

Chris Hittinger

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

95
papers

5,014
citations

38
h-index

70
g-index

117
ext. papers

6,820
ext. citations

9.9
avg, IF

5.95
L-index

#	Paper	IF	Citations
95	Microbe domestication and the identification of the wild genetic stock of lager-brewing yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 14539-44	11.5	450
94	Gene duplication and the adaptive evolution of a classic genetic switch. <i>Nature</i> , 2007 , 449, 677-81	50.4	306
93	Contentious relationships in phylogenomic studies can be driven by a handful of genes. <i>Nature Ecology and Evolution</i> , 2017 , 1, 126	12.3	246
92	Identifying genes of agronomic importance in maize by screening microsatellites for evidence of selection during domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 9650-5	11.5	241
91	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	3.2	231
90	Comparative genomics of biotechnologically important yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 9882-7	11.5	212
89	Tempo and Mode of Genome Evolution in the Budding Yeast Subphylum. <i>Cell</i> , 2018 , 175, 1533-1545.e2056.2	20.4	204
88	Parallel inactivation of multiple GAL pathway genes and ecological diversification in yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 14144-9	11.5	160
87	The Genome Sequence of <i>Saccharomyces eubayanus</i> and the Domestication of Lager-Brewing Yeasts. <i>Molecular Biology and Evolution</i> , 2015 , 32, 2818-31	8.3	140
86	A Gondwanan imprint on global diversity and domestication of wine and cider yeast <i>Saccharomyces uvarum</i> . <i>Nature Communications</i> , 2014 , 5, 4044	17.4	139
85	Benchmarking next-generation transcriptome sequencing for functional and evolutionary genomics. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2731-44	8.3	134
84	Reconstructing the Backbone of the Saccharomycotina Yeast Phylogeny Using Genome-Scale Data. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 3927-3939	3.2	126
83	<i>Saccharomyces</i> diversity and evolution: a budding model genus. <i>Trends in Genetics</i> , 2013 , 29, 309-17	8.5	126
82	Speciation driven by hybridization and chromosomal plasticity in a wild yeast. <i>Nature Microbiology</i> , 2016 , 1, 15003	26.6	120
81	Remarkably ancient balanced polymorphisms in a multi-locus gene network. <i>Nature</i> , 2010 , 464, 54-8	50.4	119
80	Population structure and reticulate evolution of <i>Saccharomyces eubayanus</i> and its lager-brewing hybrids. <i>Molecular Ecology</i> , 2014 , 23, 2031-45	5.7	103
79	Leveraging skewed transcript abundance by RNA-Seq to increase the genomic depth of the tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 1476-81	11.5	94

