

Wieland Meyer

List of Publications by Year in descending order

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216
papers

17,090
citations

20036

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123
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docs citations

227
times ranked

14576
citing authors

#	ARTICLE	IF	CITATIONS
1	In depth search of the Sequence Read Archive database reveals global distribution of the emerging pathogenic fungus <i>Scedosporium aurantiacum</i> . Medical Mycology, 2022, 60, .	0.3	2
2	Recent Advances in Cryptococcus and Cryptococcosis. Microorganisms, 2022, 10, 13.	1.6	10
3	Inferring Species Compositions of Complex Fungal Communities from Long- and Short-Read Sequence Data. MBio, 2022, 13, e0244421.	1.8	2
4	A Possible Link between the Environment and Cryptococcus gattii Nasal Colonisation in Koalas (Phascolarctos cinereus) in the Liverpool Plains, New South Wales. International Journal of Environmental Research and Public Health, 2022, 19, 4603.	1.2	2
5	Host transmission dynamics of first- and third-stage <i>Angiostrongylus cantonensis</i> larvae in <i>Bullastra lessoni</i> . Parasitology, 2022, 149, 1034-1044.	0.7	5
6	Finding a Needle in a Haystack – In Silico Search for Environmental Traces of <i>Candida auris</i> . Japanese Journal of Infectious Diseases, 2022, 75, 490-495.	0.5	8
7	Environmental Isolation of Sporothrix brasiliensis in an Area With Recurrent Feline Sporotrichosis Cases. Frontiers in Cellular and Infection Microbiology, 2022, 12, .	1.8	11
8	Clinical epidemiology and high genetic diversity amongst Cryptococcus spp. isolates infecting people living with HIV in Kinshasa, Democratic Republic of Congo. PLoS ONE, 2022, 17, e0267842.	1.1	3
9	Molecular type distribution and fluconazole susceptibility of clinical Cryptococcus gattii isolates from South African laboratory-based surveillance, 2005–2013. PLoS Neglected Tropical Diseases, 2022, 16, e0010448.	1.3	1
10	Fungal taxonomy and sequence-based nomenclature. Nature Microbiology, 2021, 6, 540-548.	5.9	101
11	Genotype, Antifungal Susceptibility, and Virulence of Clinical South African Cryptococcus neoformans Strains from National Surveillance, 2005–2009. Journal of Fungi (Basel, Switzerland), 2021, 7, 338.	1.5	5
12	Cryptococcus neoformans and Cryptococcus gattii Species Complexes in Latin America: A Map of Molecular Types, Genotypic Diversity, and Antifungal Susceptibility as Reported by the Latin American Cryptococcal Study Group. Journal of Fungi (Basel, Switzerland), 2021, 7, 282.	1.5	20
13	Nomenclatural issues concerning cultured yeasts and other fungi: why it is important to avoid unneeded name changes. IMA Fungus, 2021, 12, 18.	1.7	13
14	Scedosporium and Lomentospora Infections: Contemporary Microbiological Tools for the Diagnosis of Invasive Disease. Journal of Fungi (Basel, Switzerland), 2021, 7, 23.	1.5	37
15	Cryptococcus gattii Species Complex as an Opportunistic Pathogen: Underlying Medical Conditions Associated with the Infection. MBio, 2021, 12, e0270821.	1.8	25
16	<i>Pneumocystis jirovecii</i> genetic diversity in a Spanish tertiary hospital. Medical Mycology, 2021, 60, .	0.3	1
17	Long-Reads-Based Metagenomics in Clinical Diagnosis With a Special Focus on Fungal Infections. Frontiers in Microbiology, 2021, 12, 708550.	1.5	9
18	Consensus guidelines for the diagnosis and management of invasive fungal disease due to moulds other than <i>Aspergillus</i> in the haematology/oncology setting, 2021. Internal Medicine Journal, 2021, 51, 177-219.	0.5	25

