Teunis Boekhout

List of Publications by Year
in descending order

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343	17,808	14655 66	23533 111
papers	citations	h-index	g-index

357	357	357	14561
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Recognition of seven species in the Cryptococcus gattii/Cryptococcus neoformans species complex. Fungal Genetics and Biology, 2015, 78, 16-48.	2.1	590
2	Dectin-1 is an extracellular pathogen sensor for the induction and processing of IL-1Î² via a noncanonical caspase-8 inflammasome. Nature Immunology, 2012, 13, 246-254.	14.5	514
3	Methods for Isolation, Phenotypic Characterization and Maintenance of Yeasts. , 2011, , 87-110.		462
4	Skin diseases associated with Malassezia species. Journal of the American Academy of Dermatology, 2004, 51, 785-798.	1.2	429
5	Consensus multi-locus sequence typing scheme forCryptococcus neoformansandCryptococcus gattii. Medical Mycology, 2009, 47, 561-570.	0.7	408
6	Dandruff-associated Malassezia genomes reveal convergent and divergent virulence traits shared with plant and human fungal pathogens. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18730-18735.	7.1	396
7	Yarrowia lipolytica: Safety assessment of an oleaginous yeast with a great industrial potential. Critical Reviews in Microbiology, 2014, 40, 187-206.	6.1	369
8	Hybrid genotypes in the pathogenic yeast Cryptococcus neoformans. Microbiology (United Kingdom), 2001, 147, 891-907.	1.8	346
9	The Amsterdam Declaration on Fungal Nomenclature. IMA Fungus, 2011, 2, 105-111.	3.8	320
10	(1557) Proposal to conserve the name Cryptococcus gattii against C. hondurianus and C. bacillisporus (Basidiomycota, Hymenomycetes, Tremellomycetidae). Taxon, 2002, 51, 804-806.	0.7	281
11	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
12	Classification of marine Ascomycota, Basidiomycota, Blastocladiomycota and Chytridiomycota. Fungal Diversity, 2015, 73, 1-72.	12.3	268
13	Notes, outline and divergence times of Basidiomycota. Fungal Diversity, 2019, 99, 105-367.	12.3	256
14	Complex microbiota of a Chinese â€œFenâ€•liquor fermentation starter (Fen-Daqu), revealed by culture-dependent and culture-independent methods. Food Microbiology, 2012, 31, 293-300.	4.2	205
15	Genus-Wide Comparative Genomics of Malassezia Delineates Its Phylogeny, Physiology, and Niche Adaptation on Human Skin. PLoS Genetics, 2015, 11, e1005614.	3.5	198
16	Malassezia ecology, pathophysiology, and treatment. Medical Mycology, 2018, 56, S10-S25.	0.7	188
17	The database of the <scp>PREDICTS</scp> (Projecting Responses of Ecological Diversity In Changing) Tj ETQq1 1 0.784314 rgBT /Ov	1.9	186
18	The fatal fungal outbreak on Vancouver Island is characterized by enhanced intracellular parasitism driven by mitochondrial regulation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12980-12985.	7.1	180

#	Article	IF	Citations
19	Fast, Noninvasive Method for Molecular Detection and Differentiation of Malassezia Yeast Species on Human Skin and Application of the Method to Dandruff Microbiology. Journal of Clinical Microbiology, 2002, 40, 3350-3357.	3.9	178
20	The <scp>PREDICTS</scp> database: a global database of how local terrestrial biodiversity responds to human impacts. Ecology and Evolution, 2014, 4, 4701-4735.	1.9	178
21	Malassezia Infections in Humans and Animals: Pathophysiology, Detection, and Treatment. PLoS Pathogens, 2015, 11, e1004523.	4.7	167
22	Intestinal Fungal Dysbiosis Is Associated With Visceral Hypersensitivity in Patients With Irritable Bowel Syndrome and Rats. Gastroenterology, 2017, 153, 1026-1039.	1.3	160
23	Candida. , 2011, , 987-1278.		147
24	Selective C-Rel Activation via Malt1 Controls Anti-Fungal TH-17 Immunity by Dectin-1 and Dectin-2. PLoS Pathogens, 2011, 7, e1001259.	4.7	144
