

# Christina A Cuomo

## List of Publications by Year in descending order

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155  
papers

30,717  
citations

20036

63  
h-index

8212

153  
g-index

196  
all docs

196  
docs citations

196  
times ranked

36774  
citing authors

#	ARTICLE	IF	CITATIONS
1	Pilon: An Integrated Tool for Comprehensive Microbial Variant Detection and Genome Assembly Improvement. PLoS ONE, 2014, 9, e112963.	1.1	6,781
2	Finishing the euchromatic sequence of the human genome. Nature, 2004, 431, 931-945.	13.7	4,232
3	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . Nature, 2010, 464, 367-373.	13.7	1,442
4	Sequencing of <i>Aspergillus nidulans</i> and comparative analysis with <i>A. fumigatus</i> and <i>A. oryzae</i> . Nature, 2005, 438, 1105-1115.	13.7	1,250
5	Simultaneous Emergence of Multidrug-Resistant <i>Candida auris</i> on 3 Continents Confirmed by Whole-Genome Sequencing and Epidemiological Analyses. Clinical Infectious Diseases, 2017, 64, 134-140.	2.9	1,099
6	Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes. Nature, 2009, 459, 657-662.	13.7	963
7	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . PLoS Genetics, 2011, 7, e1002230.	1.5	902
8	The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. Science, 2007, 317, 1400-1402.	6.0	837
9	Cleavage at a V(D)J recombination signal requires only RAG1 and RAG2 proteins and occurs in two steps. Cell, 1995, 83, 387-395.	13.5	643
10	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
11	DNA-dependent kinase (p350) as a candidate gene for the murine SCID defect. Science, 1995, 267, 1178-1183.	6.0	610
12	Comparative Genomics Yields Insights into Niche Adaptation of Plant Vascular Wilt Pathogens. PLoS Pathogens, 2011, 7, e1002137.	2.1	477
13	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. PLoS Genetics, 2014, 10, e1004261.	1.5	336
14	Genomic Analysis of the Basal Lineage Fungus <i>Rhizopus oryzae</i> Reveals a Whole-Genome Duplication. PLoS Genetics, 2009, 5, e1000549.	1.5	332
15	Genetic and phenotypic intra-species variation in <i>Candida albicans</i> . Genome Research, 2015, 25, 413-425.	2.4	305
16	Genomic insights into multidrug-resistance, mating and virulence in <i>Candida auris</i> and related emerging species. Nature Communications, 2018, 9, 5346.	5.8	298
17	Threats Posed by the Fungal Kingdom to Humans, Wildlife, and Agriculture. MBio, 2020, 11, .	1.8	275
18	The Case for Adopting the "Species Complex" Nomenclature for the Etiologic Agents of Cryptococcosis. MSphere, 2017, 2, .	1.3	274

