

Gianni Liti

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3505305/publications.pdf>

Version: 2024-02-01

92
papers

8,588
citations

81900

39
h-index

53230

85
g-index

112
all docs

112
docs citations

112
times ranked

5963
citing authors

#	ARTICLE	IF	CITATIONS
1	Yeasts from temperate forests. <i>Yeast</i> , 2022, 39, 4-24.	1.7	18
2	Domestication reprogrammed the budding yeast life cycle. <i>Nature Ecology and Evolution</i> , 2022, 6, 448-460.	7.8	32
3	Extensive sampling of <i>Saccharomyces cerevisiae</i> in Taiwan reveals ecology and evolution of predomesticated lineages. <i>Genome Research</i> , 2022, , .	5.5	13
4	Unlocking the functional potential of polyploid yeasts. <i>Nature Communications</i> , 2022, 13, 2580.	12.8	10
5	RecombineX: A generalized computational framework for automatic high-throughput gamete genotyping and tetrad-based recombination analysis. <i>PLoS Genetics</i> , 2022, 18, e1010047.	3.5	5
6	Extensive simulations assess the performance of genome-wide association mapping in various <i>Saccharomyces cerevisiae</i> subpopulations. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	4.0	3
7	miRNAs Copy Number Variations Repertoire as Hallmark Indicator of Cancer Species Predisposition. <i>Genes</i> , 2022, 13, 1046.	2.4	5
8	Resistance to Arsenite and Arsenate in <i>Saccharomyces cerevisiae</i> Arises through the Subtelomeric Expansion of a Cluster of Yeast Genes. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 8119.	2.6	5
9	The budding yeast life cycle: More complex than anticipated?. <i>Yeast</i> , 2021, 38, 5-11.	1.7	18
10	Meiotic Cells Counteract Programmed Retrotransposon Activation via RNA-Binding Translational Repressor Assemblies. <i>Developmental Cell</i> , 2021, 56, 22-35.e7.	7.0	8
11	Natural variants suppress mutations in hundreds of essential genes. <i>Molecular Systems Biology</i> , 2021, 17, e10138.	7.2	13
12	Lager Yeast Design Through Meiotic Segregation of a <i>Saccharomyces cerevisiae</i> × <i>Saccharomyces eubayanus</i> Hybrid. <i>Frontiers in Fungal Biology</i> , 2021, 2, .	2.0	12
13	Aborting meiosis allows recombination in sterile diploid yeast hybrids. <i>Nature Communications</i> , 2021, 12, 6564.	12.8	14
14	Comparison of Phylogenetic Tree Topologies for Nitrogen Associated Genes Partially Reconstruct the Evolutionary History of <i>Saccharomyces cerevisiae</i> . <i>Microorganisms</i> , 2020, 8, 32.	3.6	26
15	Population Size, Sex and Purifying Selection: Comparative Genomics of Two Sister Taxa of the Wild Yeast <i>Saccharomyces paradoxus</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 1636-1645.	2.5	7
16	A yeast living ancestor reveals the origin of genomic introgressions. <i>Nature</i> , 2020, 587, 420-425.	27.8	45
17	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.	1.8	11
18	An Out-of-Patagonia migration explains the worldwide diversity and distribution of <i>Saccharomyces eubayanus</i> lineages. <i>PLoS Genetics</i> , 2020, 16, e1008777.	3.5	34