25	Phylogenetic placements of ustilaginomycetous anamorphs as deduced from nuclear LSU rDNA sequences. Mycological Research, 2000, 104, 53-60.	2.5	142
26	Cold-adapted yeasts from Antarctica and the Italian Alpsâ€"description of three novel species: Mrakia robertii sp. nov., Mrakia blollopis sp. nov. and Mrakiella niccombsii sp. nov.. Extremophiles, 2010, 14, 47-59.	2.3	137
27	Multidrug-Resistant Trichosporon asahii Infection of Nongranulocytopenic Patients in Three Intensive Care Units. Journal of Clinical Microbiology, 2001, 39, 4420-4425.	3.9	136
28	Diversidad del complejo de especies Cryptococcus neoformans-Cryptococcus gattii. Revista Iberoamericana De Micologia, 2008, 25, S4-S12.	0.9	134
29	Fungal Engagement of the C-Type Lectin Mincle Suppresses Dectin-1-Induced Antifungal Immunity. Cell Host and Microbe, 2014, 15, 494-505.	11.0	134
30	Fungi on the Skin: Dermatophytes and Malassezia. Cold Spring Harbor Perspectives in Medicine, 2014, 4, a019802-a019802.	6.2	134
31	An online resource for marine fungi. Fungal Diversity, 2019, 96, 347-433.	12.3	133
32	Autochthonous and DormantCryptococcus gattiiInfections in Europe. Emerging Infectious Diseases, 2012, 18, 1618-1624.	4.3	132
33	Sporangiospore Size Dimorphism Is Linked to Virulence of Mucor circinelloides. PLoS Pathogens, 2011, 7, e1002086.	4.7	128
34	Two new lipid-dependentMalasseziaspecies from domestic animals. FEMS Yeast Research, 2007, 7, 1064-1076.	2.3	126
35	Importance of Resolving Fungal Nomenclature: the Case of Multiple Pathogenic Species in the Cryptococcus Genus. MSphere, 2017, 2, .	2.9	124
36	Unique hybrids between the fungal pathogensCryptococcus neoformansandCryptococcus gattii. FEMS Yeast Research, 2006, 6, 599-607.	2.3	122

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37	Ancient Dispersal of the Human Fungal Pathogen Cryptococcus gattii from the Amazon Rainforest. PLoS ONE, 2013, 8, e71148.	2.5	122
38	Identification and Typing of Malassezia Species by Amplified Fragment Length Polymorphism and Sequence Analyses of the Internal Transcribed Spacer and Large-Subunit Regions of Ribosomal DNA. Journal of Clinical Microbiology, 2004, 42, 4253-4260.	3.9	121
39	In Vitro Antifungal Susceptibilities and Amplified Fragment Length Polymorphism Genotyping of a Worldwide Collection of 350 Clinical, Veterinary, and Environmental Cryptococcus gattii Isolates. Antimicrobial Agents and Chemotherapy, 2010, 54, 5139-5145.	3.2	121
40	C-type lectin Langerin is a Î²-glucan receptor on human Langerhans cells that recognizes opportunistic and pathogenic fungi. Molecular Immunology, 2010, 47, 1216-1225.	2.2	121
41	Baillon, emerging clinical yeasts. FEMS Yeast Research, 2005, 5, 1101-1113.	2.3	119
42	Genomic Insights into the Atopic Eczema-Associated Skin Commensal Yeast Malassezia sympodialis. MBio, 2013, 4, e00572-12.	4.1	118
43	Psychrophilic yeasts from Antarctica and European glaciers: description of Glaciozyma gen. nov., Glaciozyma martinii sp. nov. and Glaciozyma watsonii sp. nov.. Extremophiles, 2011, 15, 573-586.	2.3	114
44	High-throughput screening of a large collection of non-conventional yeasts reveals their potential for aroma formation in food fermentation. Food Microbiology, 2016, 60, 147-159.	4.2	110
45	Oropharyngeal candidiasis in hospitalised COVIDâ€19 patients from Iran: Species identification and antifungal susceptibility pattern. Mycoses, 2020, 63, 771-778.	4.0	106
46	Genomics and the making of yeast biodiversity. Current Opinion in Genetics and Development, 2015, 35, 100-109.	3.3	105
47	Pseudozyma Bandoni emend. Boekhout, a genus for yeast-like anamorphs of Ustilaginales.. Journal of General and Applied Microbiology, 1995, 41, 359-366.	0.7	98
48	Microbiota dynamics related to environmental conditions during the fermentative production of Fen-Daqu, a Chinese industrial fermentation starter. International Journal of Food Microbiology, 2014, 182-183, 57-62.	4.7	98