78	Evaluating Fast Maximum Likelihood-Based Phylogenetic Programs Using Empirical Phylogenomic Data Sets. <i>Molecular Biology and Evolution</i> , 2018 , 35, 486-503	8.3	82
77	Genomics and the making of yeast biodiversity. <i>Current Opinion in Genetics and Development</i> , 2015 , 35, 100-9	4.9	79
76	New yeasts-new brews: modern approaches to brewing yeast design and development. <i>FEMS Yeast Research</i> , 2017 , 17,	3.1	75
75	Complex Ancestries of Lager-Brewing Hybrids Were Shaped by Standing Variation in the Wild Yeast <i>Saccharomyces eubayanus</i> . <i>PLoS Genetics</i> , 2016 , 12, e1006155	6	72
74	Diverse yeasts for diverse fermented beverages and foods. <i>Current Opinion in Biotechnology</i> , 2018 , 49, 199-206	11.4	63
73	Toward a Fully Resolved Fungal Tree of Life. <i>Annual Review of Microbiology</i> , 2020 , 74, 291-313	17.5	61
72	Extensive loss of cell-cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. <i>PLoS Biology</i> , 2019 , 17, e3000255	9.7	59
71	Temperature and host preferences drive the diversification of <i>Saccharomyces</i> and other yeasts: a survey and the discovery of eight new yeast species. <i>FEMS Yeast Research</i> , 2015 , 15,	3.1	56
70	A Molecular Portrait of De Novo Genes in Yeasts. <i>Molecular Biology and Evolution</i> , 2018 , 35, 631-645	8.3	53
69	Hybridization and adaptive evolution of diverse species for cellulosic biofuel production. <i>Biotechnology for Biofuels</i> , 2017 , 10, 78	7.8	52
68	Horizontally acquired genes in early-diverging pathogenic fungi enable the use of host nucleosides and nucleotides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 4116-21	11.5	50
67	Local climatic adaptation in a widespread microorganism. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014 , 281, 20132472	4.4	49
66	Directed Evolution Reveals Unexpected Epistatic Interactions That Alter Metabolic Regulation and Enable Anaerobic Xylose Use by <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2016 , 12, e1006372	6	49
65	On the origins and industrial applications of <i>Saccharomyces cerevisiae</i> × <i>Saccharomyces kudriavzevii</i> hybrids. <i>Yeast</i> , 2018 , 35, 51-69	3.4	46
64	Eukaryotic Acquisition of a Bacterial Operon. <i>Cell</i> , 2019 , 176, 1356-1366.e10	56.2	45
63	Mitochondrial DNA and temperature tolerance in lager yeasts. <i>Science Advances</i> , 2019 , 5, eaav1869	14.3	44
62	Functional and evolutionary characterization of a secondary metabolite gene cluster in budding yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 11030-11035	11.5	44
61	Pleiotropic functions of a conserved insect-specific Hox peptide motif. <i>Development (Cambridge)</i> , 2005 , 132, 5261-70	6.6	43

60	Fermentation innovation through complex hybridization of wild and domesticated yeasts. <i>Nature Ecology and Evolution</i> , 2019 , 3, 1576-1586	12.3	42
59	Efficient engineering of marker-free synthetic allotetraploids of <i>Saccharomyces</i> . <i>Fungal Genetics and Biology</i> , 2016 , 89, 10-17	3.9	39
58	Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. <i>Nature Communications</i> , 2018 , 9, 1887	17.4	38
57	Evidence for loss and reacquisition of alcoholic fermentation in a fructophilic yeast lineage. <i>ELife</i> , 2018 , 7,	8.9	36
56	Genome Sequence and Analysis of a Stress-Tolerant, Wild-Derived Strain of <i>Saccharomyces cerevisiae</i> Used in Biofuels Research. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 1757-66	3.2	35
55	Mitochondria-encoded genes contribute to evolution of heat and cold tolerance in yeast. <i>Science Advances</i> , 2019 , 5, eaav1848	14.3	34
54	Dynamic Evolution of Nitric Oxide Detoxifying Flavohemoglobins, a Family of Single-Protein Metabolic Modules in Bacteria and Eukaryotes. <i>Molecular Biology and Evolution</i> , 2016 , 33, 1979-87	8.3	31
53	Genomic analysis and D-xylose fermentation of three novel <i>Spathaspora</i> species: <i>Spathaspora girioi</i> sp. nov., <i>Spathaspora hagerdaliae</i> f. a., sp. nov. and <i>Spathaspora gorwiae</i> f. a., sp. nov. <i>FEMS Yeast Research</i> , 2016 , 16,	3.1	31
52	A genome-scale phylogeny of the kingdom Fungi. <i>Current Biology</i> , 2021 , 31, 1653-1665.e5	6.3	29
51	Whole Genome Sequencer and Analyzer (iWGS): a Computational Pipeline to Guide the Design and Analysis of Genome Sequencing Studies. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 3655-3662	3.2	28
50	Pathogenic budding yeasts isolated outside of clinical settings. <i>FEMS Yeast Research</i> , 2019 , 19,	3.1	26
49	Evolution of a novel chimeric maltotriose transporter in <i>Saccharomyces eubayanus</i> from parent proteins unable to perform this function. <i>PLoS Genetics</i> , 2019 , 15, e1007786	6	25
48	Variation and selection on codon usage bias across an entire subphylum. <i>PLoS Genetics</i> , 2019 , 15, e1008304	10.4	25
47	sppIDer: A Species Identification Tool to Investigate Hybrid Genomes with High-Throughput Sequencing. <i>Molecular Biology and Evolution</i> , 2018 , 35, 2835-2849	8.3	25
46	Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. <i>Science Advances</i> , 2020 , 6,	14.3	24
45	Phylogeography of the wild Lager-brewing ancestor (<i>Saccharomyces eubayanus</i>) in Patagonia. <i>Environmental Microbiology</i> , 2018 , 20, 3732-3743	5.2	22
44	Comparative genomics provides new insights into the diversity, physiology, and sexuality of the only industrially exploited tremellomycete: <i>Phaffia rhodozyma</i> . <i>BMC Genomics</i> , 2016 , 17, 901	4.5	22
43	High-efficiency genome editing and allele replacement in prototrophic and wild strains of <i>Saccharomyces</i> . <i>Genetics</i> , 2014 , 198, 859-66	4	20

