

# Michael Zimmermann

## List of Publications by Year in descending order

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Version: 2024-02-01

34  
papers

3,728  
citations

279798

23  
h-index

377865

34  
g-index

37  
all docs

37  
docs citations

37  
times ranked

5809  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamic tracing of sugar metabolism reveals the mechanisms of action of synthetic sugar analogs. <i>Glycobiology</i> , 2022, 32, 239-250.	2.5	15
2	Metabolic reprogramming of <i>Pseudomonas aeruginosa</i> by phage-based quorum sensing modulation. <i>Cell Reports</i> , 2022, 38, 110372.	6.4	20
3	Towards a mechanistic understanding of reciprocal drug-microbiome interactions. <i>Molecular Systems Biology</i> , 2021, 17, e10116.	7.2	64
4	Methodological Advances to Study Contaminant Biotransformation: New Prospects for Understanding and Reducing Environmental Persistence?. <i>ACS ES&amp;T Water</i> , 2021, 1, 1541-1554.	4.6	35
5	Adaptive laboratory evolution of microbial co-cultures for improved metabolite secretion. <i>Molecular Systems Biology</i> , 2021, 17, e10189.	7.2	21
6	Bioaccumulation of therapeutic drugs by human gut bacteria. <i>Nature</i> , 2021, 597, 533-538.	27.8	159
7	Unravelling the collateral damage of antibiotics on gut bacteria. <i>Nature</i> , 2021, 599, 120-124.	27.8	159
8	Insights from pharmacokinetic models of host-microbiome drug metabolism. <i>Gut Microbes</i> , 2020, 11, 587-596.	9.8	27
9	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
10	The gut microbiome in solid organ transplantation. <i>Pediatric Transplantation</i> , 2020, 24, e13866.	1.0	17
11	Mapping human microbiome drug metabolism by gut bacteria and their genes. <i>Nature</i> , 2019, 570, 462-467.	27.8	666
12	<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
13	Separating host and microbiome contributions to drug pharmacokinetics and toxicity. <i>Science</i> , 2019, 363, .	12.6	281
14	Antibodies Set Boundaries Limiting Microbial Metabolite Penetration and the Resultant Mammalian Host Response. <i>Immunity</i> , 2018, 49, 545-559.e5.	14.3	121
15	The Stringent Response Determines the Ability of a Commensal Bacterium to Survive Starvation and to Persist in the Gut. <i>Cell Host and Microbe</i> , 2018, 24, 120-132.e6.	11.0	50
16	Modulation of bacterial metabolism by the microenvironment controls MAIT cell stimulation. <i>Mucosal Immunology</i> , 2018, 11, 1060-1070.	6.0	60
17	Engineered Regulatory Systems Modulate Gene Expression of Human Commensals in the Gut. <i>Cell</i> , 2017, 169, 547-558.e15.	28.9	147
18	Nontargeted Metabolomics Reveals the Multilevel Response to Antibiotic Perturbations. <i>Cell Reports</i> , 2017, 19, 1214-1228.	6.4	139

#	ARTICLE	IF	CITATIONS
19	Integration of Metabolomics and Transcriptomics Reveals a Complex Diet of Mycobacterium tuberculosis during Early Macrophage Infection. <i>MSystems</i> , 2017, 2, .	3.8	112
20	Systems Pharmacology Dissection of Cholesterol Regulation Reveals Determinants of Large Pharmacodynamic Variability between Cell Lines. <i>Cell Systems</i> , 2017, 5, 604-619.e7.	6.2	17
21	PknG senses amino acid availability to control metabolism and virulence of Mycobacterium tuberculosis. <i>PLoS Pathogens</i> , 2017, 13, e1006399.	4.7	81
22	A rheostat mechanism governs the bifurcation of carbon flux in mycobacteria. <i>Nature Communications</i> , 2016, 7, 12527.	12.8	27
23	High coverage metabolomics analysis reveals phage-specific alterations to <i>Pseudomonas aeruginosa</i> physiology during infection. <i>ISME Journal</i> , 2016, 10, 1823-1835.	9.8	126
24	Next-Generation $\alpha$ -omics Approaches Reveal a Massive Alteration of Host RNA Metabolism during Bacteriophage Infection of <i>Pseudomonas aeruginosa</i> . <i>PLoS Genetics</i> , 2016, 12, e1006134.	3.5	94
25	Dynamic exometabolome analysis reveals active metabolic pathways in non-replicating mycobacteria. <i>Environmental Microbiology</i> , 2015, 17, 4802-4815.	3.8	40
26	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of Mycobacterium tuberculosis. <i>Cell Host and Microbe</i> , 2015, 18, 96-108.	11.0	229
27	Characterization of the Mycobacterial Acyl-CoA Carboxylase Holo Complexes Reveals Their Functional Expansion into Amino Acid Catabolism. <i>PLoS Pathogens</i> , 2015, 11, e1004623.	4.7	19
28	Discovery and Characterization of Gut Microbiota Decarboxylases that Can Produce the Neurotransmitter Tryptamine. <i>Cell Host and Microbe</i> , 2014, 16, 495-503.	11.0	473
29	Quantification and Mass Isotopomer Profiling of $\beta$ -Keto Acids in Central Carbon Metabolism. <i>Analytical Chemistry</i> , 2014, 86, 3232-3237.	6.5	60
30	Nontargeted Profiling of Coenzyme A thioesters in biological samples by tandem mass spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 8284-8290.	6.5	24
31	A general strategy to characterize calmodulin-calcium complexes involved in Ca <sup>2+</sup> -target recognition: DAPK and EGFR calmodulin binding domains interact with different calmodulin-calcium complexes. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2011, 1813, 1059-1067.	4.1	20
32	Fumarate Reductase Activity Maintains an Energized Membrane in Anaerobic Mycobacterium tuberculosis. <i>PLoS Pathogens</i> , 2011, 7, e1002287.	4.7	221
33	A Family of Pyrazinone Natural Products from a Conserved Nonribosomal Peptide Synthetase in <i>Staphylococcus aureus</i> . <i>Chemistry and Biology</i> , 2010, 17, 925-930.	6.0	74
34	Homodimerization of the Death-Associated Protein Kinase Catalytic Domain: Development of a New Small Molecule Fluorescent Reporter. <i>PLoS ONE</i> , 2010, 5, e14120.	2.5	12