49	Characterization of the microbial community in different types of Daqu samples as revealed by 16S rRNA and 26S rRNA gene clone libraries. World Journal of Microbiology and Biotechnology, 2015, 31, 199-208.	3.6	98
50	Identification and typing ofMalasseziayeasts using amplified fragment length polymorphism (AFLPTm), random amplified polymorphic DNA (RAPD) and denaturing gradient gel electrophoresis (DGGE). FEMS Yeast Research, 2001, 1, 79-86.	2.3	97
51	Molecular Sequence Analyses of the Intergenic Spacer (IGS) Associated with rDNA of the Two Varieties of the Pathogenic Yeast, Cryptococcus neoformans. Systematic and Applied Microbiology, 2000, 23, 535-545.	2.8	93
52	Molecular typing ofMalasseziaspecies with PFGE and RAPD. Medical Mycology, 1998, 36, 365-372.	0.7	92
53	AIDS Patient Death Caused by NovelCryptococcus neoformansÃ—C.gattiiHybrid. Emerging Infectious Diseases, 2008, 14, 1105-1108.	4.3	91
54	Yeasts and lactic acid bacteria microbiota from masau (Ziziphus mauritiana) fruits and their fermented fruit pulp in Zimbabwe. International Journal of Food Microbiology, 2007, 120, 159-166.	4.7	89

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55	Identification of Medically Relevant Species of Arthroconidial Yeasts by Use of Matrix-Assisted Laser Desorption Ionizationâ€“Time of Flight Mass Spectrometry. Journal of Clinical Microbiology, 2013, 51, 2491-2500.	3.9	89
56	Identification of uncommon oral yeasts from cancer patients by MALDI-TOF mass spectrometry. BMC Infectious Diseases, 2018, 18, 24.	2.9	86
57	The worldâ€™s ten most feared fungi. Fungal Diversity, 2018, 93, 161-194.	12.3	85
58	Cryptococcus Vuillemin (1901). , 2011, , 1661-1737.		84
59	The Quiet and Underappreciated Rise of Drug-Resistant Invasive Fungal Pathogens. Journal of Fungi (Basel, Switzerland), 2020, 6, 138.	3.5	84
60	Polygenic analysis and targeted improvement of the complex trait of high acetic acid tolerance in the yeast Saccharomyces cerevisiae. Biotechnology for Biofuels, 2016, 9, 5.	6.2	83
61	Geographically Structured Populations of Cryptococcus neoformans Variety grubii in Asia Correlate with HIV Status and Show a Clonal Population Structure. PLoS ONE, 2013, 8, e72222.	2.5	83
62	Interaction Between Genetic Background and the Mating-Type Locus in Cryptococcus neoformans Virulence Potential. Genetics, 2005, 171, 975-983.	2.9	82
63	Comparative analysis of the intergenic spacer regions and population structure of the species complex of the pathogenic yeast. FEMS Yeast Research, 2005, 5, 1129-1140.	2.3	79
64	The reach of the genome signature in prokaryotes. BMC Evolutionary Biology, 2006, 6, 84.	3.2	79
65	Low Diversity Cryptococcus neoformans Variety grubii Multilocus Sequence Types from Thailand Are Consistent with an Ancestral African Origin. PLoS Pathogens, 2011, 7, e1001343.	4.7	74
66	Novel anamorphic mite-associated fungi belonging to the Ustilaginomycetes: Meira geulakonigii gen. nov., sp. nov., Meira argovae sp. nov. and Acaromyces ingoldii gen. nov., sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 1655-1664.	1.7	70
67	Interlaboratory Comparison of Sample Preparation Methods, Database Expansions, and Cutoff Values for Identification of Yeasts by Matrix-Assisted Laser Desorption Ionizationâ€“Time of Flight Mass Spectrometry Using a Yeast Test Panel. Journal of Clinical Microbiology, 2014, 52, 3023-3029.	3.9	69
68	Molecular identification and genetic diversity within species of the generaHanseniasporaandKloeckera. FEMS Yeast Research, 2002, 1, 279-289.	2.3	67
69	Ceratonia siliqua(carob) trees as natural habitat and source of infection byCryptococcus gattiiin the Mediterranean environment. Medical Mycology, 2012, 50, 67-73.	0.7	67
