Geraldine Butler

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3243170/publications.pdf

Version: 2024-02-01

104	6,734	66343	66911
papers	citations	42 h-index	78 g-index

119	119	119	6211
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Evolution of pathogenicity and sexual reproduction in eight Candida genomes. Nature, 2009, 459, 657-662.	27.8	963
2	A fungal phylogeny based on 42 complete genomes derived from supertree and combined gene analysis. BMC Evolutionary Biology, 2006, 6, 99.	3.2	428
3	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
4	Genus-Wide Comparative Genomics of Malassezia Delineates Its Phylogeny, Physiology, and Niche Adaptation on Human Skin. PLoS Genetics, 2015, 11, e1005614.	3.5	198
5	Comparative genomics of the fungal pathogens Candida dubliniensis and Candida albicans. Genome Research, 2009, 19, 2231-2244.	5.5	195
6	High-resolution mycobiota analysis reveals dynamic intestinal translocation preceding invasive candidiasis. Nature Medicine, 2020, 26, 59-64.	30.7	193
7	The Candida Pathogenic Species Complex. Cold Spring Harbor Perspectives in Medicine, 2014, 4, a019778-a019778.	6.2	190
8	Candida parapsilosis: from Genes to the Bedside. Clinical Microbiology Reviews, 2019, 32, .	13.6	182
9	Candida parapsilosis Is a Significant Neonatal Pathogen. Pediatric Infectious Disease Journal, 2013, 32, e206-e216.	2.0	175
10	The Candida albicans CaACE2 gene affects morphogenesis, adherence and virulence. Molecular Microbiology, 2004, 53, 969-983.	2.5	166
11	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
12	Multiple Origins of the Pathogenic Yeast Candida orthopsilosis by Separate Hybridizations between Two Parental Species. PLoS Genetics, 2016, 12, e1006404.	3.5	125
13	Overlapping and distinct roles of the duplicated yeast transcription factors Ace2p and Swi5p. Molecular Microbiology, 2001, 40, 422-432.	2.5	122
14	Candida albicans Transcription Factor Ace2 Regulates Metabolism and Is Required for Filamentation in Hypoxic Conditions. Eukaryotic Cell, 2006, 5, 2001-2013.	3.4	119
15	Regulation of the Hypoxic Response in Candida albicans. Eukaryotic Cell, 2010, 9, 1734-1746.	3.4	119
16	Genomic Insights into the Atopic Eczema-Associated Skin Commensal Yeast Malassezia sympodialis. MBio, 2013, 4, e00572-12.	4.1	118
17	Comparative Genome Analysis and Gene Finding in Candida Species Using CGOB. Molecular Biology and Evolution, 2013, 30, 1281-1291.	8.9	115
18	Yeast genome evolutionâ€"the origin of the species. Yeast, 2007, 24, 929-942.	1.7	114

#	Article	IF	Citations
19	Candida glabrata environmental stress response involves Saccharomyces cerevisiae Msn2/4 orthologous transcription factors. Molecular Microbiology, 2008, 69, 603-620.	2.5	112
20	Comparative Phenotypic Analysis of the Major Fungal Pathogens Candida parapsilosis and Candida albicans. PLoS Pathogens, 2014, 10, e1004365.	4.7	108
21	Phenotype switching affects biofilm formation by Candida parapsilosis. Microbiology (United) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.8	99
22	Evidence from comparative genomics for a complete sexual cycle in the 'asexual' pathogenic yeast Candida glabrata. Genome Biology, 2003, 4, R10.	9.6	97
23	Analysis of gene evolution and metabolic pathways using the Candida Gene Order Browser. BMC Genomics, 2010, 11, 290.	2.8	86
24	Fungal Sex and Pathogenesis. Clinical Microbiology Reviews, 2010, 23, 140-159.	13.6	84
25	Correlation between Biofilm Formation and the Hypoxic Response in Candida parapsilosis. Eukaryotic Cell, 2009, 8, 550-559.	3.4	83
26	Identification of fungi in shotgun metagenomics datasets. PLoS ONE, 2018, 13, e0192898.	2.5	83
27	Regulated nuclear localisation of the yeast transcription factor Ace2p controls expression of chitinase (CTS1) in Saccharomyces cerevisiae. Molecular Genetics and Genomics, 1999, 262, 275-282.	2.4	82
28	Development of a Gene Knockout System in Candida parapsilosis Reveals a Conserved Role for BCR1 in Biofilm Formation. Eukaryotic Cell, 2007, 6, 1310-1319.	3.4	76
29	Conserved and Divergent Roles of Bcr1 and CFEM Proteins in Candida parapsilosis and Candida albicans. PLoS ONE, 2011, 6, e28151.	2.5	76
30	Pseudomonas aeruginosa secreted factors impair biofilm development in Candida albicans. Microbiology (United Kingdom), 2010, 156, 1476-1486.	1.8	73
31	Ace2p, a regulator of CTS1 (chitinase) expression, affects pseudohyphal production in Saccharomyces cerevisiae. Current Genetics, 1998, 34, 183-191.	1.7	72
32	Inactivation of Transcription Factor Gene ACE2 in the Fungal Pathogen Candida glabrata Results in Hypervirulence. Eukaryotic Cell, 2004, 3, 546-552.	3.4	70
33	Transcriptional Response of Candida parapsilosis following Exposure to Farnesol. Antimicrobial Agents and Chemotherapy, 2007, 51, 2304-2312.	3.2	70
34	Sequence and Analysis of the Genome of the Pathogenic Yeast Candida orthopsilosis. PLoS ONE, 2012, 7, e35750.	2.5	69
35	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
36	A Genome Sequence Survey Shows that the Pathogenic Yeast Candida parapsilosis Has a Defective MTL a 1 Allele at Its Mating Type Locus. Eukaryotic Cell, 2005, 4, 1009-1017.	3.4	64