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19	Multilocus Sequence Typing Reveals Extensive Genetic Diversity of the Emerging Fungal Pathogen <i>Scedosporium aurantiacum</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 761596.	1.8	4
20	Long-read sequencing based clinical metagenomics for the detection and confirmation of <i>Pneumocystis jirovecii</i> directly from clinical specimens: A paradigm shift in mycological diagnostics. <i>Medical Mycology</i> , 2020, 58, 650-660.	0.3	28
21	Unambiguous identification of fungi: where do we stand and how accurate and precise is fungal DNA barcoding?. <i>IMA Fungus</i> , 2020, 11, 14.	1.7	232
22	Molecular Epidemiology Reveals Low Genetic Diversity among <i>Cryptococcus neoformans</i> Isolates from People Living with HIV in Lima, Peru, during the Pre-HAART Era. <i>Pathogens</i> , 2020, 9, 665.	1.2	7
23	Rearing and Maintenance of <i>Galleria mellonella</i> and Its Application to Study Fungal Virulence. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 130.	1.5	32
24	Consensus Multilocus Sequence Typing Scheme for <i>Pneumocystis jirovecii</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 130.	1.5	32
25	Indoor Dust as a Source of Virulent Strains of the Agents of Cryptococcosis in the Rio Negro Micro-Region of the Brazilian Amazon. <i>Microorganisms</i> , 2020, 8, 682.	1.6	8
26	Genetic Heterogeneity of Australian <i>Candida auris</i> Isolates: Insights From a Nonoutbreak Setting Using Whole-Genome Sequencing. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa158.	0.4	12
27	New multilocus sequence typing primers to enable genotyping of AD hybrids within the <i>Cryptococcus neoformans</i> species complex. <i>Medical Mycology</i> , 2020, 58, 1005-1009.	0.3	4
28	Molecular Detection of Antimalarial Drug Resistance in <i>Plasmodium vivax</i> from Returned Travellers to NSW, Australia during 2008–2018. <i>Pathogens</i> , 2020, 9, 101.	1.2	8
29	CCMetagen: comprehensive and accurate identification of eukaryotes and prokaryotes in metagenomic data. <i>Genome Biology</i> , 2020, 21, 103.	3.8	91
30	Molecular detection of <i>Pneumocystis</i> in the lungs of cats. <i>Medical Mycology</i> , 2019, 57, 813-824.	0.3	6
31	Molecular detection of drug resistant malaria in Southern Thailand. <i>Malaria Journal</i> , 2019, 18, 275.	0.8	28
32	Metatranscriptomics as a tool to identify fungal species and subspecies in mixed communities – a proof of concept under laboratory conditions. <i>IMA Fungus</i> , 2019, 10, 12.	1.7	20
33	Effect of peptidases secreted by the opportunistic pathogen <i>Scedosporium aurantiacum</i> on human epithelial cells. <i>Canadian Journal of Microbiology</i> , 2019, 65, 814-822.	0.8	4
34	The mycobiome of Australian tree hollows in relation to the <i>Cryptococcus gattii</i> and <i>C. neoformans</i> species complexes. <i>Ecology and Evolution</i> , 2019, 9, 9684-9700.	0.8	7
35	Dual DNA Barcoding for the Molecular Identification of the Agents of Invasive Fungal Infections. <i>Frontiers in Microbiology</i> , 2019, 10, 1647.	1.5	40
36	Identification of the environmental source of infection for a domestic ferret with cryptococcosis. <i>Journal of Veterinary Diagnostic Investigation</i> , 2019, 31, 828-835.	0.5	6

