

Daniela Delneri

List of Publications by Year in descending order

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60
papers

2,602
citations

186209

28
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214721

47
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docs citations

71
times ranked

3327
citing authors

#	ARTICLE	IF	CITATIONS
1	Aneuploidy influences the gene expression profiles in <i>Saccharomyces pastorianus</i> group I and II strains during fermentation. <i>PLoS Genetics</i> , 2022, 18, e1010149.	1.5	8
2	Functional and transcriptional profiling of non-coding RNAs in yeast reveal context-dependent phenotypes and in trans effects on the protein regulatory network. <i>PLoS Genetics</i> , 2021, 17, e1008761.	1.5	17
3	A high-throughput screening method for the discovery of <i>Saccharomyces</i> and non- <i>Saccharomyces</i> yeasts with potential in the brewing industry. <i>Engineering Biology</i> , 2021, 5, 72-80.	0.8	5
4	Restoring fertility in yeast hybrids: Breeding and quantitative genetics of beneficial traits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	21
5	Transcriptional Profile of the Industrial Hybrid <i>Saccharomyces pastorianus</i> Reveals Temperature-Dependent Allele Expression Bias and Preferential Orthologous Protein Assemblies. <i>Molecular Biology and Evolution</i> , 2021, 38, 5437-5452.	3.5	15
6	Biotechnological exploitation of <i>Saccharomyces jurei</i> and its hybrids in craft beer fermentation uncovers new aroma combinations. <i>Food Microbiology</i> , 2021, 100, 103838.	2.1	26
7	HybridMine: A Pipeline for Allele Inheritance and Gene Copy Number Prediction in Hybrid Genomes and Its Application to Industrial Yeasts. <i>Microorganisms</i> , 2020, 8, 1554.	1.6	8
8	Genomic Adaptation of <i>Saccharomyces</i> Species to Industrial Environments. <i>Frontiers in Genetics</i> , 2020, 11, 916.	1.1	25
9	An update on the diversity, ecology and biogeography of the <i>Saccharomyces</i> genus. <i>FEMS Yeast Research</i> , 2020, 20, .	1.1	35
10	Plasticity of Mitochondrial DNA Inheritance and its Impact on Nuclear Gene Transcription in Yeast Hybrids. <i>Microorganisms</i> , 2020, 8, 494.	1.6	20
11	High-throughput Gene Replacement in <i>Aspergillus fumigatus</i> . <i>Current Protocols in Microbiology</i> , 2019, 54, e88.	6.5	35
12	Fast and Reliable PCR Amplification from <i>Aspergillus fumigatus</i> Spore Suspension Without Traditional DNA Extraction. <i>Current Protocols in Microbiology</i> , 2019, 54, e89.	6.5	20
13	Targeted metagenomics approach to capture the biodiversity of <i>Saccharomyces</i> genus in wild environments. <i>Environmental Microbiology Reports</i> , 2019, 11, 206-214.	1.0	25
14	History of genome editing in yeast. <i>Yeast</i> , 2018, 35, 361-368.	0.8	40
15	Whole Genome Sequencing, <i>de Novo</i> Assembly and Phenotypic Profiling for the New Budding Yeast Species <i>Saccharomyces jurei</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2967-2977.	0.8	46
16	Large-scale profiling of noncoding RNA function in yeast. <i>PLoS Genetics</i> , 2018, 14, e1007253.	1.5	29
17	A resource for functional profiling of noncoding RNA in the yeast <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , 2017, 23, 1166-1171.	1.6	14
18	Rapid functional and evolutionary changes follow gene duplication in yeast. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171393.	1.2	41

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19	<i>Saccharomyces jurei</i> sp. nov., isolation and genetic identification of a novel yeast species from <i>Quercus robur</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 2046-2052.	0.8	69
20	Novel Intronic RNA Structures Contribute to Maintenance of Phenotype in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2016, 203, 1469-1481.	1.2	29
21	Widespread Impact of Chromosomal Inversions on Gene Expression Uncovers Robustness via Phenotypic Buffering. <i>Molecular Biology and Evolution</i> , 2016, 33, 1679-1696.	3.5	36
22	Induced expression of defence-related genes in barley is specific to aphid genotype. <i>Biological Journal of the Linnean Society</i> , 2016, 117, 672-685.	0.7	10
23	Non-coding RNAs and disease: the classical ncRNAs make a comeback. <i>Biochemical Society Transactions</i> , 2016, 44, 1073-1078.	1.6	71
24	Sequencing and Characterisation of Rearrangements in Three <i>S. pastorianus</i> Strains Reveals the Presence of Chimeric Genes and Gives Evidence of Breakpoint Reuse. <i>PLoS ONE</i> , 2014, 9, e92203.	1.1	71
25	Limb Displays of Male <i>Saitis barbipes</i> (Simon, 1868) (Araneae: Salticidae). <i>Arachnology</i> , 2014, 16, 219-224.	0.4	3
26	Intron Evolution in Saccharomycetaceae. <i>Genome Biology and Evolution</i> , 2014, 6, 2543-2556.	1.1	48
27	Environmental systems biology of cold-tolerant phenotype in <i>Saccharomyces</i> species adapted to grow at different temperatures. <i>Molecular Ecology</i> , 2014, 23, 5241-5257.	2.0	79
28	Osteoblastic cell secretome: A novel role for progranulin during risedronate treatment. <i>Bone</i> , 2014, 58, 81-91.	1.4	14
29	Chimeric Protein Complexes in Hybrid Species Generate Novel Phenotypes. <i>PLoS Genetics</i> , 2013, 9, e1003836.	1.5	49
30	Characterization and Prediction of Haploinsufficiency Using Systems-Level Gene Properties in Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1965-1977.	0.8	13
31	Non-coding RNAs in <i>Saccharomyces cerevisiae</i> : what is the function?. <i>Biochemical Society Transactions</i> , 2012, 40, 907-911.	1.6	28
32	Genome-wide analysis of longevity in nutrient-deprived <i>Saccharomyces cerevisiae</i> reveals importance of recycling in maintaining cell viability. <i>Environmental Microbiology</i> , 2012, 14, 1249-1260.	1.8	21
33	Impact of Chromosomal Inversions on the Yeast DAL Cluster. <i>PLoS ONE</i> , 2012, 7, e42022.	1.1	34
34	Knock-in reconstitution studies reveal an unexpected role of Cys-65 in regulating APE1/Ref-1 subcellular trafficking and function. <i>Molecular Biology of the Cell</i> , 2011, 22, 3887-3901.	0.9	62
35	Genome-wide analysis of yeast stress survival and tolerance acquisition to analyze the central trade-off between growth rate and cellular robustness. <i>Molecular Biology of the Cell</i> , 2011, 22, 4435-4446.	0.9	138
36	Competition Experiments Coupled with High-Throughput Analyses for Functional Genomics Studies in Yeast. <i>Methods in Molecular Biology</i> , 2011, 759, 271-282.	0.4	5

