Continents Confirmed by Whole-Genome Sequencing and Epidemiological Analyses. <i>Clinical Infectious Diseases</i> , 2017, 64, 134-140.	2.9	1,099
77	Comparative Genomics Integrated with Association Analysis Identifies Candidate Effector Genes Corresponding to Lr20 in Phenotype-Paired <i>Puccinia triticina</i> Isolates from Australia. <i>Frontiers in Plant Science</i> , 2017, 8, 148.	1.7	49
78	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
79	Fungal genome and mating system transitions facilitated by chromosomal translocations involving intercentromeric recombination. <i>PLoS Biology</i> , 2017, 15, e2002527.	2.6	67
80	A Multistate Toggle Switch Defines Fungal Cell Fates and Is Regulated by Synergistic Genetic Cues. <i>PLoS Genetics</i> , 2016, 12, e1006353.	1.5	25
81	Lower prevalence but similar fitness in a parasitic fungus at higher radiation levels near Chernobyl. <i>Molecular Ecology</i> , 2016, 25, 3370-3383.	2.0	9
82	Genome Sequence of <i>Spizellomyces punctatus</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	20
83	Microevolutionary traits and comparative population genomics of the emerging pathogenic fungus <i>Cryptococcus gattii</i> . <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20160021.	1.8	30
84	Use of Multiple Sequencing Technologies To Produce a High-Quality Genome of the Fungus <i>Pseudogymnoascus destructans</i> , the Causative Agent of Bat White-Nose Syndrome. <i>Genome Announcements</i> , 2016, 4, .	0.8	24
85	Intracellular Action of a Secreted Peptide Required for Fungal Virulence. <i>Cell Host and Microbe</i> , 2016, 19, 849-864.	5.1	93
86	Genome Diversity, Recombination, and Virulence across the Major Lineages of <i>Paracoccidioides</i> . <i>MSphere</i> , 2016, 1, .	1.3	109
87	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
88	Hsf1 and Hsp90 orchestrate temperature-dependent global transcriptional remodelling and chromatin architecture in <i>Candida albicans</i> . <i>Nature Communications</i> , 2016, 7, 11704.	5.8	77
89	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
90	50 Years of <i>Emmonsia</i> Disease in Humans: The Dramatic Emergence of a Cluster of Novel Fungal Pathogens. <i>PLoS Pathogens</i> , 2015, 11, e1005198.	2.1	57

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91	Draft Genome Sequence of the Cellulolytic Fungus <i>Chaetomium globosum</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	47
92	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
93	Finding a Missing Gene: <i>EFG1</i> Regulates Morphogenesis in <i>Candida tropicalis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 849-856.	0.8	40
94	Chaos of Rearrangements in the Mating-Type Chromosomes of the Anther-Smut Fungus <i>Microbotryum lychnidis-dioicae</i> . <i>Genetics</i> , 2015, 200, 1275-1284.	1.2	78
95	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
96	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
97	Genome Evolution and Innovation across the Four Major Lineages of <i>Cryptococcus gattii</i> . <i>MBio</i> , 2015, 6, e00868-15.	1.8	101
98	Genetic and phenotypic intra-species variation in <i>Candida albicans</i> . <i>Genome Research</i> , 2015, 25, 413-425.	2.4	305
99	The evolution of drug resistance in clinical isolates of <i>Candida albicans</i> . <i>ELife</i> , 2015, 4, e00662.	2.8	268
100	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. <i>PLoS ONE</i> , 2014, 9, e99979.	1.1	34
101	Analysis of a Food-Borne Fungal Pathogen Outbreak: Virulence and Genome of a <i>Mucor circinelloides</i> Isolate from Yogurt. <i>MBio</i> , 2014, 5, e01390-14.	1.8	106
102	Genome Update of the Dimorphic Human Pathogenic Fungi Causing Paracoccidioidomycosis. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3348.	1.3	38
103	Ubiquitin-Mediated Response to Microsporidia and Virus Infection in <i>C. elegans</i> . <i>PLoS Pathogens</i> , 2014, 10, e1004200.	2.1	184
