

# Francisco Salinas

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

1,865  
citations

361413

20  
h-index

414414

32  
g-index

36  
all docs

36  
docs citations

36  
times ranked

1365  
citing authors

#	ARTICLE	IF	CITATIONS
1	A <i>Saccharomyces eubayanus</i> haploid resource for research studies. <i>Scientific Reports</i> , 2022, 12, 5976.	3.3	8
2	Interactions between Core Elements of the <i>Botrytis cinerea</i> Circadian Clock Are Modulated by Light and Different Protein Domains. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 486.	3.5	5
3	The rise and shine of yeast optogenetics. <i>Yeast</i> , 2021, 38, 131-146.	1.7	21
4	Modular and Molecular Optimization of a LOV (Light-Oxygen-Voltage)-Based Optogenetic Switch in Yeast. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8538.	4.1	8
5	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
6	Total evidence or taxonomic congruence? A comparison of methods for combining biological evidence. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2050040.	0.8	2
7	Differential Gene Expression and Allele Frequency Changes Favour Adaptation of a Heterogeneous Yeast Population to Nitrogen-Limited Fermentations. <i>Frontiers in Microbiology</i> , 2020, 11, 1204.	3.5	3
8	GTR1 Affects Nitrogen Consumption and TORC1 Activity in <i>Saccharomyces cerevisiae</i> Under Fermentation Conditions. <i>Frontiers in Genetics</i> , 2020, 11, 519.	2.3	4
9	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
10	12 Exploiting Fungal Photobiology as a Source of Novel Bio-blocks for Optogenetic Systems. , 2020, , 297-318.		0
11	Indirect monitoring of TORC1 signalling pathway reveals molecular diversity among different yeast strains. <i>Yeast</i> , 2019, 36, 65-74.	1.7	71
12	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
13	KAE1 Allelic Variants Affect TORC1 Activation and Fermentation Kinetics in <i>Saccharomyces cerevisiae</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1686.	3.5	49
14	GPD1 and ADH3 Natural Variants Underlie Glycerol Yield Differences in Wine Fermentation. <i>Frontiers in Microbiology</i> , 2018, 9, 1460.	3.5	31
15	Fungal Light-Oxygen-Voltage Domains for Optogenetic Control of Gene Expression and Flocculation in Yeast. <i>MBio</i> , 2018, 9, .	4.1	34
16	Optogenetic switches for light-controlled gene expression in yeast. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 2629-2640.	3.6	35
17	Clonal Heterogeneity Influences the Fate of New Adaptive Mutations. <i>Cell Reports</i> , 2017, 21, 732-744.	6.4	70
18	Powerful decomposition of complex traits in a diploid model. <i>Nature Communications</i> , 2016, 7, 13311.	12.8	34

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19	Natural variation in non-coding regions underlying phenotypic diversity in budding yeast. <i>Scientific Reports</i> , 2016, 6, 21849.	3.3	100
20	<i>RIM15</i> antagonistic pleiotropy is responsible for differences in fermentation and stress response kinetics in budding yeast. <i>FEMS Yeast Research</i> , 2016, 16, fow021.	2.3	67
21	Extensive Recombination of a Yeast Diploid Hybrid through Meiotic Reversion. <i>PLoS Genetics</i> , 2016, 12, e1005781.	3.5	60
22	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
23	ATG18 and FAB1 Are Involved in Dehydration Stress Tolerance in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2015, 10, e0119606.	2.5	12
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	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
26	High-Resolution Mapping of Complex Traits with a Four-Parent Advanced Intercross Yeast Population. <i>Genetics</i> , 2013, 195, 1141-1155.	2.9	164
27	Identification of genes related to nitrogen uptake in wine strains of <i>Saccharomyces cerevisiae</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2012, 28, 1107-1113.	3.6	43
28	The Genetic Basis of Natural Variation in Oenological Traits in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2012, 7, e49640.	2.5	107
29	Revealing the genetic structure of a trait by sequencing a population under selection. <i>Genome Research</i> , 2011, 21, 1131-1138.	5.5	263
30	Cinnamic acid, ethanol and temperature interaction on coumarate decarboxylase activity and the relative expression of the putative <i>cd</i> gene in <i>D. bruxellensis</i> . <i>Electronic Journal of Biotechnology</i> , 2011, 14, .	2.2	4
31	Genomic and phenotypic comparison between similar wine yeast strains of <i>Saccharomyces cerevisiae</i> from different geographic origins. <i>Journal of Applied Microbiology</i> , 2010, 108, 1850-1858.	3.1	18
32	Taqman real-time PCR for the detection and enumeration of <i>Saccharomyces cerevisiae</i> in wine. <i>Food Microbiology</i> , 2009, 26, 328-332.	4.2	33
33	POLYMERASE CHAIN REACTION CONFIRMATORY METHOD FOR MICROBIOLOGICAL DETECTION OF <i>BRETTANOMYCES BRUXELLENSIS</i> IN WINES. <i>Journal of Rapid Methods and Automation in Microbiology</i> , 2008, 16, 308-319.	0.4	6