#	Article	IF	Citations
37	Zinc Finger Transcription Factors Displaced SREBP Proteins as the Major Sterol Regulators during Saccharomycotina Evolution. PLoS Genetics, 2014, 10, e1004076.	3.5	63
38	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
39	Molecular Genotyping of Candida parapsilosis Group I Clinical Isolates by Analysis of Polymorphic Microsatellite Markers. Journal of Clinical Microbiology, 2006, 44, 750-759.	3.9	59
40	Evidence of recent interkingdom horizontal gene transfer between bacteria and Candida parapsilosis. BMC Evolutionary Biology, 2008, 8, 181.	3.2	57
41	Evolution of Mating within the Candida parapsilosis Species Group. Eukaryotic Cell, 2011, 10, 578-587.	3.4	56
42	The CRISPR toolbox in medical mycology: State of the art and perspectives. PLoS Pathogens, 2020, 16, e1008201.	4.7	49
43	Candida 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
44	The <scp>APSES</scp> transcription factor <scp>Efg</scp>1 is a global regulator that controls morphogenesis and biofilm formation in <scp>C</scp>andida parapsilosis. Molecular Microbiology, 2013, 90, 36-53.	2.5	46
45	Hypoxia and Gene Expression in Eukaryotic Microbes. Annual Review of Microbiology, 2013, 67, 291-312.	7.3	44
46	Identification of an upstream activation site in the pyruvate decarboxylase structural gene (PDC1) of Saccharomyces cerevisiae. Current Genetics, 1988, 14, 405-412.	1.7	43
47	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
48	Plasmid-Based CRISPR-Cas9 Gene Editing in Multiple Candida Species. MSphere, 2019, 4, .	2.9	41
49	TUF factor binds to the upstream region of the pyruvate decarboxylase structural gene (PDC1) of Saccharomyces cerevisiae. Molecular Genetics and Genomics, 1990, 223, 449-456.	2.4	39
50	Identification and Characterization of MFA1, the Gene Encoding Candida albicansa-Factor Pheromone. Eukaryotic Cell, 2007, 6, 487-494.	3.4	38
51	Fluconazole and Voriconazole Resistance in Candida parapsilosis Is Conferred by Gain-of-Function Mutations inMRR1Transcription Factor Gene. Antimicrobial Agents and Chemotherapy, 2015, 59, 6629-6633.	3.2	38
52	Gene editing in clinical isolates of Candida parapsilosis using CRISPR/Cas9. Scientific Reports, 2017, 7, 8051.	3.3	36
53	Population genomics of the pathogenic yeast Candida tropicalis identifies hybrid isolates in environmental samples. PLoS Pathogens, 2021, 17, e1009138.	4.7	36
54	A Transcriptomics Approach To Unveiling the Mechanisms of In Vitro Evolution towards Fluconazole Resistance of a Candida glabrata Clinical Isolate. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	31