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19	Genomics of the fungal kingdom: Insights into eukaryotic biology. <i>Genome Research</i> , 2005, 15, 1620-1631.	2.4	269
20	The evolution of drug resistance in clinical isolates of <i>Candida albicans</i> . <i>ELife</i> , 2015, 4, e00662.	2.8	268
21	Microsporidian genome analysis reveals evolutionary strategies for obligate intracellular growth. <i>Genome Research</i> , 2012, 22, 2478-2488.	2.4	235
22	Novel, panzootic and hybrid genotypes of amphibian chytridiomycosis associated with the bullfrog trade. <i>Molecular Ecology</i> , 2012, 21, 5162-5177.	2.0	227
23	Tracing the Evolutionary History and Global Expansion of <i>Candida auris</i> Using Population Genomic Analyses. <i>MBio</i> , 2020, 11, .	1.8	224
24	One Fungus, One Name: Defining the Genus <i>Fusarium</i> in a Scientifically Robust Way That Preserves Longstanding Use. <i>Phytopathology</i> , 2013, 103, 400-408.	1.1	219
25	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
26	Comparative proteomics of extracellular proteins <i>in vitro</i> and <i>in planta</i> from the pathogenic fungus <i>Fusarium graminearum</i> . <i>Proteomics</i> , 2007, 7, 3171-3183.	1.3	196
27	Ubiquitin-Mediated Response to Microsporidia and Virus Infection in <i>C. elegans</i> . <i>PLoS Pathogens</i> , 2014, 10, e1004200.	2.1	184
28	Genome Variation in <i>Cryptococcus gattii</i> , an Emerging Pathogen of Immunocompetent Hosts. <i>MBio</i> , 2011, 2, e00342-10.	1.8	182
29	Genomic epidemiology of the UK outbreak of the emerging human fungal pathogen <i>Candida auris</i> . <i>Emerging Microbes and Infections</i> , 2018, 7, 1-12.	3.0	169
30	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
31	Comparative Genomic Analysis of Human Fungal Pathogens Causing Paracoccidioidomycosis. <i>PLoS Genetics</i> , 2011, 7, e1002345.	1.5	164
32	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
33	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
34	Fungi on the Skin: Dermatophytes and <i>Malassezia</i> . <i>Cold Spring Harbor Perspectives in Medicine</i> , 2014, 4, a019802-a019802.	2.9	134
35	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
36	Analysis of regions of RAG-2 important for V(D)J recombination. <i>Nucleic Acids Research</i> , 1994, 22, 1810-1814.	6.5	131

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37	DNA sequence of human chromosome 17 and analysis of rearrangement in the human lineage. <i>Nature</i> , 2006, 440, 1045-1049.	13.7	130
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 Structure Requirements for Cleavage of V(D)J Recombination Signal Sequences. <i>Molecular and Cellular Biology</i> , 1996, 16, 5683-5690.	1.1	124
40	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
41	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
42	DNA sequence and analysis of human chromosome 8. <i>Nature</i> , 2006, 439, 331-335.	13.7	115
43	RNAi is a critical determinant of centromere evolution in closely related fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3108-3113.	3.3	112
44	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
45	Genome Diversity, Recombination, and Virulence across the Major Lineages of <i>Paracoccidioides</i> . <i>MSphere</i> , 2016, 1, .	1.3	109
46	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
47	Approaches to Fungal Genome Annotation. <i>Mycology</i> , 2011, 2, 118-141.	2.0	109
48	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
49	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
50	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
51	Genome Evolution and Innovation across the Four Major Lineages of <i>Cryptococcus gattii</i> . <i>MBio</i> , 2015, 6, e00868-15.	1.8	101
52	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
53	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. <i>Frontiers in Plant Science</i> , 2014, 5, 759.	1.7	98
54	Genomic innovations linked to infection strategies across emerging pathogenic chytrid fungi. <i>Nature Communications</i> , 2017, 8, 14742.	5.8	96

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55	Intracellular Action of a Secreted Peptide Required for Fungal Virulence. <i>Cell Host and Microbe</i> , 2016, 19, 849-864.	5.1	93
56	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
57	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
58	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
59	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
60	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
61	Genetic Analysis of <i>Candida auris</i> Implicates Hsp90 in Morphogenesis and Azole Tolerance and Cdr1 in Azole Resistance. <i>MBio</i> , 2019, 10, .	1.8	77
62	Adaptation of the Black Yeast <i>Wangiella dermatitidis</i> to Ionizing Radiation: Molecular and Cellular Mechanisms. <i>PLoS ONE</i> , 2012, 7, e48674.	1.1	76
63	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
64	Human chromosome 11 DNA sequence and analysis including novel gene identification. <i>Nature</i> , 2006, 440, 497-500.	13.7	74
65	Antagonistic paralogs control a switch between growth and pathogen resistance in <i>C. elegans</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007528.	2.1	72
66	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
67	SREB, a GATA Transcription Factor That Directs Disparate Fates in <i>Blastomyces dermatitidis</i> Including Morphogenesis and Siderophore Biosynthesis. <i>PLoS Pathogens</i> , 2010, 6, e1000846.	2.1	68
68	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
69	Analysis of the DNA sequence and duplication history of human chromosome 15. <i>Nature</i> , 2006, 440, 671-675.	13.7	67
70	Fungal genome and mating system transitions facilitated by chromosomal translocations involving intercentromeric recombination. <i>PLoS Biology</i> , 2017, 15, e2002527.	2.6	67
71	A New Lineage of <i>Cryptococcus gattii</i> (VGV) Discovered in the Central Zambesian Miombo Woodlands. <i>MBio</i> , 2019, 10, .	1.8	66
72	Coordinated host-pathogen transcriptional dynamics revealed using sorted subpopulations and single macrophages infected with <i>Candida albicans</i> . <i>Nature Communications</i> , 2019, 10, 1607.	5.8	65