104	Using transcription of six <i>Puccinia triticina</i> races to identify the effective secretome during infection of wheat. <i>Frontiers in Plant Science</i> , 2014, 4, 520.	1.7	68
105	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
106	Highly Recombinant VGII <i>Cryptococcus gattii</i> Population Develops Clonal Outbreak Clusters through both Sexual Macroevolution and Asexual Microevolution. <i>MBio</i> , 2014, 5, e01494-14.	1.8	81
107	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
108	Genome Sequence of the Pathogenic Fungus <i>Sporothrix schenckii</i> (ATCC 58251). <i>Genome Announcements</i> , 2014, 2, .	0.8	30

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109	Fungi on the Skin: Dermatophytes and Malassezia. Cold Spring Harbor Perspectives in Medicine, 2014, 4, a019802-a019802.	2.9	134
110	Genomics of <i>Sclerotinia sclerotiorum</i> . , 2014, , 1-17.		1
111	Genome Sequence of the Microsporidian Species <i>Nematocida</i> sp1 Strain ERTm6 (ATCC PRA-372). Genome Announcements, 2014, 2, .	0.8	14
112	Comparative genomics of Australian isolates of the wheat stem rust pathogen <i>Puccinia graminis</i> f. sp. <i>tritici</i> reveals extensive polymorphism in candidate effector genes. Frontiers in Plant Science, 2014, 5, 759.	1.7	98
113	<i>Puccinia graminis</i> . , 2014, , 177-196.		9
114	Pilon: An Integrated Tool for Comprehensive Microbial Variant Detection and Genome Assembly Improvement. PLoS ONE, 2014, 9, e112963.	1.1	6,781
115	Conserved loci of leaf and stem rust fungi of wheat share synteny interrupted by lineage-specific influx of repeat elements. BMC Genomics, 2013, 14, 60.	1.2	20
116	Identification of the Mating-Type (<i>MAT</i>) Locus That Controls Sexual Reproduction of <i>Blastomyces dermatitidis</i> . Eukaryotic Cell, 2013, 12, 109-117.	3.4	38
117	Sequencing and characterization of the complete mitochondrial genomes of three <i>Pneumocystis</i> species provide new insights into divergence between human and rodent <i>Pneumocystis</i> . FASEB Journal, 2013, 27, 1962-1972.	0.2	40
118	Isolation of <i>Blastomyces dermatitidis</i> yeast from lung tissue during murine infection for in vivo transcriptional profiling. Fungal Genetics and Biology, 2013, 56, 1-8.	0.9	7
119	One Fungus, One Name: Defining the Genus <i>Fusarium</i> in a Scientifically Robust Way That Preserves Longstanding Use. Phytopathology, 2013, 103, 400-408.	1.1	219
120	Complete Genome Sequences from Three Genetically Distinct Strains Reveal High Intraspecies Genetic Diversity in the Microsporidian <i>Encephalitozoon cuniculi</i> . Eukaryotic Cell, 2013, 12, 503-511.	3.4	57
121	Comparative Genome Analysis of <i>Trichophyton rubrum</i> and Related Dermatophytes Reveals Candidate Genes Involved in Infection. MBio, 2012, 3, e00259-12.	1.8	211
122	Adaptation of the Black Yeast <i>Wangiella dermatitidis</i> to Ionizing Radiation: Molecular and Cellular Mechanisms. PLoS ONE, 2012, 7, e48674.	1.1	76
123	Microsporidian genome analysis reveals evolutionary strategies for obligate intracellular growth. Genome Research, 2012, 22, 2478-2488.	2.4	235
124	Novel, panzootic and hybrid genotypes of amphibian chytridiomycosis associated with the bullfrog trade. Molecular Ecology, 2012, 21, 5162-5177.	2.0	227
125	LINKAGE TO THE MATING-TYPE LOCUS ACROSS THE GENUS <i>MICROBOTRYUM</i> : INSIGHTS INTO NONRECOMBINING CHROMOSOMES. Evolution; International Journal of Organic Evolution, 2012, 66, 3519-3533.	1.1	32
126	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . PLoS Genetics, 2011, 7, e1002230.	1.5	902

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127	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9166-9171.	3.3	640
128	Genome Variation in <i>Cryptococcus gattii</i> , an Emerging Pathogen of Immunocompetent Hosts. MBio, 2011, 2, e00342-10.	1.8	182
