

# Maitreya J Dunham

## List of Publications by Year in descending order

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94  
papers

8,382  
citations

81900

39  
h-index

54911

84  
g-index

122  
all docs

122  
docs citations

122  
times ranked

10556  
citing authors

#	ARTICLE	IF	CITATIONS
1	Effects of Aneuploidy on Cellular Physiology and Cell Division in Haploid Yeast. <i>Science</i> , 2007, 317, 916-924.	12.6	811
2	Asymmetric leaves1 mediates leaf patterning and stem cell function in Arabidopsis. <i>Nature</i> , 2000, 408, 967-971.	27.8	716
3	Single-molecule sequencing and chromatin conformation capture enable de novo reference assembly of the domestic goat genome. <i>Nature Genetics</i> , 2017, 49, 643-650.	21.4	600
4	Characteristic genome rearrangements in experimental evolution of <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16144-16149.	7.1	514
5	The Repertoire and Dynamics of Evolutionary Adaptations to Controlled Nutrient-Limited Environments in Yeast. <i>PLoS Genetics</i> , 2008, 4, e1000303.	3.5	417
6	Identification of Aneuploidy-Tolerating Mutations. <i>Cell</i> , 2010, 143, 71-83.	28.9	352
7	The Awesome Power of Yeast Evolutionary Genetics: New Genome Sequences and Strain Resources for the <i>Saccharomyces sensu stricto</i> Genus. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 11-25.	1.8	348
8	Variant Interpretation: Functional Assays to the Rescue. <i>American Journal of Human Genetics</i> , 2017, 101, 315-325.	6.2	275
9	Transcriptional consequences of aneuploidy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12644-12649.	7.1	250
10	Genome-Wide Detection of Polymorphisms at Nucleotide Resolution with a Single DNA Microarray. <i>Science</i> , 2006, 311, 1932-1936.	12.6	242
11	Comparing whole genomes using DNA microarrays. <i>Nature Reviews Genetics</i> , 2008, 9, 291-302.	16.3	194
12	Species-Level Deconvolution of Metagenome Assemblies with Hi-C-Based Contact Probability Maps. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1339-1346.	1.8	177
13	Genome-wide Consequences of Deleting Any Single Gene. <i>Molecular Cell</i> , 2013, 52, 485-494.	9.7	163
14	Functional Analysis of Gene Duplications in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2007, 175, 933-943.	2.9	148
15	Loss of Heterozygosity Drives Adaptation in Hybrid Yeast. <i>Molecular Biology and Evolution</i> , 2017, 34, 1596-1612.	8.9	147
16	Integrative phenomics reveals insight into the structure of phenotypic diversity in budding yeast. <i>Genome Research</i> , 2013, 23, 1496-1504.	5.5	138
17	Accurate detection of aneuploidies in array CGH and gene expression microarray data. <i>Bioinformatics</i> , 2004, 20, 3533-3543.	4.1	109
18	A Low Cost, Customizable Turbidostat for Use in Synthetic Circuit Characterization. <i>ACS Synthetic Biology</i> , 2015, 4, 32-38.	3.8	108

