

Wieland Meyer

List of Publications by Year in descending order

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216
papers

17,090
citations

17440

63
h-index

16650

123
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227
all docs

227
docs citations

227
times ranked

13438
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	7.1	4,012
2	A rare genotype of <i>Cryptococcus gattii</i> caused the cryptococcosis outbreak on Vancouver Island (British Columbia, Canada). Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 17258-17263.	7.1	698
3	Molecular Typing of IberoAmerican <i>Cryptococcus neoformans</i> Isolates. Emerging Infectious Diseases, 2003, 9, 189-195.	4.3	468
4	Consensus multi-locus sequence typing scheme for <i>Cryptococcus neoformans</i> and <i>Cryptococcus gattii</i> . Medical Mycology, 2009, 47, 561-570.	0.7	408
5	Hybrid genotypes in the pathogenic yeast <i>Cryptococcus neoformans</i> . Microbiology (United Kingdom), 2001, 147, 891-907.	1.8	346
6	<i>Cryptococcus gattii</i> Infections. Clinical Microbiology Reviews, 2014, 27, 980-1024.	13.6	327
7	The Amsterdam Declaration on Fungal Nomenclature. IMA Fungus, 2011, 2, 105-111.	3.8	320
8	Sequence-Based Identification of <i>Aspergillus</i> , <i>Fusarium</i> , and <i>Mucorales</i> Species in the Clinical Mycology Laboratory: Where Are We and Where Should We Go from Here?. Journal of Clinical Microbiology, 2009, 47, 877-884.	3.9	299
9	The Case for Adopting the "Species Complex" Nomenclature for the Etiologic Agents of Cryptococcosis. MSphere, 2017, 2, .	2.9	274
10	Finding needles in haystacks: linking scientific names, reference specimens and molecular data for Fungi. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau061-bau061.	3.0	272
11	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. Medical Mycology, 2015, 53, 313-337.	0.7	252
12	Unambiguous identification of fungi: where do we stand and how accurate and precise is fungal DNA barcoding?. IMA Fungus, 2020, 11, 14.	3.8	232
13	Survey of Simple Sequence Repeats in Completed Fungal Genomes. Molecular Biology and Evolution, 2005, 22, 639-649.	8.9	221
14	Molecular typing of global isolates of <i>Cryptococcus neoformans</i> var. <i>neoformans</i> by polymerase chain reaction fingerprinting and randomly amplified polymorphic DNA—a pilot study to standardize techniques on which to base a detailed epidemiological survey. Electrophoresis, 1999, 20, 1790-1799.	2.4	210
15	<i>Scedosporium</i> and <i>Lomentospora</i> : an updated overview of underrated opportunists. Medical Mycology, 2018, 56, S102-S125.	0.7	186
16	Genome Variation in <i>Cryptococcus gattii</i> , an Emerging Pathogen of Immunocompetent Hosts. MBio, 2011, 2, e00342-10.	4.1	182
17	Not Just Little Adults: Candidemia Epidemiology, Molecular Characterization, and Antifungal Susceptibility in Neonatal and Pediatric Patients. Pediatrics, 2009, 123, 1360-1368.	2.1	171
18	Clinical Manifestations of <i>Cryptococcus gattii</i> Infection: Determinants of Neurological Sequelae and Death. Clinical Infectious Diseases, 2012, 55, 789-798.	5.8	171

