

Gianni Liti

List of Publications by Year in descending order

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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	Population genomics of domestic and wild yeasts. <i>Nature</i> , 2009, 458, 337-341.	27.8	1,391
2	Genome evolution across 1,011 <i>Saccharomyces cerevisiae</i> isolates. <i>Nature</i> , 2018, 556, 339-344.	27.8	952
3	Contrasting evolutionary genome dynamics between domesticated and wild yeasts. <i>Nature Genetics</i> , 2017, 49, 913-924.	21.4	340
4	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
5	Trait Variation in Yeast Is Defined by Population History. <i>PLoS Genetics</i> , 2011, 7, e1002111.	3.5	311
6	Sequence Diversity, Reproductive Isolation and Species Concepts in <i>Saccharomyces</i> . <i>Genetics</i> , 2006, 174, 839-850.	2.9	283
7	Revealing the genetic structure of a trait by sequencing a population under selection. <i>Genome Research</i> , 2011, 21, 1131-1138.	5.5	263
8	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
9	Elucidating the molecular architecture of adaptation via evolve and resequence experiments. <i>Nature Reviews Genetics</i> , 2015, 16, 567-582.	16.3	236
10	Assessing the complex architecture of polygenic traits in diverged yeast populations. <i>Molecular Ecology</i> , 2011, 20, 1401-1413.	3.9	194
11	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
12	Advances in Quantitative Trait Analysis in Yeast. <i>PLoS Genetics</i> , 2012, 8, e1002912.	3.5	167
13	High-Resolution Mapping of Complex Traits with a Four-Parent Advanced Intercross Yeast Population. <i>Genetics</i> , 2013, 195, 1141-1155.	2.9	164
14	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
15	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
16	The fascinating and secret wild life of the budding yeast <i>S. cerevisiae</i> . <i>ELife</i> , 2015, 4, .	6.0	147
17	De novo yeast genome assemblies from MinION, PacBio and MiSeq platforms. <i>Scientific Reports</i> , 2017, 7, 3935.	3.3	146
18	High-quality genome (re)assembly using chromosomal contact data. <i>Nature Communications</i> , 2014, 5, 5695.	12.8	142

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19	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
20	YEAST EVOLUTION AND COMPARATIVE GENOMICS. <i>Annual Review of Microbiology</i> , 2005, 59, 135-153.	7.3	113
21	<i>Saccharomyces pastorianus</i> : genomic insights inspiring innovation for industry. <i>Yeast</i> , 2014, 32, n/a-n/a.	1.7	111
22	The Genetic Basis of Natural Variation in Oenological Traits in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2012, 7, e49640.	2.5	107
23	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
24	Mapping Genetic Variants Underlying Differences in the Central Nitrogen Metabolism in Fermenter Yeasts. <i>PLoS ONE</i> , 2014, 9, e86533.	2.5	96
25	High quality de novo sequencing and assembly of the <i>Saccharomyces arboricolus</i> genome. <i>BMC Genomics</i> , 2013, 14, 69.	2.8	87
26	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
27	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
28	Ancient Evolutionary Trade-Offs between Yeast Ploidy States. <i>PLoS Genetics</i> , 2013, 9, e1003388.	3.5	85
29	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
30	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
31	Ploidy influences the functional attributes of de novo lager yeast hybrids. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 7203-7222.	3.6	75
32	Clonal Heterogeneity Influences the Fate of New Adaptive Mutations. <i>Cell Reports</i> , 2017, 21, 732-744.	6.4	70
33	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
34	Tetrad analysis in plants and fungi finds large differences in gene conversion rates but no GC bias. <i>Nature Ecology and Evolution</i> , 2018, 2, 164-173.	7.8	65
35	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
36	Extensive Recombination of a Yeast Diploid Hybrid through Meiotic Reversion. <i>PLoS Genetics</i> , 2016, 12, e1005781.	3.5	60

