

# R Blake Billmyre

## List of Publications by Year in descending order

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Version: 2024-02-01

27  
papers

1,958  
citations

304743

22  
h-index

526287

27  
g-index

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, .	6.0	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.	12.8	73
3	A Novel Resistance Pathway for Calcineurin Inhibitors in the Human-Pathogenic Mucorales <i>Mucor circinelloides</i> . <i>MBio</i> , 2020, 11, .	4.1	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.	2.9	29
5	Gastrointestinal microbiota alteration induced by <i>Mucor circinelloides</i> in a murine model. <i>Journal of Microbiology</i> , 2019, 57, 509-520.	2.8	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.	3.5	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.	7.1	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.	2.9	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.	2.9	34
10	Identification of small RNAs in extracellular vesicles from the commensal yeast <i>Malassezia sympodialis</i> . <i>Scientific Reports</i> , 2017, 7, 39742.	3.3	69
11	Importance of Resolving Fungal Nomenclature: the Case of Multiple Pathogenic Species in the <i>Cryptococcus</i> Genus. <i>MSphere</i> , 2017, 2, .	2.9	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.	14.5	47
13	Fungal genome and mating system transitions facilitated by chromosomal translocations involving intercentromeric recombination. <i>PLoS Biology</i> , 2017, 15, e2002527.	5.6	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.	3.5	90
15	Genetic and epigenetic engines of diversity in pathogenic microbes. <i>PLoS Pathogens</i> , 2017, 13, e1006468.	4.7	7
16	Natural mismatch repair mutations mediate phenotypic diversity and drug resistance in <i>Cryptococcus deuterogattii</i> . <i>ELife</i> , 2017, 6, .	6.0	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.	3.5	43
18	Cancer-associated isocitrate dehydrogenase mutations induce mitochondrial DNA instability. <i>Human Molecular Genetics</i> , 2016, 25, 3524-3538.	2.9	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. MBio, 2014, 5, e01390-14.	4.1	106
20	Cryptococcus gattii VGIII Isolates Causing Infections in HIV/AIDS Patients in Southern California: Identification of the Local Environmental Source as Arboreal. PLoS Pathogens, 2014, 10, e1004285.	4.7	85
21	Analysis of the Genome and Transcriptome of Cryptococcus neoformans var. grubii Reveals Complex RNA Expression and Microevolution Leading to Virulence Attenuation. PLoS Genetics, 2014, 10, e1004261.	3.5	336
22	Unisexual Reproduction Drives Meiotic Recombination and Phenotypic and Karyotypic Plasticity in Cryptococcus neoformans. PLoS Genetics, 2014, 10, e1004849.	3.5	71
23	Highly Recombinant VGII Cryptococcus gattii Population Develops Clonal Outbreak Clusters through both Sexual Macroevolution and Asexual Microevolution. MBio, 2014, 5, e01494-14.	4.1	81
24	RNAi function, diversity, and loss in the fungal kingdom. Chromosome Research, 2013, 21, 561-572.	2.2	95
25	Generators of Phenotypic Diversity in the Evolution of Pathogenic Microorganisms. PLoS Pathogens, 2013, 9, e1003181.	4.7	37
26	Cryptococcus gattii, No Longer an Accidental Pathogen?. Current Fungal Infection Reports, 2012, 6, 245-256.	2.6	39
27	Photosynthetic microbial fuel cells with positive light response. Biotechnology and Bioengineering, 2009, 104, 939-946.	3.3	174