#	Article	IF	Citations
55	Spatial inter-centromeric interactions facilitated the emergence of evolutionary new centromeres. ELife, 2020, 9, .	6.0	31
56	TPP riboswitch-dependent regulation of an ancient thiamin transporter in Candida. PLoS Genetics, 2018, 14, e1007429.	3.5	29
57	Comparative genomic and transcriptomic analyses unveil novel features of azole resistance and adaptation to the human host in Candida glabrata. FEMS Yeast Research, 2018, 18, .	2.3	28
58	Cloning and Analysis of the Genes for a Novel Electron-transferring Flavoprotein from Megasphaera elsdenii. Journal of Biological Chemistry, 1998, 273, 21015-21024.	3.4	26
59	Coverage-Versus-Length Plots, a Simple Quality Control Step for de Novo Yeast Genome Sequence Assemblies. G3: Genes, Genomes, Genetics, 2019, 9, 879-887.	1.8	26
60	Synthesis, structures and antimicrobial activity of novel NHCâ^—- and Ph3P-Ag(I)-Benzoate derivatives. Inorganica Chimica Acta, 2019, 486, 294-303.	2.4	25
61	Evolution of the complex transcription network controlling biofilm formation in Candida species. ELife, 2021, 10, .	6.0	25
62	The CgHaa1-Regulon Mediates Response and Tolerance to Acetic Acid Stress in the Human Pathogen Candida glabrata. G3: Genes, Genomes, Genetics, 2017, 7, 1-18.	1.8	24
63	Impact of the transcriptional regulator, Ace2, on theCandida glabratasecretome. Proteomics, 2010, 10, 212-223.	2.2	23
64	Evolution of Mating in the Saccharomycotina. Annual Review of Microbiology, 2017, 71, 197-214.	7.3	22
65	Polymorphic centromere locations in the pathogenic yeast Candida parapsilosis. Genome Research, 2020, 30, 684-696.	5.5	22
66	The Evolution ofMAT: The Ascomycetes. , 0, , 1-18.		22
67	Precise genome editing using a CRISPR-Cas9 method highlights the role of CoERG11 amino acid substitutions in azole resistance in Candida orthopsilosis. Journal of Antimicrobial Chemotherapy, 2019, 74, 2230-2238.	3.0	20
68	Candida glabrata Transcription Factor Rpn4 Mediates Fluconazole Resistance through Regulation of Ergosterol Biosynthesis and Plasma Membrane Permeability. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	20
69	Characterization of carboxylate nanoparticle adhesion with the fungal pathogen Candida albicans. Nanoscale, 2017, 9, 15911-15922.	5.6	15
70	Draft Genome Sequence of a Highly Heterozygous Yeast Strain from the Metschnikowia pulcherrima Subclade, UCD127. Genome Announcements, 2018, 6, .	0.8	14
71	Genome analysis of the yeast Diutina catenulata, a member of the Debaryomycetaceae/Metschnikowiaceae (CTG-Ser) clade. PLoS ONE, 2018, 13, e0198957.	2.5	13
72	Cloning, sequencing and expression of the gene for flavodoxin from Megasphaera elsdenii and the effects of removing the protein negative charge that is closest to N(1) of the bound FMN. FEBS Journal, 2000, 267, 4434-4444.	0.2	11

