

Jonas Warringer

List of Publications by Year in descending order

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72
papers

6,176
citations

117453

34
h-index

85405

71
g-index

88
all docs

88
docs citations

88
times ranked

5972
citing authors

#	ARTICLE	IF	CITATIONS
1	Domestication reprogrammed the budding yeast life cycle. <i>Nature Ecology and Evolution</i> , 2022, 6, 448-460.	3.4	32
2	Genome-Wide Association Study Reveals Host Factors Affecting Conjugation in <i>Escherichia coli</i> . <i>Microorganisms</i> , 2022, 10, 608.	1.6	3
3	Genomic Epidemiology and Evolution of <i>Escherichia coli</i> in Wild Animals in Mexico. <i>MSphere</i> , 2021, 6, .	1.3	19
4	Mutagenic mechanisms of cancer-associated DNA polymerase β alleles. <i>Nucleic Acids Research</i> , 2021, 49, 3919-3931.	6.5	12
5	Machine Learning Prediction of Resistance to Subinhibitory Antimicrobial Concentrations from <i>Escherichia coli</i> Genomes. <i>MSystems</i> , 2021, 6, e0034621.	1.7	6
6	Aborting meiosis allows recombination in sterile diploid yeast hybrids. <i>Nature Communications</i> , 2021, 12, 6564.	5.8	14
7	Protein kinase A controls yeast growth in visible light. <i>BMC Biology</i> , 2020, 18, 168.	1.7	17
8	A yeast living ancestor reveals the origin of genomic introgressions. <i>Nature</i> , 2020, 587, 420-425.	13.7	45
9	Intragenic repeat expansion in the cell wall protein gene <i>HPF1</i> controls yeast chronological aging. <i>Genome Research</i> , 2020, 30, 697-710.	2.4	23
10	A High-Throughput Method for Screening for Genes Controlling Bacterial Conjugation of Antibiotic Resistance. <i>MSystems</i> , 2020, 5, .	1.7	10
11	Shared Molecular Targets Confer Resistance over Short and Long Evolutionary Timescales. <i>Molecular Biology and Evolution</i> , 2019, 36, 691-708.	3.5	43
12	Inhibiting conjugation as a tool in the fight against antibiotic resistance. <i>Drug Development Research</i> , 2019, 80, 19-23.	1.4	48
13	Prediction of antibiotic resistance in <i>Escherichia coli</i> from large-scale pan-genome data. <i>PLoS Computational Biology</i> , 2018, 14, e1006258.	1.5	127
14	Contrasting evolutionary genome dynamics between domesticated and wild yeasts. <i>Nature Genetics</i> , 2017, 49, 913-924.	9.4	340
15	Clonal Heterogeneity Influences the Fate of New Adaptive Mutations. <i>Cell Reports</i> , 2017, 21, 732-744.	2.9	70
16	Isolation and Laboratory Domestication of Natural Yeast Strains. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot089052.	0.2	16
17	Mapping Quantitative Trait Loci in Yeast. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot089060.	0.2	6
18	Budding Yeast Strains and Genotype-Phenotype Mapping. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.top077735.	0.2	6