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19	The enduring utility of continuous culturing in experimental evolution. <i>Genomics</i> , 2014, 104, 399-405.	2.9	104
20	Predicting Cellular Growth from Gene Expression Signatures. <i>PLoS Computational Biology</i> , 2009, 5, e1000257.	3.2	97
21	Evolution of protein phosphorylation across 18 fungal species. <i>Science</i> , 2016, 354, 229-232.	12.6	93
22	The Fitness Consequences of Aneuploidy Are Driven by Condition-Dependent Gene Effects. <i>PLoS Biology</i> , 2015, 13, e1002155.	5.6	90
23	Whole-genome sequencing of a laboratory-evolved yeast strain. <i>BMC Genomics</i> , 2010, 11, 88.	2.8	88
24	Mapping Novel Traits by Array-Assisted Bulk Segregant Analysis in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2006, 173, 1813-1816.	2.9	86
25	The Yeast Alix Homolog Bro1 Functions as a Ubiquitin Receptor for Protein Sorting into Multivesicular Endosomes. <i>Developmental Cell</i> , 2013, 25, 520-533.	7.0	83
26	Fis1 deficiency selects for compensatory mutations responsible for cell death and growth control defects. <i>Cell Death and Differentiation</i> , 2008, 15, 1838-1846.	11.2	77
27	Design and Use of Multiplexed Chemostat Arrays. <i>Journal of Visualized Experiments</i> , 2013, , e50262.	0.3	73
28	The Dynamics of Diverse Segmental Amplifications in Populations of <i>Saccharomyces cerevisiae</i> Adapting to Strong Selection. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 399-409.	1.8	73
29	High-Throughput Identification of Adaptive Mutations in Experimentally Evolved Yeast Populations. <i>PLoS Genetics</i> , 2016, 12, e1006339.	3.5	72
30	Experimental Evolution Reveals Favored Adaptive Routes to Cell Aggregation in Yeast. <i>Genetics</i> , 2017, 206, 1153-1167.	2.9	69
31	Genetic Analysis of Desiccation Tolerance in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2011, 189, 507-519.	2.9	65
32	Accurate identification of centromere locations in yeast genomes using Hi-C. <i>Nucleic Acids Research</i> , 2015, 43, 5331-5339.	14.5	61
33	A polyploid admixed origin of beer yeasts derived from European and Asian wine populations. <i>PLoS Biology</i> , 2019, 17, e3000147.	5.6	58
34	The dynamic three-dimensional organization of the diploid yeast genome. <i>ELife</i> , 2017, 6, .	6.0	57
35	An autonomously replicating sequence for use in a wide range of budding yeasts. <i>FEMS Yeast Research</i> , 2014, 14, 364-367.	2.3	55
36	Competitive Repair by Naturally Dispersed Repetitive DNA during Non-Allelic Homologous Recombination. <i>PLoS Genetics</i> , 2010, 6, e1001228.	3.5	54

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37	High-resolution mapping, characterization, and optimization of autonomously replicating sequences in yeast. <i>Genome Research</i> , 2013, 23, 698-704.	5.5	53
38	Massively parallel characterization of CYP2C9 variant enzyme activity and abundance. <i>American Journal of Human Genetics</i> , 2021, 108, 1735-1751.	6.2	53
39	Origin-Dependent Inverted-Repeat Amplification: A Replication-Based Model for Generating Palindromic Amplicons. <i>PLoS Genetics</i> , 2011, 7, e1002016.	3.5	51
40	Global Mapping of Transposon Location. <i>PLoS Genetics</i> , 2006, 2, e212.	3.5	45
41	GC-Rich DNA Elements Enable Replication Origin Activity in the Methylophilic Yeast <i>Pichia pastoris</i> . <i>PLoS Genetics</i> , 2014, 10, e1004169.	3.5	44
42	Origin-Dependent Inverted-Repeat Amplification: Tests of a Model for Inverted DNA Amplification. <i>PLoS Genetics</i> , 2015, 11, e1005699.	3.5	42
43	Synthetic ecology: A model system for cooperation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1741-1742.	7.1	39
44	Ploidy-Regulated Variation in Biofilm-Related Phenotypes in Natural Isolates of <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1773-1786.	1.8	39
45	Control of Plasma Membrane Permeability by ABC Transporters. <i>Eukaryotic Cell</i> , 2015, 14, 442-453.	3.4	39
46	Characterization of a panARS-based episomal vector in the methylotrophic yeast <i>Pichia pastoris</i> for recombinant protein production and synthetic biology applications. <i>Microbial Cell Factories</i> , 2016, 15, 139.	4.0	38
47	Translocation and Assembly of Mitochondrially Coded <i>Saccharomyces cerevisiae</i> Cytochrome <i>c</i> Oxidase Subunit Cox2 by Oxa1 and Yme1 in the Absence of Cox18. <i>Genetics</i> , 2009, 182, 519-528.	2.9	36
48	Expression and Functional Characterization of Breast Cancer-Associated Cytochrome P450 4Z1 in <i>Saccharomyces cerevisiae</i> . <i>Drug Metabolism and Disposition</i> , 2017, 45, 1364-1371.	3.3	35
49	Contemporary, yeast-based approaches to understanding human genetic variation. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 658-664.	3.3	34
50	Neocentromeres Provide Chromosome Segregation Accuracy and Centromere Clustering to Multiple Loci along a <i>Candida albicans</i> Chromosome. <i>PLoS Genetics</i> , 2016, 12, e1006317.	3.5	34
51	Evolutionary engineering of a wine yeast strain revealed a key role of inositol and mannoprotein metabolism during low-temperature fermentation. <i>BMC Genomics</i> , 2015, 16, 537.	2.8	33
52	The Hidden Complexity of Mendelian Traits across Natural Yeast Populations. <i>Cell Reports</i> , 2016, 16, 1106-1114.	6.4	31
53	Identification of a novel interspecific hybrid yeast from a metagenomic spontaneously inoculated beer sample using Hi-C. <i>Yeast</i> , 2018, 35, 71-84.	1.7	31
54	Temperature preference can bias parental genome retention during hybrid evolution. <i>PLoS Genetics</i> , 2019, 15, e1008383.	3.5	30