#	ARTICLE	IF	CITATIONS
19	Discordant evolution of mitochondrial and nuclear yeast genomes at population level. BMC Biology, 2020, 18, 49.	3.8	42
20	Differential Gene Expression and Allele Frequency Changes Favour Adaptation of a Heterogeneous Yeast Population to Nitrogen-Limited Fermentations. Frontiers in Microbiology, 2020, 11, 1204.	3.5	3
21	Human <i>RAP80</i> specifically protects telomeres of senescent cells from DNA damage. EMBO Reports, 2020, 21, e49076.	4.5	43
22	Intragenic repeat expansion in the cell wall protein gene <i>HPF1</i> controls yeast chronological aging. Genome Research, 2020, 30, 697-710.	5.5	23
23	Transcriptional Activity and Protein Levels of Horizontally Acquired Genes in Yeast Reveal Hallmarks of Adaptation to Fermentative Environments. Frontiers in Genetics, 2020, 11, 293.	2.3	16
24	Genetic variants of TORC1 signaling pathway affect nitrogen consumption in <i>Saccharomyces cerevisiae</i> during alcoholic fermentation. PLoS ONE, 2019, 14, e0220515.	2.5	55
25	simuG: a general-purpose genome simulator. Bioinformatics, 2019, 35, 4442-4444.	4.1	41
26	Accurate Tracking of the Mutational Landscape of Diploid Hybrid Genomes. Molecular Biology and Evolution, 2019, 36, 2861-2877.	8.9	41
27	Shared Molecular Targets Confer Resistance over Short and Long Evolutionary Timescales. Molecular Biology and Evolution, 2019, 36, 691-708.	8.9	43
28	André Goffeau's imprinting on second generation yeast <i>œgenomologists</i> . Yeast, 2019, 36, 167-175.	1.7	1
29	Genome evolution across 1,011 <i>Saccharomyces cerevisiae</i> isolates. Nature, 2018, 556, 339-344.	27.8	952
30	Long-read sequencing data analysis for yeasts. Nature Protocols, 2018, 13, 1213-1231.	12.0	43
31	Tetrad analysis in plants and fungi finds large differences in gene conversion rates but no GC bias. Nature Ecology and Evolution, 2018, 2, 164-173.	7.8	65
32	Yeast chromosome numbers minimized using genome editing. Nature, 2018, 560, 317-318.	27.8	3
33	The genetic architecture of low-temperature adaptation in the wine yeast <i>Saccharomyces cerevisiae</i> . BMC Genomics, 2017, 18, 159.	2.8	58
34	Contrasting evolutionary genome dynamics between domesticated and wild yeasts. Nature Genetics, 2017, 49, 913-924.	21.4	340
35	De novo yeast genome assemblies from MinION, PacBio and MiSeq platforms. Scientific Reports, 2017, 7, 3935.	3.3	146
36	Mismatch Repair Incompatibilities in Diverse Yeast Populations. Genetics, 2017, 205, 1459-1471.	2.9	22

#	ARTICLE	IF	CITATIONS
37	Clonal Heterogeneity Influences the Fate of New Adaptive Mutations. <i>Cell Reports</i> , 2017, 21, 732-744.	6.4	70
38	Isolation and Laboratory Domestication of Natural Yeast Strains. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot089052.	0.3	16
39	Mapping Quantitative Trait Loci in Yeast. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot089060.	0.3	6
40	Budding Yeast Strains and Genotype-Phenotype Mapping. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.top077735.	0.3	6
41	Yeast Reciprocal Hemizygosity to Confirm the Causality of a Quantitative Trait Loci-Associated Gene. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot089078.	0.3	7
42	de novo assembly and population genomic survey of natural yeast isolates with the Oxford Nanopore MinION sequencer. <i>GigaScience</i> , 2017, 6, 1-13.	6.4	123
43	Identification of Nitrogen Consumption Genetic Variants in Yeast Through QTL Mapping and Bulk Segregant RNA-Seq Analyses. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1693-1705.	1.8	87
44	Predicting quantitative traits from genome and phenome with near perfect accuracy. <i>Nature Communications</i> , 2016, 7, 11512.	12.8	32
45	Ploidy influences the functional attributes of de novo lager yeast hybrids. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 7203-7222.	3.6	75
46	Yeast2.0: a new chapter. <i>Yeast</i> , 2016, 33, 3-4.	1.7	1
47	Powerful decomposition of complex traits in a diploid model. <i>Nature Communications</i> , 2016, 7, 13311.	12.8	34
48	Extensive Recombination of a Yeast Diploid Hybrid through Meiotic Reversion. <i>PLoS Genetics</i> , 2016, 12, e1005781.	3.5	60
49	The fascinating and secret wild life of the budding yeast <i>S. cerevisiae</i> . <i>ELife</i> , 2015, 4, .	6.0	147
50	Elucidating the molecular architecture of adaptation via evolve and resequence experiments. <i>Nature Reviews Genetics</i> , 2015, 16, 567-582.	16.3	236
51	Concerted Evolution of Life Stage Performances Signals Recent Selection on Yeast Nitrogen Use. <i>Molecular Biology and Evolution</i> , 2015, 32, 153-161.	8.9	86
52	ATG18 and FAB1 Are Involved in Dehydration Stress Tolerance in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2015, 10, e0119606.	2.5	12
53	Mapping Genetic Variants Underlying Differences in the Central Nitrogen Metabolism in Fermenter Yeasts. <i>PLoS ONE</i> , 2014, 9, e86533.	2.5	96
54	Kinetochore assembly and heterochromatin formation occur autonomously in <i>Schizosaccharomyces pombe</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1903-1908.	7.1	16

