

Massimo Cigliati

List of Publications by Year in descending order

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49

papers

2,083

citations

331670

21

h-index

243625

44

g-index

51

all docs

51

docs citations

51

times ranked

1701

citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Trichophyton tonsurans</i> in Chile: Genotyping in search of an origin. Medical Mycology, 2022, 60, .	0.7	3
2	Azole resistance in <i>Aspergillus</i> isolates by different types of patients and correlation with environment – An Italian prospective multicentre study (ARIa study). Mycoses, 2021, 64, 528-536.	4.0	9
3	Global warming impact on the expansion of fundamental niche of <i>Cryptococcus gattii</i> VGI in Europe. Environmental Microbiology Reports, 2021, 13, 375-383.	2.4	19
4	The need for environmental surveillance to understand the ecology, epidemiology and impact of <i>Cryptococcus</i> infection in Africa. FEMS Microbiology Ecology, 2021, 97, .	2.7	9
5	Multi-locus sequence typing reveals genotypic similarity in Nigerian Cryptococcus neoformans AFLP1/VNI of environmental and clinical origin. Journal of Medical Microbiology, 2021, 70, .	1.8	2
6	Spatial Quantification of the Population Exposed to Cryptococcus neoformans and Cryptococcus gattii Species Complexes in Europe: Estimating the Immunocompetent and HIV/AIDS Patients Under Risk. Risk Analysis, 2020, 40, 524-533.	2.7	10
7	First Autochthonous Case of Cryptococcal Meningitis in an Immunocompetent Host Due to Cryptococcus gattii VGI in Northern Italy. SN Comprehensive Clinical Medicine, 2020, 2, 237-241.	0.6	2
8	Cryptococcus gattii infection in an immunocompetent host in Greece. Medical Mycology Case Reports, 2020, 27, 1-3.	1.3	22
9	Cryptococcus neoformans species complex isolates living in a tree micro-ecosystem. Fungal Ecology, 2020, 44, 100889.	1.6	4
10	Expansion of the Emerging Fungal Pathogen Cryptococcus bacillisporus Into America: Linking Phylogenetic Origin, Geographical Spread and Population Under Exposure Risk. Frontiers in Microbiology, 2020, 11, 2117.	3.5	7
11	New multilocus sequence typing primers to enable genotyping of AD hybrids within the Cryptococcus neoformans species complex. Medical Mycology, 2020, 58, 1005-1009.	0.7	4
12	Epidemiological characteristics of cryptococcal meningoencephalitis associated with Cryptococcus neoformans var. grubii from HIV-infected patients in Madagascar: A cross-sectional study. PLoS Neglected Tropical Diseases, 2020, 14, e0007984.	3.0	10
13	Molecular-Type Specific Multiplex PCR produces a distinct VNII PCR pattern among Cryptococcus neoformans species complex. Medical Mycology, 2019, 57, 384-386.	0.7	5
14	Comment on: T2Candida MR as a predictor of outcome in patients with suspected invasive candidiasis starting empirical antifungal treatment: a prospective pilot study. Journal of Antimicrobial Chemotherapy, 2019, 74, 532-533.	3.0	3
15	Cryptococcus neoformans and Cryptococcus gattii Species Complex Isolates on the Slopes of Mount Etna, SICILY, Italy. Frontiers in Microbiology, 2019, 10, 2390.	3.5	4
16	Genotypes and population genetics of cryptococcus neoformans and cryptococcus gattii species complexes in Europe and the mediterranean area. Fungal Genetics and Biology, 2019, 129, 16-29.	2.1	37
17	First Isolation, Antifungal Susceptibility, and Molecular Characterization of Cryptococcus neoformans from the Environment in Croatia. Journal of Fungi (Basel, Switzerland), 2019, 5, 99.	3.5	4
18	Epidemiological trends of cryptococcosis in Italy: Molecular typing and susceptibility pattern of Cryptococcus neoformans isolates collected during a 20-year period. Medical Mycology, 2018, 56, 963-971.	0.7	12