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55	Fitness benefits of loss of heterozygosity in <i>Saccharomyces</i> hybrids. <i>Genome Research</i> , 2019, 29, 1685-1692.	5.5	29
56	Aneuploidy shortens replicative lifespan in <i>Saccharomyces cerevisiae</i> . <i>Aging Cell</i> , 2016, 15, 317-324.	6.7	28
57	The environmental stress response causes ribosome loss in aneuploid yeast cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17031-17040.	7.1	28
58	A modified fluctuation assay reveals a natural mutator phenotype that drives mutation spectrum variation within <i>Saccharomyces cerevisiae</i> . <i>ELife</i> , 2021, 10, .	6.0	28
59	A New System for Comparative Functional Genomics of <i>Saccharomyces</i> Yeasts. <i>Genetics</i> , 2013, 195, 275-287.	2.9	27
60	Transposable Element Mobilization in Interspecific Yeast Hybrids. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	26
61	The Ras/cAMP Pathway and the CDK-Like Kinase Ime2 Regulate the MAPK Smk1 and Spore Morphogenesis in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2009, 181, 511-523.	2.9	25
62	Differential paralog divergence modulates genome evolution across yeast species. <i>PLoS Genetics</i> , 2017, 13, e1006585.	3.5	25
63	Transposon insertional mutagenesis in <i>Saccharomyces uvarum</i> reveals <i>trans</i> -acting effects influencing species-dependent essential genes. <i>Genome Research</i> , 2019, 29, 396-406.	5.5	24
64	Systematic Planning of Genome-Scale Experiments in Poorly Studied Species. <i>PLoS Computational Biology</i> , 2010, 6, e1000698.	3.2	22
65	Comprehensive Analysis of the <i>SUL1</i> Promoter of <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2016, 203, 191-202.	2.9	22
66	Comparative gene expression between two yeast species. <i>BMC Genomics</i> , 2013, 14, 33.	2.8	21
67	Coupling Unbiased Mutagenesis to High-throughput DNA Sequencing Uncovers Functional Domains in the Ndc80 Kinetochore Protein of <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2013, 195, 159-170.	2.9	21
68	Phased polyploid genomes provide deeper insight into the multiple origins of domesticated <i>Saccharomyces cerevisiae</i> beer yeasts. <i>Current Biology</i> , 2022, 32, 1350-1361.e3.	3.9	19
69	Mutability and mutational spectrum of chromosome transmission fidelity genes. <i>Chromosoma</i> , 2012, 121, 263-275.	2.2	17
70	A combination of transcription factors mediates inducible interchromosomal contacts. <i>ELife</i> , 2019, 8, .	6.0	16
71	Applying Multiplex Assays to Understand Variation in Pharmacogenes. <i>Clinical Pharmacology and Therapeutics</i> , 2019, 106, 290-294.	4.7	15
72	Multiplexing mutation rate assessment: determining pathogenicity of Msh2 variants in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2021, 218, .	2.9	12