129	Comparative Genomic Analysis of Human Fungal Pathogens Causing Paracoccidioidomycosis. PLoS Genetics, 2011, 7, e1002345.	1.5	164
130	Comparative Genomics Yields Insights into Niche Adaptation of Plant Vascular Wilt Pathogens. PLoS Pathogens, 2011, 7, e1002137.	2.1	477
131	Approaches to Fungal Genome Annotation. Mycology, 2011, 2, 118-141.	2.0	109
132	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . Nature, 2010, 464, 367-373.	13.7	1,442
133	The Fungal Genome Initiative and Lessons Learned from Genome Sequencing. Methods in Enzymology, 2010, 470, 833-855.	0.4	58
134	SREB, a GATA Transcription Factor That Directs Disparate Fates in <i>Blastomyces dermatitidis</i> Including Morphogenesis and Siderophore Biosynthesis. PLoS Pathogens, 2010, 6, e1000846.	2.1	68
135	Genomic Analysis of the Basal Lineage Fungus <i>Rhizopus oryzae</i> Reveals a Whole-Genome Duplication. PLoS Genetics, 2009, 5, e1000549.	1.5	332
136	Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes. Nature, 2009, 459, 657-662.	13.7	963
137	CandidaDB: a multi-genome database for <i>Candida</i> species and related Saccharomycotina. Nucleic Acids Research, 2007, 36, D557-D561.	6.5	26
138	The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. Science, 2007, 317, 1400-1402.	6.0	837
139	Comparative proteomics of extracellular proteins <i>in vitro</i> and <i>in planta</i> from the pathogenic fungus <i>Fusarium graminearum</i> . Proteomics, 2007, 7, 3171-3183.	1.3	196
140	DNA sequence and analysis of human chromosome 8. Nature, 2006, 439, 331-335.	13.7	115
141	Analysis of the DNA sequence and duplication history of human chromosome 15. Nature, 2006, 440, 671-675.	13.7	67
142	Human chromosome 11 DNA sequence and analysis including novel gene identification. Nature, 2006, 440, 497-500.	13.7	74
143	DNA sequence of human chromosome 17 and analysis of rearrangement in the human lineage. Nature, 2006, 440, 1045-1049.	13.7	130
144	DNA sequence and analysis of human chromosome 18. Nature, 2005, 437, 551-555.	13.7	53

#	ARTICLE	IF	CITATIONS
145	Sequencing of <i>Aspergillus nidulans</i> and comparative analysis with <i>A. fumigatus</i> and <i>A. oryzae</i> . <i>Nature</i> , 2005, 438, 1105-1115.	13.7	1,250
146	Genomics of the fungal kingdom: Insights into eukaryotic biology. <i>Genome Research</i> , 2005, 15, 1620-1631.	2.4	269
147	Finishing the euchromatic sequence of the human genome. <i>Nature</i> , 2004, 431, 931-945.	13.7	4,232
148	The Breakpoint Region of the Most Common Isochromosome, i(17q), in Human Neoplasia Is Characterized by a Complex Genomic Architecture with Large, Palindromic, Low-Copy Repeats. <i>American Journal of Human Genetics</i> , 2004, 74, 1-10.	2.6	122
149	DNA Sequence and Structure Requirements for Cleavage of V(D)J Recombination Signal Sequences. <i>Molecular and Cellular Biology</i> , 1996, 16, 5683-5690.	1.1	124
150	DNA-dependent kinase (p350) as a candidate gene for the murine SCID defect. <i>Science</i> , 1995, 267, 1178-1183.	6.0	610
151	Cleavage at a V(D)J recombination signal requires only RAG1 and RAG2 proteins and occurs in two steps. <i>Cell</i> , 1995, 83, 387-395.	13.5	643
152	Analysis of regions of RAG-2 important for V(D)J recombination. <i>Nucleic Acids Research</i> , 1994, 22, 1810-1814.	6.5	131
153	Rch1, a protein that specifically interacts with the RAG-1 recombination-activating protein.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 6156-6160.	3.3	167
154	Fungi Are What They Secrete: Evolution of Zygomycete Secretomes and the Origins of Terrestrial Fungal Ecologies. <i>SSRN Electronic Journal</i> , 0, , .	0.4	4
155	Obligate sexual reproduction of a homothallic fungus closely related to the <i>Cryptococcus</i> pathogenic species complex. <i>ELife</i> , 0, 11, .	2.8	4