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19	MycoBank gearing up for new horizons. <i>IMA Fungus</i> , 2013, 4, 371-379.	3.8	170
20	Proposed nomenclature for <i>Pseudallescheria</i> , <i>Scedosporium</i> and related genera. <i>Fungal Diversity</i> , 2014, 67, 1-10.	12.3	152
21	Genetic Diversity of the <i>Cryptococcus</i> Species Complex Suggests that <i>Cryptococcus gattii</i> Deserves to Have Varieties. <i>PLoS ONE</i> , 2009, 4, e5862.	2.5	144
22	Rapid identification and differentiation of yeasts by DNA and PCR fingerprinting. <i>Journal of Basic Microbiology</i> , 1993, 33, 413-425.	3.3	137
23	Regional pattern of the molecular types of <i>Cryptococcus neoformans</i> and <i>Cryptococcus gattii</i> in Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2008, 103, 455-462.	1.6	131
24	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.	6.0	129
25	<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.	4.1	126
26	Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry Identification of Yeasts Is Contingent on Robust Reference Spectra. <i>PLoS ONE</i> , 2011, 6, e25712.	2.5	123
27	Ancient Dispersal of the Human Fungal Pathogen <i>Cryptococcus gattii</i> from the Amazon Rainforest. <i>PLoS ONE</i> , 2013, 8, e71148.	2.5	122
28	Clonality and Recombination in Genetically Differentiated Subgroups of <i>Cryptococcus gattii</i> . <i>Eukaryotic Cell</i> , 2005, 4, 1403-1409.	3.4	117
29	Revision of <i>Trichoderma</i> sect. <i>Longibrachiatum</i> including related teleomorphs based on analysis of ribosomal DNA internal transcribed spacer sequences. <i>Mycologia</i> , 1997, 89, 442-460.	1.9	116
30	A review of nucleic acid-based diagnostic tests for systemic mycoses with an emphasis on polymerase chain reaction-based assays. <i>Medical Mycology</i> , 2002, 40, 333-357.	0.7	116
31	MALDI-TOF MS Enables the Rapid Identification of the Major Molecular Types within the <i>Cryptococcus neoformans/C. gattii</i> Species Complex. <i>PLoS ONE</i> , 2012, 7, e37566.	2.5	113
32	Polymerase chain reaction fingerprinting in fungi using single primers specific to minisatellites and simple repetitive DNA sequences: Strain variation in <i>Cryptococcus neoformans</i> . <i>Electrophoresis</i> , 1995, 16, 1648-1656.	2.4	112
33	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.	2.6	109
34	The D1/D2 domain of the large-subunit rDNA of the yeast species is unusually polymorphic. <i>FEMS Yeast Research</i> , 2003, 4, 253-258.	2.3	107
35	Antifungal Therapy and Management of Complications of Cryptococcosis due to <i>Cryptococcus gattii</i> . <i>Clinical Infectious Diseases</i> , 2013, 57, 543-551.	5.8	106
36	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.	2.9	105