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73	Experimental Evolution in Yeast. <i>Methods in Enzymology</i> , 2010, 470, 487-507.	1.0	11
74	Population Genomics and Transcriptional Consequences of Regulatory Motif Variation in Globally Diverse <i>Saccharomyces cerevisiae</i> Strains. <i>Molecular Biology and Evolution</i> , 2013, 30, 1605-1613.	8.9	11
75	High Throughput Analyses of Budding Yeast ARSs Reveal New DNA Elements Capable of Conferring Centromere-Independent Plasmid Propagation. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 993-1012.	1.8	11
76	Chemostat Culture for Yeast Physiology and Experimental Evolution. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.top077610.	0.3	10
77	A multiplex culture system for the long-term growth of fission yeast cells. <i>Yeast</i> , 2017, 34, 343-355.	1.7	9
78	Phenotypic and Genotypic Consequences of CRISPR/Cas9 Editing of the Replication Origins in the rDNA of <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2019, 213, 229-249.	2.9	9
79	Measuring Pharmacogene Variant Function at Scale Using Multiplexed Assays. <i>Annual Review of Pharmacology and Toxicology</i> , 2022, 62, 531-550.	9.4	9
80	Telomere behavior in a hybrid yeast. <i>Cell Research</i> , 2009, 19, 910-912.	12.0	8
81	Nucleosome-coupled expression differences in closely-related species. <i>BMC Genomics</i> , 2011, 12, 466.	2.8	7
82	Assembly of a Mini-Chemostat Array. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot088997.	0.3	7
83	Effect of the Ala234Asp replacement in mitochondrial branched-chain amino acid aminotransferase on the production of BCAAs and fusel alcohols in yeast. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 7915-7925.	3.6	7
84	Viewing the Larger Context of Genomic Data through Horizontal Integration. <i>Proceedings / International Conference on Information Visualisation</i> , 2007, , .	0.0	6
85	Two Flavors of Bulk Segregant Analysis in Yeast. <i>Methods in Molecular Biology</i> , 2012, 871, 41-54.	0.9	6
86	Multiple Pathways Regulate Minisatellite Stability During Stationary Phase in Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1185-1195.	1.8	5
87	PacRAT: a program to improve barcode-variant mapping from PacBio long reads using multiple sequence alignment. <i>Bioinformatics</i> , 2022, 38, 2927-2929.	4.1	5
88	Chemostat Culture for Yeast Experimental Evolution. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot089011.	0.3	3
89	Dietary Change Enables Robust Growth-Coupling of Heterologous Methyltransferase Activity in Yeast. <i>ACS Synthetic Biology</i> , 2020, 9, 3408-3415.	3.8	3
90	Experimental Evolution and Resequencing Analysis of Yeast. <i>Methods in Molecular Biology</i> , 2016, 1361, 361-374.	0.9	3

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91	Directed evolution as an approach to increase fructose utilization in synthetic grape juice by wine yeast AWRI 796. FEMS Yeast Research, 2022, 22, .	2.3	3
92	Chemostat Culture for Yeast Physiology. Cold Spring Harbor Protocols, 2017, 2017, pdb.prot089003.	0.3	2
93	Scalable, Dynamic Analysis and Visualization for Genomic Datasets. , 2007, , .		1
94	University of Washington Nathan Shock Center: innovation to advance aging research. GeroScience, 2021, 43, 2161-2165.	4.6	1