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37	Jet-Setting Koalas Spread <i>Cryptococcus gattii</i> VGII in Australia. <i>MSphere</i> , 2019, 4, .	1.3	8
38	Clonal Dispersal of <i>Cryptococcus gattii</i> VGII in an Endemic Region of Cryptococcosis in Colombia. <i>Journal of Fungi</i> (Basel, Switzerland), 2019, 5, 32.	1.5	10
39	A novel multilocus sequence typing scheme identifying genetic diversity amongst <i>Leishmania donovani</i> isolates from a genetically homogeneous population in the Indian subcontinent. <i>International Journal for Parasitology</i> , 2019, 49, 555-567.	1.3	15
40	Cryptococcosis due to <i>Cryptococcus gattii</i> VGII in southeast Brazil: The One Health approach revealing a possible role for domestic cats. <i>Medical Mycology Case Reports</i> , 2019, 24, 61-64.	0.7	9
41	Interactions of an Emerging Fungal Pathogen <i>Scedosporium aurantiacum</i> with Human Lung Epithelial Cells. <i>Scientific Reports</i> , 2019, 9, 5035.	1.6	11
42	Genotypes and population genetics of <i>cryptococcus neoformans</i> and <i>cryptococcus gattii</i> species complexes in Europe and the mediterranean area. <i>Fungal Genetics and Biology</i> , 2019, 129, 16-29.	0.9	37
43	Genetic differences in <i>Chlamydia pecorum</i> between neighbouring sub-populations of koalas (<i>Phascolarctos cinereus</i>). <i>Veterinary Microbiology</i> , 2019, 231, 264-270.	0.8	14
44	A New Lineage of <i>Cryptococcus gattii</i> (VGV) Discovered in the Central Zambezi Miombo Woodlands. <i>MBio</i> , 2019, 10, .	1.8	66
45	Preliminary study of the oral mycobiome of children with and without dental caries. <i>Journal of Oral Microbiology</i> , 2019, 11, 1536182.	1.2	30
46	Database establishment for the secondary fungal DNA barcode<i>translational elongation factor 1 \pm </i> (<i>TEF1 \pm </i>). <i>Genome</i> , 2019, 62, 160-169.	0.9	41
47	Prevalence of cryptococcal antigenemia and nasal colonization in a free-ranging koala population. <i>Medical Mycology</i> , 2019, 57, 848-857.	0.3	15
48	Prevalence, geographic risk factor, and development of a standardized protocol for fungal isolation in cystic fibrosis: Results from the international prospective study &œMFIP&œ. <i>Journal of Cystic Fibrosis</i> , 2019, 18, 212-220.	0.3	38
49	Multi-locus sequence typing as a tool to investigate environmental sources of infection for cryptococcosis in captive birds. <i>Medical Mycology</i> , 2019, 57, 653-657.	0.3	3
50	A New Age in Molecular Diagnostics for Invasive Fungal Disease: Are We Ready?. <i>Frontiers in Microbiology</i> , 2019, 10, 2903.	1.5	94
51	Australian medical mycology culture collections: fundamental resources for mycological diagnosis and research. <i>Microbiology Australia</i> , 2019, 40, 130.	0.1	0
52	Cryptococcosis in the koala (<i>Phascolarctos cinereus</i>): pathogenesis and treatment in the context of two atypical cases. <i>Medical Mycology</i> , 2018, 56, 926-936.	0.3	7
53	Dating the <i>Cryptococcus gattii</i> Dispersal to the North American Pacific Northwest. <i>MSphere</i> , 2018, 3, .	1.3	20
54	Biological, biochemical and molecular aspects of <i>Scedosporium aurantiacum</i> , a primary and opportunistic fungal pathogen. <i>Fungal Biology Reviews</i> , 2018, 32, 156-165.	1.9	4