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37	The genetic architecture of low-temperature adaptation in the wine yeast <i>Saccharomyces cerevisiae</i> . <i>BMC Genomics</i> , 2017, 18, 159.	2.8	58
38	Genetic variants of TORC1 signaling pathway affect nitrogen consumption in <i>Saccharomyces cerevisiae</i> during alcoholic fermentation. <i>PLoS ONE</i> , 2019, 14, e0220515.	2.5	55
39	NEJ1 Prevents NHEJ-Dependent Telomere Fusions in Yeast without Telomerase. <i>Molecular Cell</i> , 2003, 11, 1373-1378.	9.7	53
40	Segregating YKU80 and TLC1 Alleles Underlying Natural Variation in Telomere Properties in Wild Yeast. <i>PLoS Genetics</i> , 2009, 5, e1000659.	3.5	46
41	A yeast living ancestor reveals the origin of genomic introgressions. <i>Nature</i> , 2020, 587, 420-425.	27.8	45
42	Long-read sequencing data analysis for yeasts. <i>Nature Protocols</i> , 2018, 13, 1213-1231.	12.0	43
43	Shared Molecular Targets Confer Resistance over Short and Long Evolutionary Timescales. <i>Molecular Biology and Evolution</i> , 2019, 36, 691-708.	8.9	43
44	Human <i>RAP80</i> specifically protects telomeres of senescent cells from DNA damage. <i>EMBO Reports</i> , 2020, 21, e49076.	4.5	43
45	Discordant evolution of mitochondrial and nuclear yeast genomes at population level. <i>BMC Biology</i> , 2020, 18, 49.	3.8	42
46	simuG: a general-purpose genome simulator. <i>Bioinformatics</i> , 2019, 35, 4442-4444.	4.1	41
47	Accurate Tracking of the Mutational Landscape of Diploid Hybrid Genomes. <i>Molecular Biology and Evolution</i> , 2019, 36, 2861-2877.	8.9	41
48	Filling annotation gaps in yeast genomes using genome-wide contact maps. <i>Bioinformatics</i> , 2014, 30, 2105-2113.	4.1	36
49	Deletion of the <i>Saccharomyces cerevisiae</i> <i>ARO8</i> gene, encoding an aromatic amino acid transaminase, enhances phenylethanol production from glucose. <i>Yeast</i> , 2014, 32, n/a-n/a.	1.7	35
50	The rise of yeast population genomics. <i>Comptes Rendus - Biologies</i> , 2011, 334, 612-619.	0.2	34
51	Powerful decomposition of complex traits in a diploid model. <i>Nature Communications</i> , 2016, 7, 13311.	12.8	34
52	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
53	Predicting quantitative traits from genome and phenome with near perfect accuracy. <i>Nature Communications</i> , 2016, 7, 11512.	12.8	32
54	Domestication reprogrammed the budding yeast life cycle. <i>Nature Ecology and Evolution</i> , 2022, 6, 448-460.	7.8	32

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55	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
56	Inferring Genome-Wide Recombination Landscapes from Advanced Intercross Lines: Application to Yeast Crosses. <i>PLoS ONE</i> , 2013, 8, e62266.	2.5	29
57	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
58	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
59	Intragenic repeat expansion in the cell wall protein gene <i>HPF1</i> controls yeast chronological aging. <i>Genome Research</i> , 2020, 30, 697-710.	5.5	23
60	Mismatch Repair Incompatibilities in Diverse Yeast Populations. <i>Genetics</i> , 2017, 205, 1459-1471.	2.9	22
61	The budding yeast life cycle: More complex than anticipated?. <i>Yeast</i> , 2021, 38, 5-11.	1.7	18
62	Yeasts from temperate forests. <i>Yeast</i> , 2022, 39, 4-24.	1.7	18
63	Kinetochores 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
64	Isolation and Laboratory Domestication of Natural Yeast Strains. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot089052.	0.3	16
65	Transcriptional Activity and Protein Levels of Horizontally Acquired Genes in Yeast Reveal Hallmarks of Adaptation to Fermentative Environments. <i>Frontiers in Genetics</i> , 2020, 11, 293.	2.3	16
66	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
67	Aborting meiosis allows recombination in sterile diploid yeast hybrids. <i>Nature Communications</i> , 2021, 12, 6564.	12.8	14
68	Natural variants suppress mutations in hundreds of essential genes. <i>Molecular Systems Biology</i> , 2021, 17, e10138.	7.2	13
69	Extensive sampling of <i>Saccharomyces cerevisiae</i> in Taiwan reveals ecology and evolution of predomesticated lineages. <i>Genome Research</i> , 2022, , .	5.5	13
70	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
71	ATG18 and FAB1 Are Involved in Dehydration Stress Tolerance in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2015, 10, e0119606.	2.5	12
72	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

