

Christina A Cuomo

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169
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144
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196
ext. papers

27,189
ext. citations

10.5
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L-index

#	Paper	IF	Citations
169	Finishing the euchromatic sequence of the human genome. <i>Nature</i> , 2004 , 431, 931-45	50.4	3444
168	Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. <i>PLoS ONE</i> , 2014 , 9, e112963	3.7	3418
167	Sequencing of <i>Aspergillus nidulans</i> and comparative analysis with <i>A. fumigatus</i> and <i>A. oryzae</i> . <i>Nature</i> , 2005 , 438, 1105-15	50.4	1094
166	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010 , 464, 367-73	50.4	1085
165	Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes. <i>Nature</i> , 2009 , 459, 657-62	50.4	764
164	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	11.6	753
163	The <i>Fusarium graminearum</i> genome reveals a link between localized polymorphism and pathogen specialization. <i>Science</i> , 2007 , 317, 1400-2	33.3	668
162	Genomic analysis of the necrotrophic fungal pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011 , 7, e1002230	6	659
161	Cleavage at a V(D)J recombination signal requires only RAG1 and RAG2 proteins and occurs in two steps. <i>Cell</i> , 1995 , 83, 387-95	56.2	594
160	DNA-dependent kinase (p350) as a candidate gene for the murine SCID defect. <i>Science</i> , 1995 , 267, 1178-83	33.3	541
159	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 9166-71	11.5	479
158	Comparative genomics yields insights into niche adaptation of plant vascular wilt pathogens. <i>PLoS Pathogens</i> , 2011 , 7, e1002137	7.6	335
157	Genomic analysis of the basal lineage fungus <i>Rhizopus oryzae</i> reveals a whole-genome duplication. <i>PLoS Genetics</i> , 2009 , 5, e1000549	6	273
156	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	6	260
155	Genomics of the fungal kingdom: insights into eukaryotic biology. <i>Genome Research</i> , 2005 , 15, 1620-31	9.7	222
154	Microsporidian genome analysis reveals evolutionary strategies for obligate intracellular growth. <i>Genome Research</i> , 2012 , 22, 2478-88	9.7	191
153	The Case for Adopting the "Species Complex" Nomenclature for the Etiologic Agents of Cryptococcosis. <i>MSphere</i> , 2017 , 2,	5	185

152	Novel, panzootic and hybrid genotypes of amphibian chytridiomycosis associated with the bullfrog trade. <i>Molecular Ecology</i> , 2012 , 21, 5162-77	5.7	183
151	Comparative proteomics of extracellular proteins in vitro and in planta from the pathogenic fungus <i>Fusarium graminearum</i> . <i>Proteomics</i> , 2007 , 7, 3171-83	4.8	178
150	Genomic insights into multidrug-resistance, mating and virulence in <i>Candida auris</i> and related emerging species. <i>Nature Communications</i> , 2018 , 9, 5346	17.4	174
149	The evolution of drug resistance in clinical isolates of <i>Candida albicans</i> . <i>ELife</i> , 2015 , 4, e00662	8.9	168
148	Genetic and phenotypic intra-species variation in <i>Candida albicans</i> . <i>Genome Research</i> , 2015 , 25, 413-25	9.7	166
147	Comparative genome analysis of <i>Trichophyton rubrum</i> and related dermatophytes reveals candidate genes involved in infection. <i>MBio</i> , 2012 , 3, e00259-12	7.8	162
146	One fungus, one name: defining the genus <i>Fusarium</i> in a scientifically robust way that preserves longstanding use. <i>Phytopathology</i> , 2013 , 103, 400-8	3.8	155
145	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, 6156-60	11.5	154
144	Genome variation in <i>Cryptococcus gattii</i> , an emerging pathogen of immunocompetent hosts. <i>MBio</i> , 2011 , 2, e00342-10	7.8	137
143	Comparative genomic analysis of human fungal pathogens causing paracoccidioidomycosis. <i>PLoS Genetics</i> , 2011 , 7, e1002345	6	132
142	Analysis of regions of RAG-2 important for V(D)J recombination. <i>Nucleic Acids Research</i> , 1994 , 22, 1810-4	120.1	124
141	DNA sequence and structure requirements for cleavage of V(D)J recombination signal sequences. <i>Molecular and Cellular Biology</i> , 1996 , 16, 5683-90	4.8	119
140	Ubiquitin-mediated response to microsporidia and virus infection in <i>C. elegans</i> . <i>PLoS Pathogens</i> , 2014 , 10, e1004200	7.6	118
139	Genomic epidemiology of the UK outbreak of the emerging human fungal pathogen <i>Candida auris</i> . <i>Emerging Microbes and Infections</i> , 2018 , 7, 43	18.9	117
138	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	11	116
137	DNA sequence of human chromosome 17 and analysis of rearrangement in the human lineage. <i>Nature</i> , 2006 , 440, 1045-9	50.4	114
136	Threats Posed by the Fungal Kingdom to Humans, Wildlife, and Agriculture. <i>MBio</i> , 2020 , 11,	7.8	94
135	Exploring the genomic diversity of black yeasts and relatives (,). <i>Studies in Mycology</i> , 2017 , 86, 1-28	22.2	93