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19	Molecular characterization of <i>Cryptococcus neoformans</i> and <i>Cryptococcus gattii</i> from environmental sources and genetic comparison with clinical isolates in Apulia, Italy. Environmental Research, 2018, 160, 347-352.	7.5	24
20	Genetic Factors and Genotype-Environment Interactions Contribute to Variation in Melanin Production in the Fungal Pathogen <i>Cryptococcus neoformans</i> . Scientific Reports, 2018, 8, 9824.	3.3	16
21	Determining the analytical specificity of PCR-based assays for the diagnosis of IA: What is <i>Aspergillus</i> ? Medical Mycology, 2017, 55, myw093.	0.7	24
22	The Case for Adopting the "Species Complex" Nomenclature for the Etiologic Agents of Cryptococcosis. MSphere, 2017, 2, .	2.9	274
23	First report of two cases of cryptococcosis in Tripoli, Libya, infected with <i>Cryptococcus neoformans</i> isolates present in the urban area. Journal De Mycologie Medicale, 2017, 27, 421-424.	1.5	9
24	Fundamental niche prediction of the pathogenic yeasts <i>Cryptococcus neoformans</i> and <i>Cryptococcus gattii</i> in Europe. Environmental Microbiology, 2017, 19, 4318-4325.	3.8	44
25	MLST-Based Population Genetic Analysis in a Global Context Reveals Clonality amongst <i>Cryptococcus neoformans</i> var. <i>grubii</i> VNI Isolates from HIV Patients in Southeastern Brazil. PLoS Neglected Tropical Diseases, 2017, 11, e0005223.	3.0	59
26	Environmental distribution of <i>Cryptococcus neoformans</i> and <i>C. gattii</i> around the Mediterranean basin. FEMS Yeast Research, 2016, 16, fow045.	2.3	57
27	Molecular characterization of environmental <i>Cryptococcus neoformans</i> VNII isolates in Jos, Plateau State, Nigeria. Journal De Mycologie Medicale, 2016, 26, 306-311.	1.5	16
28	Multilocus sequence typing analysis reveals that <i>Cryptococcus neoformans</i> var. <i>neoformans</i> is a recombinant population. Fungal Genetics and Biology, 2016, 87, 22-29.	2.1	34
29	Isolation, Identification and Molecular Typing of <i>Cryptococcus neoformans</i> from Pigeon Droppings and Other Environmental Sources in Tripoli, Libya. Mycopathologia, 2016, 181, 603-608.	3.1	29
30	Azole Resistance in <i>Aspergillus fumigatus</i> Clinical Isolates from an Italian Culture Collection. Antimicrobial Agents and Chemotherapy, 2016, 60, 682-685.	3.2	32
31	Identification and Characterization of VNI/VNII and Novel VNII/VNIV Hybrids and Impact of Hybridization on Virulence and Antifungal Susceptibility Within the <i>C. neoformans/C. gattii</i> Species Complex. PLoS ONE, 2016, 11, e0163955.	2.5	12
32	<i>Cryptococcus gattii</i> sero-mating type allelic pattern determined by multiplex PCR. Clinical Microbiology and Infection, 2015, 21, 190.e1-190.e4.	6.0	7
33	Multilocus sequence typing (MLST) and M13 PCR fingerprinting revealed heterogeneity amongst <i>Cryptococcus</i> species obtained from Italian veterinary isolates. FEMS Yeast Research, 2014, 14, 897-909.	2.3	36
34	A case of <i>Histoplasma capsulatum</i> endophthalmitis diagnosed in Italy. Travel Medicine and Infectious Disease, 2013, 11, 256-258.	3.0	3
35	Molecular epidemiology of Italian clinical <i>Cryptococcus neoformans</i> var. <i>grubii</i> isolates. Medical Mycology, 2013, 51, 499-506.	0.7	33
36	Global Molecular Epidemiology of <i>Cryptococcus neoformans</i> and <i>Cryptococcus gattii</i> : An Atlas of the Molecular Types. Scientifica, 2013, 2013, 1-23.	1.7	226

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37	Autochthonous and Dormant <i>Cryptococcus gattii</i> Infections in Europe. <i>Emerging Infectious Diseases</i> , 2012, 18, 1618-1624.	4.3	132
38	Matrix-Assisted Laser Desorption Ionization-â€“Time of Flight Mass Spectrometry-Based Method for Discrimination between Molecular Types of <i>Cryptococcus neoformans</i> and <i>Cryptococcus gattii</i> . <i>Journal of Clinical Microbiology</i> , 2012, 50, 2472-2476.	3.9	87
39	Heterozygosity and Pathogenicity of <i>Cryptococcus neoformans</i> AD-Hybrid Isolates. <i>Mycopathologia</i> , 2012, 173, 347-357.	3.1	20
40	< i> <i>Cryptococcus gattii</i> serotype C strains isolated in Bangalore, Karnataka, India. <i>Mycoses</i> , 2012, 55, 262-268.	4.0	25
41	Electrophoretic karyotyping of < i> <i>Cryptococcus neoformans</i> AD-hybrid strains. <i>Mycoses</i> , 2009, 52, 16-23.	4.0	5
42	Consensus multi-locus sequence typing scheme for < i> <i>Cryptococcus neoformans</i> and < i> <i>Cryptococcus gattii</i> . <i>Medical Mycology</i> , 2009, 47, 561-570.	0.7	408
43	< i> <i>Cryptococcus neoformans</i> Typing by PCR Fingerprinting Using (GACA) ₄ Primers Based on < i> <i>C. neoformans</i> Genome Project Data. <i>Journal of Clinical Microbiology</i> , 2007, 45, 3427-3430.	3.9	6
44	Molecular analysis of 311 <i>Cryptococcus neoformans</i> isolates from a 30-month ECMM survey of cryptococcosis in Europe. <i>FEMS Yeast Research</i> , 2006, 6, 614-619.	2.3	134
45	<i>Cryptococcus neoformans</i> population includes hybrid strains homozygous at mating-type locus. <i>FEMS Yeast Research</i> , 2006, 6, 608-613.	2.3	39
46	Four-Year Persistence of a Single <i>Candida albicans</i> Genotype Causing Bloodstream Infections in a Surgical Ward Proven by Multilocus Sequence Typing. <i>Journal of Clinical Microbiology</i> , 2006, 44, 218-221.	3.9	24
47	Origin of <i>Cryptococcus neoformans</i> var. <i>neoformans</i> Diploid Strains. <i>Journal of Clinical Microbiology</i> , 2001, 39, 3889-3894.	3.9	73
48	Comparison of Three Methods for Testing Azole Susceptibilities of < i> <i>Candida albicans</i> Strains Isolated Sequentially from Oral Cavities of AIDS Patients. <i>Journal of Clinical Microbiology</i> , 1998, 36, 1578-1583.	3.9	17
49	Hybridization and Its Importance in the <i>Cryptococcus</i> Species Complex. , 0, , 359-370.		2