#	ARTICLE	IF	CITATIONS
19	Yeast Reciprocal Hemizygoty to Confirm the Causality of a Quantitative Trait Loci-Associated Gene. Cold Spring Harbor Protocols, 2017, 2017, pdb.prot089078.	0.2	7
20	Scan-o-matic: High-Resolution Microbial Phenomics at a Massive Scale. G3: Genes, Genomes, Genetics, 2016, 6, 3003-3014.	0.8	69
21	Disentangling genetic and epigenetic determinants of ultrafast adaptation. Molecular Systems Biology, 2016, 12, 892.	3.2	9
22	Predicting quantitative traits from genome and phenome with near perfect accuracy. Nature Communications, 2016, 7, 11512.	5.8	32
23	PRECOC: a tool for automated extraction and visualization of fitness components in microbial growth phenomics. BMC Bioinformatics, 2016, 17, 249.	1.2	51
24	Powerful decomposition of complex traits in a diploid model. Nature Communications, 2016, 7, 13311.	5.8	34
25	Replenishment and mobilization of intracellular nitrogen pools decouples wine yeast nitrogen uptake from growth. Applied Microbiology and Biotechnology, 2016, 100, 3255-3265.	1.7	24
26	The cellular growth rate controls overall mRNA turnover, and modulates either transcription or degradation rates of particular gene regulons. Nucleic Acids Research, 2016, 44, 3643-3658.	6.5	45
27	High-Throughput Biochemical Fingerprinting of <i>Saccharomyces cerevisiae</i> by Fourier Transform Infrared Spectroscopy. PLoS ONE, 2015, 10, e0118052.	1.1	38
28	Concerted Evolution of Life Stage Performances Signals Recent Selection on Yeast Nitrogen Use. Molecular Biology and Evolution, 2015, 32, 153-161.	3.5	86
29	Kinetochores assembly and heterochromatin formation occur autonomously in <i>Schizosaccharomyces pombe</i> . Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1903-1908.	3.3	16
30	A High-Definition View of Functional Genetic Variation from Natural Yeast Genomes. Molecular Biology and Evolution, 2014, 31, 872-888.	3.5	328
31	High quality de novo sequencing and assembly of the <i>Saccharomyces arboricolus</i> genome. BMC Genomics, 2013, 14, 69.	1.2	87
32	A role for Myh1 in DNA repair after treatment with strand-breaking and crosslinking chemotherapeutic agents. Environmental and Molecular Mutagenesis, 2013, 54, 327-337.	0.9	7
33	High-Resolution Mapping of Complex Traits with a Four-Parent Advanced Intercross Yeast Population. Genetics, 2013, 195, 1141-1155.	1.2	164
34	Ancient Evolutionary Trade-Offs between Yeast Ploidy States. PLoS Genetics, 2013, 9, e1003388.	1.5	85
35	Genetic Basis of Variations in Nitrogen Source Utilization in Four Wine Commercial Yeast Strains. PLoS ONE, 2013, 8, e67166.	1.1	88
36	Abundant Gene-by-Environment Interactions in Gene Expression Reaction Norms to Copper within <i>Saccharomyces cerevisiae</i> . Genome Biology and Evolution, 2012, 4, 1061-1079.	1.1	37

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37	Life History Shapes Trait Heredity by Accumulation of Loss-of-Function Alleles in Yeast. <i>Molecular Biology and Evolution</i> , 2012, 29, 1781-1789.	3.5	76
38	Exploration of multivariate analysis in microbial coding sequence modeling. <i>BMC Bioinformatics</i> , 2012, 13, 97.	1.2	8
39	Improving stability and understandability of genotype-phenotype mapping in <i>Saccharomyces</i> using regularized variable selection in L-PLS regression. <i>BMC Bioinformatics</i> , 2012, 13, 327.	1.2	10
40	The Genetic Basis of Natural Variation in Oenological Traits in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2012, 7, e49640.	1.1	107
41	Assessing the complex architecture of polygenic traits in diverged yeast populations. <i>Molecular Ecology</i> , 2011, 20, 1401-1413.	2.0	194
42	Quantitative Proteomics of Yeast Post-Golgi Vesicles Reveals a Discriminating Role for Sro7p in Protein Secretion. <i>Traffic</i> , 2011, 12, 740-753.	1.3	20
43	Systematic exploration of essential yeast gene function with temperature-sensitive mutants. <i>Nature Biotechnology</i> , 2011, 29, 361-367.	9.4	352
44	A Partial Least Squares based algorithm for parsimonious variable selection. <i>Algorithms for Molecular Biology</i> , 2011, 6, 27.	0.3	71
45	The <i>Ashbya gossypii</i> EF-1 promoter of the ubiquitously used MX cassettes is toxic to <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 2011, 585, 3907-3913.	1.3	5
46	Mining for genotype-phenotype relations in <i>Saccharomyces</i> using partial least squares. <i>BMC Bioinformatics</i> , 2011, 12, 318.	1.2	20
47	Depletion of eIF4G from yeast cells narrows the range of translational efficiencies genome-wide. <i>BMC Genomics</i> , 2011, 12, 68.	1.2	60
48	Revealing the genetic structure of a trait by sequencing a population under selection. <i>Genome Research</i> , 2011, 21, 1131-1138.	2.4	263
49	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.	0.8	75
50	Trait Variation in Yeast Is Defined by Population History. <i>PLoS Genetics</i> , 2011, 7, e1002111.	1.5	311
51	The HOG Pathway Dictates the Short-Term Translational Response after Hyperosmotic Shock. <i>Molecular Biology of the Cell</i> , 2010, 21, 3080-3092.	0.9	67
52	Sulfate Assimilation Mediates Tellurite Reduction and Toxicity in <i>Saccharomyces cerevisiae</i> . <i>Eukaryotic Cell</i> , 2010, 9, 1635-1647.	3.4	22
53	Robustness and fragility in the yeast high osmolarity glycerol (HOG) signal transduction pathway. <i>Molecular Systems Biology</i> , 2009, 5, 281.	3.2	56
54	mRNA stability changes precede changes in steady-state mRNA amounts during hyperosmotic stress. <i>Rna</i> , 2009, 15, 600-614.	1.6	80

