

Rui Pereira

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

750
citations

840776

11
h-index

1199594

12
g-index

14
all docs

14
docs citations

14
times ranked

1141
citing authors

#	ARTICLE	IF	CITATIONS
1	Reprogramming Yeast Metabolism from Alcoholic Fermentation to Lipogenesis. <i>Cell</i> , 2018, 174, 1549-1558.e14.	28.9	215
2	Complete genomic and transcriptional landscape analysis using third-generation sequencing: a case study of <i>Saccharomyces cerevisiae</i> CEN.PK113-7D. <i>Nucleic Acids Research</i> , 2018, 46, e38-e38.	14.5	116
3	Multidimensional engineering of <i>Saccharomyces cerevisiae</i> for efficient synthesis of medium-chain fatty acids. <i>Nature Catalysis</i> , 2020, 3, 64-74.	34.4	80
4	Production of Î²-ionone by combined expression of carotenogenic and plant CCD1 genes in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2015, 14, 84.	4.0	71
5	Adaptive laboratory evolution of tolerance to dicarboxylic acids in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2019, 56, 130-141.	7.0	63
6	Improving the flux distributions simulated with genome-scale metabolic models of <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering Communications</i> , 2016, 3, 153-163.	3.6	51
7	Nitrogen limitation reveals large reserves in metabolic and translational capacities of yeast. <i>Nature Communications</i> , 2020, 11, 1881.	12.8	51
8	Elucidating aromatic acid tolerance at low pH in <i>Saccharomyces cerevisiae</i> using adaptive laboratory evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27954-27961.	7.1	40
9	Stress-induced expression is enriched for evolutionarily young genes in diverse budding yeasts. <i>Nature Communications</i> , 2020, 11, 2144.	12.8	24
10	Metabolic network remodelling enhances yeast's fitness on xylose using aerobic glycolysis. <i>Nature Catalysis</i> , 2021, 4, 783-796.	34.4	23
11	Optimization Approaches for the <i>In Silico</i> Discovery of Optimal Targets for Gene Over/Underexpression. <i>Journal of Computational Biology</i> , 2012, 19, 102-114.	1.6	14
12	Turnover Dependent Phenotypic Simulation: A Quantitative Constraint-Based Simulation Method That Accommodates All Main Strain Design Strategies. <i>ACS Synthetic Biology</i> , 2019, 8, 976-988.	3.8	1