134	Genome analysis of three <i>Pneumocystis</i> species reveals adaptation mechanisms to life exclusively in mammalian hosts. <i>Nature Communications</i> , 2016 , 7, 10740	17.4	93
133	Tracing the Evolutionary History and Global Expansion of <i>Candida auris</i> Using Population Genomic Analyses. <i>MBio</i> , 2020 , 11,	7.8	92
132	Approaches to Fungal Genome Annotation. <i>Mycology</i> , 2011 , 2, 118-141	3.7	92
131	Fungi on the skin: dermatophytes and <i>Malassezia</i> . <i>Cold Spring Harbor Perspectives in Medicine</i> , 2014 , 4,	5.4	90
130	DNA sequence and analysis of human chromosome 8. <i>Nature</i> , 2006 , 439, 331-5	50.4	86
129	Population genomics and the evolution of virulence in the fungal pathogen. <i>Genome Research</i> , 2017 , 27, 1207-1219	9.7	85
128	Novel taxa of thermally dimorphic systemic pathogens in the Ajellomycetaceae (Onygenales). <i>Mycoses</i> , 2017 , 60, 296-309	5.2	82
127	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	7.8	82
126	Genome Evolution and Innovation across the Four Major Lineages of <i>Cryptococcus gattii</i> . <i>MBio</i> , 2015 , 6, e00868-15	7.8	70
125	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	11.5	69
124	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	3.2	67
123	Genome Diversity, Recombination, and Virulence across the Major Lineages of. <i>MSphere</i> , 2016 , 1,	5	67
122	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	7.6	65
121	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	6.2	64
120	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	7.8	63
119	Adaptation of the black yeast <i>Wangiella dermatitidis</i> to ionizing radiation: molecular and cellular mechanisms. <i>PLoS ONE</i> , 2012 , 7, e48674	3.7	61
118	Chaos of Rearrangements in the Mating-Type Chromosomes of the Anther-Smut Fungus <i>Microbotryum lychnidis-dioicae</i> . <i>Genetics</i> , 2015 , 200, 1275-84	4	60
117	Intracellular Action of a Secreted Peptide Required for Fungal Virulence. <i>Cell Host and Microbe</i> , 2016 , 19, 849-64	23.4	59

