

Mattia Zampieri

List of Publications by Year in descending order

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Version: 2024-02-01

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 | Combining CRISPRi and metabolomics for functional annotation of compound libraries. <i>Nature Chemical Biology</i> , 2022, 18, 482-491. | 8.0 | 33 |
| 2 | Expanding the search for small-molecule antibacterials by multidimensional profiling. <i>Nature Chemical Biology</i> , 2022, 18, 584-595. | 8.0 | 6 |
| 3 | The genetic underground of antibiotic resistance. <i>Science</i> , 2021, 371, 783-784. | 12.6 | 9 |
| 4 | Pareto optimality between growth-rate and lag-time couples metabolic noise to phenotypic heterogeneity in <i>Escherichia coli</i> . <i>Nature Communications</i> , 2021, 12, 3204. | 12.8 | 13 |
| 5 | Expression Dysregulation as a Mediator of Fitness Costs in Antibiotic Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0050421. | 3.2 | 5 |
| 6 | Model-based integration of genomics and metabolomics reveals SNP functionality in <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8494-8502. | 7.1 | 24 |
| 7 | Regulatory mechanisms underlying coordination of amino acid and glucose catabolism in <i>Escherichia coli</i> . <i>Nature Communications</i> , 2019, 10, 3354. | 12.8 | 101 |
| 8 | Metabolic profiling of cancer cells reveals genome-wide crosstalk between transcriptional regulators and metabolism. <i>Nature Communications</i> , 2019, 10, 1841. | 12.8 | 108 |
| 9 | Metabolomics-Driven Exploration of the Chemical Drug Space to Predict Combination Antimicrobial Therapies. <i>Molecular Cell</i> , 2019, 74, 1291-1303.e6. | 9.7 | 57 |
| 10 | High-throughput metabolomic analysis predicts mode of action of uncharacterized antimicrobial compounds. <i>Science Translational Medicine</i> , 2018, 10, . | 12.4 | 102 |
| 11 | From the metabolic profiling of drug response to drug mode of action. <i>Current Opinion in Systems Biology</i> , 2018, 10, 26-33. | 2.6 | 6 |
| 12 | A framework for large-scale metabolome drug profiling links coenzyme A metabolism to the toxicity of anti-cancer drug dichloroacetate. <i>Communications Biology</i> , 2018, 1, 101. | 4.4 | 26 |
| 13 | Genomewide landscape of gene-metabolome associations in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2017, 13, 907. | 7.2 | 109 |
| 14 | Nontargeted Metabolomics Reveals the Multilevel Response to Antibiotic Perturbations. <i>Cell Reports</i> , 2017, 19, 1214-1228. | 6.4 | 139 |
| 15 | Metabolic constraints on the evolution of antibiotic resistance. <i>Molecular Systems Biology</i> , 2017, 13, 917. | 7.2 | 151 |
| 16 | Frontiers of high-throughput metabolomics. <i>Current Opinion in Chemical Biology</i> , 2017, 36, 15-23. | 6.1 | 139 |
| 17 | Metabolomics-driven understanding of genotype-phenotype relations in model organisms. <i>Current Opinion in Systems Biology</i> , 2017, 6, 28-36. | 2.6 | 17 |
| 18 | Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005297. | 3.2 | 51 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Model-based media selection to minimize the cost of metabolic cooperation in microbial ecosystems. <i>Bioinformatics</i> , 2016, 32, 1733-1739. | 4.1 | 13 |
| 20 | Dynamic phosphoproteomics reveals TORC1-dependent regulation of yeast nucleotide and amino acid biosynthesis. <i>Science Signaling</i> , 2015, 8, rs4. | 3.6 | 64 |
| 21 | Large-scale functional analysis of the roles of phosphorylation in yeast metabolic pathways. <i>Science Signaling</i> , 2014, 7, rs6. | 3.6 | 32 |
| 22 | Detection of transcriptional triggers in the dynamics of microbial growth: application to the respiratorily versatile bacterium <i>Shewanella oneidensis</i> . <i>Nucleic Acids Research</i> , 2012, 40, 7132-7149. | 14.5 | 20 |
| 23 | Predicting and characterizing selective multiple drug treatments for metabolic diseases and cancer. <i>BMC Systems Biology</i> , 2012, 6, 115. | 3.0 | 26 |
| 24 | Multidimensional Optimality of Microbial Metabolism. <i>Science</i> , 2012, 336, 601-604. | 12.6 | 360 |
| 25 | A system-level approach for deciphering the transcriptional response to prion infection. <i>Bioinformatics</i> , 2011, 27, 3407-3414. | 4.1 | 10 |
| 26 | Gene expression profiling to identify druggable targets in prion diseases. <i>Expert Opinion on Drug Discovery</i> , 2010, 5, 177-202. | 5.0 | 7 |
| 27 | A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets. <i>Nucleic Acids Research</i> , 2009, 37, 5057-5070. | 14.5 | 27 |
| 28 | Investigating the Conformational Stability of Prion Strains through a Kinetic Replication Model. <i>PLoS Computational Biology</i> , 2009, 5, e1000420. | 3.2 | 15 |
| 29 | mRNA stability and the unfolding of gene expression in the long-period yeast metabolic cycle. <i>BMC Systems Biology</i> , 2009, 3, 18. | 3.0 | 6 |
| 30 | Discerning static and causal interactions in genome-wide reverse engineering problems. <i>Bioinformatics</i> , 2008, 24, 1510-1515. | 4.1 | 31 |
| 31 | Origin of Co-Expression Patterns in <i>E.coli</i> and <i>S.cerevisiae</i> Emerging from Reverse Engineering Algorithms. <i>PLoS ONE</i> , 2008, 3, e2981. | 2.5 | 11 |