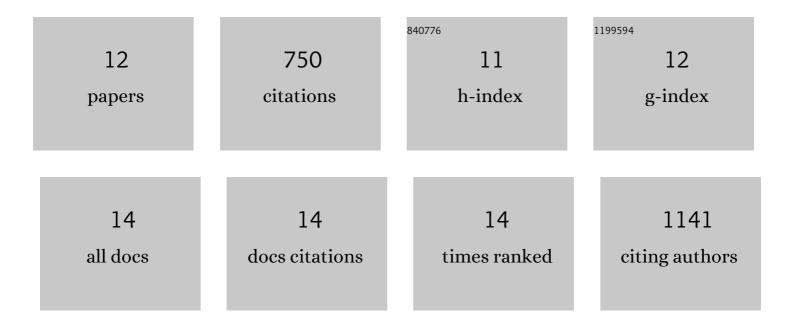
Rui Pereira

List of Publications by Year in descending order

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