

Hans-Joachim Ruscheweyh

List of Publications by Year in descending order

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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	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	19.0	133
2	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome. <i>Science</i> , 2022, 376, 156-162.	12.6	124
3	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
4	Terrestrial and marine influence on atmospheric bacterial diversity over the north Atlantic and Pacific Oceans. <i>Communications Earth & Environment</i> , 2022, 3, .	6.8	13
5	Biosynthetic potential of the global ocean microbiome. <i>Nature</i> , 2022, 607, 111-118.	27.8	128
6	High throughput sequencing provides exact genomic locations of inducible prophages and accurate phage-to-host ratios in gut microbial strains. <i>Microbiome</i> , 2021, 9, 77.	11.1	20
7	Impact of manipulation of glycerol/diol dehydratase activity on intestinal microbiota ecology and metabolism. <i>Environmental Microbiology</i> , 2021, 23, 1765-1779.	3.8	10
8	mTAGs: taxonomic profiling using degenerate consensus reference sequences of ribosomal RNA genes. <i>Bioinformatics</i> , 2021, 38, 270-272.	4.1	5
9	Multi-omics data integration reveals novel drug targets in hepatocellular carcinoma. <i>BMC Genomics</i> , 2021, 22, 592.	2.8	12
10	mOTUs: Profiling Taxonomic Composition, Transcriptional Activity and Strain Populations of Microbial Communities. <i>Current Protocols</i> , 2021, 1, e218.	2.9	8
11	The rumen microbiome inhibits methane formation through dietary choline supplementation. <i>Scientific Reports</i> , 2021, 11, 21761.	3.3	3
12	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
13	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	28.9	268
14	Gut microbial beta-glucuronidase and glycerol/diol dehydratase activity contribute to dietary heterocyclic amine biotransformation. <i>BMC Microbiology</i> , 2019, 19, 99.	3.3	42
15	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019, 10, 1014.	12.8	298
16	Bioinformatics for precision oncology. <i>Briefings in Bioinformatics</i> , 2019, 20, 778-788.	6.5	49
17	NGS-pipe: a flexible, easily extendable and highly configurable framework for NGS analysis. <i>Bioinformatics</i> , 2018, 34, 107-108.	4.1	25
18	Intestinal Dysbiosis, Barrier Dysfunction, and Bacterial Translocation Account for CKD-Related Systemic Inflammation. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 76-83.	6.1	196

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19	Trophic Interactions of Infant Bifidobacteria and <i>Eubacterium hallii</i> during L-Fucose and Fucosyllactose Degradation. <i>Frontiers in Microbiology</i> , 2017, 8, 95.	3.5	131
20	The Common Gut Microbe <i>Eubacterium hallii</i> also Contributes to Intestinal Propionate Formation. <i>Frontiers in Microbiology</i> , 2016, 7, 713.	3.5	224
21	Accurate and predictive antibody repertoire profiling by molecular amplification fingerprinting. <i>Science Advances</i> , 2016, 2, e1501371.	10.3	131
22	MEGAN Community Edition - Interactive Exploration and Analysis of Large-Scale Microbiome Sequencing Data. <i>PLoS Computational Biology</i> , 2016, 12, e1004957.	3.2	1,500
23	Integrative analysis of environmental sequences using MEGAN4. <i>Genome Research</i> , 2011, 21, 1552-1560.	5.5	1,245