

# Michael MÃ¼ller

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2294873/publications.pdf>

Version: 2024-02-01

33  
papers

3,091  
citations

331670

21  
h-index

414414

32  
g-index

48  
all docs

48  
docs citations

48  
times ranked

4651  
citing authors

#	ARTICLE	IF	CITATIONS
1	A proteomic survival predictor for COVID-19 patients in intensive care. , 2022, 1, e0000007.		28
2	Complement activation induces excessive T cell cytotoxicity in severe COVID-19. Cell, 2022, 185, 493-512.e25.	28.9	122
3	Microbial communities form rich extracellular metabolomes that foster metabolic interactions and promote drug tolerance. Nature Microbiology, 2022, 7, 542-555.	13.3	58
4	A multiplex protein panel assay for severity prediction and outcome prognosis in patients with COVID-19: An observational multi-cohort study. EclinicalMedicine, 2022, 49, 101495.	7.1	17
5	dia-PASEF data analysis using FragPipe and DIA-NN for deep proteomics of low sample amounts. Nature Communications, 2022, 13, .	12.8	120
6	Effects of CGRP receptor antagonism on glucose and bone metabolism in mice with diet-induced obesity. Bone, 2021, 143, 115646.	2.9	7
7	Ribosome profiling reveals ribosome stalling on tryptophan codons and ribosome queuing upon oxidative stress in fission yeast. Nucleic Acids Research, 2021, 49, 383-399.	14.5	40
8	Amino Acids Whose Intracellular Levels Change Most During Aging Alter Chronological Life Span of Fission Yeast. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 205-210.	3.6	9
9	Ultra-fast proteomics with Scanning SWATH. Nature Biotechnology, 2021, 39, 846-854.	17.5	173
10	Dietary-challenged mice with Alzheimer-like pathology show increased energy expenditure and reduced adipocyte hypertrophy and steatosis. Aging, 2021, 13, 10891-10919.	3.1	2
11	A time-resolved proteomic and prognostic map of COVID-19. Cell Systems, 2021, 12, 780-794.e7.	6.2	125
12	Virus-induced senescence is a driver and therapeutic target in COVID-19. Nature, 2021, 599, 283-289.	27.8	195
13	The metabolic growth limitations of petite cells lacking the mitochondrial genome. Nature Metabolism, 2021, 3, 1521-1535.	11.9	29
14	Slow Growth and Increased Spontaneous Mutation Frequency in Respiratory Deficient afo1- Yeast Suppressed by a Dominant Mutation in ATP3. G3: Genes, Genomes, Genetics, 2020, 10, 4637-4648.	1.8	7
15	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. Cell Systems, 2020, 11, 11-24.e4.	6.2	439
16	Pyruvate kinase variant of fission yeast tunes carbon metabolism, cell regulation, growth and stress resistance. Molecular Systems Biology, 2020, 16, e9270.	7.2	27
17	Lysine harvesting is an antioxidant strategy and triggers underground polyamine metabolism. Nature, 2019, 572, 249-253.	27.8	99
18	Low catalytic activity is insufficient to induce disease pathology in triosephosphate isomerase deficiency. Journal of Inherited Metabolic Disease, 2019, 42, 839-849.	3.6	13

#	ARTICLE	IF	CITATIONS
19	Ice-Age Climate Adaptations Trap the Alpine Marmot in a State of Low Genetic Diversity. <i>Current Biology</i> , 2019, 29, 1712-1720.e7.	3.9	27
20	Cost-effective generation of precise label-free quantitative proteomes in high-throughput by microLC and data-independent acquisition. <i>Scientific Reports</i> , 2018, 8, 4346.	3.3	66
21	Machine Learning Predicts the Yeast Metabolome from the Quantitative Proteome of Kinase Knockouts. <i>Cell Systems</i> , 2018, 7, 269-283.e6.	6.2	80
22	Yeast Creates a Niche for Symbiotic Lactic Acid Bacteria through Nitrogen Overflow. <i>Cell Systems</i> , 2017, 5, 345-357.e6.	6.2	247
23	Metabolomics in Yeast. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.top083576.	0.3	6
24	A High-Throughput Method for the Quantitative Determination of Free Amino Acids in <i>Saccharomyces cerevisiae</i> by Hydrophilic Interaction Chromatography-Tandem Mass Spectrometry. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot089094.	0.3	21
25	Functional Metabolomics Describes the Yeast Biosynthetic Regulome. <i>Cell</i> , 2016, 167, 553-565.e12.	28.9	137
26	The metabolic background is a global player in <i>Saccharomyces</i> gene expression epistasis. <i>Nature Microbiology</i> , 2016, 1, 15030.	13.3	76
27	<i>Saccharomyces cerevisiae</i> single-copy plasmids for auxotrophy compensation, multiple marker selection, and for designing metabolically cooperating communities. <i>F1000Research</i> , 2016, 5, 2351.	1.6	30
28	Self-establishing communities enable cooperative metabolite exchange in a eukaryote. <i>ELife</i> , 2015, 4, .	6.0	81
29	The genomic and phenotypic diversity of <i>Schizosaccharomyces pombe</i> . <i>Nature Genetics</i> , 2015, 47, 235-241.	21.4	174
30	Cytosine DNA Methylation Is Found in <i>Drosophila melanogaster</i> but Absent in <i>Saccharomyces cerevisiae</i> , <i>Schizosaccharomyces pombe</i> , and Other Yeast Species. <i>Analytical Chemistry</i> , 2014, 86, 3697-3702.	6.5	225
31	Tpo1-mediated spermine and spermidine export controls cell cycle delay and times antioxidant protein expression during the oxidative stress response. <i>EMBO Reports</i> , 2013, 14, 1113-1119.	4.5	52
32	A prototrophic deletion mutant collection for yeast metabolomics and systems biology. <i>Nature Biotechnology</i> , 2012, 30, 1176-1178.	17.5	107
33	Pyruvate Kinase Triggers a Metabolic Feedback Loop that Controls Redox Metabolism in Respiring Cells. <i>Cell Metabolism</i> , 2011, 14, 415-427.	16.2	185