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73	The Fungal Genome Initiative and Lessons Learned from Genome Sequencing. <i>Methods in Enzymology</i> , 2010, 470, 833-855.	0.4	58
74	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
75	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
76	Complete Genome Sequences from Three Genetically Distinct Strains Reveal High Intraspecies Genetic Diversity in the Microsporidian Encephalitozoon cuniculi. <i>Eukaryotic Cell</i> , 2013, 12, 503-511.	3.4	57
77	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
78	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
79	<i>Emergomyces</i> : The global rise of new dimorphic fungal pathogens. <i>PLoS Pathogens</i> , 2019, 15, e1007977.	2.1	54
80	Clade-specific chromosomal rearrangements and loss of subtelomeric adhesins in <i>Candida auris</i> . <i>Genetics</i> , 2021, 218, .	1.2	54
81	DNA sequence and analysis of human chromosome 18. <i>Nature</i> , 2005, 437, 551-555.	13.7	53
82	Best practices on the differential expression analysis of multi-species RNA-seq. <i>Genome Biology</i> , 2021, 22, 121.	3.8	51
83	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
84	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
85	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
86	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
87	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
88	Draft Genome Sequence of the Cellulolytic Fungus <i>Chaetomium globosum</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	47
89	Identification of <i>Candida auris</i> by Use of the Updated Vitek 2 Yeast Identification System, Version 8.01: a Multilaboratory Evaluation Study. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	47
90	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

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91	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> . <i>FASEB Journal</i> , 2013, 27, 1962-1972.	0.2	40
92	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
93	Genomic Understanding of an Infectious Brain Disease from the Desert. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 909-922.	0.8	39
94	Identification of the Mating-Type ( <i>MAT</i> ) Locus That Controls Sexual Reproduction of <i>Blastomyces dermatitidis</i> . <i>Eukaryotic Cell</i> , 2013, 12, 109-117.	3.4	38
95	Genome Update of the Dimorphic Human Pathogenic Fungi Causing Paracoccidioidomycosis. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3348.	1.3	38
96	Genetic and Genomic Analyses Reveal Boundaries between Species Closely Related to <i>Cryptococcus</i> Pathogens. <i>MBio</i> , 2019, 10, .	1.8	37
97	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
98	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. <i>PLoS ONE</i> , 2014, 9, e99979.	1.1	34
99	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
100	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
101	LINKAGE TO THE MATING-TYPE LOCUS ACROSS THE GENUS <i>MICROBOTRYUM</i> : INSIGHTS INTO NONRECOMBINING CHROMOSOMES. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 3519-3533.	1.1	32
102	Zinc Cluster Transcription Factors Alter Virulence in <i>Candida albicans</i> . <i>Genetics</i> , 2017, 205, 559-576.	1.2	31
103	Whole Genome Sequence of the Heterozygous Clinical Isolate <i>Candida krusei</i> 81-B-5. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2883-2889.	0.8	31
104	In vivo 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
105	Genome Sequence of the Pathogenic Fungus <i>Sporothrix schenckii</i> (ATCC 58251). <i>Genome Announcements</i> , 2014, 2, .	0.8	30
106	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
107	Genome analysis reveals evolutionary mechanisms of adaptation in systemic dimorphic fungi. <i>Scientific Reports</i> , 2018, 8, 4473.	1.6	28
108	Amoeba Predation of <i>Cryptococcus neoformans</i> Results in Pleiotropic Changes to Traits Associated with Virulence. <i>MBio</i> , 2021, 12, .	1.8	27

