

Melanie Schirmer

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

27
papers

6,539
citations

23
h-index

29
g-index

29
ext. papers

9,499
ext. citations

21.1
avg, IF

5.55
L-index

#	Paper	IF	Citations
27	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016 , 352, 565-9	33.3	929
26	Binning metagenomic contigs by coverage and composition. <i>Nature Methods</i> , 2014 , 11, 1144-6	21.6	872
25	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019 , 569, 655-662	50.4	761
24	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018 , 15, 962-968	21.6	608
23	Insight into biases and sequencing errors for amplicon sequencing with the Illumina MiSeq platform. <i>Nucleic Acids Research</i> , 2015 , 43, e37	20.1	461
22	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , 2016 , 167, 1125-1136	16.4	497
21	The effect of host genetics on the gut microbiome. <i>Nature Genetics</i> , 2016 , 48, 1407-1412	36.3	434
20	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	40	315
19	Dynamics of metatranscription in the inflammatory bowel disease gut microbiome. <i>Nature Microbiology</i> , 2018 , 3, 337-346	26.6	249
18	A comprehensive benchmarking study of protocols and sequencing platforms for 16S rRNA community profiling. <i>BMC Genomics</i> , 2016 , 17, 55	4.5	237
17	Illumina error profiles: resolving fine-scale variation in metagenomic sequencing data. <i>BMC Bioinformatics</i> , 2016 , 17, 125	3.6	208
16	Microbial genes and pathways in inflammatory bowel disease. <i>Nature Reviews Microbiology</i> , 2019 , 17, 497-511	22.2	187
15	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	23.4	120
14	Ulcerative colitis mucosal transcriptomes reveal mitochondriopathy and personalized mechanisms underlying disease severity and treatment response. <i>Nature Communications</i> , 2019 , 10, 38	17.4	98
13	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	23.4	93
12	Spatial and Temporal Mapping of Human Innate Lymphoid Cells Reveals Elements of Tissue Specificity. <i>Immunity</i> , 2019 , 50, 505-519.e4	32.3	91
11	PhyloPythiaS+: a self-training method for the rapid reconstruction of low-ranking taxonomic bins from metagenomes. <i>PeerJ</i> , 2016 , 4, e1603	3.1	66

10	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	40	61
9	Benchmarking of viral haplotype reconstruction programmes: an overview of the capacities and limitations of currently available programmes. <i>Briefings in Bioinformatics</i> , 2014 , 15, 431-42	13.4	47
8	Understanding human immune function using the resources from the Human Functional Genomics Project. <i>Nature Medicine</i> , 2016 , 22, 831-3	50.5	43
7	The kinase DYRK1A reciprocally regulates the differentiation of Th17 and regulatory T cells. <i>ELife</i> , 2015 , 4,	8.9	33
6	Stable-isotope probing and metagenomics reveal predation by protozoa drives E. coli removal in slow sand filters. <i>ISME Journal</i> , 2015 , 9, 797-808	11.9	32
5	The causes and consequences of variation in human cytokine production in health. <i>Current Opinion in Immunology</i> , 2018 , 54, 50-58	7.8	21
4	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	9.2	11
3	Population Structure Discovery in Meta-Analyzed Microbial Communities and Inflammatory Bowel Disease		3
2	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	2.4	1
1	Deciphering mechanisms and implications of bacterial translocation in human health and disease.. <i>Current Opinion in Microbiology</i> , 2022 , 67, 102147	7.9	0