70	Bloodstream infections by Malassezia and Candida species in critical care patients. Medical Mycology, 2014, 52, 264-269.	0.7	67
71	Fungal genome and mating system transitions facilitated by chromosomal translocations involving intercentromeric recombination. PLoS Biology, 2017, 15, e2002527.	5.6	67
72	Phylogenomics reveal a robust fungal tree of life. FEMS Yeast Research, 2006, 6, 1213-1220.	2.3	66

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73	Molecular Identification and Susceptibility ofTrichosporonSpecies Isolated from Clinical Specimens in Qatar: Isolation ofTrichosporon dohaenseTaj-Aldeen, Meis & Boekhout sp. nov. Journal of Clinical Microbiology, 2009, 47, 1791-1799.	3.9	66
74	In Vitro Activity of the New Azole Isavuconazole (BAL4815) Compared with Six Other Antifungal Agents against 162 Cryptococcus neoformans Isolates from Cuba. Antimicrobial Agents and Chemotherapy, 2008, 52, 1580-1582.	3.2	65
75	Whole-Genome Sequencing of the Opportunistic Yeast Pathogen Candida inconspicua Uncovers Its Hybrid Origin. Frontiers in Genetics, 2019, 10, 383.	2.3	63
76	Temperate Climate Niche forCryptococcus gattiiin Northern Europe. Emerging Infectious Diseases, 2012, 18, 172-174.	4.3	62
77	Definition, Classification and Nomenclature of the Yeasts. , 2011, , 3-5.		59
78	Phylogeny of the industrial relevant, thermophilic genera Myceliophthora and Corynascus. Fungal Diversity, 2012, 52, 197-207.	12.3	59
79	Uncommon opportunistic yeast bloodstream infections from Qatar. Medical Mycology, 2014, 52, 552-556.	0.7	59
80	MLST-Based Population Genetic Analysis in a Global Context Reveals Clonality amongst Cryptococcus neoformans var. grubii VNI Isolates from HIV Patients in Southeastern Brazil. PLoS Neglected Tropical Diseases, 2017, 11, e0005223.	3.0	59
81	Environmental distribution ofCryptococcus neoformansandC. gattiiaround the Mediterranean basin. FEMS Yeast Research, 2016, 16, fow045.	2.3	57
82	First Report of Candidemia Clonal Outbreak Caused by Emerging Fluconazole-Resistant Candida parapsilosis Isolates Harboring Y132F and/or Y132F+K143R in Turkey. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	57
83	Karyotyping of Malassezia Yeasts: Taxonomic and Epidemiological Implications. Systematic and Applied Microbiology, 1994, 17, 146-153.	2.8	56
84	Gut feeling for yeasts. Nature, 2005, 434, 449-451.	27.8	56
85	Discussion of Teleomorphic and Anamorphic Basidiomycetous Yeasts. , 2011, , 1339-1372.		56
86	Phylogenetic relationships of Rhizoctonia fungi within the Cantharellales. Fungal Biology, 2016, 120, 603-619.	2.5	56
87	Cryptococcus randhawai sp. nov., a novel anamorphic basidiomycetous yeast isolated from tree trunk hollow of Ficus religiosa (peepal tree) from New Delhi, India. Antonie Van Leeuwenhoek, 2010, 97, 253-259.	1.7	55
88	Advances in yeast systematics and phylogeny and their use as predictors of biotechnologically important metabolic pathways. FEMS Yeast Research, 2015, 15, fov050.	2.3	55
89	Antifungal susceptibility, genotyping, resistance mechanism, and clinical profile of Candida tropicalis blood isolates. Medical Mycology, 2020, 58, 766-773.	0.7	54
90	Extensive Genetic Diversity within the Dutch Clinical Cryptococcus neoformans Population. Journal of Clinical Microbiology, 2012, 50, 1918-1926.	3.9	53

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91	Phylogenetic Relationships in the Genus Hebeloma Based on ITS1 and 2 Sequences, with Special Emphasis on the Hebeloma crustuliniforme Complex. Mycologia, 2000, 92, 269.	1.9	52
92	Proof of Concept for MBT ASTRA, a Rapid Matrix-Assisted Laser Desorption Ionizationâ€“Time of Flight Mass Spectrometry (MALDI-TOF MS)-Based Method To Detect Caspofungin Resistance in Candida albicans and Candida glabrata. Journal of Clinical Microbiology, 2018, 56, .	3.9	52