116	Tracing Genetic Exchange and Biogeography of var. at the Global Population Level. <i>Genetics</i> , 2017 , 207, 327-346	4	57
115	Analysis of the DNA sequence and duplication history of human chromosome 15. <i>Nature</i> , 2006 , 440, 671-50.4	50.4	57
114	Human chromosome 11 DNA sequence and analysis including novel gene identification. <i>Nature</i> , 2006 , 440, 497-500	50.4	57
113	Contrasting host-pathogen interactions and genome evolution in two generalist and specialist microsporidian pathogens of mosquitoes. <i>Nature Communications</i> , 2015 , 6, 7121	17.4	56
112	Genomic innovations linked to infection strategies across emerging pathogenic chytrid fungi. <i>Nature Communications</i> , 2017 , 8, 14742	17.4	55
111	Hsf1 and Hsp90 orchestrate temperature-dependent global transcriptional remodelling and chromatin architecture in <i>Candida albicans</i> . <i>Nature Communications</i> , 2016 , 7, 11704	17.4	55
110	Mutations in : a Novel Genetic Determinant of Clinical Fluconazole Resistance in <i>Candida auris</i> . <i>MBio</i> , 2020 , 11,	7.8	52
109	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	7.6	52
108	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	11.5	52
107	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	6	51
106	Genetic Analysis of Implicates Hsp90 in Morphogenesis and Azole Tolerance and Cdr1 in Azole Resistance. <i>MBio</i> , 2019 , 10,	7.8	49
105	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	56.2	46
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	6.2	45
103	DNA sequence and analysis of human chromosome 18. <i>Nature</i> , 2005 , 437, 551-5	50.4	45
102	Microevolution of Serial Clinical Isolates of var. and. <i>MBio</i> , 2017 , 8,	7.8	44
101	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	4.5	44
100	Fungal genome and mating system transitions facilitated by chromosomal translocations involving intercentromeric recombination. <i>PLoS Biology</i> , 2017 , 15, e2002527	9.7	44
99	Complete genome sequences from three genetically distinct strains reveal high intraspecies genetic diversity in the microsporidian <i>Encephalitozoon cuniculi</i> . <i>Eukaryotic Cell</i> , 2013 , 12, 503-11		43

98	The fungal genome initiative and lessons learned from genome sequencing. <i>Methods in Enzymology</i> , 2010 , 470, 833-55	1.7	43
97	50 Years of Emmonsia Disease in Humans: The Dramatic Emergence of a Cluster of Novel Fungal Pathogens. <i>PLoS Pathogens</i> , 2015 , 11, e1005198	7.6	41
96	Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic that Includes the Species Complex. <i>Phytopathology</i> , 2021 , 111, 1064-1079	3.8	39
95	Comparative genomic and transcriptomic analysis of wangiella dermatitidis, a major cause of phaeohyphomycosis and a model black yeast human pathogen. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 561-78	3.2	38
94	Antagonistic paralogs control a switch between growth and pathogen resistance in <i>C. elegans</i> . <i>PLoS Pathogens</i> , 2019 , 15, e1007528	7.6	37
93	Whole-Genome Analysis Illustrates Global Clonal Population Structure of the Ubiquitous Dermatophyte Pathogen. <i>Genetics</i> , 2018 , 208, 1657-1669	4	36
92	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, 1962-72	0.9	36
91	Degeneration of the nonrecombining regions in the mating-type chromosomes of the anther-smut fungi. <i>Molecular Biology and Evolution</i> , 2015 , 32, 928-43	8.3	36
90	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	17.4	35
89	A New Lineage of <i>Cryptococcus gattii</i> (VGV) Discovered in the Central Zambebian Miombo Woodlands. <i>MBio</i> , 2019 , 10,	7.8	34
88	Finding a Missing Gene: EFG1 Regulates Morphogenesis in <i>Candida tropicalis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 849-56	3.2	31
87	Genome update of the dimorphic human pathogenic fungi causing paracoccidioidomycosis. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e3348	4.8	31
86	Identification of the mating-type (MAT) locus that controls sexual reproduction of <i>Blastomyces dermatitidis</i> . <i>Eukaryotic Cell</i> , 2013 , 12, 109-17		30
85	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,	9.7	29
84	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, 3519-33	3.8	27
83	<i>Emergomyces</i> : The global rise of new dimorphic fungal pathogens. <i>PLoS Pathogens</i> , 2019 , 15, e1007977	7.6	26
82	Comparative Genomics Integrated with Association Analysis Identifies Candidate Effector Genes Corresponding to in Phenotype-Paired Isolates from Australia. <i>Frontiers in Plant Science</i> , 2017 , 8, 148	6.2	26
81	Genome Sequence of the Pathogenic Fungus <i>Sporothrix schenckii</i> (ATCC 58251). <i>Genome Announcements</i> , 2014 , 2,		26

