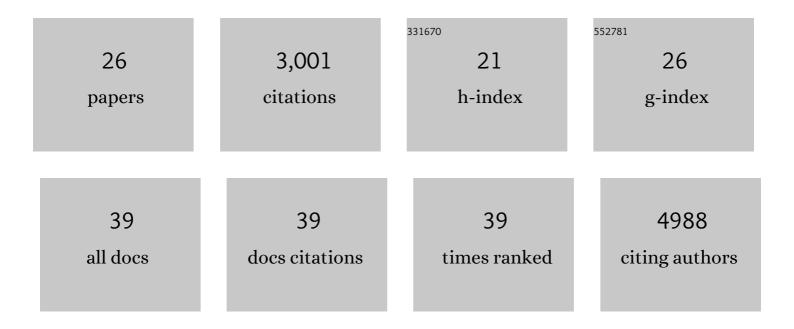
Thomas Sb Schmidt

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1718889/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Microbiome and metabolome features of the cardiometabolic disease spectrum. Nature Medicine, 2022, 28, 303-314.	30.7	102
2	Landscape of mobile genetic elements and their antibiotic resistance cargo in prokaryotic genomes. Nucleic Acids Research, 2022, 50, 3155-3168.	14.5	34
3	A faecal microbiota signature with high specificity for pancreatic cancer. Gut, 2022, 71, 1359-1372.	12.1	104
4	Metagenomic Identification of Microbial Signatures Predicting Pancreatic Cancer From a Multinational Study. Gastroenterology, 2022, 163, 222-238.	1.3	61
5	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses. Genome Biology, 2021, 22, 157.	8.8	7
6	GUNC: detection of chimerism and contamination in prokaryotic genomes. Genome Biology, 2021, 22, 178.	8.8	94
7	Combinatorial, additive and dose-dependent drug–microbiome associations. Nature, 2021, 600, 500-505.	27.8	102
8	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. Nucleic Acids Research, 2020, 48, D621-D625.	14.5	60
9	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. ISME Journal, 2020, 14, 1247-1259.	9.8	74
10	Disentangling the mechanisms shaping the surface ocean microbiota. Microbiome, 2020, 8, 55.	11.1	154
11	Microbial abundance, activity and population genomic profiling with mOTUs2. Nature Communications, 2019, 10, 1014.	12.8	298
12	Protein tyrosine phosphatase non-receptor type 22 modulates colitis in a microbiota-dependent manner. Journal of Clinical Investigation, 2019, 129, 2527-2541.	8.2	15
13	Extensive transmission of microbes along the gastrointestinal tract. ELife, 2019, 8, .	6.0	313
14	The Human Gut Microbiome: From Association to Modulation. Cell, 2018, 172, 1198-1215.	28.9	558
15	Ecologically informed microbial biomarkers and accurate classification of mixed and unmixed samples in an extensive cross-study of human body sites. Microbiome, 2018, 6, 192.	11.1	25
16	Similarity of the dog and human gut microbiomes in gene content and response to diet. Microbiome, 2018, 6, 72.	11.1	211
17	A family of interaction-adjusted indices of community similarity. ISME Journal, 2017, 11, 791-807.	9.8	39
18	MAPseq: highly efficient k-mer search with confidence estimates, for rRNA sequence analysis. Bioinformatics, 2017, 33, 3808-3810.	4.1	98

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#	Article	IF	CITATIONS
19	Effects of oral antibiotics and isotretinoin on the murine gut microbiota. International Journal of Antimicrobial Agents, 2017, 50, 342-351.	2.5	27
20	Preventive Trichuris suis ova (TSO) treatment protects immunocompetent rabbits from DSS colitis but may be detrimental under conditions of immunosuppression. Scientific Reports, 2017, 7, 16500.	3.3	17
21	Limits to robustness and reproducibility in the demarcation of operational taxonomic units. Environmental Microbiology, 2015, 17, 1689-1706.	3.8	95
22	Pseudo-transition Analysis Identifies the Key Regulators of Dynamic Metabolic Adaptations from Steady-State Data. Cell Systems, 2015, 1, 270-282.	6.2	133
23	Ecological Consistency of SSU rRNA-Based Operational Taxonomic Units at a Global Scale. PLoS Computational Biology, 2014, 10, e1003594.	3.2	85
24	Analyses of dryland biological soil crusts highlight lichens as an important regulator of microbial communities. Biodiversity and Conservation, 2014, 23, 1735-1755.	2.6	72
25	Microbiota-Derived Hydrogen Fuels Salmonella Typhimurium Invasion of the Gut Ecosystem. Cell Host and Microbe, 2013, 14, 641-651.	11.0	145
26	Grasp Detection from Human ECoG during Natural Reach-to-Grasp Movements. PLoS ONE, 2013, 8, e54658.	2.5	40