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109	CandidaDB: a multi-genome database for Candida species and related Saccharomycotina. Nucleic Acids Research, 2007, 36, D557-D561.	6.5	26
110	A Multistate Toggle Switch Defines Fungal Cell Fates and Is Regulated by Synergistic Genetic Cues. PLoS Genetics, 2016, 12, e1006353.	1.5	25
111	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. Genome Announcements, 2016, 4, .	0.8	24
112	Understanding the Emergence of Multidrug-Resistant Candida: Using Whole-Genome Sequencing to Describe the Population Structure of Candida haemulonii Species Complex. Frontiers in Genetics, 2020, 11, 554.	1.1	24
113	Landscape of gene expression variation of natural isolates of Cryptococcus neoformans in response to biologically relevant stresses. Microbial Genomics, 2020, 6, .	1.0	24
114	Comparative Population Genomics Analysis of the Mammalian Fungal Pathogen <i>Pneumocystis</i> . MBio, 2018, 9, .	1.8	23
115	Genomic insights into the host specific adaptation of the Pneumocystis genus. Communications Biology, 2021, 4, 305.	2.0	23
116	Gene Expression of Diverse Cryptococcus Isolates during Infection of the Human Central Nervous System. MBio, 2021, 12, e0231321.	1.8	23
117	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
118	Genome Sequence of <i>Spizellomyces punctatus</i> . Genome Announcements, 2016, 4, .	0.8	20
119	Harnessing Whole Genome Sequencing in Medical Mycology. Current Fungal Infection Reports, 2017, 11, 52-59.	0.9	20
120	Pathways of Pathogenicity: Transcriptional Stages of Germination in the Fatal Fungal Pathogen <i>Rhizopus delemar</i> . MSphere, 2018, 3, .	1.3	19
121	Blastomycosis in Africa and the Middle East: A Comprehensive Review of Reported Cases and Reanalysis of Historical Isolates Based on Molecular Data. Clinical Infectious Diseases, 2021, 73, e1560-e1569.	2.9	19
122	Paracoccidioides spp. catalases and their role in antioxidant defense against host defense responses. Fungal Genetics and Biology, 2017, 100, 22-32.	0.9	16
123	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. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	16
124	Inter-species geographic signatures for tracing horizontal gene transfer and long-term persistence of carbapenem resistance. Genome Medicine, 2022, 14, 37.	3.6	15
125	Genome Sequence of the Microsporidian Species <i>Nematocida</i> sp1 Strain ERTm6 (ATCC PRA-372). Genome Announcements, 2014, 2, .	0.8	14
126	Genome Sequence for Candida albicans Clinical Oral Isolate 529L. Microbiology Resource Announcements, 2019, 8, .	0.3	13



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127	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
128	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
129	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
130	<i>Cryptococcus neoformans</i> Recovered From Olive Trees ( <i>Olea europaea</i> ) in Turkey Reveal Allopatry With African and South American Lineages. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 384.	1.8	12
131	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
132	Diversity, multifaceted evolution, and facultative saprotrophism in the European <i>Batrachochytrium salamandrivorans</i> epidemic. <i>Nature Communications</i> , 2021, 12, 6688.	5.8	11
133	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
134	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
135	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
136	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
137	<i>Puccinia graminis</i> . , 2014, , 177-196.		9
138	Tracking a Global Threat: a New Genotyping Method for <i>Candida auris</i> . <i>MBio</i> , 2020, 11, .	1.8	9
139	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
140	Diagnostic Allele-Specific PCR for the Identification of <i>Candida auris</i> Clades. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 1078.	1.5	8
141	Isolation of <i>Blastomyces dermatitidis</i> yeast from lung tissue during murine infection for in vivo transcriptional profiling. <i>Fungal Genetics and Biology</i> , 2013, 56, 1-8.	0.9	7
142	Genome Sequence of the Black Yeast <i>Exophiala lecanii-corni</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	7
143	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
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