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37	Molecular epidemiology of clinical and environmental isolates of the <i>Cryptococcus neoformans</i> species complex reveals a high genetic diversity and the presence of the molecular type VGII mating type a in Colombia. <i>FEMS Yeast Research</i> , 2006, 6, 625-635.	2.3	104
38	Differentiation of species and strains among filamentous fungi by DNA fingerprinting. <i>Current Genetics</i> , 1991, 19, 239-242.	1.7	103
39	The internal transcribed spacers and 5.8S rRNA gene show extensive diversity among isolates of the species complex. <i>FEMS Yeast Research</i> , 2004, 4, 377-388.	2.3	103
40	Population-based surveillance for scedosporiosis in Australia: epidemiology, disease manifestations and emergence of <i>Scedosporium aurantiacum</i> infection. <i>Clinical Microbiology and Infection</i> , 2009, 15, 689-693.	6.0	102
41	Fungal taxonomy and sequence-based nomenclature. <i>Nature Microbiology</i> , 2021, 6, 540-548.	13.3	101
42	Evaluation of ribosomal RNA and actin gene sequences for the identification of ascomycetous yeasts. <i>International Journal of Food Microbiology</i> , 2003, 86, 61-78.	4.7	94
43	A New Age in Molecular Diagnostics for Invasive Fungal Disease: Are We Ready?. <i>Frontiers in Microbiology</i> , 2019, 10, 2903.	3.5	94
44	Molecular typing of clinical and environmental isolates in the Brazilian state Rio Grande do Sul. <i>FEMS Yeast Research</i> , 2003, 3, 405-415.	2.3	93
45	Clinical associations and prevalence of <i>Scedosporium</i> spp. in Australian cystic fibrosis patients: identification of novel risk factors?. <i>Medical Mycology</i> , 2010, 48, S37-S44.	0.7	93
46	CCMetagen: comprehensive and accurate identification of eukaryotes and prokaryotes in metagenomic data. <i>Genome Biology</i> , 2020, 21, 103.	8.8	91
47	The Trehalose Synthesis Pathway Is an Integral Part of the Virulence Composite for <i>Cryptococcus gattii</i> . <i>Infection and Immunity</i> , 2009, 77, 4584-4596.	2.2	88
48	Prevalence of the VNlc genotype of <i>Cryptococcus neoformans</i> in non-HIV-associated cryptococcosis in the Republic of Korea. <i>FEMS Yeast Research</i> , 2010, 10, 769-778.	2.3	87
49	<i>SEC14</i> is a specific requirement for secretion of phospholipase B1 and pathogenicity of <i>Cryptococcus neoformans</i> . <i>Molecular Microbiology</i> , 2011, 80, 1088-1101.	2.5	87
50	Correlation of antifungal susceptibility and molecular type within the <i>Cryptococcus neoformans</i> / <i>C. gattii</i> species complex. <i>Medical Mycology</i> , 2012, 50, 328-332.	0.7	86
51	Clinical Signs, Imaging Features, Neuropathology, and Outcome in Cats and Dogs with Central Nervous System Cryptococcosis from California. <i>Journal of Veterinary Internal Medicine</i> , 2010, 24, 1427-1438.	1.6	84
52	Geographically Structured Populations of <i>Cryptococcus neoformans</i> Variety <i>grubii</i> in Asia Correlate with HIV Status and Show a Clonal Population Structure. <i>PLoS ONE</i> , 2013, 8, e72222.	2.5	83
53	Nosocomial <i>Pneumocystis jirovecii</i> Pneumonia: Lessons From a Cluster in Kidney Transplant Recipients. <i>Transplantation</i> , 2011, 92, 1327-1334.	1.0	82
54	Clinical features and epidemiology of cryptococcosis in cats and dogs in California: 93 cases (1988-2010). <i>Journal of the American Veterinary Medical Association</i> , 2011, 239, 357-369.	0.5	80

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55	Candidaemia with uncommon <i>Candida</i> species: predisposing factors, outcome, antifungal susceptibility, and implications for management. <i>Clinical Microbiology and Infection</i> , 2009, 15, 662-669.	6.0	79
56	Species and Genotypic Diversities and Similarities of Pathogenic Yeasts Colonizing Women. <i>Journal of Clinical Microbiology</i> , 1999, 37, 3835-3843.	3.9	76
57	Molecular Typing of Australian <i>Scedosporium</i> Isolates Showing Genetic Variability and Numerous <i>S. aurantiacum</i> . <i>Emerging Infectious Diseases</i> , 2008, 14, 282-290.	4.3	74
58	Detection of Occult <i>Scedosporium</i> Species in Respiratory Tract Specimens from Patients with Cystic Fibrosis by Use of Selective Media. <i>Journal of Clinical Microbiology</i> , 2010, 48, 314-316.	3.9	74
59	Primary endemic <i>Cryptococcus gattii</i> by molecular type VGII in the state of Pará, Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2008, 103, 813-818.	1.6	72
60	Clonality and \pm -a Recombination in the Australian <i>Cryptococcus gattii</i> VGII Population - An Emerging Outbreak in Australia. <i>PLoS ONE</i> , 2011, 6, e16936.	2.5	71
61	Abundance of <i>Pseudallescheria</i> / <i>Scedosporium</i> species in the Australian urban environment suggests a possible source for scedosporiosis including the colonization of airways in cystic fibrosis. <i>Medical Mycology</i> , 2010, 48, S70-S76.	0.7	69
62	DNA barcoding of fungi causing infections in humans and animals. <i>Fungal Biology</i> , 2016, 120, 125-136.	2.5	67
63	The use of DNA-fingerprint analysis in the classification of some species of the <i>Trichoderma</i> aggregate. <i>Current Genetics</i> , 1992, 21, 27-30.	1.7	66
64	A New Lineage of <i>Cryptococcus gattii</i> (VGV) Discovered in the Central Zambesian Miombo Woodlands. <i>MBio</i> , 2019, 10, .	4.1	66
65	Commentaries: Name Changes in Medically Important Fungi and Their Implications for Clinical Practice. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1056-1062.	3.9	65
66	Delimitation of <i>Umbelopsis</i> (<i>Mucorales</i> , <i>Umbelopsidaceae</i> fam. nov.) based on ITS sequence and RFLP data. <i>Mycological Research</i> , 2003, 107, 339-350.	2.5	64
67	Global VGIIa isolates are of comparable virulence to the major fatal <i>Cryptococcus gattii</i> Vancouver Island outbreak genotype. <i>Clinical Microbiology and Infection</i> , 2011, 17, 251-258.	6.0	60
68	Molecular mycology: DNA probes and applications of PCR technology. <i>Medical Mycology</i> , 1994, 32, 351-366.	0.7	59
69	Hyperbranched rolling circle amplification as a rapid and sensitive method for species identification within the <i>Cryptococcus</i> species complex. <i>Electrophoresis</i> , 2008, 29, 3183-3191.	2.4	59
70	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.	3.0	59
71	Revision of <i>Trichoderma</i> sect. <i>Longibrachiatum</i> Including Related Teleomorphs Based on Analysis of Ribosomal DNA Internal Transcribed Spacer Sequences. <i>Mycologia</i> , 1997, 89, 442.	1.9	58
72	Environmental distribution of <i>Cryptococcus neoformans</i> and <i>C. gattii</i> around the Mediterranean basin. <i>FEMS Yeast Research</i> , 2016, 16, fow045.	2.3	57