93	Constructing Level-2 Phylogenetic Networks from Triplets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 667-681.	3.0	51
94	Microsatellite Typing of Clinical and Environmental Cryptococcus neoformans var. grubii Isolates from Cuba Shows Multiple Genetic Lineages. PLoS ONE, 2010, 5, e9124.	2.5	51
95	Fermentation characteristics of yeasts isolated from traditionally fermented masau (Ziziphus) Tj ETQq1 1 0.784314 rgBT /Overlock 10	4.7	50
96	Cryptococcus gattiiRisk for Tourists Visiting Vancouver Island, Canada. Emerging Infectious Diseases, 2007, 13, 178-179.	4.3	49
97	Malassezia spp. Yeasts of Emerging Concern in Fungemia. Frontiers in Cellular and Infection Microbiology, 2020, 10, 370.	3.9	49
98	Candida auris Identification and Rapid Antifungal Susceptibility Testing Against Echinocandins by MALDI-TOF MS. Frontiers in Cellular and Infection Microbiology, 2019, 9, 20.	3.9	48
99	The septal pore cap is an organelle that functions in vegetative growth and mushroom formation of the woodâ€rot fungus Schizophyllum commune. Environmental Microbiology, 2010, 12, 833-844.	3.8	47
100	Proteogenomics produces comprehensive and highly accurate protein-coding gene annotation in a complete genome assembly ofMalassezia sympodialis. Nucleic Acids Research, 2017, 45, gkx006.	14.5	47
101	Structural and phylogenetic analysis of the actin gene from the yeast Phaffia rhodozyma. Yeast, 1996, 12, 641-651.	1.7	45
102	Cryptotrichosporon anacardiigen. nov., sp. nov., a new trichosporonoid capsulate basidiomycetous yeast from Nigeria that is able to form melanin on niger seed agar. FEMS Yeast Research, 2007, 7, 339-350.	2.3	45
103	In vitro resistance of clinical Fusarium species to amphotericin B and voriconazole using the EUCAST antifungal susceptibility method. Diagnostic Microbiology and Infectious Disease, 2016, 85, 438-443.	1.8	45
104	Evaluation of non-Saccharomyces yeasts in the fermentation of wine, beer and cider for the development of new beverages. Journal of the Institute of Brewing, 2018, 124, 389-402.	2.3	45
105	Considerations and consequences of allowing DNA sequence data as types of fungal taxa. IMA Fungus, 2018, 9, 167-175.	3.8	45
106	Penicillium araracuarense sp. nov., Penicillium elleniae sp. nov., Penicillium penarojense sp. nov., Penicillium vanderhammenii sp. nov. and Penicillium wotroi sp. nov., isolated from leaf litter. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 1462-1475.	1.7	44
107	Description of Holtermanniella gen. nov., including Holtermanniella takashimae sp. nov. and four new combinations, and proposal of the order Holtermanniales to accommodate tremellomycetous yeasts of the Holtermannia clade. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 680-689.	1.7	44
108	Macrofungal diversity in Colombian Amazon forests varies with regions and regimes of disturbance. Biodiversity and Conservation, 2012, 21, 2221-2243.	2.6	44

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109	Dissimilatory nitrate reduction by Aspergillus terreus isolated from the seasonal oxygen minimum zone in the Arabian Sea. BMC Microbiology, 2014, 14, 35.	3.3	44
110	Use of non-conventional yeast improves the wine aroma profile of Ribolla Gialla. Journal of Industrial Microbiology and Biotechnology, 2015, 42, 997-1010.	3.0	44
111	Characterization of Saccharomyces uvarum (Beijerinck, 1898) and related hybrids: assessment of molecular markers that predict the parent and hybrid genomes and a proposal to name yeast hybrids. FEMS Yeast Research, 2017, 17, .	2.3	44
112	Fundamental niche prediction of the pathogenic yeasts Cryptococcus neoformans and Cryptococcus gattii in Europe. Environmental Microbiology, 2017, 19, 4318-4325.	3.8	44