#	Article	IF	Citations
73	Identification of Non-Coding RNAs in the Candida parapsilosis Species Group. PLoS ONE, 2016, 11, e0163235.	2.5	11
74	Dal81 Regulates Expression of Arginine Metabolism Genes in Candida parapsilosis. MSphere, 2018, 3, .	2.9	11
75	Draft Genome Sequence of the Yeast Kazachstania telluris CBS 16338 Isolated from Forest Soil in Ireland. Mycopathologia, 2020, 185, 587-590.	3.1	11
76	Using RNA-seq for Analysis of Differential Gene Expression in Fungal Species. Methods in Molecular Biology, 2016, 1361, 1-40.	0.9	10
77	Identification of an Exceptionally Long Intron in the HAC1 Gene of Candida parapsilosis. MSphere, 2018, 3, .	2.9	10
78	Susceptibility to Medium-Chain Fatty Acids Is Associated with Trisomy of Chromosome 7 in Candida albicans. MSphere, 2019, 4, .	2.9	9
79	From the first touch to biofilm establishment by the human pathogen Candida glabrata: a genome-wide to nanoscale view. Communications Biology, 2021, 4, 886.	4.4	9
80	Correlating Genotype and Phenotype in the Asexual Yeast Candida orthopsilosis Implicates ZCF29 in Sensitivity to Caffeine. G3: Genes, Genomes, Genetics, 2019, 9, 3035-3043.	1.8	8
81	Effect of progesterone on Candida albicans biofilm formation under acidic conditions: A transcriptomic analysis. International Journal of Medical Microbiology, 2020, 310, 151414.	3.6	8
82	Draft Genome Sequences of Two Isolates of the Yeast Kazachstania servazzii Recovered from Soil in Ireland. Microbiology Resource Announcements, 2019, 8, .	0.6	7
83	Genomic differences betweenCandida glabrata andSaccharomyces cerevisiae around theMRPL28 andGCN3 loci. Yeast, 2002, 19, 991-994.	1.7	6
84	Identification of a novel Candida metapsilosis isolate reveals multiple hybridization events. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	6
85	Draft Genome Sequence of the Yeast Nadsonia starkeyi-henricii UCD142, Isolated from Forest Soil in Ireland. Genome Announcements, 2018, 6, .	0.8	5
86	Regulation of expression of the chitinase gene CTS1 in Saccharomyces cerevisiae. Biochemical Society Transactions, 1997, 25, 555S-555S.	3.4	4
87	Draft Genome Sequence of the Birch Tree Fungal Pathogen Taphrina betulina UCD315. Microbiology Resource Announcements, 2019, 8, .	0.6	4
88	Mating-Type Switching in Budding Yeasts, from Flip/Flop Inversion to Cassette Mechanisms. Microbiology and Molecular Biology Reviews, 2022, 86, e0000721.	6.6	4
89	Cloning of Electron-Transferring Flavoprotein from Megasphaera elsdenii. Biochemical Society Transactions, 1995, 23, 379S-379S.	3.4	3
90	93 Inappropriate expression of the yeast transcription factor Ace2p affects cell growth. Biochemical Society Transactions, 1998, 26, S78-S78.	3.4	3

#	Article	IF	Citations
91	Comparative Genomic Analysis of Pathogenic Yeasts and the Evolution of Virulence. , 2010, , 1-18.		3
92	Role of Genomics and RNA-seq in Studies of Fungal Virulence. Current Fungal Infection Reports, 2012, 6, 267-274.	2.6	3
93	Candida Intestinal Domination Precedes Fungal Infections Bloodstream in Allogeneic Hematopoietic Cell Transplant Patients. Biology of Blood and Marrow Transplantation, 2019, 25, S340-S341.	2.0	3
94	Cloning of the gene for flavodoxin from the anaerobic bacterium Megasphaera elsdenii. Biochemical Society Transactions, 1995, 23, 384S-384S.	3.4	2
95	Draft Genome Sequence of a Diploid and Hybrid Candida Strain, Candida sanyaensis UCD423, Isolated from Compost in Ireland. Microbiology Resource Announcements, 2021, 10, e0076121.	0.6	2
96	Draft Genome Sequence of the Yeast Ogataea degrootiae Strain UCD465, Isolated from Soil in Ireland. Microbiology Resource Announcements, 2021, 10, e0073621.	0.6	2
97	Draft Genome Sequence of a Red Basidiomycete Yeast, Symmetrospora coprosmae Strain UCD350, Isolated from Soil in Ireland. Microbiology Resource Announcements, 2019, 8, .	0.6	2
98	Transcriptional Response of Candida parapsilosis following Exposure to Farnesol. Antimicrobial Agents and Chemotherapy, 2008, 52, 2296-2296.	3.2	1
99	Draft Genome Sequences of Two Natural Isolates of the Yeast Barnettozyma californica from Ireland, UCD09 and UCD89. Genome Announcements, 2018, 6, .	0.8	1
100	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
101	Regulated nuclear entry of a yeast transcription factor. Biochemical Society Transactions, 1995, 23, 346S-346S.	3.4	0
102	Potential role of extracellular L-glutamine in the host immune response to yeast infection. Biochemical Society Transactions, 2000, 28, A255-A255.	3.4	0
103	Comparative Genomics of Candida Species. , 0, , 27-43.		0
104	Characterization of the Candida glabrata Transcription Factor CgMar1: Role in Azole Susceptibility. Journal of Fungi (Basel, Switzerland), 2022, 8, 61.	3.5	0