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73	PCR-Restriction Fragment Length Polymorphism Analysis of the Phospholipase B (PLB1) Gene for Subtyping of <i>Cryptococcus neoformans</i> Isolates. <i>Applied and Environmental Microbiology</i> , 2003, 69, 2080-2086.	3.1	56
74	<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.	2.5	56
75	<i>Cryptococcus gattii</i> Virulence Composite: Candidate Genes Revealed by Microarray Analysis of High and Less Virulent Vancouver Island Outbreak Strains. <i>PLoS ONE</i> , 2011, 6, e16076.	2.5	56
76	Re-examining the phylogeny of clinically relevant <i>Candida</i> species and allied genera based on multigene analyses. <i>FEMS Yeast Research</i> , 2008, 8, 651-659.	2.3	54
77	Molecular Epidemiology Reveals Genetic Diversity amongst Isolates of the <i>Cryptococcus neoformans/C. gattii</i> Species Complex in Thailand. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2297.	3.0	54
78	Molecular epidemiology of <i>Cryptococcus neoformans</i> isolates from AIDS patients of the Brazilian city, Rio de Janeiro. <i>Medical Mycology</i> , 2004, 42, 229-238.	0.7	53
79	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.	3.0	52
80	Retrospective Study of the Epidemiology and Clinical Manifestations of <i>Cryptococcus gattii</i> Infections in Colombia from 1997 to 2011. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3272.	3.0	51
81	Identification of pathogenic yeasts of the imperfect genus <i>Candida</i> by polymerase chain reaction fingerprinting. <i>Electrophoresis</i> , 1997, 18, 1548-1559.	2.4	49
82	Feline Cryptococcosis. <i>Journal of Feline Medicine and Surgery</i> , 2011, 13, 163-172.	1.6	49
83	Identification of Novel Hybrids Between <i>Cryptococcus neoformans</i> var. <i>grubii</i> VNI and <i>Cryptococcus gattii</i> VGII. <i>Mycopathologia</i> , 2012, 173, 337-346.	3.1	49
84	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.	3.0	49
85	Fingerprinting reveals gamma-ray induced mutations in fungal DNA: implications for identification of patent strains of <i>Trichoderma harzianum</i> . <i>Current Genetics</i> , 1994, 26, 74-78.	1.7	44
86	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.	3.8	44
87	Online Databases for Taxonomy and Identification of Pathogenic Fungi and Proposal for a Cloud-Based Dynamic Data Network Platform. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1011-1024.	3.9	43
88	Clinical Significance and Phylogenetic Relationship of Novel Australian <i>Pneumocystis jirovecii</i> Genotypes. <i>Journal of Clinical Microbiology</i> , 2009, 47, 1818-1823.	3.9	42
89	Draft Genome Sequence of the Pathogenic Fungus <i>Scedosporium apiospermum</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	42
90	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.	2.5	42

