

# Geraldine Butler

## List of Publications by Year in descending order

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104  
papers

6,734  
citations

66343

42  
h-index

66911

78  
g-index

119  
all docs

119  
docs citations

119  
times ranked

6211  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of a novel <i>Candida metapsilosis</i> isolate reveals multiple hybridization events. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	6
2	Characterization of the <i>Candida glabrata</i> Transcription Factor CgMar1: Role in Azole Susceptibility. Journal of Fungi (Basel, Switzerland), 2022, 8, 61.	3.5	0
3	Mating-Type Switching in Budding Yeasts, from Flip/Flop Inversion to Cassette Mechanisms. Microbiology and Molecular Biology Reviews, 2022, 86, e0000721.	6.6	4
4	<i>Candida</i> pathogens induce protective mitochondria-associated type I interferon signalling and a damage-driven response in vaginal epithelial cells. Nature Microbiology, 2021, 6, 643-657.	13.3	49
5	Population genomics of the pathogenic yeast <i>Candida tropicalis</i> identifies hybrid isolates in environmental samples. PLoS Pathogens, 2021, 17, e1009138.	4.7	36
6	Evolution of the complex transcription network controlling biofilm formation in <i>Candida</i> species. ELife, 2021, 10, .	6.0	25
7	From the first touch to biofilm establishment by the human pathogen <i>Candida glabrata</i> : a genome-wide to nanoscale view. Communications Biology, 2021, 4, 886.	4.4	9
8	On a Special Collection in MMBR on Sex in Fungi: Molecular Mechanisms and Evolutionary Implications. Microbiology and Molecular Biology Reviews, 2021, 85, e0009421.	6.6	1
9	Draft Genome Sequence of a Diploid and Hybrid <i>Candida</i> Strain, <i>Candida sanyaensis</i> UCD423, Isolated from Compost in Ireland. Microbiology Resource Announcements, 2021, 10, e0076121.	0.6	2
10	Draft Genome Sequence of the Yeast <i>Ogataea degrootiae</i> Strain UCD465, Isolated from Soil in Ireland. Microbiology Resource Announcements, 2021, 10, e0073621.	0.6	2
11	High-resolution mycobiota analysis reveals dynamic intestinal translocation preceding invasive candidiasis. Nature Medicine, 2020, 26, 59-64.	30.7	193
12	Draft Genome Sequence of the Yeast <i>Kazachstania telluris</i> CBS 16338 Isolated from Forest Soil in Ireland. Mycopathologia, 2020, 185, 587-590.	3.1	11
13	Polymorphic centromere locations in the pathogenic yeast <i>Candida parapsilosis</i> . Genome Research, 2020, 30, 684-696.	5.5	22
14	<i>Candida glabrata</i> Transcription Factor Rpn4 Mediates Fluconazole Resistance through Regulation of Ergosterol Biosynthesis and Plasma Membrane Permeability. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	20
15	Effect of progesterone on <i>Candida albicans</i> biofilm formation under acidic conditions: A transcriptomic analysis. International Journal of Medical Microbiology, 2020, 310, 151414.	3.6	8
16	The CRISPR toolbox in medical mycology: State of the art and perspectives. PLoS Pathogens, 2020, 16, e1008201.	4.7	49
17	Spatial inter-centromeric interactions facilitated the emergence of evolutionary new centromeres. ELife, 2020, 9, .	6.0	31
18	Susceptibility to Medium-Chain Fatty Acids Is Associated with Trisomy of Chromosome 7 in <i>Candida albicans</i> . MSphere, 2019, 4, .	2.9	9