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73	Telomeres in fungi. , 0, , 101-130.		10
74	Unlocking the functional potential of polyploid yeasts. Nature Communications, 2022, 13, 2580.	12.8	10
75	Genetically controlled mtDNA deletions prevent ROS damage by arresting oxidative phosphorylation. ELife, 0, 11, .	6.0	9
76	Meiotic Cells Counteract Programmed Retrotransposon Activation via RNA-Binding Translational Repressor Assemblies. Developmental Cell, 2021, 56, 22-35.e7.	7.0	8
77	Yeast Reciprocal Hemizygoty to Confirm the Causality of a Quantitative Trait Loci-Associated Gene. Cold Spring Harbor Protocols, 2017, 2017, pdb.prot089078.	0.3	7
78	Population Size, Sex and Purifying Selection: Comparative Genomics of Two Sister Taxa of the Wild Yeast <i>Saccharomyces paradoxus</i> . Genome Biology and Evolution, 2020, 12, 1636-1645.	2.5	7
79	Mapping Quantitative Trait Loci in Yeast. Cold Spring Harbor Protocols, 2017, 2017, pdb.prot089060.	0.3	6
80	Budding Yeast Strains and Genotype-Phenotype Mapping. Cold Spring Harbor Protocols, 2017, 2017, pdb.top077735.	0.3	6
81	RecombineX: A generalized computational framework for automatic high-throughput gamete genotyping and tetrad-based recombination analysis. PLoS Genetics, 2022, 18, e1010047.	3.5	5
82	miRNAs Copy Number Variations Repertoire as Hallmark Indicator of Cancer Species Predisposition. Genes, 2022, 13, 1046.	2.4	5
83	Resistance to Arsenite and Arsenate in <i>Saccharomyces cerevisiae</i> Arises through the Subtelomeric Expansion of a Cluster of Yeast Genes. International Journal of Environmental Research and Public Health, 2022, 19, 8119.	2.6	5
84	Yeast chromosome numbers minimized using genome editing. Nature, 2018, 560, 317-318.	27.8	3
85	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
86	Apparent Ploidy Effects on Silencing Are Post-Transcriptional at HML and Telomeres in <i>Saccharomyces cerevisiae</i> . PLoS ONE, 2012, 7, e39044.	2.5	3
87	Extensive simulations assess the performance of genome-wide association mapping in various <i>Saccharomyces cerevisiae</i> subpopulations. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, .	4.0	3
88	Population genomics of domestic and wild yeasts. Nature Precedings, 2008, , .	0.1	1
89	Budding Topics: insights from emerging scientists. Yeast, 2014, 31, 195-195.	1.7	1
90	Yeast2.0: a new chapter. Yeast, 2016, 33, 3-4.	1.7	1

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91	Andr� Goffeau's imprinting on second generation yeast â€œgenomologistsâ€. Yeast, 2019, 36, 167-175.	1.7	1
92	â€Newâ€™ yeasts for a newYeast. Yeast, 2012, 29, 407-407.	1.7	0