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91	Database establishment for the secondary fungal DNA barcode< i>translational elongation factor 1Î±< /i> (< i>TEF1Î±< /i>). Genome, 2019, 62, 160-169.	2.0	41
92	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.	2.5	41
93	Genotyping of< i>Scedosporium< /i> species: a review of molecular approaches. Medical Mycology, 2009, 47, 406-414.	0.7	40
94	Antifungal Drug Susceptibility and Phylogenetic Diversity among Cryptococcus Isolates from Dogs and Cats in North America. Journal of Clinical Microbiology, 2014, 52, 2061-2070.	3.9	40
95	Dual DNA Barcoding for the Molecular Identification of the Agents of Invasive Fungal Infections. Frontiers in Microbiology, 2019, 10, 1647.	3.5	40
96	Development and Validation of a Multiplex PCR for Detection of Scedosporium spp. in Respiratory Tract Specimens from Patients with Cystic Fibrosis. Journal of Clinical Microbiology, 2011, 49, 1508-1512.	3.9	39
97	Identification of the Major Molecular Types of Cryptococcus neoformans and C. gattii by Hyperbranched Rolling Circle Amplification. PLoS ONE, 2014, 9, e94648.	2.5	39
98	Fatal Disseminated Cryptococcus gattii Infection in New Mexico. PLoS ONE, 2011, 6, e28625.	2.5	38
99	Fungal infections and treatment in cystic fibrosis. Current Opinion in Pulmonary Medicine, 2013, 19, 670-675.	2.6	38
100	Prevalence, geographic risk factor, and development of a standardized protocol for fungal isolation in cystic fibrosis: Results from the international prospective study â€œMFIPâ€• Journal of Cystic Fibrosis, 2019, 18, 212-220.	0.7	38
101	Comparison of Different DNA-Based Methods for Molecular Typing of < i>Histoplasma capsulatum< /i>. Applied and Environmental Microbiology, 2010, 76, 4438-4447.	3.1	37
102	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
103	Scedosporium and Lomentospora Infections: Contemporary Microbiological Tools for the Diagnosis of Invasive Disease. Journal of Fungi (Basel, Switzerland), 2021, 7, 23.	3.5	37
104	Genotyping of Mexican Cryptococcus neoformans and C. gattii isolates by PCR-fingerprinting. Medical Mycology, 2009, 47, 713-721.	0.7	36
105	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
106	Multilocus microsatellite typing for< i>Cryptococcus neoformans< /i> var.< i>grubii< /i>. Medical Mycology, 2008, 46, 685-696.	0.7	35
107	Pathogenesis of Pulmonary Cryptococcus gattii Infection: A Rat Model. Mycopathologia, 2010, 170, 315-330.	3.1	34
108	Phenotypic Differences of Cryptococcus Molecular Types and Their Implications for Virulence in a Drosophila Model of Infection. Infection and Immunity, 2014, 82, 3058-3065.	2.2	33