#	ARTICLE	IF	CITATIONS
55	High-quality genome (re)assembly using chromosomal contact data. <i>Nature Communications</i> , 2014, 5, 5695.	12.8	142
56	A High-Definition View of Functional Genetic Variation from Natural Yeast Genomes. <i>Molecular Biology and Evolution</i> , 2014, 31, 872-888.	8.9	328
57	Filling annotation gaps in yeast genomes using genome-wide contact maps. <i>Bioinformatics</i> , 2014, 30, 2105-2113.	4.1	36
58	Deletion of the <i>Saccharomyces cerevisiae</i> ARO8 gene, encoding an aromatic amino acid transaminase, enhances phenylethanol production from glucose. <i>Yeast</i> , 2014, 32, n/a-n/a.	1.7	35
59	A set of genetically diverged <i>Saccharomyces cerevisiae</i> strains with markerless deletions of multiple auxotrophic genes. <i>Yeast</i> , 2014, 31, 91-101.	1.7	15
60	Budding Topics: insights from emerging scientists. <i>Yeast</i> , 2014, 31, 195-195.	1.7	1
61	Standing Genetic Variation Drives Repeatable Experimental Evolution in Outcrossing Populations of <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 3228-3239.	8.9	157
62	<i>Saccharomyces pastorianus</i> : genomic insights inspiring innovation for industry. <i>Yeast</i> , 2014, 32, n/a-n/a.	1.7	111
63	Phenotypic characterisation of <i>Saccharomyces</i> spp. yeast for tolerance to stresses encountered during fermentation of lignocellulosic residues to produce bioethanol. <i>Microbial Cell Factories</i> , 2014, 13, 47.	4.0	68
64	High quality de novo sequencing and assembly of the <i>Saccharomyces arboricolus</i> genome. <i>BMC Genomics</i> , 2013, 14, 69.	2.8	87
65	High-Resolution Mapping of Complex Traits with a Four-Parent Advanced Intercross Yeast Population. <i>Genetics</i> , 2013, 195, 1141-1155.	2.9	164
66	Ancient Evolutionary Trade-Offs between Yeast Ploidy States. <i>PLoS Genetics</i> , 2013, 9, e1003388.	3.5	85
67	Recurrent Rearrangement during Adaptive Evolution in an Interspecific Yeast Hybrid Suggests a Model for Rapid Introgression. <i>PLoS Genetics</i> , 2013, 9, e1003366.	3.5	102
68	Inferring Genome-Wide Recombination Landscapes from Advanced Intercross Lines: Application to Yeast Crosses. <i>PLoS ONE</i> , 2013, 8, e62266.	2.5	29
69	Advances in Quantitative Trait Analysis in Yeast. <i>PLoS Genetics</i> , 2012, 8, e1002912.	3.5	167
70	Quantifying Selection Acting on a Complex Trait Using Allele Frequency Time Series Data. <i>Molecular Biology and Evolution</i> , 2012, 29, 1187-1197.	8.9	64
71	Surprisingly diverged populations of <i>Saccharomyces cerevisiae</i> in natural environments remote from human activity. <i>Molecular Ecology</i> , 2012, 21, 5404-5417.	3.9	257
72	Life History Shapes Trait Heredity by Accumulation of Loss-of-Function Alleles in Yeast. <i>Molecular Biology and Evolution</i> , 2012, 29, 1781-1789.	8.9	76