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55	Evolutionary ARMS Race: Antimalarial Resistance Molecular Surveillance. Trends in Parasitology, 2018, 34, 322-334.	1.5	9
56	Developing collaborative works for faster progress on fungal respiratory infections in cystic fibrosis. Medical Mycology, 2018, 56, S42-S59.	0.3	27
57	Scedosporium and Lomentospora: an updated overview of underrated opportunists. Medical Mycology, 2018, 56, S102-S125.	0.3	186
58	Pseudomonas aeruginosa Inhibits the Growth of Scedosporium and Lomentospora In Vitro. Mycopathologia, 2018, 183, 251-261.	1.3	32
59	Challenges in Laboratory Detection of Fungal Pathogens in the Airways of Cystic Fibrosis Patients. Mycopathologia, 2018, 183, 89-100.	1.3	21
60	Whole Genome Sequencing of Australian Candida glabrata Isolates Reveals Genetic Diversity and Novel Sequence Types. Frontiers in Microbiology, 2018, 9, 2946.	1.5	31
61	Resistance screening and trend analysis of imported falciparum malaria in NSW, Australia (2010 to) Tj ETQq1 1 0.784314 rgBT /Overl	1.1	13
62	Flucytosine resistance in <i>Cryptococcus gattii</i> is indirectly mediated by the FCY2-FCY1-FUR1 pathway. Medical Mycology, 2018, 56, 857-867.	0.3	18
63	Molecular identification and antifungal susceptibility profiles of clinical strains of Fonsecaea spp. isolated from patients with chromoblastomycosis in Rio de Janeiro, Brazil. PLoS Neglected Tropical Diseases, 2018, 12, e0006675.	1.3	23
64	Taxonomic annotation of public fungal ITS sequences from the built environment – a report from an April 10–11, 2017 workshop (Aberdeen, UK). MycoKeys, 2018, 28, 65-82.	0.8	33
65	NGS barcode sequencing in taxonomy and diagnostics, an application in <i>Candida</i> -pathogenic yeasts with a metagenomic perspective. IMA Fungus, 2018, 9, 91-105.	1.7	20
66	Growth and protease secretion of Scedosporium aurantiacum under conditions of hypoxia. Microbiological Research, 2018, 216, 23-29.	2.5	5
67	Identification of 14- β -Lanosterol Demethylase (CYP51) in Scedosporium Species. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	8
68	Challenges in Laboratory Detection of Fungal Pathogens in the Airways of Cystic Fibrosis Patients. , 2018, 183, 89.		1
69	Genotypic analysis of clinical and environmental Cryptococcus neoformans isolates from Brazil reveals the presence of VNB isolates and a correlation with biological factors. PLoS ONE, 2018, 13, e0193237.	1.1	41
70	The Case for Adopting the <i>Species Complex</i> Nomenclature for the Etiologic Agents of Cryptococcosis. MSphere, 2017, 2, .	1.3	274
71	Online Databases for Taxonomy and Identification of Pathogenic Fungi and Proposal for a Cloud-Based Dynamic Data Network Platform. Journal of Clinical Microbiology, 2017, 55, 1011-1024.	1.8	43
72	Molecular diagnosis of Pneumocystis pneumonia in dogs. Medical Mycology, 2017, 55, 828-842.	0.3	28

