

JosÃ© F Muñoz

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

2,117
citations

236612

25
h-index

264894

42
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54
all docs

54
docs citations

54
times ranked

1793
citing authors

#	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	InÃvivo 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
3	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
4	Clade-specific chromosomal rearrangements and loss of subtelomeric adhesins in <i>Candida auris</i> . <i>Genetics</i> , 2021, 218, .	1.2	54
5	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
6	Best practices on the differential expression analysis of multi-species RNA-seq. <i>Genome Biology</i> , 2021, 22, 121.	3.8	51
7	<i>In Vitro</i> Antifungal Resistance of <i>Candida auris</i> Isolates from Bloodstream Infections, South Africa. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0051721.	1.4	38
8	Diversity, multifaceted evolution, and facultative saprotrophism in the European <i>Batrachochytrium salamandrivorans</i> epidemic. <i>Nature Communications</i> , 2021, 12, 6688.	5.8	11
9	Human Blastomycosis in South Africa Caused by <i>Blastomyces percursor</i> and <i>Blastomyces emzantsi</i> sp. nov., 1967 to 2014. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	35
10	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
11	Mitochondrial Genome Sequences of the Emerging Fungal Pathogen <i>Candida auris</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 560332.	1.5	6
12	Updates and Comparative Analysis of the Mitochondrial Genomes of <i>Paracoccidioides</i> spp. Using Oxford Nanopore MinION Sequencing. <i>Frontiers in Microbiology</i> , 2020, 11, 1751.	1.5	12
13	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
14	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
15	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
16	Tracing the Evolutionary History and Global Expansion of <i>Candida auris</i> Using Population Genomic Analyses. <i>MBio</i> , 2020, 11, .	1.8	224
17	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
18	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

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19	Emergomycetes: The global rise of new dimorphic fungal pathogens. PLoS Pathogens, 2019, 15, e1007977.	2.1	54
20	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
21	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
22	Genome analysis reveals evolutionary mechanisms of adaptation in systemic dimorphic fungi. Scientific Reports, 2018, 8, 4473.	1.6	28
23	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
24	Pathways of Pathogenicity: Transcriptional Stages of Germination in the Fatal Fungal Pathogen <i>Rhizopus delemar</i> . MSphere, 2018, 3, .	1.3	19
25	Draft Genome Sequences of Two <i>Sporothrix schenckii</i> Clinical Isolates Associated with Human Sporotrichosis in Colombia. Genome Announcements, 2018, 6, .	0.8	10
26	Phylogeny, ecology and taxonomy of systemic pathogens and their relatives in Ajellomycetaceae (Onygenales): Blastomyces, Emergomycetes, Emmonsia, Emmonsiiellosis. Fungal Diversity, 2018, 90, 245-291.	4.7	71
27	Paracoccidioides spp. catalases and their role in antioxidant defense against host defense responses. Fungal Genetics and Biology, 2017, 100, 22-32.	0.9	16
28	Novel taxa of thermally dimorphic systemic pathogens in the Ajellomycetaceae (Onygenales). Mycoses, 2017, 60, 296-309.	1.8	111
29	Genome Diversity, Recombination, and Virulence across the Major Lineages of <i>Paracoccidioides</i> . MSphere, 2016, 1, .	1.3	109
30	From NGS assembly challenges to instability of fungal mitochondrial genomes: A case study in genome complexity. Computational Biology and Chemistry, 2016, 61, 258-269.	1.1	13
31	Identification and Analysis of the Role of Superoxide Dismutases Isoforms in the Pathogenesis of <i>Paracoccidioides</i> spp.. PLoS Neglected Tropical Diseases, 2016, 10, e0004481.	1.3	58
32	The Dynamic Genome and Transcriptome of the Human Fungal Pathogen Blastomyces and Close Relative Emmonsia. PLoS Genetics, 2015, 11, e1005493.	1.5	57
33	50 Years of Emmonsia Disease in Humans: The Dramatic Emergence of a Cluster of Novel Fungal Pathogens. PLoS Pathogens, 2015, 11, e1005198.	2.1	57
34	Genome Update of the Dimorphic Human Pathogenic Fungi Causing Paracoccidioidomycosis. PLoS Neglected Tropical Diseases, 2014, 8, e3348.	1.3	38
35	<i>Paracoccidioides brasiliensis</i> PbP27 gene: knockdown procedures and functional characterization. FEMS Yeast Research, 2014, 14, 270-280.	1.1	17
36	The complex task of choosing a de novo assembly: Lessons from fungal genomes. Computational Biology and Chemistry, 2014, 53, 97-107.	1.1	6

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37	The eukaryotic genome, its reads, and the unfinished assembly. FEBS Letters, 2013, 587, 2090-2093.	1.3	3
38	Involvement of the 90kDa heat shock protein during adaptation of <i>Paracoccidioides brasiliensis</i> to different environmental conditions. Fungal Genetics and Biology, 2013, 51, 34-41.	0.9	35
39	Inhibition of PbGP43 Expression May Suggest that gp43 is a Virulence Factor in <i>Paracoccidioides brasiliensis</i> . PLoS ONE, 2013, 8, e68434.	1.1	43
40	RNAi technology targeting PbGP43 and PbP27 in <i>Paracoccidioides brasiliensis</i> . Open Journal of Genetics, 2013, 03, 1-8.	0.1	2
41	Differential PbP27 expression in the yeast and mycelial forms of the <i>Paracoccidioides brasiliensis</i> species complex. Fungal Genetics and Biology, 2011, 48, 1087-1095.	0.9	6