

R Blake Billmyre

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

1,958
citations

304368

22
h-index

525886

27
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37
all docs

37
docs citations

37
times ranked

2530
citing authors

#	ARTICLE	IF	CITATIONS
1	Diverse mating phenotypes impact the spread of wtf meiotic drivers in <i>Schizosaccharomyces pombe</i> . <i>ELife</i> , 2021, 10, .	2.8	11
2	5-fluorocytosine resistance is associated with hypermutation and alterations in capsule biosynthesis in <i>Cryptococcus</i> . <i>Nature Communications</i> , 2020, 11, 127.	5.8	73
3	A Novel Resistance Pathway for Calcineurin Inhibitors in the Human-Pathogenic Mucorales <i>Mucor circinelloides</i> . <i>MBio</i> , 2020, 11, .	1.8	29
4	Roles for Stress Response and Cell Wall Biosynthesis Pathways in Caspofungin Tolerance in <i>Cryptococcus neoformans</i> . <i>Genetics</i> , 2019, 213, 213-227.	1.2	29
5	Gastrointestinal microbiota alteration induced by <i>Mucor circinelloides</i> in a murine model. <i>Journal of Microbiology</i> , 2019, 57, 509-520.	1.3	18
6	Broad antifungal resistance mediated by RNAi-dependent epimutation in the basal human fungal pathogen <i>Mucor circinelloides</i> . <i>PLoS Genetics</i> , 2019, 15, e1007957.	1.5	46
7	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
8	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
9	A High-Resolution Map of Meiotic Recombination in <i>Cryptococcus deneoformans</i> Demonstrates Decreased Recombination in Unisexual Reproduction. <i>Genetics</i> , 2018, 209, 567-578.	1.2	34
10	Identification of small RNAs in extracellular vesicles from the commensal yeast <i>Malassezia sympodialis</i> . <i>Scientific Reports</i> , 2017, 7, 39742.	1.6	69
11	Importance of Resolving Fungal Nomenclature: the Case of Multiple Pathogenic Species in the <i>Cryptococcus</i> Genus. <i>MSphere</i> , 2017, 2, .	1.3	124
12	Proteogenomics produces comprehensive and highly accurate protein-coding gene annotation in a complete genome assembly of <i>Malassezia sympodialis</i> . <i>Nucleic Acids Research</i> , 2017, 45, gkx006.	6.5	47
13	Fungal genome and mating system transitions facilitated by chromosomal translocations involving intercentromeric recombination. <i>PLoS Biology</i> , 2017, 15, e2002527.	2.6	67
14	Elucidation of the calcineurin-Crz1 stress response transcriptional network in the human fungal pathogen <i>Cryptococcus neoformans</i> . <i>PLoS Genetics</i> , 2017, 13, e1006667.	1.5	90
15	Genetic and epigenetic engines of diversity in pathogenic microbes. <i>PLoS Pathogens</i> , 2017, 13, e1006468.	2.1	7
16	Natural mismatch repair mutations mediate phenotypic diversity and drug resistance in <i>Cryptococcus deuterogattii</i> . <i>ELife</i> , 2017, 6, .	2.8	74
17	Gene Network Polymorphism Illuminates Loss and Retention of Novel RNAi Silencing Components in the <i>Cryptococcus</i> Pathogenic Species Complex. <i>PLoS Genetics</i> , 2016, 12, e1005868.	1.5	43
18	Cancer-associated isocitrate dehydrogenase mutations induce mitochondrial DNA instability. <i>Human Molecular Genetics</i> , 2016, 25, 3524-3538.	1.4	8

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19	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
20	<i>Cryptococcus gattii</i> VGIII Isolates Causing Infections in HIV/AIDS Patients in Southern California: Identification of the Local Environmental Source as Arboreal. <i>PLoS Pathogens</i> , 2014, 10, e1004285.	2.1	85
21	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
22	Unisexual Reproduction Drives Meiotic Recombination and Phenotypic and Karyotypic Plasticity in <i>Cryptococcus neoformans</i> . <i>PLoS Genetics</i> , 2014, 10, e1004849.	1.5	71
23	Highly Recombinant VGIII <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
24	RNAi function, diversity, and loss in the fungal kingdom. <i>Chromosome Research</i> , 2013, 21, 561-572.	1.0	95
25	Generators of Phenotypic Diversity in the Evolution of Pathogenic Microorganisms. <i>PLoS Pathogens</i> , 2013, 9, e1003181.	2.1	37
26	<i>Cryptococcus gattii</i> , No Longer an Accidental Pathogen?. <i>Current Fungal Infection Reports</i> , 2012, 6, 245-256.	0.9	39
27	Photosynthetic microbial fuel cells with positive light response. <i>Biotechnology and Bioengineering</i> , 2009, 104, 939-946.	1.7	174