

Christopher A Desjardins

List of Publications by Year in descending order

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35
papers

5,437
citations

201385

27
h-index

360668

35
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docs citations

37
times ranked

8074
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	2.9	1,099
2	Functional and Evolutionary Insights from the Genomes of Three Parasitoid <i>Nasonia</i> Species. <i>Science</i> , 2010, 327, 343-348.	6.0	808
3	Comparative Functional Genomics of the Fission Yeasts. <i>Science</i> , 2011, 332, 930-936.	6.0	458
4	Comparative Genomics of Enterococci: Variation in <i>Enterococcus faecalis</i> , Clade Structure in <i>E. faecium</i> , and Defining Characteristics of <i>E. gallinarum</i> and <i>E. casseliflavus</i> . <i>MBio</i> , 2012, 3, e00318-11.	1.8	259
5	Genomic analysis of globally diverse <i>Mycobacterium tuberculosis</i> strains provides insights into the emergence and spread of multidrug resistance. <i>Nature Genetics</i> , 2017, 49, 395-402.	9.4	258
6	Evolution of Extensively Drug-Resistant Tuberculosis over Four Decades: Whole Genome Sequencing and Dating Analysis of <i>Mycobacterium tuberculosis</i> Isolates from KwaZulu-Natal. <i>PLoS Medicine</i> , 2015, 12, e1001880.	3.9	236
7	Microsporidian genome analysis reveals evolutionary strategies for obligate intracellular growth. <i>Genome Research</i> , 2012, 22, 2478-2488.	2.4	235
8	Ubiquitin-Mediated Response to Microsporidia and Virus Infection in <i>C. elegans</i> . <i>PLoS Pathogens</i> , 2014, 10, e1004200.	2.1	184
9	Genomics of <i>Loa loa</i> , a <i>Wolbachia</i> -free filarial parasite of humans. <i>Nature Genetics</i> , 2013, 45, 495-500.	9.4	173
10	Comparative Genomic Analysis of Human Fungal Pathogens Causing Paracoccidioidomycosis. <i>PLoS Genetics</i> , 2011, 7, e1002345.	1.5	164
11	Genomic and functional analyses of <i>Mycobacterium tuberculosis</i> strains implicate <i>ald</i> in D-cycloserine resistance. <i>Nature Genetics</i> , 2016, 48, 544-551.	9.4	145
12	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
13	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
14	The mushroom habitat as an ecological arena for global exchange of <i>Wolbachia</i> . <i>Molecular Ecology</i> , 2010, 19, 1940-1952.	2.0	118
15	Comparative and Functional Genomics of <i>Rhodococcus opacus</i> PD630 for Biofuels Development. <i>PLoS Genetics</i> , 2011, 7, e1002219.	1.5	109
16	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
17	Genome Evolution and Innovation across the Four Major Lineages of <i>Cryptococcus gattii</i> . <i>MBio</i> , 2015, 6, e00868-15.	1.8	101
18	SER-109, an Investigational Microbiome Drug to Reduce Recurrence After <i>Clostridioides difficile</i> Infection: Lessons Learned From a Phase 2 Trial. <i>Clinical Infectious Diseases</i> , 2021, 72, 2132-2140.	2.9	96

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19	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
20	Recombination and Its Impact on the Genome of the Haplodiploid Parasitoid Wasp <i>Nasonia</i> . <i>PLoS ONE</i> , 2010, 5, e8597.	1.1	66
21	Evolutionary Dynamics of the Accessory Genome of <i>Listeria monocytogenes</i> . <i>PLoS ONE</i> , 2013, 8, e67511.	1.1	63
22	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
23	Longitudinal multi-omics analyses link gut microbiome dysbiosis with recurrent urinary tract infections in women. <i>Nature Microbiology</i> , 2022, 7, 630-639.	5.9	54
24	Whole-Genome Sequencing of <i>Mycobacterium tuberculosis</i> Provides Insight into the Evolution and Genetic Composition of Drug-Resistant Tuberculosis in Belarus. <i>Journal of Clinical Microbiology</i> , 2017, 55, 457-469.	1.8	47
25	Baeyer-Villiger Monooxygenases EthA and MymA Are Required for Activation of Replicating and Non-replicating <i>Mycobacterium tuberculosis</i> Inhibitors. <i>Cell Chemical Biology</i> , 2016, 23, 666-677.	2.5	46
26	Whole Genome Sequencing of <i>Mycobacterium africanum</i> Strains from Mali Provides Insights into the Mechanisms of Geographic Restriction. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004332.	1.3	41
27	Phylogeny of pteromalid parasitic wasps (Hymenoptera: Pteromalidae): Initial evidence from four protein-coding nuclear genes. <i>Molecular Phylogenetics and Evolution</i> , 2007, 45, 454-469.	1.2	34
28	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
29	Extensive global movement of multidrug-resistant <i>M. tuberculosis</i> strains revealed by whole-genome analysis. <i>Thorax</i> , 2019, 74, 882-889.	2.7	24
30	Landscape of gene expression variation of natural isolates of <i>Cryptococcus neoformans</i> in response to biologically relevant stresses. <i>Microbial Genomics</i> , 2020, 6, .	1.0	24
31	Limited effects of long-term daily cranberry consumption on the gut microbiome in a placebo-controlled study of women with recurrent urinary tract infections. <i>BMC Microbiology</i> , 2021, 21, 53.	1.3	21
32	Genomic Analysis of the Evolution of Fluoroquinolone Resistance in <i>Mycobacterium tuberculosis</i> Prior to Tuberculosis Diagnosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6600-6608.	1.4	19
33	Epidemiologic Investigation of a Cluster of Neuroinvasive <i>Bacillus cereus</i> Infections in 5 Patients With Acute Myelogenous Leukemia. <i>Open Forum Infectious Diseases</i> , 2015, 2, ofv096.	0.4	13
34	Fatal Nosocomial MDR TB Identified through Routine Genetic Analysis and Whole-Genome Sequencing. <i>Emerging Infectious Diseases</i> , 2015, 21, 1082-1084.	2.0	12
35	High quality draft genome sequence of <i>Segniliparus rugosus</i> CDC 945T= (ATCC BAA-974T). <i>Standards in Genomic Sciences</i> , 2011, 5, 389-397.	1.5	6