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55	Population genomics of domestic and wild yeasts. <i>Nature</i> , 2009, 458, 337-341.	13.7	1,391
56	A phenotypic study of TFS1 mutants differentially altered in the inhibition of Ira2p or CPY. <i>FEMS Yeast Research</i> , 2009, 9, 867-874.	1.1	5
57	Reducing Inter-Replicate Variation in Fourier Transform Infrared Spectroscopy by Extended Multiplicative Signal Correction. <i>Applied Spectroscopy</i> , 2009, 63, 296-305.	1.2	38
58	Chemogenetic fingerprinting by analysis of cellular growth dynamics. <i>BMC Chemical Biology</i> , 2008, 8, 3.	1.6	37
59	The sodium pump Ena1p provides mechanistic insight into the salt sensitivity of vacuolar protein sorting mutants. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2008, 1783, 974-984.	1.9	18
60	The tumor suppressor homolog in fission yeast, myh1+, displays a strong interaction with the checkpoint gene rad1+. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2008, 644, 48-55.	0.4	8
61	Functional importance of individual rRNA 2'-O-ribose methylations revealed by high-resolution phenotyping. <i>Rna</i> , 2008, 14, 649-656.	1.6	59
62	Population genomics of domestic and wild yeasts. <i>Nature Precedings</i> , 2008, .	0.1	1
63	PROPHECY—a yeast phenome database, update 2006. <i>Nucleic Acids Research</i> , 2007, 35, D463-D467.	6.5	28
64	Involvement of yeast YOL151W/GRE2 in ergosterol metabolism. <i>Yeast</i> , 2006, 23, 389-398.	0.8	29
65	Genetic pleiotropy in <i>Saccharomyces cerevisiae</i> quantified by high-resolution phenotypic profiling. <i>Molecular Genetics and Genomics</i> , 2006, 275, 605-614.	1.0	19
66	Evolutionary constraints on yeast protein size. <i>BMC Evolutionary Biology</i> , 2006, 6, 61.	3.2	64
67	Phenotypic effects of membrane protein overexpression in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11148-11153.	3.3	36
68	Physiological Importance and Identification of Novel Targets for the N-Terminal Acetyltransferase NatB. <i>Eukaryotic Cell</i> , 2006, 5, 368-378.	3.4	40
69	PROPHECY—a database for high-resolution phenomics. <i>Nucleic Acids Research</i> , 2004, 33, D369-D373.	6.5	30
70	Automated screening in environmental arrays allows analysis of quantitative phenotypic profiles in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2003, 20, 53-67.	0.8	266
71	High-resolution yeast phenomics resolves different physiological features in the saline response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15724-15729.	3.3	207
72	Genetically controlled mtDNA deletions prevent ROS damage by arresting oxidative phosphorylation. <i>ELife</i> , 0, 11, .	2.8	9