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19	Coverage-Versus-Length Plots, a Simple Quality Control Step for <i>de Novo</i> Yeast Genome Sequence Assemblies. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 879-887.	1.8	26
20	Precise genome editing using a CRISPR-Cas9 method highlights the role of CoERG11 amino acid substitutions in azole resistance in <i>Candida orthopsilosis</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2230-2238.	3.0	20
21	<i>Candida</i> Intestinal Domination Precedes Fungal Infections Bloodstream in Allogeneic Hematopoietic Cell Transplant Patients. <i>Biology of Blood and Marrow Transplantation</i> , 2019, 25, S340-S341.	2.0	3
22	Plasmid-Based CRISPR-Cas9 Gene Editing in Multiple <i>Candida</i> Species. <i>MSphere</i> , 2019, 4, .	2.9	41
23	<i>Candida parapsilosis</i> : from Genes to the Bedside. <i>Clinical Microbiology Reviews</i> , 2019, 32, .	13.6	182
24	Correlating Genotype and Phenotype in the Asexual Yeast <i>Candida orthopsilosis</i> Implicates ZCF29 in Sensitivity to Caffeine. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3035-3043.	1.8	8
25	Draft Genome Sequence of the Birch Tree Fungal Pathogen <i>Taphrina betulina</i> UCD315. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
26	Synthesis, structures and antimicrobial activity of novel NHC <sup>+</sup> and Ph3P-Ag(I)-Benzoate derivatives. <i>Inorganica Chimica Acta</i> , 2019, 486, 294-303.	2.4	25
27	A Transcriptomics Approach To Unveiling the Mechanisms of <i>In Vitro</i> Evolution towards Fluconazole Resistance of a <i>Candida glabrata</i> Clinical Isolate. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	31
28	Draft Genome Sequences of Two Isolates of the Yeast <i>Kazachstania servazzii</i> Recovered from Soil in Ireland. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	7
29	Draft Genome Sequence of a Red Basidiomycete Yeast, <i>Symmetrospora coprosmae</i> Strain UCD350, Isolated from Soil in Ireland. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
30	Dal81 Regulates Expression of Arginine Metabolism Genes in <i>Candida parapsilosis</i> . <i>MSphere</i> , 2018, 3, .	2.9	11
31	Comparative genomic and transcriptomic analyses unveil novel features of azole resistance and adaptation to the human host in <i>Candida glabrata</i> . <i>FEMS Yeast Research</i> , 2018, 18, .	2.3	28
32	Draft Genome Sequences of Two Natural Isolates of the Yeast <i>Barnettozyma californica</i> from Ireland, UCD09 and UCD89. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
33	Identification of an Exceptionally Long Intron in the <i>HAC1</i> Gene of <i>Candida parapsilosis</i> . <i>MSphere</i> , 2018, 3, .	2.9	10
34	Draft Genome Sequence of the Yeast <i>Nadsonia starkeyi-henricii</i> UCD142, Isolated from Forest Soil in Ireland. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
35	Genome analysis of the yeast <i>Diutina catenulata</i> , a member of the <i>Debaryomycetaceae</i> / <i>Metschnikowiaceae</i> (CTG-Ser) clade. <i>PLoS ONE</i> , 2018, 13, e0198957.	2.5	13
36	Draft Genome Sequence of a Highly Heterozygous Yeast Strain from the <i>Metschnikowia pulcherrima</i> Subclade, UCD127. <i>Genome Announcements</i> , 2018, 6, .	0.8	14