42	Natural Variation in the Multidrug Efflux Pump Underlies Ionic Liquid Tolerance in Yeast. <i>Genetics</i> , 2018 , 210, 219-234	4	19
41	Ongoing resolution of duplicate gene functions shapes the diversification of a metabolic network. <i>ELife</i> , 2016 , 5,	8.9	18
40	Synthetic hybrids of six yeast species. <i>Nature Communications</i> , 2020 , 11, 2085	17.4	17
39	Multiple Reinventions of Mating-type Switching during Budding Yeast Evolution. <i>Current Biology</i> , 2019 , 29, 2555-2562.e8	6.3	16
38	ESTs from the basidiomycete Schizophyllum commune grown on nitrogen-replete and nitrogen-limited media. <i>Fungal Genetics and Biology</i> , 2003 , 39, 191-8	3.9	16
37	Towards yeast taxogenomics: lessons from novel species descriptions based on complete genome sequences. <i>FEMS Yeast Research</i> , 2020 , 20,	3.1	16
36	Factors driving metabolic diversity in the budding yeast subphylum. <i>BMC Biology</i> , 2018 , 16, 26	7.3	15
35	Transcriptional rewiring: the proof is in the eating. <i>Current Biology</i> , 2007 , 17, R626-8	6.3	15
34	Genomic content of a novel yeast species <i>Hanseniaspora gamundiae</i> sp. nov. from fungal stromata (Cyttaria) associated with a unique fermented beverage in Andean Patagonia, Argentina. <i>PLoS ONE</i> , 2019 , 14, e0210792	3.7	14
33	Microbial Diversity Associated with the Pollen Stores of Captive-Bred Bumble Bee Colonies. <i>Insects</i> , 2020 , 11,	2.8	14
32	<i>Spathaspora boniae</i> sp. nov., a D-xylose-fermenting species in the <i>Candida albicans</i> / <i>Lodderomyces</i> clade. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017 , 67, 3798-3805	2.2	14
31	Repeated Cis-Regulatory Tuning of a Metabolic Bottleneck Gene during Evolution. <i>Molecular Biology and Evolution</i> , 2018 , 35, 1968-1981	8.3	12
30	Into the wild: new yeast genomes from natural environments and new tools for their analysis. <i>FEMS Yeast Research</i> , 2020 , 20,	3.1	11
29	Population genomics of the pathogenic yeast <i>Candida tropicalis</i> identifies hybrid isolates in environmental samples. <i>PLoS Pathogens</i> , 2021 , 17, e1009138	7.6	11
28	Postglacial migration shaped the genomic diversity and global distribution of the wild ancestor of lager-brewing hybrids. <i>PLoS Genetics</i> , 2020 , 16, e1008680	6	11
27	Genome sequence and physiological analysis of <i>Yamadazyma laniorum</i> f.a. sp. nov. and a reevaluation of the apocryphal xylose fermentation of its sister species, <i>Candida tenuis</i> . <i>FEMS Yeast Research</i> , 2017 , 17,	3.1	9
26	Evolution of an insect-specific GROUCHO-interaction motif in the ENGRAILED selector protein. <i>Evolution & Development</i> , 2008 , 10, 537-45	2.6	9
25	An investigation of irreproducibility in maximum likelihood phylogenetic inference. <i>Nature Communications</i> , 2020 , 11, 6096	17.4	9