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73	Fundamental niche prediction of the pathogenic yeasts <i>Cryptococcus neoformans</i> and <i>Cryptococcus gattii</i> in Europe. <i>Environmental Microbiology</i> , 2017, 19, 4318-4325.	1.8	44
74	Advances in the understanding of the <i>Cryptococcus neoformans</i> and <i>C. gattii</i> species complexes and cryptococcosis. <i>Microbiology Australia</i> , 2017, 38, 106.	0.1	1
75	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
76	Furthering the Continental Drift Speciation Hypothesis in the Pathogenic <i>Cryptococcus</i> Species Complexes. <i>MSphere</i> , 2017, 2, .	1.3	6
77	Fungal Contaminants in Drinking Water Regulation? A Tale of Ecology, Exposure, Purification and Clinical Relevance. <i>International Journal of Environmental Research and Public Health</i> , 2017, 14, 636.	1.2	109
78	Differential Antifungal Activity of Human and Cryptococcal Melanins with Structural Discrepancies. <i>Frontiers in Microbiology</i> , 2017, 8, 1292.	1.5	24
79	Preheating of urine improves the specificity of urinary cryptococcal antigen testing using the lateral flow assay. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005304.	1.3	7
80	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. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005223.	1.3	59
81	Cytokine patterns in a prospective cohort of HIV-infected patients with cryptococcal meningitis following initiation of antifungal and antiretroviral therapy. <i>PLoS ONE</i> , 2017, 12, e0176304.	1.1	11
82	Detection of <i>Leishmania donovani</i> in peripheral blood of asymptomatic individuals in contact with patients with visceral leishmaniasis. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2016, 110, 286-293.	0.7	14
83	Environmental distribution of <i>Cryptococcus neoformans</i> and <i>C. gattii</i> around the Mediterranean basin. <i>FEMS Yeast Research</i> , 2016, 16, fow045.	1.1	57
84	Exploring ecological modelling to investigate factors governing the colonization success in nosocomial environment of <i>Candida albicans</i> and other pathogenic yeasts. <i>Scientific Reports</i> , 2016, 6, 26860.	1.6	19
85	Stimulation with lysates of <i>Aspergillus terreus</i> , <i>Candida krusei</i> and <i>Rhizopus oryzae</i> maximizes cross-reactivity of anti-fungal T cells. <i>Cytotherapy</i> , 2016, 18, 65-79.	0.3	18
86	DNA barcoding of fungi causing infections in humans and animals. <i>Fungal Biology</i> , 2016, 120, 125-136.	1.1	67
87	MLST and Whole-Genome-Based Population Analysis of <i>Cryptococcus gattii</i> VGIII Links Clinical, Veterinary and Environmental Strains, and Reveals Divergent Serotype Specific Sub-populations and Distant Ancestors. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004861.	1.3	49
88	Population Genetic Analysis Reveals a High Genetic Diversity in the Brazilian <i>Cryptococcus gattii</i> VGII Population and Shifts the Global Origin from the Amazon Rainforest to the Semi-arid Desert in the Northeast of Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004885.	1.3	52
89	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</i> / <i>C. gattii</i> Species Complex. <i>PLoS ONE</i> , 2016, 11, e0163955.	1.1	12
90	Medical and veterinary mycology. <i>Microbiology Australia</i> , 2015, 36, 42.	0.1	0

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91	Colonisation with <i>Pneumocystis jirovecii</i> in Australian infants. <i>Pathology</i> , 2015, 47, 489-490.	0.3	2
92	Pathogenic diversity amongst serotype C VGIII and VGIV <i>Cryptococcus gattii</i> isolates. <i>Scientific Reports</i> , 2015, 5, 11717.	1.6	15
93	<i>Cryptococcus gattii</i> in the Age of Whole-Genome Sequencing. <i>MBio</i> , 2015, 6, e01761-15.	1.8	16
94	Draft Genome of Australian Environmental Strain WM 09.24 of the Opportunistic Human Pathogen <i>Scedosporium aurantiacum</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	21
95	Environmental Isolation of <i>Cryptococcus gattii</i> VGII from Indoor Dust from Typical Wooden Houses in the Deep Amazonas of the Rio Negro Basin. <i>PLoS ONE</i> , 2015, 10, e0115866.	1.1	42
96	Phenotypic Profiling of <i>Scedosporium aurantiacum</i> , an Opportunistic Pathogen Colonizing Human Lungs. <i>PLoS ONE</i> , 2015, 10, e0122354.	1.1	22
97	Invasive infections due to filamentous fungi other than <i>Aspergillus</i> : epidemiology and determinants of mortality. <i>Clinical Microbiology and Infection</i> , 2015, 21, 490.e1-490.e10.	2.8	129
98	Australia in the global picture of the molecular epidemiology of <i>Cryptococcus gattii</i> molecular type VGII. <i>Microbiology Australia</i> , 2015, 36, 67.	0.1	3
99	International Society of Human and Animal Mycology (ISHAM)-ITS reference DNA barcoding database—the quality controlled standard tool for routine identification of human and animal pathogenic fungi. <i>Medical Mycology</i> , 2015, 53, 313-337.	0.3	252
100	Fatal Case of Polymicrobial Meningitis Caused by <i>Cryptococcus liquefaciens</i> and <i>Mycobacterium tuberculosis</i> Complex in a Human Immunodeficiency Virus-Infected Patient. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2753-2755.	1.8	16
101	Commentaries: Name Changes in Medically Important Fungi and Their Implications for Clinical Practice. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1056-1062.	1.8	65
102	DNA barcoding of human and animal pathogenic fungi: the ISHAM-ITS database. <i>Microbiology Australia</i> , 2015, 36, 44.	0.1	1
103	The Westmead Medical Mycology Collection: basis for research and diagnosis of fungal diseases. <i>Microbiology Australia</i> , 2015, 36, 60.	0.1	0
104	<i>Galleria mellonella</i> Model Identifies Highly Virulent Strains among All Major Molecular Types of <i>Cryptococcus gattii</i> . <i>PLoS ONE</i> , 2014, 9, e105076.	1.1	56
105	<i>Cryptococcus gattii</i> in North American Pacific Northwest: Whole-Population Genome Analysis Provides Insights into Species Evolution and Dispersal. <i>MBio</i> , 2014, 5, e01464-14.	1.8	126
106	Draft Genome Sequence of the Pathogenic Fungus <i>Scedosporium apiospermum</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	42
107	Retrospective Study of the Epidemiology and Clinical Manifestations of <i>Cryptococcus gattii</i> Infections in Colombia from 1997–2011. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3272.	1.3	51
108	Phenotypic Differences of <i>Cryptococcus</i> Molecular Types and Their Implications for Virulence in a <i>Drosophila</i> Model of Infection. <i>Infection and Immunity</i> , 2014, 82, 3058-3065.	1.0	33

