

# Michael MÃ¼ller

## List of Publications by Year in descending order

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33  
papers

3,091  
citations

331670

21  
h-index

414414

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g-index

48  
all docs

48  
docs citations

48  
times ranked

4651  
citing authors

#	ARTICLE	IF	CITATIONS
1	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. <i>Cell Systems</i> , 2020, 11, 11-24.e4.	6.2	439
2	Yeast Creates a Niche for Symbiotic Lactic Acid Bacteria through Nitrogen Overflow. <i>Cell Systems</i> , 2017, 5, 345-357.e6.	6.2	247
3	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
4	Virus-induced senescence is a driver and therapeutic target in COVID-19. <i>Nature</i> , 2021, 599, 283-289.	27.8	195
5	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
6	The genomic and phenotypic diversity of <i>Schizosaccharomyces pombe</i> . <i>Nature Genetics</i> , 2015, 47, 235-241.	21.4	174
7	Ultra-fast proteomics with Scanning SWATH. <i>Nature Biotechnology</i> , 2021, 39, 846-854.	17.5	173
8	Functional Metabolomics Describes the Yeast Biosynthetic Regulome. <i>Cell</i> , 2016, 167, 553-565.e12.	28.9	137
9	A time-resolved proteomic and prognostic map of COVID-19. <i>Cell Systems</i> , 2021, 12, 780-794.e7.	6.2	125
10	Complement activation induces excessive T cell cytotoxicity in severe COVID-19. <i>Cell</i> , 2022, 185, 493-512.e25.	28.9	122
11	dia-PASEF data analysis using FragPipe and DIA-NN for deep proteomics of low sample amounts. <i>Nature Communications</i> , 2022, 13, .	12.8	120
12	A prototrophic deletion mutant collection for yeast metabolomics and systems biology. <i>Nature Biotechnology</i> , 2012, 30, 1176-1178.	17.5	107
13	Lysine harvesting is an antioxidant strategy and triggers underground polyamine metabolism. <i>Nature</i> , 2019, 572, 249-253.	27.8	99
14	Self-establishing communities enable cooperative metabolite exchange in a eukaryote. <i>ELife</i> , 2015, 4, .	6.0	81
15	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
16	The metabolic background is a global player in <i>Saccharomyces</i> gene expression epistasis. <i>Nature Microbiology</i> , 2016, 1, 15030.	13.3	76
17	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
18	Microbial communities form rich extracellular metabolomes that foster metabolic interactions and promote drug tolerance. <i>Nature Microbiology</i> , 2022, 7, 542-555.	13.3	58

#	ARTICLE	IF	CITATIONS
19	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
20	Ribosome profiling reveals ribosome stalling on tryptophan codons and ribosome queuing upon oxidative stress in fission yeast. <i>Nucleic Acids Research</i> , 2021, 49, 383-399.	14.5	40
21	<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
22	The metabolic growth limitations of petite cells lacking the mitochondrial genome. <i>Nature Metabolism</i> , 2021, 3, 1521-1535.	11.9	29
23	A proteomic survival predictor for COVID-19 patients in intensive care. , 2022, 1, e0000007.		28
24	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
25	Pyruvate kinase variant of fission yeast tunes carbon metabolism, cell regulation, growth and stress resistance. <i>Molecular Systems Biology</i> , 2020, 16, e9270.	7.2	27
26	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
27	A multiplex protein panel assay for severity prediction and outcome prognosis in patients with COVID-19: An observational multi-cohort study. <i>EClinicalMedicine</i> , 2022, 49, 101495.	7.1	17
28	Low catalytic activity is insufficient to induce disease pathology in triosephosphate isomerase deficiency. <i>Journal of Inherited Metabolic Disease</i> , 2019, 42, 839-849.	3.6	13
29	Amino Acids Whose Intracellular Levels Change Most During Aging Alter Chronological Life Span of Fission Yeast. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021, 76, 205-210.	3.6	9
30	Slow Growth and Increased Spontaneous Mutation Frequency in Respiratory Deficient <i>afp1</i> - Yeast Suppressed by a Dominant Mutation in <i>ATP3</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4637-4648.	1.8	7
31	Effects of CGRP receptor antagonism on glucose and bone metabolism in mice with diet-induced obesity. <i>Bone</i> , 2021, 143, 115646.	2.9	7
32	Metabolomics in Yeast. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.top083576.	0.3	6
33	Dietary-challenged mice with Alzheimer-like pathology show increased energy expenditure and reduced adipocyte hypertrophy and steatosis. <i>Aging</i> , 2021, 13, 10891-10919.	3.1	2