Meleah A Hickman

List of Publications by Year
in descending order

20	745	759233 12	794594 19
papers	citations	h-index	g-index

25	25	25	808
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The â€˜obligate diploidâ€™ Candida albicans forms mating-competent haploids. Nature, 2013, 494, 55-59.	27.8	246
2	Parasexual Ploidy Reduction Drives Population Heterogeneity Through Random and Transient Aneuploidy in Candida albicans. Genetics, 2015, 200, 781-794.	2.9	98
3	High-Resolution SNP/CGH Microarrays Reveal the Accumulation of Loss of Heterozygosity in Commonly UsedCandida albicansStrains. G3: Genes, Genomes, Genetics, 2011, 1, 523-530.	1.8	64
4	Substitution as a Mechanism for Genetic Robustness: The Duplicated Deacetylases Hst1p and Sir2p in Saccharomyces cerevisiae. PLoS Genetics, 2007, 3, e126.	3.5	48
5	Transcriptional silencing functions of the yeast protein Orc1/Sir3 subfunctionalized after gene duplication. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19384-19389.	7.1	48
6	Reinventing Heterochromatin in Budding Yeasts: Sir2 and the Origin Recognition Complex Take Center Stage. Eukaryotic Cell, 2011, 10, 1183-1192.	3.4	47
7	Ploidy tug-of-war: Evolutionary and genetic environments influence the rate of ploidy drive in a human fungal pathogen. Evolution; International Journal of Organic Evolution, 2017, 71, 1025-1038.	2.3	42
8	Phenotypic Consequences of a Spontaneous Loss of Heterozygosity in a Common Laboratory Strain of Candida albicans. Genetics, 2016, 203, 1161-1176.	2.9	28
9	The Sir2-Sum1 Complex Represses Transcription Using Both Promoter-Specific and Long-Range Mechanisms to Regulate Cell Identity and Sexual Cycle in the Yeast Kluyveromyces lactis. PLoS Genetics, 2009, 5, e1000710.	3.5	26
10	Origin Replication Complex Binding, Nucleosome Depletion Patterns, and a Primary Sequence Motif Can Predict Origins of Replication in a Genome with Epigenetic Centromeres. MBio, 2014, 5, e01703-14.	4.1	21
11	A Novel Virulence Phenotype Rapidly Assesses Candida Fungal Pathogenesis in Healthy and Immunocompromised Caenorhabditis elegans Hosts. MSphere, 2019, 4, .	2.9	21
12	The Magnitude ofCandida albicansStress-Induced Genome Instability Results from an Interaction Between Ploidy and Antifungal Drugs. G3: Genes, Genomes, Genetics, 2019, 9, 4019-4027.	1.8	17
13	Host-Induced Genome Instability Rapidly Generates Phenotypic Variation across Candida albicans Strains and Ploidy States. MSphere, 2020, 5, .	2.9	12
14	Host Defense Mechanisms Induce Genome Instability Leading to Rapid Evolution in an Opportunistic Fungal Pathogen. Infection and Immunity, 2022, 90, IAI0032821.	2.2	7
15	Evolution of Distinct Responses to Low NAD+ Stress by Rewiring the Sir2 Deacetylase Network in Yeasts. Genetics, 2020, 214, 855-868.	2.9	6
16	Assessment of Course-Based Research Modules Based on Faculty Research in Introductory Biology. Journal of Microbiology and Biology Education, 2021, 22, .	1.0	4
17	Virulence phenotypes result from interactions between pathogen ploidy and genetic background. Ecology and Evolution, 2020, 10, 9326-9338.	1.9	3
18	The Interplay Between Neutral and Adaptive Processes Shapes Genetic Variation During Candida Species Evolution. Current Clinical Microbiology Reports, 2021, 8, 129-138.	3.4	3

#	Article	IF	Citations
19	Two Infection Assays to Study Non-Lethal Virulence Phenotypes in C. Albicans using C. Elegans. Journal of Visualized Experiments, 2021, , .	0.3	1
20	Increased Virulence and Large-Scale Reduction in Genome Size of Tetraploid Candida albicans Evolved in Nematode Hosts. Frontiers in Fungal Biology, 0, 3, .	2.0	0