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37	TPP riboswitch-dependent regulation of an ancient thiamin transporter in <i>Candida</i> . <i>PLoS Genetics</i> , 2018, 14, e1007429.	3.5	29
38	Identification of fungi in shotgun metagenomics datasets. <i>PLoS ONE</i> , 2018, 13, e0192898.	2.5	83
39	The CgHaa1-Regulon Mediates Response and Tolerance to Acetic Acid Stress in the Human Pathogen <i>Candida glabrata</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1-18.	1.8	24
40	Characterization of carboxylate nanoparticle adhesion with the fungal pathogen <i>Candida albicans</i> . <i>Nanoscale</i> , 2017, 9, 15911-15922.	5.6	15
41	Gene editing in clinical isolates of <i>Candida parapsilosis</i> using CRISPR/Cas9. <i>Scientific Reports</i> , 2017, 7, 8051.	3.3	36
42	Evolution of Mating in the Saccharomycotina. <i>Annual Review of Microbiology</i> , 2017, 71, 197-214.	7.3	22
43	Multiple Origins of the Pathogenic Yeast <i>Candida orthopsilosis</i> by Separate Hybridizations between Two Parental Species. <i>PLoS Genetics</i> , 2016, 12, e1006404.	3.5	125
44	Identification of Non-Coding RNAs in the <i>Candida parapsilosis</i> Species Group. <i>PLoS ONE</i> , 2016, 11, e0163235.	2.5	11
45	Using RNA-seq for Analysis of Differential Gene Expression in Fungal Species. <i>Methods in Molecular Biology</i> , 2016, 1361, 1-40.	0.9	10
46	Genus-Wide Comparative Genomics of <i>Malassezia</i> Delineates Its Phylogeny, Physiology, and Niche Adaptation on Human Skin. <i>PLoS Genetics</i> , 2015, 11, e1005614.	3.5	198
47	Fluconazole and Voriconazole Resistance in <i>Candida parapsilosis</i> Is Conferred by Gain-of-Function Mutations in MRR1 Transcription Factor Gene. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 6629-6633.	3.2	38
48	Comparative Phenotypic Analysis of the Major Fungal Pathogens <i>Candida parapsilosis</i> and <i>Candida albicans</i> . <i>PLoS Pathogens</i> , 2014, 10, e1004365.	4.7	108
49	Zinc Finger Transcription Factors Displaced SREBP Proteins as the Major Sterol Regulators during Saccharomycotina Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004076.	3.5	63
50	The <i>Candida</i> Pathogenic Species Complex. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2014, 4, a019778-a019778.	6.2	190
51	Hypoxia and Gene Expression in Eukaryotic Microbes. <i>Annual Review of Microbiology</i> , 2013, 67, 291-312.	7.3	44
52	The <i>APSES</i> transcription factor <i>Efg1</i> is a global regulator that controls morphogenesis and biofilm formation in <i>Candida parapsilosis</i> . <i>Molecular Microbiology</i> , 2013, 90, 36-53.	2.5	46
53	Comparative Genome Analysis and Gene Finding in <i>Candida</i> Species Using CCOB. <i>Molecular Biology and Evolution</i> , 2013, 30, 1281-1291.	8.9	115
54	Genomic Insights into the Atopic Eczema-Associated Skin Commensal Yeast <i>Malassezia sympodialis</i> . <i>MBio</i> , 2013, 4, e00572-12.	4.1	118