#	ARTICLE	IF	CITATIONS
73	â€™Newâ€™ yeasts for a newYeast. <i>Yeast</i> , 2012, 29, 407-407.	1.7	0
74	Apparent Ploidy Effects on Silencing Are Post-Transcriptional at HML and Telomeres in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2012, 7, e39044.	2.5	3
75	The Genetic Basis of Natural Variation in Oenological Traits in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2012, 7, e49640.	2.5	107
76	The rise of yeast population genomics. <i>Comptes Rendus - Biologies</i> , 2011, 334, 612-619.	0.2	34
77	From sequence to function: Insights from natural variation in budding yeasts. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2011, 1810, 959-966.	2.4	28
78	Assessing the complex architecture of polygenic traits in diverged yeast populations. <i>Molecular Ecology</i> , 2011, 20, 1401-1413.	3.9	194
79	Revealing the genetic structure of a trait by sequencing a population under selection. <i>Genome Research</i> , 2011, 21, 1131-1138.	5.5	263
80	A Geographically Diverse Collection of <i>Schizosaccharomyces pombe</i> Isolates Shows Limited Phenotypic Variation but Extensive Karyotypic Diversity. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 615-626.	1.8	75
81	Trait Variation in Yeast Is Defined by Population History. <i>PLoS Genetics</i> , 2011, 7, e1002111.	3.5	311
82	Segregating YKU80 and TLC1 Alleles Underlying Natural Variation in Telomere Properties in Wild Yeast. <i>PLoS Genetics</i> , 2009, 5, e1000659.	3.5	46
83	Population genomics of domestic and wild yeasts. <i>Nature</i> , 2009, 458, 337-341.	27.8	1,391
84	Generation of a large set of genetically tractable haploid and diploid <i>Saccharomyces</i> strains. <i>FEMS Yeast Research</i> , 2009, 9, 1217-1225.	2.3	187
85	Population genomics of domestic and wild yeasts. <i>Nature Precedings</i> , 2008, , .	0.1	1
86	Sequence Diversity, Reproductive Isolation and Species Concepts in <i>Saccharomyces</i> . <i>Genetics</i> , 2006, 174, 839-850.	2.9	283
87	YEAST EVOLUTION AND COMPARATIVE GENOMICS. <i>Annual Review of Microbiology</i> , 2005, 59, 135-153.	7.3	113
88	Inferences of evolutionary relationships from a population survey of LTR-retrotransposons and telomeric-associated sequences in the <i>Saccharomyces sensu stricto</i> complex. <i>Yeast</i> , 2005, 22, 177-192.	1.7	148
89	Analysis of a Ty1-less variant of <i>Saccharomyces paradoxus</i> : the gain and loss of Ty1 elements. <i>Yeast</i> , 2004, 21, 649-660.	1.7	29
90	NEJ1 Prevents NHEJ-Dependent Telomere Fusions in Yeast without Telomerase. <i>Molecular Cell</i> , 2003, 11, 1373-1378.	9.7	53

#	ARTICLE	IF	CITATIONS
91	Telomeres in fungi. , 0, , 101-130.		10
92	Genetically controlled mtDNA deletions prevent ROS damage by arresting oxidative phosphorylation. ELife, 0, 11, .	6.0	9