

Stefan Janssen

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

20,673
citations

304602

22
h-index

395590

33
g-index

41
all docs

41
docs citations

41
times ranked

25781
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into the genome and secretome of <i>Fusarium metavorans</i> DSM105788 by cultivation on agro-residual biomass and synthetic nutrient sources. <i>Biotechnology for Biofuels</i> , 2021, 14, 74.	6.2	9
2	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	1.7	36
3	Description and comparison of the skin and ear canal microbiota of non-allergic and allergic German shepherd dogs using next generation sequencing. <i>PLoS ONE</i> , 2021, 16, e0250695.	1.1	9
4	Results from a pilot study on the oral microbiome in children and adolescents with chronic nonbacterial osteomyelitis. <i>Zeitschrift Fur Rheumatologie</i> , 2021, , 1.	0.5	4
5	The Microbiome in Childhood Acute Lymphoblastic Leukemia. <i>Cancers</i> , 2021, 13, 4947.	1.7	17
6	Vitamin D metabolites and the gut microbiome in older men. <i>Nature Communications</i> , 2020, 11, 5997.	5.8	88
7	An intact gut microbiome protects genetically predisposed mice against leukemia. <i>Blood</i> , 2020, 136, 2003-2017.	0.6	64
8	Microbiome analyses of blood and tissues suggest cancer diagnostic approach. <i>Nature</i> , 2020, 579, 567-574.	13.7	691
9	The effect of legume supplementation on the gut microbiota in rural Malawian infants aged 6 to 12 months. <i>American Journal of Clinical Nutrition</i> , 2020, 111, 884-892.	2.2	10
10	A gut bacterial amyloid promotes α -synuclein aggregation and motor impairment in mice. <i>ELife</i> , 2020, 9, .	2.8	251
11	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
12	The impact of skin care products on skin chemistry and microbiome dynamics. <i>BMC Biology</i> , 2019, 17, 47.	1.7	101
13	Environmental toxicants in breast milk of Norwegian mothers and gut bacteria composition and metabolites in their infants at 1 month. <i>Microbiome</i> , 2019, 7, 34.	4.9	115
14	Assessing taxonomic metagenome profilers with OPAL. <i>Genome Biology</i> , 2019, 20, 51.	3.8	67
15	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	5.8	197
16	Infectious stimuli promote malignant B-cell acute lymphoblastic leukemia in the absence of AID. <i>Nature Communications</i> , 2019, 10, 5563.	5.8	21
17	Creating a 3D microbial and chemical snapshot of a human habitat. <i>Scientific Reports</i> , 2018, 8, 3669.	1.6	34
18	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , 2018, 3, .	1.7	376

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19	KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. <i>MSystems</i> , 2018, 3, .	1.7	123
20	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018, 15, 796-798.	9.0	459
21	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
22	Critical Assessment of Metagenome Interpretationâ€”a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	9.0	635
23	A communal catalogue reveals Earthâ€™s multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
24	Gut Microbiota Regulate Motor Deficits and Neuroinflammation in a Model of Parkinsonâ€™s Disease. <i>Cell</i> , 2016, 167, 1469-1480.e12.	13.5	2,399
25	Ambivalent covariance models. <i>BMC Bioinformatics</i> , 2015, 16, 178.	1.2	4
26	The RNA shapes studio. <i>Bioinformatics</i> , 2015, 31, 423-425.	1.8	113
27	Abstract Shape Analysis of RNA. <i>Methods in Molecular Biology</i> , 2014, 1097, 215-245.	0.4	3
28	Bellmanâ€™s GAPâ€”a language and compiler for dynamic programming in sequence analysis. <i>Bioinformatics</i> , 2013, 29, 551-560.	1.8	15
29	Lost in folding space? Comparing four variants of the thermodynamic model for RNA secondary structure prediction. <i>BMC Bioinformatics</i> , 2011, 12, 429.	1.2	24
30	A genome-wide survey of sRNAs in the symbiotic nitrogen-fixing alpha-proteobacterium <i>Sinorhizobium meliloti</i> . <i>BMC Genomics</i> , 2010, 11, 245.	1.2	104
31	Faster computation of exact RNA shape probabilities. <i>Bioinformatics</i> , 2010, 26, 632-639.	1.8	21
32	Shape based indexing for faster search of RNA family databases. <i>BMC Bioinformatics</i> , 2008, 9, 131.	1.2	23