113	Evaluation of Molecular Epidemiology, Clinical Characteristics, Antifungal Susceptibility Profiles, and Molecular Mechanisms of Antifungal Resistance of Iranian Candida parapsilosis Species Complex Blood Isolates. Frontiers in Cellular and Infection Microbiology, 2020, 10, 206.	3.9	44
114	Biodiversity, Phylogeny and Ultrastructure. , 2010, , 17-63.		43
115	Nutritive value of masau (Ziziphus mauritiana) fruits from Zambezi Valley in Zimbabwe. Food Chemistry, 2013, 138, 168-172.	8.2	43
116	Epidemiology of Malassezia-Related Skin Diseases. , 2010, , 65-119.		42
117	Identification of Mycoses in Developing Countries. Journal of Fungi (Basel, Switzerland), 2019, 5, 90.	3.5	42
118	YEAST PANEL multiplex PCR for identification of clinically important yeast species: stepwise diagnostic strategy, useful for developing countries. Diagnostic Microbiology and Infectious Disease, 2019, 93, 112-119.	1.8	42
119	Resistance of Asian Cryptococcus neoformans Serotype A Is Confined to Few Microsatellite Genotypes. PLoS ONE, 2012, 7, e32868.	2.5	42
120	The Potential Role of Marine Fungi in Plastic Degradation â€“ A Review. Frontiers in Marine Science, 2021, 8, .	2.5	42
121	Antifungal susceptibility, serotyping, and genotyping of clinicalCryptococcus neoformansisolates collected during 18 years in a single institution in Madrid, Spain. Medical Mycology, 2010, 48, 942-948.	0.7	41
122	Activated dormantCryptococcus gattiiinfection in a Dutch tourist who visited Vancouver Island (Canada): a molecular epidemiological approach. Medical Mycology, 2010, 48, 528-531.	0.7	41
123	Structural differences between two types of basidiomycete septal pore caps. Microbiology (United) Tj ETQq1 1 0.784314 rgBT /Overlo	1.8	40
124	Candida nivariensis Isolated from an Indonesian Human Immunodeficiency Virus-Infected Patient Suffering from Oropharyngeal Candidiasis. Journal of Clinical Microbiology, 2008, 46, 388-391.	3.9	40
125	Microcoding and flow cytometry as a high-throughput fungal identification system for Malassezia species. Journal of Medical Microbiology, 2006, 55, 1197-1209.	1.8	39
126	Complete DNA Sequence of Kuraishia capsulata Illustrates Novel Genomic Features among Budding Yeasts (Saccharomycotina). Genome Biology and Evolution, 2013, 5, 2524-2539.	2.5	39

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127	Tuberculosis/cryptococcosis co-infection in China between 1965 and 2016. Emerging Microbes and Infections, 2017, 6, 1-7.	6.5	39
128	Low Level of Antifungal Resistance in Iranian Isolates of Candida glabrata Recovered from Blood Samples in a Multicenter Study from 2015 to 2018 and Potential Prognostic Values of Genotyping and Sequencing of PDR1. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	39
129	Candida tropicalis is the most prevalent yeast species causing candidemia in Algeria: the urgent need for antifungal stewardship and infection control measures. Antimicrobial Resistance and Infection Control, 2020, 9, 50.	4.1	39
130	Antifungal and antioxidant activities of the phytomedicine pipsissewa, Chimaphila umbellata. Phytochemistry, 2008, 69, 738-746.	2.9	38
131	Adding Flavor to Beverages with Non-Conventional Yeasts. Fermentation, 2018, 4, 15.	3.0	38
132	Novel multiplex real-time quantitative PCR detecting system approach for direct detection of Candida auris and its relatives in spiked serum samples. Future Microbiology, 2019, 14, 33-45.	2.0	38
133	Bulleromyces genus novum (Tremellales), a teleomorph for Bullera alba, and the occurrence of mating in Bullera variabilis. Antonie Van Leeuwenhoek, 1991, 59, 81-93.	1.7	37
134	Four novel Talaromyces species isolated from leaf litter from Colombian Amazon rain forests. Mycological Progress, 2016, 15, 1041-1056.	1.4	37
135	Kazachstania gamospora and Wickerhamomyces subpelliculosus : Two alternative bakerâ€™s yeasts in the modern bakery. International Journal of Food Microbiology, 2017, 250, 45-58.	4.7	37
