

# Michael Zimmermann

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5170740/publications.pdf>

Version: 2024-02-01

34  
papers

3,728  
citations

279778

23  
h-index

377849

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. MSystems, 2017, 2, .	3.8	112
20	Systems Pharmacology Dissection of Cholesterol Regulation Reveals Determinants of Large Pharmacodynamic Variability between Cell Lines. Cell Systems, 2017, 5, 604-619.e7.	6.2	17
21	PknG senses amino acid availability to control metabolism and virulence of Mycobacterium tuberculosis. PLoS Pathogens, 2017, 13, e1006399.	4.7	81
22	A rheostat mechanism governs the bifurcation of carbon flux in mycobacteria. Nature Communications, 2016, 7, 12527.	12.8	27
23	High coverage metabolomics analysis reveals phage-specific alterations to <i>Pseudomonas aeruginosa</i> physiology during infection. ISME Journal, 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> . PLoS Genetics, 2016, 12, e1006134.	3.5	94
25	Dynamic exometabolome analysis reveals active metabolic pathways in non-replicating mycobacteria. Environmental Microbiology, 2015, 17, 4802-4815.	3.8	40
26	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of Mycobacterium tuberculosis. Cell Host and Microbe, 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. PLoS Pathogens, 2015, 11, e1004623.	4.7	19
28	Discovery and Characterization of Gut Microbiota Decarboxylases that Can Produce the Neurotransmitter Tryptamine. Cell Host and Microbe, 2014, 16, 495-503.	11.0	473
29	Quantification and Mass Isotopomer Profiling of $\pm$ -Keto Acids in Central Carbon Metabolism. Analytical Chemistry, 2014, 86, 3232-3237.	6.5	60
30	Nontargeted Profiling of Coenzyme A thioesters in biological samples by tandem mass spectrometry. Analytical Chemistry, 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. Biochimica Et Biophysica Acta - Molecular Cell Research, 2011, 1813, 1059-1067.	4.1	20
32	Fumarate Reductase Activity Maintains an Energized Membrane in Anaerobic Mycobacterium tuberculosis. PLoS Pathogens, 2011, 7, e1002287.	4.7	221
33	A Family of Pyrazinone Natural Products from a Conserved Nonribosomal Peptide Synthetase in Staphylococcus aureus. Chemistry and Biology, 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. PLoS ONE, 2010, 5, e14120.	2.5	12