80	Standardized metadata for human pathogen/vector genomic sequences. <i>PLoS ONE</i> , 2014 , 9, e99979	3.7	25
79	Phenotypic Variability Correlates with Clinical Outcome in Isolates Obtained from Botswanan HIV/AIDS Patients. <i>MBio</i> , 2018 , 9,	7.8	24
78	Clade-specific chromosomal rearrangements and loss of subtelomeric adhesins in <i>Candida auris</i> . <i>Genetics</i> , 2021 , 218,	4	22
77	Draft Genome Sequence of the Cellulolytic Fungus <i>Chaetomium globosum</i> . <i>Genome Announcements</i> , 2015 , 3,		21
76	Genomic diversity of the human pathogen <i>Paracoccidioides</i> across the South American continent. <i>Fungal Genetics and Biology</i> , 2020 , 140, 103395	3.9	20
75	<i>CandidaDB</i> : a multi-genome database for <i>Candida</i> species and related Saccharomycotina. <i>Nucleic Acids Research</i> , 2008 , 36, D557-61	20.1	20
74	Human Blastomycosis in South Africa Caused by and sp. nov., 1967 to 2014. <i>Journal of Clinical Microbiology</i> , 2020 , 58,	9.7	20
73	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,	5.8	20
72	Genome analysis reveals evolutionary mechanisms of adaptation in systemic dimorphic fungi. <i>Scientific Reports</i> , 2018 , 8, 4473	4.9	19
71	Comparative Population Genomics Analysis of the Mammalian Fungal Pathogen. <i>MBio</i> , 2018 , 9,	7.8	19
70	Genome-Wide Analysis of Experimentally Evolved <i>Candida auris</i> Reveals Multiple Novel Mechanisms of Multidrug Resistance. <i>MBio</i> , 2021 , 12,	7.8	19
69	Genomic Understanding of an Infectious Brain Disease from the Desert. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 909-922	3.2	18
68	Genetic and Genomic Analyses Reveal Boundaries between Species Closely Related to Pathogens. <i>MBio</i> , 2019 , 10,	7.8	17
67	A Multistate Toggle Switch Defines Fungal Cell Fates and Is Regulated by Synergistic Genetic Cues. <i>PLoS Genetics</i> , 2016 , 12, e1006353	6	17
66	Zinc Cluster Transcription Factors Alter Virulence in <i>Candida albicans</i> . <i>Genetics</i> , 2017 , 205, 559-576	4	16
65	Experimental Evolution Identifies Adaptive Aneuploidy as a Mechanism of Fluconazole Resistance in <i>Candida auris</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020 , 65,	5.9	16
64	Genome Sequence of <i>Spizellomyces punctatus</i> . <i>Genome Announcements</i> , 2016 , 4,		16
63	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,		16

