

# Hans-Joachim Ruscheweyh

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1184246/publications.pdf>

Version: 2024-02-01

23  
papers

4,574  
citations

567281

15  
h-index

642732

23  
g-index

23  
all docs

23  
docs citations

23  
times ranked

8322  
citing authors

#	ARTICLE	IF	CITATIONS
1	MEGAN Community Edition - Interactive Exploration and Analysis of Large-Scale Microbiome Sequencing Data. PLoS Computational Biology, 2016, 12, e1004957.	3.2	1,500
2	Integrative analysis of environmental sequences using MEGAN4. Genome Research, 2011, 21, 1552-1560.	5.5	1,245
3	Microbial abundance, activity and population genomic profiling with mOTUs2. Nature Communications, 2019, 10, 1014.	12.8	298
4	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. Cell, 2019, 179, 1068-1083.e21.	28.9	268
5	The Common Gut Microbe Eubacterium hallii also Contributes to Intestinal Propionate Formation. Frontiers in Microbiology, 2016, 7, 713.	3.5	224
6	Intestinal Dysbiosis, Barrier Dysfunction, and Bacterial Translocation Account for CKD-Related Systemic Inflammation. Journal of the American Society of Nephrology: JASN, 2017, 28, 76-83.	6.1	196
7	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	19.0	133
8	Accurate and predictive antibody repertoire profiling by molecular amplification fingerprinting. Science Advances, 2016, 2, e1501371.	10.3	131
9	Trophic Interactions of Infant Bifidobacteria and Eubacterium hallii during L-Fucose and Fucosyllactose Degradation. Frontiers in Microbiology, 2017, 8, 95.	3.5	131
10	Biosynthetic potential of the global ocean microbiome. Nature, 2022, 607, 111-118.	27.8	128
11	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome. Science, 2022, 376, 156-162.	12.6	124
12	Bioinformatics for precision oncology. Briefings in Bioinformatics, 2019, 20, 778-788.	6.5	49
13	Gut microbial beta-glucuronidase and glycerol/diol dehydratase activity contribute to dietary heterocyclic amine biotransformation. BMC Microbiology, 2019, 19, 99.	3.3	42
14	NGS-pipe: a flexible, easily extendable and highly configurable framework for NGS analysis. Bioinformatics, 2018, 34, 107-108.	4.1	25
15	High throughput sequencing provides exact genomic locations of inducible prophages and accurate phage-to-host ratios in gut microbial strains. Microbiome, 2021, 9, 77.	11.1	20
16	Terrestrial and marine influence on atmospheric bacterial diversity over the north Atlantic and Pacific Oceans. Communications Earth & Environment, 2022, 3, .	6.8	13
17	Multi-omics data integration reveals novel drug targets in hepatocellular carcinoma. BMC Genomics, 2021, 22, 592.	2.8	12
18	Impact of manipulation of glycerol/diol dehydratase activity on intestinal microbiota ecology and metabolism. Environmental Microbiology, 2021, 23, 1765-1779.	3.8	10

#	ARTICLE	IF	CITATIONS
19	mOTUs: Profiling Taxonomic Composition, Transcriptional Activity and Strain Populations of Microbial Communities. <i>Current Protocols</i> , 2021, 1, e218.	2.9	8
20	Methylation of CpG 5962 in L1 of the human papillomavirus 16 genome as a potential predictive marker for viral persistence: A prospective large cohort study using cervical swab samples. <i>Cancer Medicine</i> , 2020, 9, 1058-1068.	2.8	7
21	mTAGs: taxonomic profiling using degenerate consensus reference sequences of ribosomal RNA genes. <i>Bioinformatics</i> , 2021, 38, 270-272.	4.1	5
22	The rumen microbiome inhibits methane formation through dietary choline supplementation. <i>Scientific Reports</i> , 2021, 11, 21761.	3.3	3
23	Long-term daily high-protein, drained yoghurt consumption alters abundance of selected functional groups of the human gut microbiota and fecal short-chain fatty acid profiles in a cohort of overweight and obese women. <i>Journal of Functional Foods</i> , 2022, 93, 105089.	3.4	2