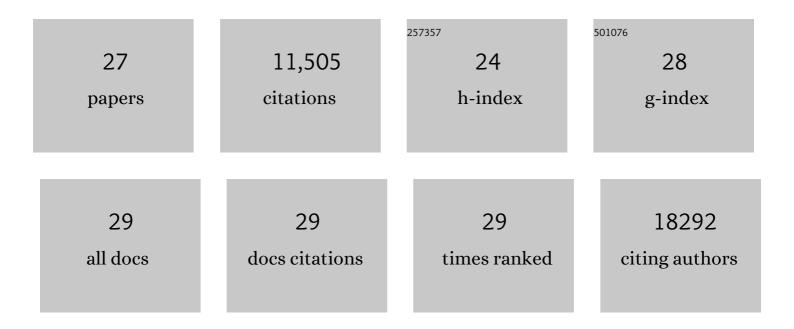
## Melanie Schirmer

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/696678/publications.pdf Version: 2024-02-01



MELANIE SCHIDMED

#	Article	IF	CITATIONS
1	Binning metagenomic contigs by coverage and composition. Nature Methods, 2014, 11, 1144-1146.	9.0	1,709
2	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. Nature, 2019, 569, 655-662.	13.7	1,638
3	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science, 2016, 352, 565-569.	6.0	1,398
4	Species-level functional profiling of metagenomes and metatranscriptomes. Nature Methods, 2018, 15, 962-968.	9.0	1,125
5	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. Cell, 2016, 167, 1125-1136.e8.	13.5	806
6	The effect of host genetics on the gut microbiome. Nature Genetics, 2016, 48, 1407-1412.	9.4	672
7	Insight into biases and sequencing errors for amplicon sequencing with the Illumina MiSeq platform. Nucleic Acids Research, 2015, 43, e37-e37.	6.5	626
8	Prediction of complicated disease course for children newly diagnosed with Crohn's disease: a multicentre inception cohort study. Lancet, The, 2017, 389, 1710-1718.	6.3	482
9	Microbial genes and pathways inÂinflammatory bowel disease. Nature Reviews Microbiology, 2019, 17, 497-511.	13.6	447
10	Dynamics of metatranscription in the inflammatory bowel disease gut microbiome. Nature Microbiology, 2018, 3, 337-346.	5.9	408
11	A comprehensive benchmarking study of protocols and sequencing platforms for 16S rRNA community profiling. BMC Genomics, 2016, 17, 55.	1.2	387
12	Illumina error profiles: resolving fine-scale variation in metagenomic sequencing data. BMC Bioinformatics, 2016, 17, 125.	1.2	303
13	Obese Individuals with and without Type 2 Diabetes Show Different Gut Microbial Functional Capacity and Composition. Cell Host and Microbe, 2019, 26, 252-264.e10.	5.1	274
14	Ulcerative colitis mucosal transcriptomes reveal mitochondriopathy and personalized mechanisms underlying disease severity and treatment response. Nature Communications, 2019, 10, 38.	5.8	215
15	Compositional and Temporal Changes in the Gut Microbiome of Pediatric Ulcerative Colitis Patients Are Linked to Disease Course. Cell Host and Microbe, 2018, 24, 600-610.e4.	5.1	193
16	Spatial and Temporal Mapping of Human Innate Lymphoid Cells Reveals Elements of Tissue Specificity. Immunity, 2019, 50, 505-519.e4.	6.6	139
17	Clinical and biological predictors of response to standardised paediatric colitis therapy (PROTECT): a multicentre inception cohort study. Lancet, The, 2019, 393, 1708-1720.	6.3	121
18	<i>PhyloPythiaS+</i> : a self-training method for the rapid reconstruction of low-ranking taxonomic bins from metagenomes. PeerJ, 2016, 4, e1603.	0.9	87

Melanie Schirmer

#	Article	IF	CITATIONS
19	Understanding human immune function using the resources from the Human Functional Genomics Project. Nature Medicine, 2016, 22, 831-833.	15.2	63
20	Benchmarking of viral haplotype reconstruction programmes: an overview of the capacities and limitations of currently available programmes. Briefings in Bioinformatics, 2014, 15, 431-442.	3.2	59
21	The kinase DYRK1A reciprocally regulates the differentiation of Th17 and regulatory T cells. ELife, 2015, 4, .	2.8	48
22	The causes and consequences of variation in human cytokine production in health. Current Opinion in Immunology, 2018, 54, 50-58.	2.4	40
23	Stable-isotope probing and metagenomics reveal predation by protozoa drives <i>E. coli</i> removal in slow sand filters. ISME Journal, 2015, 9, 797-808.	4.4	36
24	Age-of-diagnosis dependent ileal immune intensification and reduced alpha-defensin in older versus younger pediatric Crohn Disease patients despite already established dysbiosis. Mucosal Immunology, 2019, 12, 491-502.	2.7	18
25	Deciphering mechanisms and implications of bacterial translocation in human health and disease. Current Opinion in Microbiology, 2022, 67, 102147.	2.3	16
26	Untargeted Plasma Metabolomics and Gut Microbiome Profiling Provide Novel Insights into the Regulation of Platelet Reactivity in Healthy Individuals. Thrombosis and Haemostasis, 2022, 122, 529-539.	1.8	3
27	Metagenomic Sequencing Unravels Gene Fragments with Phylogenetic Signatures of O2-Tolerant NiFe Membrane-Bound Hydrogenases in Lacustrine Sediment. Current Microbiology, 2015, 71, 296-302.	1.0	1