

Tomer Shlomi

List of Publications by Year in descending order

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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	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
2	Glycine decarboxylase maintains mitochondrial protein lipoylation to support tumor growth. <i>Cell Metabolism</i> , 2022, 34, 775-782.e9.	16.2	20
3	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
4	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
5	Mind your media. <i>Nature Metabolism</i> , 2020, 2, 1369-1372.	11.9	34
6	Fast and sensitive flow-injection mass spectrometry metabolomics by analyzing sample-specific ion distributions. <i>Nature Communications</i> , 2020, 11, 3186.	12.8	50
7	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
8	Studying metabolic flux adaptations in cancer through integrated experimental-computational approaches. <i>BMC Biology</i> , 2019, 17, 51.	3.8	20
9	Blimp1+ cells generate functional mouse sebaceous gland organoids in vitro. <i>Nature Communications</i> , 2019, 10, 2348.	12.8	30
10	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
11	Inferring cancer dependencies on metabolic genes from large-scale genetic screens. <i>BMC Biology</i> , 2019, 17, 37.	3.8	16
12	Spatial-fluxomics provides a subcellular-compartmentalized view of reductive glutamine metabolism in cancer cells. <i>Nature Communications</i> , 2019, 10, 1351.	12.8	56
13	A new ESI-LC/MS approach for comprehensive metabolic profiling of phytocannabinoids in Cannabis. <i>Scientific Reports</i> , 2018, 8, 14280.	3.3	186
14	Transfer of miRNA in Macrophage-Derived Exosomes Induces Drug Resistance in Pancreatic Adenocarcinoma. <i>Cancer Research</i> , 2018, 78, 5287-5299.	0.9	248
15	Temporal fluxomics reveals oscillations in TCA cycle flux throughout the mammalian cell cycle. <i>Molecular Systems Biology</i> , 2017, 13, 953.	7.2	72
16	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
17	Metabolite concentrations, fluxes and free energies imply efficient enzyme usage. <i>Nature Chemical Biology</i> , 2016, 12, 482-489.	8.0	332
18	Global characterization of in vivo enzyme catalytic rates and their correspondence to in vitro catalytic measurements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3401-3406.	7.1	212

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19	Efficient Modeling of MS/MS Data for Metabolic Flux Analysis. PLoS ONE, 2015, 10, e0130213.	2.5	14
20	Quantitation of Cellular Metabolic Fluxes of Methionine. Analytical Chemistry, 2014, 86, 1583-1591.	6.5	42
21	Quantitative flux analysis reveals folate-dependent NADPH production. Nature, 2014, 510, 298-302.	27.8	892
22	Fatty Acid Labeling from Glutamine in Hypoxia Can Be Explained by Isotope Exchange without Net Reductive Isocitrate Dehydrogenase (IDH) Flux. Journal of Biological Chemistry, 2013, 288, 31363-31369.	3.4	56
23	Glutamine-driven oxidative phosphorylation is a major ATP source in transformed mammalian cells in both normoxia and hypoxia. Molecular Systems Biology, 2013, 9, 712.	7.2	338
24	Steady-State Metabolite Concentrations Reflect a Balance between Maximizing Enzyme Efficiency and Minimizing Total Metabolite Load. PLoS ONE, 2013, 8, e75370.	2.5	67
25	Prediction of Microbial Growth Rate versus Biomass Yield by a Metabolic Network with Kinetic Parameters. PLoS Computational Biology, 2012, 8, e1002575.	3.2	148
26	Computational Design of Auxotrophy-Dependent Microbial Biosensors for Combinatorial Metabolic Engineering Experiments. PLoS ONE, 2011, 6, e16274.	2.5	20
27	Predicting selective drug targets in cancer through metabolic networks. Molecular Systems Biology, 2011, 7, .	7.2	48
28	Haem oxygenase is synthetically lethal with the tumour suppressor fumarate hydratase. Nature, 2011, 477, 225-228.	27.8	433
29	Predicting selective drug targets in cancer through metabolic networks. Molecular Systems Biology, 2011, 7, 501.	7.2	418
30	Genome-Scale Metabolic Modeling Elucidates the Role of Proliferative Adaptation in Causing the Warburg Effect. PLoS Computational Biology, 2011, 7, e1002018.	3.2	201
31	iMAT: an integrative metabolic analysis tool. Bioinformatics, 2010, 26, 3140-3142.	4.1	330
32	Computational reconstruction of tissue-specific metabolic models: application to human liver metabolism. Molecular Systems Biology, 2010, 6, 401.	7.2	335
33	Integrating quantitative proteomics and metabolomics with a genome-scale metabolic network model. Bioinformatics, 2010, 26, i255-i260.	4.1	219
34	Metabolic Network-Based Interpretation of Gene Expression Data Elucidates Human Cellular Metabolism. Biotechnology and Genetic Engineering Reviews, 2009, 26, 281-296.	6.2	8
35	Predicting metabolic biomarkers of human inborn errors of metabolism. Molecular Systems Biology, 2009, 5, 263.	7.2	149
36	Network-based prediction of human tissue-specific metabolism. Nature Biotechnology, 2008, 26, 1003-1010.	17.5	594

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37	Systematic condition-dependent annotation of metabolic genes. <i>Genome Research</i> , 2007, 17, 1626-1633.	5.5	22
38	QPath: a method for querying pathways in a protein-protein interaction network. <i>BMC Bioinformatics</i> , 2006, 7, 199.	2.6	140
39	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
40	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