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109	Taxonomic annotation of public fungal ITS sequences from the built environment – a report from an April 10–11, 2017 workshop (Aberdeen, UK). <i>MycoKeys</i> , 2018, 28, 65-82.	1.9	33
110	Differentiation of <i>Cryptococcus neoformans</i> varieties and <i>Cryptococcus gattii</i> using CAP59-based loop-mediated isothermal DNA amplification. <i>Clinical Microbiology and Infection</i> , 2010, 16, 711-714.	6.0	32
111	<i>Pseudomonas aeruginosa</i> Inhibits the Growth of <i>Scedosporium</i> and <i>Lomentospora</i> In Vitro. <i>Mycopathologia</i> , 2018, 183, 251-261.	3.1	32
112	Rearing and Maintenance of <i>Galleria mellonella</i> and Its Application to Study Fungal Virulence. <i>Journal of Fungi</i> (Basel, Switzerland), 2020, 6, 130.	3.5	32
113	Taxonomy of medically important fungi in the molecular era. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 385-386.	9.1	31
114	Whole Genome Sequencing of Australian <i>Candida glabrata</i> Isolates Reveals Genetic Diversity and Novel Sequence Types. <i>Frontiers in Microbiology</i> , 2018, 9, 2946.	3.5	31
115	Preliminary study of the oral mycobiome of children with and without dental caries. <i>Journal of Oral Microbiology</i> , 2019, 11, 1536182.	2.7	30
116	<i>Scedosporium aurantiacumis</i> as virulent as <i>S. prolificans</i> , and shows strain-specific virulence differences, in a mouse model. <i>Medical Mycology</i> , 2010, 48, S45-S51.	0.7	29
117	Robust polyfunctional T-helper 1 responses to multiple fungal antigens from a cell population generated using an environmental strain of <i>Aspergillus fumigatus</i> . <i>Cytotherapy</i> , 2012, 14, 1119-1130.	0.7	29
118	Molecular diagnosis of <i>Pneumocystis pneumonia</i> in dogs. <i>Medical Mycology</i> , 2017, 55, 828-842.	0.7	28
119	Molecular detection of drug resistant malaria in Southern Thailand. <i>Malaria Journal</i> , 2019, 18, 275.	2.3	28
120	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.	0.7	28
121	Developing collaborative works for faster progress on fungal respiratory infections in cystic fibrosis. <i>Medical Mycology</i> , 2018, 56, S42-S59.	0.7	27
122	Association between fertility and molecular sub-type of global isolates of <i>Cryptococcus gattii</i> molecular type VGII. <i>Medical Mycology</i> , 2008, 46, 665-673.	0.7	26
123	<i>Cryptococcus gattii</i> Species Complex as an Opportunistic Pathogen: Underlying Medical Conditions Associated with the Infection. <i>MBio</i> , 2021, 12, e0270821.	4.1	25
124	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. <i>Internal Medicine Journal</i> , 2021, 51, 177-219.	0.8	25
125	Isolation and characterisation of the phospholipase B gene of <i>Cryptococcus neoformans</i> var. <i>gattii</i> . <i>FEMS Yeast Research</i> , 2002, 2, 551-561.	2.3	24
126	Fatal Mycotic Aneurysms Due to <i>Scedosporium</i> and <i>Pseudallescheria</i> Infection. <i>Journal of Clinical Microbiology</i> , 2011, 49, 2067-2071.	3.9	24

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127	Differential Antifungal Activity of Human and Cryptococcal Melanins with Structural Discrepancies. <i>Frontiers in Microbiology</i> , 2017, 8, 1292.	3.5	24
128	Molecular identification and antifungal susceptibility profiles of clinical strains of <i>Fonsecaea</i> spp. isolated from patients with chromoblastomycosis in Rio de Janeiro, Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006675.	3.0	23
129	Phenotypic Profiling of <i>Scedosporium aurantiacum</i> , an Opportunistic Pathogen Colonizing Human Lungs. <i>PLoS ONE</i> , 2015, 10, e0122354.	2.5	22
130	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
131	Challenges in Laboratory Detection of Fungal Pathogens in the Airways of Cystic Fibrosis Patients. <i>Mycopathologia</i> , 2018, 183, 89-100.	3.1	21
132	Dating the <i>Cryptococcus gattii</i> Dispersal to the North American Pacific Northwest. <i>MSphere</i> , 2018, 3, .	2.9	20
133	NGS barcode sequencing in taxonomy and diagnostics, an application in “ <i>Candida</i> ” pathogenic yeasts with a metagenomic perspective. <i>IMA Fungus</i> , 2018, 9, 91-105.	3.8	20
134	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.	3.8	20
135	<i>Cryptococcus neoformans</i> and <i>Cryptococcus gattii</i> Species Complexes in Latin America: A Map of Molecular Types, Genotypic Diversity, and Antifungal Susceptibility as Reported by the Latin American Cryptococcal Study Group. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 282.	3.5	20
136	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.	3.3	19
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