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37	Gene Duplication and Environmental Adaptation within Yeast Populations. <i>Genome Biology and Evolution</i> , 2010, 2, 591-601.	1.1	44
38	New generation of <i>loxP</i> -mutated deletion cassettes for the genetic manipulation of yeast natural isolates. <i>Yeast</i> , 2010, 27, 765-775.	0.8	68
39	Barcode technology in yeast: application to pharmacogenomics. <i>FEMS Yeast Research</i> , 2010, 10, 1083-1089.	1.1	15
40	Evolutionary Systems Biology of Amino Acid Biosynthetic Cost in Yeast. <i>PLoS ONE</i> , 2010, 5, e11935.	1.1	57
41	Genome-wide analysis and proteomic studies reveal APE1/Ref1 multifunctional role in mammalian cells. <i>Proteomics</i> , 2009, 9, 1058-1074.	1.3	90
42	Transcriptome and Proteome Analysis of Osteocytes Treated with Nitrogen-Containing Bisphosphonates. <i>Journal of Proteome Research</i> , 2009, 8, 1131-1142.	1.8	20
43	Identification of secondary targets of N-containing bisphosphonates in mammalian cells via parallel competition analysis of the barcoded yeast deletion collection. <i>Genome Biology</i> , 2009, 10, R93.	13.9	24
44	Identification and characterization of high-flux-control genes of yeast through competition analyses in continuous cultures. <i>Nature Genetics</i> , 2008, 40, 113-117.	9.4	93
45	Probing (macro)molecular transport through cell walls. <i>Faraday Discussions</i> , 2008, 139, 199.	1.6	18
46	Systems biology of energetic and atomic costs in the yeast transcriptome, proteome, and metabolome. <i>Nature Precedings</i> , 2008, , .	0.1	3
47	Plasticity of genetic interactions in metabolic networks of yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2307-2312.	3.3	185
48	Cellular Processes and Pathways That Protect <i>Saccharomyces cerevisiae</i> Cells against the Plasma Membrane-Perturbing Compound Chitosan. <i>Eukaryotic Cell</i> , 2007, 6, 600-608.	3.4	62
49	Application of the comprehensive set of heterozygous yeast deletion mutants to elucidate the molecular basis of cellular chromium toxicity. <i>Genome Biology</i> , 2007, 8, R268.	13.9	57
50	Development of novel guanidino-labelling derivatisation (GLaD) reagents for liquid chromatography/matrix-assisted laser desorption/ionisation analysis. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 3069-3076.	0.7	5
51	Effects of reciprocal chromosomal translocations on the fitness of <i>Saccharomyces cerevisiae</i> . <i>EMBO Reports</i> , 2004, 5, 392-398.	2.0	45
52	The Use of Yeast Mutant Collections in Genome Profiling and Large-Scale Functional Analysis. <i>Current Genomics</i> , 2004, 5, 59-65.	0.7	5
53	GIMS: an integrated data storage and analysis environment for genomic and functional data. <i>Yeast</i> , 2003, 20, 1291-1306.	0.8	39
54	Engineering evolution to study speciation in yeasts. <i>Nature</i> , 2003, 422, 68-72.	13.7	232

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55	Tools for the study of genome rearrangements in laboratory and industrial yeast strains. <i>Yeast</i> , 2002, 19, 441-448.	0.8	4
56	Towards a truly integrative biology through the functional genomics of yeast. <i>Current Opinion in Biotechnology</i> , 2001, 12, 87-91.	3.3	75
57	Exploring redundancy in the yeast genome: an improved strategy for use of the cre-loxP system. <i>Gene</i> , 2000, 252, 127-135.	1.0	120
58	Disruption of seven hypothetical aryl alcohol dehydrogenase genes from <i>Saccharomyces cerevisiae</i> and construction of a multiple knock-out strain. <i>Yeast</i> , 1999, 15, 1681-1689.	0.8	60
59	Analysis of the Seven-Member AAD Gene Set Demonstrates That Genetic Redundancy in Yeast May Be More Apparent Than Real. <i>Genetics</i> , 1999, 153, 1591-1600.	1.2	62
60	Sequencing of a 40.5 kb Fragment Located on the Left Arm of Chromosome VII from <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 1997, 13, 55-64.	0.8	6