

Tomer Shlomi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8852322/publications.pdf>

Version: 2024-02-01

40
papers

6,604
citations

172457

29
h-index

276875

41
g-index

41
all docs

41
docs citations

41
times ranked

8818
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Quantitative flux analysis reveals folate-dependent NADPH production. <i>Nature</i> , 2014, 510, 298-302. | 27.8 | 892 |
| 2 | Network-based prediction of human tissue-specific metabolism. <i>Nature Biotechnology</i> , 2008, 26, 1003-1010. | 17.5 | 594 |
| 3 | Haem oxygenase is synthetically lethal with the tumour suppressor fumarate hydratase. <i>Nature</i> , 2011, 477, 225-228. | 27.8 | 433 |
| 4 | Regulatory on/off minimization of metabolic flux changes after genetic perturbations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7695-7700. | 7.1 | 427 |
| 5 | Predicting selective drug targets in cancer through metabolic networks. <i>Molecular Systems Biology</i> , 2011, 7, 501. | 7.2 | 418 |
| 6 | Glutamine-driven oxidative phosphorylation is a major ATP source in transformed mammalian cells in both normoxia and hypoxia. <i>Molecular Systems Biology</i> , 2013, 9, 712. | 7.2 | 338 |
| 7 | Computational reconstruction of tissue-specific metabolic models: application to human liver metabolism. <i>Molecular Systems Biology</i> , 2010, 6, 401. | 7.2 | 335 |
| 8 | Metabolite concentrations, fluxes and free energies imply efficient enzyme usage. <i>Nature Chemical Biology</i> , 2016, 12, 482-489. | 8.0 | 332 |
| 9 | iMAT: an integrative metabolic analysis tool. <i>Bioinformatics</i> , 2010, 26, 3140-3142. | 4.1 | 330 |
| 10 | Transfer of miRNA in Macrophage-Derived Exosomes Induces Drug Resistance in Pancreatic Adenocarcinoma. <i>Cancer Research</i> , 2018, 78, 5287-5299. | 0.9 | 248 |
| 11 | Integrating quantitative proteomics and metabolomics with a genome-scale metabolic network model. <i>Bioinformatics</i> , 2010, 26, i255-i260. | 4.1 | 219 |
| 12 | Global characterization of in vivo enzyme catalytic rates and their correspondence to in vitro k_{cat} measurements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3401-3406. | 7.1 | 212 |
| 13 | Genome-Scale Metabolic Modeling Elucidates the Role of Proliferative Adaptation in Causing the Warburg Effect. <i>PLoS Computational Biology</i> , 2011, 7, e1002018. | 3.2 | 201 |
| 14 | A new ESI-LC/MS approach for comprehensive metabolic profiling of phytocannabinoids in Cannabis. <i>Scientific Reports</i> , 2018, 8, 14280. | 3.3 | 186 |
| 15 | Predicting metabolic biomarkers of human inborn errors of metabolism. <i>Molecular Systems Biology</i> , 2009, 5, 263. | 7.2 | 149 |
| 16 | Prediction of Microbial Growth Rate versus Biomass Yield by a Metabolic Network with Kinetic Parameters. <i>PLoS Computational Biology</i> , 2012, 8, e1002575. | 3.2 | 148 |
| 17 | QPath: a method for querying pathways in a protein-protein interaction network. <i>BMC Bioinformatics</i> , 2006, 7, 199. | 2.6 | 140 |
| 18 | Intra-Tumoral Metabolic Zonation and Resultant Phenotypic Diversification Are Dictated by Blood Vessel Proximity. <i>Cell Metabolism</i> , 2019, 30, 201-211.e6. | 16.2 | 86 |