24	Empirical, Metagenomic, and Computational Techniques Illuminate the Mechanisms by which Fungicides Compromise Bee Health. <i>Journal of Visualized Experiments</i> , 2017 ,	1.6	8
23	Draft Genome Sequence of <i>Sporidiobolus salmonicolor</i> CBS 6832, a Red-Pigmented Basidiomycetous Yeast. <i>Genome Announcements</i> , 2015 , 3,		6
22	A genome-scale phylogeny of Fungi; insights into early evolution, radiations, and the relationship between taxonomy and phylogeny		6
21	Evolution. Endless rots most beautiful. <i>Science</i> , 2012 , 336, 1649-50	33.3	4
20	Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota		4
19	Mitochondrial DNA and temperature tolerance in lager yeasts		3
18	in silico Whole Genome Sequencer & Analyzer (iWGS): a computational pipeline to guide the design and analysis of de novo genome sequencing studies		3
17	Evaluating fast maximum likelihood-based phylogenetic programs using empirical phylogenomic data sets		3
16	Nomenclatural issues concerning cultured yeasts and other fungi: why it is important to avoid unneeded name changes. <i>IMA Fungus</i> , 2021 , 12, 18	6.8	3
15	sp. nov., a Novel Apiculate Yeast Species From Patagonian Forests That Lacks the Typical Genomic Domestication Signatures for Fermentative Environments. <i>Frontiers in Microbiology</i> , 2021 , 12, 679894	5.7	3
14	Crabtree/Warburg-like aerobic xylose fermentation by engineered <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2021 , 68, 119-130	9.7	3
13	Evolution of a novel chimeric maltotriose transporter in <i>Saccharomyces eubayanus</i> from parent proteins unable to perform this function		2
12	CRISpy-Pop: A Web Tool for Designing CRISPR/Cas9-Driven Genetic Modifications in Diverse Populations. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 4287-4294	3.2	2
11	Signatures of optimal codon usage in metabolic genes inform budding yeast ecology. <i>PLoS Biology</i> , 2021 , 19, e3001185	9.7	2
10	sppIDer: a species identification tool to investigate hybrid genomes with high-throughput sequencing		1
9	Mitochondria-encoded genes contribute to the evolution of heat and cold tolerance among <i>Saccharomyces</i> species		1
8	Genomic diversity and global distribution of <i>Saccharomyces eubayanus</i> , the wild ancestor of hybrid lager-brewing yeasts		1
7	CRISpy-pop: a web tool for designing CRISPR/Cas9-driven genetic modifications in diverse populations		1

6	Repeated horizontal gene transfer of GALactose metabolism genes violates Dollo's law of irreversible loss. <i>Genetics</i> , 2021 , 217,	4	1
5	Reconstructing the backbone of the Saccharomycotina yeast phylogeny using genome-scale data		1
4	Synthetic hybrids of six yeast species		1
3	An orthologous gene coevolution network provides insight into eukaryotic cellular and genomic structure and function.. <i>Science Advances</i> , 2022 , 8, eabn0105	14.3	0
2	Evaluation of Kuroda et al.: Insight into Yeast Isobutanol Tolerance with Advances Still Needed. <i>Cell Systems</i> , 2020 , 10, 124	10.6	
1	Comparative functional genomics identifies an iron-limited bottleneck in a strain with a cytosolic-localized isobutanol pathway.. <i>Synthetic and Systems Biotechnology</i> , 2022 , 7, 738-749	4.2	