136	Antifungal susceptibility testing of Candida species isolated from the immunocompromised patients admitted to ten university hospitals in Iran: comparison of colonizing and infecting isolates. BMC Infectious Diseases, 2017, 17, 727.	2.9	37
137	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
138	The evolving species concepts used for yeasts: from phenotypes and genomes to speciation networks. Fungal Diversity, 2021, 109, 27-55.	12.3	37
139	Interactions between yeasts, fungicides and apple fruit russeting. FEMS Yeast Research, 2006, 6, 1149-1156.	2.3	36
140	Cryptococcus gattii Induces a Cytokine Pattern That Is Distinct from Other Cryptococcal Species. PLoS ONE, 2013, 8, e55579.	2.5	36
141	The use of karyotyping in the systematics of yeasts. Antonie Van Leeuwenhoek, 1993, 63, 157-163.	1.7	35
142	Phylogenetic diversity of human pathogenic Fusarium and emergence of uncommon virulent species. Journal of Infection, 2015, 71, 658-666.	3.3	35
143	The global catalogue of microorganisms 10K type strain sequencing project: closing the genomic gaps for the validly published prokaryotic and fungi species. GigaScience, 2018, 7, .	6.4	35
144	Extensive colonization of apples by smut anamorphs causes a new postharvest disorder. FEMS Yeast Research, 2006, 6, 63-76.	2.3	34

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145	Cytoplasmic Continuity Revisited: Closure of Septa of the Filamentous Fungus Schizophyllum commune in Response to Environmental Conditions. PLoS ONE, 2009, 4, e5977.	2.5	34
146	Septal pore complex morphology in the Agaricomycotina (Basidiomycota) with emphasis on the Cantharellales and Hymenochaetales. Mycological Research, 2009, 113, 559-576.	2.5	34
147	Gene Sequence Analyses and other DNA-Based Methods for Yeast Species Recognition. , 2011, , 137-144.		34
148	Molecular Identification, Genotypic Diversity, Antifungal Susceptibility, and Clinical Outcomes of Infections Caused by Clinically Underrated Yeasts, Candida orthopsilosis, and Candida metapsilosis: An Iranian Multicenter Study (2014â€“2019). Frontiers in Cellular and Infection Microbiology, 2019, 9, 264.	3.9	34
149	Differentiation of clinically relevant Mucorales Rhizopus microsporus and R. arrhizus by matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS). Journal of Medical Microbiology, 2015, 64, 694-701.	1.8	33
150	Skin Fungi from Colonization to Infection. Microbiology Spectrum, 2017, 5, .	3.0	33
151	Identification of nine cryptic species of Candida albicans, C. glabrata, and C. parapsilosis complexes using one-step multiplex PCR. BMC Infectious Diseases, 2018, 18, 480.	2.9	33
152	Microsatellite typing and susceptibilities of serial Cryptococcus neoformansisolates from Cuban patients with recurrent cryptococcal meningitis. BMC Infectious Diseases, 2010, 10, 289.	2.9	32
153	DNA barcoding survey of Trichoderma diversity in soil and litter of the Colombian lowland Amazonian rainforest reveals Trichoderma strigosellum sp. nov. and other species. Antonie Van Leeuwenhoek, 2013, 104, 657-674.	1.7	32
154	Multilocus sequence typing of Candida albicans isolates from a burn intensive care unit in Iran. Journal of Medical Microbiology, 2015, 64, 248-253.	1.8	32
155	Reclassification of the Sporobolomyces roseus and Sporidiobolus pararoseus complexes, with the description of Sporobolomyces phaffii sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 2309-2314.	1.7	32
156	Automated Electron Tomography of the Septal Pore Cap in Rhizoctonia solani. Journal of Structural Biology, 2000, 131, 10-18.	2.8	31
157	Septal Pore Cap Protein SPC18, Isolated from the Basidiomycetous Fungus Rhizoctonia solani , Also Resides in Pore Plugs. Eukaryotic Cell, 2008, 7, 1865-1873.	3.4	31
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