

# Tobias Fuhrer

## List of Publications by Year in descending order

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Version: 2024-02-01

50  
papers

6,986  
citations

109321

35  
h-index

197818

49  
g-index

55  
all docs

55  
docs citations

55  
times ranked

11845  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide RNAi screen identifies novel players in human 60S subunit biogenesis including key enzymes of polyamine metabolism. <i>Nucleic Acids Research</i> , 2022, 50, 2872-2888.	14.5	11
2	Glycolysis/gluconeogenesis specialization in microbes is driven by biochemical constraints of flux sensing. <i>Molecular Systems Biology</i> , 2022, 18, e10704.	7.2	21
3	High-Throughput Metabolomics and Diabetic Kidney Disease Progression: Evidence from the Chronic Renal Insufficiency (CRIC) Study. <i>American Journal of Nephrology</i> , 2022, 53, 215-225.	3.1	14
4	Distinct N and C Cross-Feeding Networks in a Synthetic Mouse Gut Consortium. <i>MSystems</i> , 2022, 7, e0148421.	3.8	9
5	Dynamic 3D proteomes reveal protein functional alterations at high resolution in situ. <i>Cell</i> , 2021, 184, 545-559.e22.	28.9	82
6	Reconfiguration of metabolic fluxes in <i>Pseudomonas putida</i> as a response to sub-lethal oxidative stress. <i>ISME Journal</i> , 2021, 15, 1751-1766.	9.8	79
7	Long-term evolution and short-term adaptation of microbiota strains and sub-strains in mice. <i>Cell Host and Microbe</i> , 2021, 29, 650-663.e9.	11.0	58
8	Bifunctional Malic/Malolactic Enzyme Provides a Novel Mechanism for NADPH-Balancing in <i>Bacillus subtilis</i> . <i>MBio</i> , 2021, 12, .	4.1	6
9	Metabolomic Markers of Kidney Function Decline in Patients With Diabetes: Evidence From the Chronic Renal Insufficiency Cohort (CRIC) Study. <i>American Journal of Kidney Diseases</i> , 2020, 76, 511-520.	1.9	45
10	Co-catabolism of arginine and succinate drives symbiotic nitrogen fixation. <i>Molecular Systems Biology</i> , 2020, 16, e9419.	7.2	33
11	Reserve Flux Capacity in the Pentose Phosphate Pathway by NADPH Binding Is Conserved across Kingdoms. <i>IScience</i> , 2019, 19, 1133-1144.	4.1	44
12	Derailing the aspartate pathway of <i>Mycobacterium tuberculosis</i> to eradicate persistent infection. <i>Nature Communications</i> , 2019, 10, 4215.	12.8	48
13	<i>Escherichia coli</i> limits <i>Salmonella Typhimurium</i> infections after diet shifts and fat-mediated microbiota perturbation in mice. <i>Nature Microbiology</i> , 2019, 4, 2164-2174.	13.3	88
14	<sup>2</sup> H/ <sup>1</sup> H variation in microbial lipids is controlled by NADPH metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12173-12182.	7.1	27
15	(p)ppGpp Regulates a Bacterial Nucleosidase by an Allosteric Two-Domain Switch. <i>Molecular Cell</i> , 2019, 74, 1239-1249.e4.	9.7	39
16	Hidden resources in the <i>Escherichia coli</i> genome restore PLP synthesis and robust growth after deletion of the essential gene <i>pdxB</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24164-24173.	7.1	23
17	Purity by design: Reducing impurities in bioproduction by stimulus-controlled global translational downregulation of non-product proteins. <i>Metabolic Engineering</i> , 2019, 52, 110-123.	7.0	10
18	A Map of Protein-Metabolite Interactions Reveals Principles of Chemical Communication. <i>Cell</i> , 2018, 172, 358-372.e23.	28.9	350