62	An oxindole efflux inhibitor potentiates azoles and impairs virulence in the fungal pathogen <i>Candida auris</i> . <i>Nature Communications</i> , 2020 , 11, 6429	17.4	15
61	Harnessing Whole Genome Sequencing in Medical Mycology. <i>Current Fungal Infection Reports</i> , 2017 , 11, 52-59	1.4	14
60	Genome Sequence of the Microsporidian Species <i>Nematocida</i> sp1 Strain ERTm6 (ATCC PRA-372). <i>Genome Announcements</i> , 2014 , 2,		14
59	Advances in <i>Cryptococcus</i> genomics: insights into the evolution of pathogenesis. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2018 , 113, e170473	2.6	13
58	<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	3.9	12
57	Conserved loci of leaf and stem rust fungi of wheat share synteny interrupted by lineage-specific influx of repeat elements. <i>BMC Genomics</i> , 2013 , 14, 60	4.5	12
56	Whole Genome Sequence of the Heterozygous Clinical Isolate 81-B-5. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 2883-2889	3.2	12
55	Landscape of gene expression variation of natural isolates of in response to biologically relevant stresses. <i>Microbial Genomics</i> , 2020 , 6,	4.4	12
54	Understanding the Emergence of Multidrug-Resistant : Using Whole-Genome Sequencing to Describe the Population Structure of Species Complex. <i>Frontiers in Genetics</i> , 2020 , 11, 554	4.5	9
53	Genomic basis of multidrug-resistance, mating, and virulence in <i>Candida auris</i> and related emerging species		9
52	Transcriptional Heterogeneity of VGII Compared with Non-VGII Lineages Underpins Key Pathogenicity Pathways. <i>MSphere</i> , 2018 , 3,	5	9
51	Pathways of Pathogenicity: Transcriptional Stages of Germination in the Fatal Fungal Pathogen. <i>MSphere</i> , 2018 , 3,	5	9
50	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	11.6	8
49	Lower prevalence but similar fitness in a parasitic fungus at higher radiation levels near Chernobyl. <i>Molecular Ecology</i> , 2016 , 25, 3370-83	5.7	8
48	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	3.9	7
47	Transcriptional analysis of mating and pre-infection stages of the anther smut,. <i>Microbiology (United Kingdom)</i> , 2017 , 163, 410-420	2.9	7
46	Chromosomal rearrangements and loss of subtelomeric adhesins linked to clade-specific phenotypes in <i>Candida auris</i>		7
45	Tracking a Global Threat: a New Genotyping Method for <i>Candida auris</i> . <i>MBio</i> , 2020 , 11,	7.8	6

44	Tracing the evolutionary history and global expansion of <i>Candida auris</i> using population genomic analyses		6
43	Best practices on the differential expression analysis of multi-species RNA-seq. <i>Genome Biology</i> , 2021 , 22, 121	18.3	6
42	Genome Sequence for <i>Candida albicans</i> Clinical Oral Isolate 529L. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	5
41	<i>Puccinia graminis</i> 2014 , 177-196		5
40	Genomic insights into the host specific adaptation of the <i>Pneumocystis</i> genus. <i>Communications Biology</i> , 2021 , 4, 305	6.7	5
39	Genome Sequence of the Black Yeast <i>Exophiala lecanii-corni</i> . <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	4
38	Comparative analysis highlights variable genome content of wheat rusts and divergence of the mating loci		4
37	Amoeba Predation of <i>Cryptococcus neoformans</i> Results in Pleiotropic Changes to Traits Associated with Virulence. <i>MBio</i> , 2021 , 12,	7.8	4
36	Recovered From Olive Trees () in Turkey Reveal Allopatry With African and South American Lineages. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019 , 9, 384	5.9	4
35	: An Intricate Dance of Anther Smut and Its Host. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 505-518	3.2	4
34	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,	3.2	4
33	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> , 2021 ,	9.5	4
32	Gene Expression of Diverse <i>Cryptococcus</i> Isolates during Infection of the Human Central Nervous System. <i>MBio</i> , 2021 , e0231321	7.8	3
31	Mutations in TAC1B: a novel genetic determinant of clinical fluconazole resistance in <i>C. auris</i>		3
30	Genome-wide analysis of experimentally evolved <i>Candida auris</i> reveals multiple novel mechanisms of multidrug-resistance		3
29	Dissecting the first phased dikaryotic genomes of the wheat rust pathogen <i>Puccinia triticina</i> reveals the mechanisms of somatic exchange in nature		3
28	Diversity and Complexity of the Large Surface Protein Family in the Compacted Genomes of Multiple Species. <i>MBio</i> , 2020 , 11,	7.8	3
27	Whole-genome sequencing of multiple isolates of <i>Puccinia triticina</i> reveals asexual lineages evolving by recurrent mutations		2

