Mattia Zampieri

List of Publications by Year
in descending order

31 papers	1,729 citations	430874 18 h-index	414414 32 g-index
37 all docs	37 docs citations	37 times ranked	2744 citing authors

#	Article	IF	Citations
1	Multidimensional Optimality of Microbial Metabolism. Science, 2012, 336, 601-604.	12.6	360
2	Metabolic constraints on the evolution of antibiotic resistance. Molecular Systems Biology, 2017, 13, 917.	7.2	151
3	Nontargeted Metabolomics Reveals the Multilevel Response to Antibiotic Perturbations. Cell Reports, 2017, 19, 1214-1228.	6.4	139
4	Frontiers of high-throughput metabolomics. Current Opinion in Chemical Biology, 2017, 36, 15-23.	6.1	139
5	Genomewide landscape of gene–metabolome associations in *Escherichia coli*. Molecular Systems Biology, 2017, 13, 907.	7.2	109
6	Metabolic profiling of cancer cells reveals genome-wide crosstalk between transcriptional regulators and metabolism. Nature Communications, 2019, 10, 1841.	12.8	108
7	High-throughput metabolomic analysis predicts mode of action of uncharacterized antimicrobial compounds. Science Translational Medicine, 2018, 10, .	12.4	102
8	Regulatory mechanisms underlying coordination of amino acid and glucose catabolism in Escherichia coli. Nature Communications, 2019, 10, 3354.	12.8	101
9	Dynamic phosphoproteomics reveals TORC1-dependent regulation of yeast nucleotide and amino acid biosynthesis. Science Signaling, 2015, 8, rs4.	3.6	64
10	Metabolomics-Driven Exploration of the Chemical Drug Space to Predict Combination Antimicrobial Therapies. Molecular Cell, 2019, 74, 1291-1303.e6.	9.7	57
11	Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. PLoS Computational Biology, 2017, 13, e1005297.	3.2	51
12	Combining CRISPRi and metabolomics for functional annotation of compound libraries. Nature Chemical Biology, 2022, 18, 482-491.	8.0	33
13	Large-scale functional analysis of the roles of phosphorylation in yeast metabolic pathways. Science Signaling, 2014, 7, rs6.	3.6	32
14	Discerning static and causal interactions in genome-wide reverse engineering problems. Bioinformatics, 2008, 24, 1510-1515.	4.1	31
15	A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets â€. Nucleic Acids Research, 2009, 37, 5057-5070.	14.5	27
16	Predicting and characterizing selective multiple drug treatments for metabolicdiseases and cancer. BMC Systems Biology, 2012, 6, 115.	3.0	26
17	A framework for large-scale metabolome drug profiling links coenzyme A metabolism to the toxicity of anti-cancer drug dichloroacetate. Communications Biology, 2018, 1, 101.	4.4	26
18	Model-based integration of genomics and metabolomics reveals SNP functionality in *Mycobacterium tuberculosis*. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 8494-8502.	7.1	24

#	ARTICLE	IF	CITATIONS
19	Detection of transcriptional triggers in the dynamics of microbial growth: application to the respiratorily versatile bacterium Shewanella oneidensis. Nucleic Acids Research, 2012, 40, 7132-7149.	14.5	20
20	Metabolomics-driven understanding of genotype-phenotype relations in model organisms. Current Opinion in Systems Biology, 2017, 6, 28-36.	2.6	17
21	Investigating the Conformational Stability of Prion Strains through a Kinetic Replication Model. PLoS Computational Biology, 2009, 5, e1000420.	3.2	15
22	Model-based media selection to minimize the cost of metabolic cooperation in microbial ecosystems. Bioinformatics, 2016, 32, 1733-1739.	4.1	13
23	Pareto optimality between growth-rate and lag-time couples metabolic noise to phenotypic heterogeneity in Escherichia coli. Nature Communications, 2021, 12, 3204.	12.8	13
24	Origin of Co-Expression Patterns in E.coli and S.cerevisiae Emerging from Reverse Engineering Algorithms. PLoS ONE, 2008, 3, e2981.	2.5	11
25	A system-level approach for deciphering the transcriptional response to prion infection. Bioinformatics, 2011, 27, 3407-3414.	4.1	10
26	The genetic underground of antibiotic resistance. Science, 2021, 371, 783-784.	12.6	9
27	Gene expression profiling to identify druggable targets in prion diseases. Expert Opinion on Drug Discovery, 2010, 5, 177-202.	5.0	7
28	mRNA stability and the unfolding of gene expression in the long-period yeast metabolic cycle. BMC Systems Biology, 2009, 3, 18.	3.0	6
29	From the metabolic profiling of drug response to drug mode of action. Current Opinion in Systems Biology, 2018, 10, 26-33.	2.6	6
30	Expanding the search for small-molecule antibacterials by multidimensional profiling. Nature Chemical Biology, 2022, 18, 584-595.	8.0	6
31	Expression Dysregulation as a Mediator of Fitness Costs in Antibiotic Resistance. Antimicrobial Agents and Chemotherapy, 2021, 65, e0050421.	3.2	5