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109	Insights on the Genotype Distribution Among <i>Cryptococcus neoformans</i> and <i>C. gattii</i> Portuguese Clinical Isolates. <i>Current Microbiology</i> , 2014, 68, 199-203.	1.0	11
110	Proposed nomenclature for <i>Pseudallescheria</i> , <i>Scedosporium</i> and related genera. <i>Fungal Diversity</i> , 2014, 67, 1-10.	4.7	152
111	<i>Cryptococcus gattii</i> Infections. <i>Clinical Microbiology Reviews</i> , 2014, 27, 980-1024.	5.7	327
112	MALDI-TOF MS for the identification of veterinary non- <i>C. neoformans</i> - <i>C. gattii</i> <i>Cryptococcus</i> spp. isolates from Italy. <i>Medical Mycology</i> , 2014, 52, 659-666.	0.3	4
113	Current Status in Diagnosis of <i>Scedosporium</i> Infections: What Is the Impact of New Molecular Methods?. <i>Current Fungal Infection Reports</i> , 2014, 8, 220-226.	0.9	2
114	The Genus <i>Scedosporium</i> and <i>Pseudallescheria</i> : Current Challenges in Laboratory Diagnosis. <i>Current Clinical Microbiology Reports</i> , 2014, 1, 27-36.	1.8	9
115	Multilocus sequence typing (MLST) and M13 PCR fingerprinting revealed heterogeneity amongst <i>Cryptococcus</i> species obtained from Italian veterinary isolates. <i>FEMS Yeast Research</i> , 2014, 14, 897-909.	1.1	36
116	Antifungal Drug Susceptibility and Phylogenetic Diversity among <i>Cryptococcus</i> Isolates from Dogs and Cats in North America. <i>Journal of Clinical Microbiology</i> , 2014, 52, 2061-2070.	1.8	40
117	Molecular Typing of the <i>Cryptococcus neoformans</i> / <i>Cryptococcus gattii</i> Species Complex. , 2014, , 327-357.		18
118	Finding needles in haystacks: linking scientific names, reference specimens and molecular data for Fungi. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau061-bau061.	1.4	272
119	Hospital-acquired <i>Pneumocystis pneumonia</i> : a renewed concern?. <i>Microbiology Australia</i> , 2014, 35, 57.	0.1	1
120	Identification of the Major Molecular Types of <i>Cryptococcus neoformans</i> and <i>C. gattii</i> by Hyperbranched Rolling Circle Amplification. <i>PLoS ONE</i> , 2014, 9, e94648.	1.1	39
121	Taxonomy of medically important fungi in the molecular era. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 385-386.	4.6	31
122	MycoBank gearing up for new horizons. <i>IMA Fungus</i> , 2013, 4, 371-379.	1.7	170
123	Molecular Epidemiology Reveals Genetic Diversity amongst Isolates of the <i>Cryptococcus neoformans</i> / <i>C. gattii</i> Species Complex in Thailand. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2297.	1.3	54
124	Molecular Epidemiology Linking Multihospital Clusters of Opportunistic <i>Pneumocystis jirovecii</i> Pneumonia. <i>Clinical Infectious Diseases</i> , 2013, 57, 1058-1059.	2.9	17
125	Fungal infections and treatment in cystic fibrosis. <i>Current Opinion in Pulmonary Medicine</i> , 2013, 19, 670-675.	1.2	38
126	Antifungal Therapy and Management of Complications of Cryptococcosis due to <i>Cryptococcus gattii</i> . <i>Clinical Infectious Diseases</i> , 2013, 57, 543-551.	2.9	106