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19	Synthesis and degradation of FtsZ quantitatively predict the first cell division in starved bacteria. <i>Molecular Systems Biology</i> , 2018, 14, e8623.	7.2	66
20	Metabolic Remodeling during Liver Regeneration. <i>Developmental Cell</i> , 2018, 47, 425-438.e5.	7.0	86
21	Antibodies Set Boundaries Limiting Microbial Metabolite Penetration and the Resultant Mammalian Host Response. <i>Immunity</i> , 2018, 49, 545-559.e5.	14.3	121
22	Reserve Flux Capacity in the Pentose Phosphate Pathway Enables <i>Escherichia coli</i> 's Rapid Response to Oxidative Stress. <i>Cell Systems</i> , 2018, 6, 569-578.e7.	6.2	162
23	The thioredoxin-1 system is essential for fueling DNA synthesis during T-cell metabolic reprogramming and proliferation. <i>Nature Communications</i> , 2018, 9, 1851.	12.8	77
24	Genomewide landscape of gene-metabolome associations in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2017, 13, 907.	7.2	109
25	Maternal microbiota and antibodies as advocates of neonatal health. <i>Gut Microbes</i> , 2017, 8, 479-485.	9.8	21
26	Glycolysis without pyruvate kinase in <i>Clostridium thermocellum</i> . <i>Metabolic Engineering</i> , 2017, 39, 169-180.	7.0	62
27	Nontargeted in vitro metabolomics for high-throughput identification of novel enzymes in <i>Escherichia coli</i> . <i>Nature Methods</i> , 2017, 14, 187-194.	19.0	125
28	L-Arginine Modulates T Cell Metabolism and Enhances Survival and Anti-tumor Activity. <i>Cell</i> , 2016, 167, 829-842.e13.	28.9	1,077
29	The maternal microbiota drives early postnatal innate immune development. <i>Science</i> , 2016, 351, 1296-1302.	12.6	871
30	<i>Pseudomonas putida</i> KT2440 Strain Metabolizes Glucose through a Cycle Formed by Enzymes of the Entner-Doudoroff, Embden-Meyerhof-Parnas, and Pentose Phosphate Pathways. <i>Journal of Biological Chemistry</i> , 2015, 290, 25920-25932.	3.4	269
31	The outer mucus layer hosts a distinct intestinal microbial niche. <i>Nature Communications</i> , 2015, 6, 8292.	12.8	390
32	Real-time metabolome profiling of the metabolic switch between starvation and growth. <i>Nature Methods</i> , 2015, 12, 1091-1097.	19.0	209
33	High-throughput discovery metabolomics. <i>Current Opinion in Biotechnology</i> , 2015, 31, 73-78.	6.6	203
34	Protein acetylation affects acetate metabolism, motility and acid stress response in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2014, 10, 762.	7.2	159
35	Hepatic mTORC1 controls locomotor activity, body temperature, and lipid metabolism through FGF21. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11592-11599.	7.1	134
36	Identification of Transcriptional and Metabolic Programs Related to Mammalian Cell Size. <i>Current Biology</i> , 2014, 24, 598-608.	3.9	108

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37	Cra regulates the cross-talk between the two branches of the phosphoenolpyruvateâ€ƒphosphotransferase system of <i>Pseudomonas putida</i> . <i>Environmental Microbiology</i> , 2013, 15, 121-132.	3.8	18
38	Global probabilistic annotation of metabolic networks enables enzyme discovery. <i>Nature Chemical Biology</i> , 2012, 8, 848-854.	8.0	53
39	Acetate scavenging activity in <i>Escherichia coli</i> : interplay of acetylâ€ƒCoA synthetase and the PEPâ€ƒglyoxylate cycle in chemostat cultures. <i>Applied Microbiology and Biotechnology</i> , 2012, 93, 2109-2124.	3.6	71
40	High-Throughput, Accurate Mass Metabolome Profiling of Cellular Extracts by Flow Injectionâ€ƒTime-of-Flight Mass Spectrometry. <i>Analytical Chemistry</i> , 2011, 83, 7074-7080.	6.5	324
41	The Nonphosphorylative Entner-Doudoroff Pathway in the Thermoacidophilic Euryarchaeon <i>Picrophilus torridus</i> Involves a Novel 2-Keto-3-Deoxygluconate-Specific Aldolase. <i>Journal of Bacteriology</i> , 2010, 192, 964-974.	2.2	50
42	Metabolism of Pentose Sugars in the Hyperthermophilic Archaea <i>Sulfolobus solfataricus</i> and <i>Sulfolobus acidocaldarius</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 33701-33709.	3.4	76
43	Different Biochemical Mechanisms Ensure Network-Wide Balancing of Reducing Equivalents in Microbial Metabolism. <i>Journal of Bacteriology</i> , 2009, 191, 2112-2121.	2.2	136
44	d-Xylose Degradation Pathway in the Halophilic Archaeon <i>Haloferax volcanii</i> . <i>Journal of Biological Chemistry</i> , 2009, 284, 27290-27303.	3.4	92
45	Computational Prediction and Experimental Verification of the Gene Encoding the NAD <sup>+</sup> /NADP <sup>+</sup> -Dependent Succinate Semialdehyde Dehydrogenase in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2007, 189, 8073-8078.	2.2	57
46	Convergent Peripheral Pathways Catalyze Initial Glucose Catabolism in <i>Pseudomonas putida</i> : Genomic and Flux Analysis. <i>Journal of Bacteriology</i> , 2007, 189, 5142-5152.	2.2	231
47	Determination of Metabolic Flux Ratios From <sup>13</sup> C-Experiments and Gas Chromatography-Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2007, 358, 177-197.	0.9	168
48	Multiple and Interconnected Pathways for l-Lysine Catabolism in <i>Pseudomonas putida</i> KT2440. <i>Journal of Bacteriology</i> , 2005, 187, 7500-7510.	2.2	122
49	Experimental Identification and Quantification of Glucose Metabolism in Seven Bacterial Species. <i>Journal of Bacteriology</i> , 2005, 187, 1581-1590.	2.2	340
50	Determination of Metabolic Flux Ratios From <sup>13</sup> C-Experiments and Gas Chromatography-Mass Spectrometry Data: Protocol and Principles. , 0, , 177-198.		4