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55	Candida parapsilosis Is a Significant Neonatal Pathogen. Pediatric Infectious Disease Journal, 2013, 32, e206-e216.	2.0	175
56	Sequence and Analysis of the Genome of the Pathogenic Yeast Candida orthopsilosis. PLoS ONE, 2012, 7, e35750.	2.5	69
57	Role of Genomics and RNA-seq in Studies of Fungal Virulence. Current Fungal Infection Reports, 2012, 6, 267-274.	2.6	3
58	Conserved and Divergent Roles of Bcr1 and CFEM Proteins in Candida parapsilosis and Candida albicans. PLoS ONE, 2011, 6, e28151.	2.5	76
59	Using RNA-seq to determine the transcriptional landscape and the hypoxic response of the pathogenic yeast Candida parapsilosis. BMC Genomics, 2011, 12, 628.	2.8	68
60	Evolution of Mating within the Candida parapsilosis Species Group. Eukaryotic Cell, 2011, 10, 578-587.	3.4	56
61	Chromosomal G + C Content Evolution in Yeasts: Systematic Interspecies Differences, and GC-Poor Troughs at Centromeres. Genome Biology and Evolution, 2010, 2, 572-583.	2.5	62
62	Analysis of gene evolution and metabolic pathways using the Candida Gene Order Browser. BMC Genomics, 2010, 11, 290.	2.8	86
63	Impact of the transcriptional regulator, Ace2, on the <i>Candida glabrata</i> secretome. Proteomics, 2010, 10, 212-223.	2.2	23
64	Regulation of the Hypoxic Response in Candida albicans. Eukaryotic Cell, 2010, 9, 1734-1746.	3.4	119
65	Pseudomonas aeruginosa secreted factors impair biofilm development in Candida albicans. Microbiology (United Kingdom), 2010, 156, 1476-1486.	1.8	73
66	Fungal Sex and Pathogenesis. Clinical Microbiology Reviews, 2010, 23, 140-159.	13.6	84
67	Comparative Genomic Analysis of Pathogenic Yeasts and the Evolution of Virulence. , 2010, , 1-18.		3
68	Correlation between Biofilm Formation and the Hypoxic Response in <i>Candida parapsilosis</i> . Eukaryotic Cell, 2009, 8, 550-559.	3.4	83
69	Evolution of pathogenicity and sexual reproduction in eight Candida genomes. Nature, 2009, 459, 657-662.	27.8	963
70	Comparative genomics of the fungal pathogens <i>Candida dubliniensis</i> and <i>Candida albicans</i> . Genome Research, 2009, 19, 2231-2244.	5.5	195
71	<i>Candida glabrata</i> environmental stress response involves <i>Saccharomyces cerevisiae</i> Msn2/4 orthologous transcription factors. Molecular Microbiology, 2008, 69, 603-620.	2.5	112
72	Evidence of recent interkingdom horizontal gene transfer between bacteria and Candida parapsilosis. BMC Evolutionary Biology, 2008, 8, 181.	3.2	57

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73	Transcriptional Response of <i>Candida parapsilosis</i> following Exposure to Farnesol. Antimicrobial Agents and Chemotherapy, 2008, 52, 2296-2296.	3.2	1
74	Identification and Characterization of MFA1, the Gene Encoding <i>Candida albicans</i> -Factor Pheromone. Eukaryotic Cell, 2007, 6, 487-494.	3.4	38
75	Development of a Gene Knockout System in <i>Candida parapsilosis</i> Reveals a Conserved Role for BCR1 in Biofilm Formation. Eukaryotic Cell, 2007, 6, 1310-1319.	3.4	76
76	Transcriptional Response of <i>Candida parapsilosis</i> following Exposure to Farnesol. Antimicrobial Agents and Chemotherapy, 2007, 51, 2304-2312.	3.2	70
77	Yeast genome evolution—the origin of the species. Yeast, 2007, 24, 929-942.	1.7	114
78	A fungal phylogeny based on 42 complete genomes derived from supertree and combined gene analysis. BMC Evolutionary Biology, 2006, 6, 99.	3.2	428
79	Molecular Genotyping of <i>Candida parapsilosis</i> Group I Clinical Isolates by Analysis of Polymorphic Microsatellite Markers. Journal of Clinical Microbiology, 2006, 44, 750-759.	3.9	59
80	<i>Candida albicans</i> Transcription Factor Ace2 Regulates Metabolism and Is Required for Filamentation in Hypoxic Conditions. Eukaryotic Cell, 2006, 5, 2001-2013.	3.4	119
81	Different Consequences of ACE2 and SWI5 Gene Disruptions for Virulence of Pathogenic and Nonpathogenic Yeasts. Infection and Immunity, 2006, 74, 5244-5248.	2.2	42
82	Phenotype switching affects biofilm formation by <i>Candida parapsilosis</i> . Microbiology (United Kingdom), 2007, 157, 1899-1909.	1.8	99
83	A Genome Sequence Survey Shows that the Pathogenic Yeast <i>Candida parapsilosis</i> Has a Defective MTL a1 Allele at Its Mating Type Locus. Eukaryotic Cell, 2005, 4, 1009-1017.	3.4	64
84	Evolution of the MAT locus and its Ho endonuclease in yeast species. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1632-1637.	7.1	217
85	Inactivation of Transcription Factor Gene ACE2 in the Fungal Pathogen <i>Candida glabrata</i> Results in Hypervirulence. Eukaryotic Cell, 2004, 3, 546-552.	3.4	70
86	The <i>Candida albicans</i> CaACE2 gene affects morphogenesis, adherence and virulence. Molecular Microbiology, 2004, 53, 969-983.	2.5	166
87	Evidence from comparative genomics for a complete sexual cycle in the 'asexual' pathogenic yeast <i>Candida glabrata</i> . Genome Biology, 2003, 4, R10.	9.6	97
88	Gene order evolution and paleopolyploidy in hemiascomycete yeasts. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9272-9277.	7.1	131
89	Genomic differences between <i>Candida glabrata</i> and <i>Saccharomyces cerevisiae</i> around the MRPL28 and GCN3 loci. Yeast, 2002, 19, 991-994.	1.7	6
90	Overlapping and distinct roles of the duplicated yeast transcription factors Ace2p and Swi5p. Molecular Microbiology, 2001, 40, 422-432.	2.5	122