26	Diversity, multifaceted evolution, and facultative saprotrophism in the European Batrachochytrium salamandrivorans epidemic. <i>Nature Communications</i> , 2021 , 12, 6688	17.4	2
25	Genetic and genomic analyses reveal boundaries between species closely related to <i>Cryptococcus</i> pathogens		2
24	Population genomics of <i>Cryptococcus neoformans</i> var. <i>grubii</i> reveals new biogeographic relationships and finely maps hybridization		2
23	Titan cells formation in <i>Cryptococcus neoformans</i> is finely tuned by environmental conditions and modulated by positive and negative genetic regulators		2
22	Genome analysis reveals evolutionary mechanisms of adaptation in systemic dimorphic fungi		2
21	Bacterial endosymbionts influence fungal transcriptional profiles with implications for host response in the human fungal pathogens <i>Rhizopus microsporus</i> and <i>Rhizopus delemar</i>		2
20	Genomic epidemiology of a case cluster in Glasgow, Scotland, 2018. <i>Microbial Genomics</i> , 2021 , 7,	4.4	2
19	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,	3.2	2
18	Genomic characterization of recurrent mold infections in thoracic transplant recipients. <i>Transplant Infectious Disease</i> , 2018 , 20, e12935	2.7	2
17	Inter-species geographic signatures for tracing horizontal gene transfer and long-term persistence of carbapenem resistance.. <i>Genome Medicine</i> , 2022 , 14, 37	14.4	2
16	Complete Genome Sequences for Two Clinical Isolates from Northern and Southern Vietnam. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
15	Genomics of <i>Sclerotinia sclerotiorum</i> 2014 , 1-17		1
14	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		1
13	Chromosome-Level Genome Assembly of a Human Fungal Pathogen Reveals Synteny among Geographically Distinct Species.. <i>MBio</i> , 2022 , e0257421	7.8	1
12	Evolutionary persistence of DNA methylation for millions of years after ancient loss of a de novo methyltransferase		
11	Rapid genome sequencing for outbreak analysis of the emerging human fungal pathogen <i>Candida auris</i>		1
10	Coordinated host-pathogen transcriptional dynamics revealed using sorted subpopulations and single, <i>Candida albicans</i> infected macrophages		1
9	Transcriptional heterogeneity of <i>Cryptococcus gattii</i> VGII compared with non-VGII lineages underpins key pathogenicity pathways		1

8	Phenotypic variability correlates with clinical outcome in <i>Cryptococcus</i> isolates obtained from Botswanan HIV/AIDS patients		1
7	Population genomics and the evolution of virulence in the fungal pathogen <i>Cryptococcus neoformans</i>		1
6	Chromosome-level genome assembly of a human fungal pathogen reveals synteny among geographically distinct species		1
5	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,	3.2	1
4	Diagnostic Allele-Specific PCR for the Identification of Clades. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021 , 7,	5.6	1
3	MycosNP: A Portable Workflow for Performing Whole-Genome Sequencing Analysis of <i>Candida auris</i> . <i>Methods in Molecular Biology</i> , 2022 , 215-228	1.4	1
2	738. A Novel Molecular Diagnostic Assay for Identification of Fungal Pathogens. <i>Open Forum Infectious Diseases</i> , 2020 , 7, S418-S419	1	
1	Generating Complete Genome Assemblies of <i>Candida auris</i> . <i>Methods in Molecular Biology</i> , 2022 , 205-214	1.4	