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127	Ancient Dispersal of the Human Fungal Pathogen <i>Cryptococcus gattii</i> from the Amazon Rainforest. PLoS ONE, 2013, 8, e71148.	1.1	122
128	Geographically Structured Populations of <i>Cryptococcus neoformans</i> Variety <i>grubii</i> in Asia Correlate with HIV Status and Show a Clonal Population Structure. PLoS ONE, 2013, 8, e72222.	1.1	83
129	PRESHIPMENT TESTING SUCCESS: RESOLUTION OF A NASAL SINUS GRANULOMA IN A CAPTIVE KOALA (<i>PHASCOLARCTOS CINEREUS</i>) CAUSED BY <i>CRYPTOCOCCUS GATTII</i> . Journal of Zoo and Wildlife Medicine, 2012, 43, 939-942.	0.3	12
130	Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for <i>Fungi</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6241-6246.	3.3	4,012
131	Clinical Manifestations of <i>Cryptococcus gattii</i> Infection: Determinants of Neurological Sequelae and Death. Clinical Infectious Diseases, 2012, 55, 789-798.	2.9	171
132	Correlation of antifungal susceptibility and molecular type within the <i>Cryptococcus neoformans/C. gattii</i> species complex. Medical Mycology, 2012, 50, 328-332.	0.3	86
133	Robust polyfunctional T-helper 1 responses to multiple fungal antigens from a cell population generated using an environmental strain of <i>Aspergillus fumigatus</i> . Cytotherapy, 2012, 14, 1119-1130.	0.3	29
134	Identification of Novel Hybrids Between <i>Cryptococcus neoformans</i> var. <i>grubii</i> VNI and <i>Cryptococcus gattii</i> VGII. Mycopathologia, 2012, 173, 337-346.	1.3	49
135	MALDI-TOF MS Enables the Rapid Identification of the Major Molecular Types within the <i>Cryptococcus neoformans/C. gattii</i> Species Complex. PLoS ONE, 2012, 7, e37566.	1.1	113
136	Feline Cryptococcosis. Journal of Feline Medicine and Surgery, 2011, 13, 163-172.	0.6	49
137	Nosocomial <i>Pneumocystis jirovecii</i> Pneumonia: Lessons From a Cluster in Kidney Transplant Recipients. Transplantation, 2011, 92, 1327-1334.	0.5	82
138	Making Moulds Meet Information retrieval as a basis for understanding <i>Pseudallescheria</i> and <i>Scedosporium</i> . Mycoses, 2011, 54, 1-4.	1.8	3
139	<i>SEC14</i> is a specific requirement for secretion of phospholipase B1 and pathogenicity of <i>Cryptococcus neoformans</i> . Molecular Microbiology, 2011, 80, 1088-1101.	1.2	87
140	Global VGIIa isolates are of comparable virulence to the major fatal <i>Cryptococcus gattii</i> Vancouver Island outbreak genotype. Clinical Microbiology and Infection, 2011, 17, 251-258.	2.8	60
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