

Melanie Schirmer

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

11,505
citations

257357

24
h-index

501076

28
g-index

29
all docs

29
docs citations

29
times ranked

18292
citing authors

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

#	ARTICLE	IF	CITATIONS
19	Understanding human immune function using the resources from the Human Functional Genomics Project. <i>Nature Medicine</i> , 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. <i>Briefings in Bioinformatics</i> , 2014, 15, 431-442.	3.2	59
21	The kinase DYRK1A reciprocally regulates the differentiation of Th17 and regulatory T cells. <i>ELife</i> , 2015, 4, .	2.8	48
22	The causes and consequences of variation in human cytokine production in health. <i>Current Opinion in Immunology</i> , 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. <i>ISME Journal</i> , 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. <i>Mucosal Immunology</i> , 2019, 12, 491-502.	2.7	18
25	Deciphering mechanisms and implications of bacterial translocation in human health and disease. <i>Current Opinion in Microbiology</i> , 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. <i>Thrombosis and Haemostasis</i> , 2022, 122, 529-539.	1.8	3
27	Metagenomic Sequencing Unravels Gene Fragments with Phylogenetic Signatures of O ₂ -Tolerant NiFe Membrane-Bound Hydrogenases in Lacustrine Sediment. <i>Current Microbiology</i> , 2015, 71, 296-302.	1.0	1