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|----|--|------|-----------|
| 19 | Temporal fluxomics reveals oscillations in TCA cycle flux throughout the mammalian cell cycle. <i>Molecular Systems Biology</i> , 2017, 13, 953. | 7.2 | 72 |
| 20 | Steady-State Metabolite Concentrations Reflect a Balance between Maximizing Enzyme Efficiency and Minimizing Total Metabolite Load. <i>PLoS ONE</i> , 2013, 8, e75370. | 2.5 | 67 |
| 21 | Fatty Acid Labeling from Glutamine in Hypoxia Can Be Explained by Isotope Exchange without Net Reductive Isocitrate Dehydrogenase (IDH) Flux. <i>Journal of Biological Chemistry</i> , 2013, 288, 31363-31369. | 3.4 | 56 |
| 22 | Spatial-fluxomics provides a subcellular-compartmentalized view of reductive glutamine metabolism in cancer cells. <i>Nature Communications</i> , 2019, 10, 1351. | 12.8 | 56 |
| 23 | Fast and sensitive flow-injection mass spectrometry metabolomics by analyzing sample-specific ion distributions. <i>Nature Communications</i> , 2020, 11, 3186. | 12.8 | 50 |
| 24 | Predicting selective drug targets in cancer through metabolic networks. <i>Molecular Systems Biology</i> , 2011, 7, . | 7.2 | 48 |
| 25 | Targeted Inhibition of Glutamine-Dependent Glutathione Metabolism Overcomes Death Resistance Induced by Chronic Cycling Hypoxia. <i>Antioxidants and Redox Signaling</i> , 2016, 25, 89-107. | 5.4 | 47 |
| 26 | Quantitation of Cellular Metabolic Fluxes of Methionine. <i>Analytical Chemistry</i> , 2014, 86, 1583-1591. | 6.5 | 42 |
| 27 | Mind your media. <i>Nature Metabolism</i> , 2020, 2, 1369-1372. | 11.9 | 34 |
| 28 | Conservation of Expression and Sequence of Metabolic Genes Is Reflected by Activity Across Metabolic States. <i>PLoS Computational Biology</i> , 2006, 2, e106. | 3.2 | 32 |
| 29 | Tumor Reliance on Cytosolic versus Mitochondrial One-Carbon Flux Depends on Folate Availability. <i>Cell Metabolism</i> , 2021, 33, 190-198.e6. | 16.2 | 31 |
| 30 | Blimp1+ cells generate functional mouse sebaceous gland organoids in vitro. <i>Nature Communications</i> , 2019, 10, 2348. | 12.8 | 30 |
| 31 | Systematic condition-dependent annotation of metabolic genes. <i>Genome Research</i> , 2007, 17, 1626-1633. | 5.5 | 22 |
| 32 | Computational Design of Auxotrophy-Dependent Microbial Biosensors for Combinatorial Metabolic Engineering Experiments. <i>PLoS ONE</i> , 2011, 6, e16274. | 2.5 | 20 |
| 33 | Studying metabolic flux adaptations in cancer through integrated experimental-computational approaches. <i>BMC Biology</i> , 2019, 17, 51. | 3.8 | 20 |
| 34 | Glycine decarboxylase maintains mitochondrial protein lipoylation to support tumor growth. <i>Cell Metabolism</i> , 2022, 34, 775-782.e9. | 16.2 | 20 |
| 35 | Inferring cancer dependencies on metabolic genes from large-scale genetic screens. <i>BMC Biology</i> , 2019, 17, 37. | 3.8 | 16 |
| 36 | Efficient Modeling of MS/MS Data for Metabolic Flux Analysis. <i>PLoS ONE</i> , 2015, 10, e0130213. | 2.5 | 14 |

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|----|---|-----|-----------|
| 37 | Increasing mTORC1 Pathway Activity or Methionine Supplementation during Pregnancy Reverses the Negative Effect of Maternal Malnutrition on the Developing Kidney. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 1898-1912. | 6.1 | 11 |
| 38 | Metabolic Network-Based Interpretation of Gene Expression Data Elucidates Human Cellular Metabolism. <i>Biotechnology and Genetic Engineering Reviews</i> , 2009, 26, 281-296. | 6.2 | 8 |
| 39 | Sensitivity of pituitary gonadotropes to hyperglycemia leads to epigenetic aberrations and reduced follicle-stimulating hormone levels. <i>FASEB Journal</i> , 2019, 33, 1020-1032. | 0.5 | 6 |
| 40 | Genomic alterations drive metastases formation in pancreatic ductal adenocarcinoma cancer: deciphering the role of CDKN2A and CDKN2B in mediating liver tropism. <i>Oncogene</i> , 2022, 41, 1468-1481. | 5.9 | 4 |