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91	Potential role of extracellular L-glutamine in the host immune response to yeast infection. <i>Biochemical Society Transactions</i> , 2000, 28, A255-A255.	3.4	0
92	Cloning, sequencing and expression of the gene for flavodoxin from <i>Megasphaera elsdenii</i> and the effects of removing the protein negative charge that is closest to N(1) of the bound FMN. <i>FEBS Journal</i> , 2000, 267, 4434-4444.	0.2	11
93	Regulated nuclear localisation of the yeast transcription factor Ace2p controls expression of chitinase (CTS1) in <i>Saccharomyces cerevisiae</i> . <i>Molecular Genetics and Genomics</i> , 1999, 262, 275-282.	2.4	82
94	Ace2p, a regulator of CTS1 (chitinase) expression, affects pseudohyphal production in <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 1998, 34, 183-191.	1.7	72
95	Cloning and Analysis of the Genes for a Novel Electron-transferring Flavoprotein from <i>Megasphaera elsdenii</i> . <i>Journal of Biological Chemistry</i> , 1998, 273, 21015-21024.	3.4	26
96	93 Inappropriate expression of the yeast transcription factor Ace2p affects cell growth. <i>Biochemical Society Transactions</i> , 1998, 26, S78-S78.	3.4	3
97	Regulation of expression of the chitinase gene <i>CTS1</i> in <i>Saccharomyces cerevisiae</i> . <i>Biochemical Society Transactions</i> , 1997, 25, 555S-555S.	3.4	4
98	Regulated nuclear entry of a yeast transcription factor. <i>Biochemical Society Transactions</i> , 1995, 23, 346S-346S.	3.4	0
99	Cloning of Electron-Transferring Flavoprotein from <i>Megasphaera elsdenii</i> . <i>Biochemical Society Transactions</i> , 1995, 23, 379S-379S.	3.4	3
100	Cloning of the gene for flavodoxin from the anaerobic bacterium <i>Megasphaera elsdenii</i> . <i>Biochemical Society Transactions</i> , 1995, 23, 384S-384S.	3.4	2
101	TUF factor binds to the upstream region of the pyruvate decarboxylase structural gene (PDC1) of <i>Saccharomyces cerevisiae</i> . <i>Molecular Genetics and Genomics</i> , 1990, 223, 449-456.	2.4	39
102	Identification of an upstream activation site in the pyruvate decarboxylase structural gene (PDC1) of <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 1988, 14, 405-412.	1.7	43
103	The Evolution of <i>MAT</i> : The Ascomycetes. , 0, , 1-18.		22
104	Comparative Genomics of <i>Candida</i> Species. , 0, , 27-43.		0