

# Jon G Sanders

## List of Publications by Year in descending order

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Version: 2024-02-01

63  
papers

11,993  
citations

116194

36  
h-index

120465

65  
g-index

81  
all docs

81  
docs citations

81  
times ranked

17721  
citing authors

#	ARTICLE	IF	CITATIONS
1	Culture-enriched community profiling improves resolution of the vertebrate gut microbiota. <i>Molecular Ecology Resources</i> , 2022, 22, 122-136.	2.2	12
2	Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort. <i>Nature Genetics</i> , 2022, 54, 134-142.	9.4	164
3	Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting. <i>Cell Metabolism</i> , 2022, 34, 719-730.e4.	7.2	35
4	Turtle ants harbor metabolically versatile microbiomes with conserved functions across development and phylogeny. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	3
5	Gastrointestinal Surgery for Inflammatory Bowel Disease Persistently Lowers Microbiome and Metabolome Diversity. <i>Inflammatory Bowel Diseases</i> , 2021, 27, 603-616.	0.9	25
6	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , 2021, 19, 20.	2.2	19
7	Localization of Bacterial Communities within Gut Compartments across <i>Cephalotes</i> Turtle Ants. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	14
8	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	1.7	36
9	Associations of healthy food choices with gut microbiota profiles. <i>American Journal of Clinical Nutrition</i> , 2021, 114, 605-616.	2.2	42
10	Taxonomic signatures of cause-specific mortality risk in human gut microbiome. <i>Nature Communications</i> , 2021, 12, 2671.	5.8	55
11	Predictable and host-species specific humanization of the gut microbiota in captive primates. <i>Molecular Ecology</i> , 2021, 30, 3677-3687.	2.0	24
12	Cooccurring Activities of Two Autotrophic Pathways in Symbionts of the Hydrothermal Vent Tubeworm <i>Riftia pachyptila</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0079421.	1.4	3
13	Association Between the Gut Microbiota and Blood Pressure in a Population Cohort of 6953 Individuals. <i>Journal of the American Heart Association</i> , 2020, 9, e016641.	1.6	67
14	Roles of the gut microbiota in the adaptive evolution of mammalian species. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190597.	1.8	83
15	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	5.8	368
16	Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence between Birds and Bats. <i>MBio</i> , 2020, 11, .	1.8	204
17	Evolutionary trends in host physiology outweigh dietary niche in structuring primate gut microbiomes. <i>ISME Journal</i> , 2019, 13, 576-587.	4.4	236
18	MetaMiner: A Scalable Peptidogenomics Approach for Discovery of Ribosomal Peptide Natural Products with Blind Modifications from Microbial Communities. <i>Cell Systems</i> , 2019, 9, 600-608.e4.	2.9	46

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19	Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. <i>Genome Biology</i> , 2019, 20, 226.	3.8	47
20	Quantifying and Understanding Well-to-Well Contamination in Microbiome Research. <i>MSystems</i> , 2019, 4, .	1.7	132
21	Not all animals need a microbiome. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	189
22	Is there convergence of gut microbes in blood-feeding vertebrates?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180249.	1.8	21
23	Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , 2019, 4, .	1.7	28
24	The genetic basis for adaptation of model-designed syntrophic co-cultures. <i>PLoS Computational Biology</i> , 2019, 15, e1006213.	1.5	17
25	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	5.8	197
26	Adapterama I: universal stubs and primers for 384 unique dual-indexed or 147,456 combinatorially-indexed Illumina libraries (iTru & iNext). <i>PeerJ</i> , 2019, 7, e7755.	0.9	243
27	Herbivorous turtle ants obtain essential nutrients from a conserved nitrogen-recycling gut microbiome. <i>Nature Communications</i> , 2018, 9, 964.	5.8	115
28	Gut microbiota utilize immunoglobulin A for mucosal colonization. <i>Science</i> , 2018, 360, 795-800.	6.0	447
29	Social behaviour in bees influences the abundance of <i>Sodalis</i> (Enterobacteriaceae) symbionts. <i>Royal Society Open Science</i> , 2018, 5, 180369.	1.1	23
30	High-Throughput Miniaturized 16S rRNA Amplicon Library Preparation Reduces Costs while Preserving Microbiome Integrity. <i>MSystems</i> , 2018, 3, .	1.7	58
31	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018, 15, 796-798.	9.0	459
32	Genome Evolution of Bartonellaceae Symbionts of Ants at the Opposite Ends of the Trophic Scale. <i>Genome Biology and Evolution</i> , 2018, 10, 1687-1704.	1.1	26
33	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018, 16, 410-422.	13.6	1,138
34	Methods for phylogenetic analysis of microbiome data. <i>Nature Microbiology</i> , 2018, 3, 652-661.	5.9	68
35	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , 2018, 44, 61-69.	2.3	27
36	Improving saliva shotgun metagenomics by chemical host DNA depletion. <i>Microbiome</i> , 2018, 6, 42.	4.9	218

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37	Balance Trees Reveal Microbial Niche Differentiation. <i>MSystems</i> , 2017, 2, .	1.7	284
38	Unraveling the processes shaping mammalian gut microbiomes over evolutionary time. <i>Nature Communications</i> , 2017, 8, 14319.	5.8	357
39	The structured diversity of specialized gut symbionts of the New World army ants. <i>Molecular Ecology</i> , 2017, 26, 3808-3825.	2.0	62
40	By their own devices: invasive Argentine ants have shifted diet without clear aid from symbiotic microbes. <i>Molecular Ecology</i> , 2017, 26, 1608-1630.	2.0	36
41	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
42	Ant-plant mutualism: a dietary by-product of a tropical ant's macronutrient requirements. <i>Ecology</i> , 2017, 98, 3141-3151.	1.5	10
43	Dramatic Differences in Gut Bacterial Densities Correlate with Diet and Habitat in Rainforest Ants. <i>Integrative and Comparative Biology</i> , 2017, 57, 705-722.	0.9	77
44	The Effects of Captivity on the Mammalian Gut Microbiome. <i>Integrative and Comparative Biology</i> , 2017, 57, 690-704.	0.9	301
45	The microbiome and big data. <i>Current Opinion in Systems Biology</i> , 2017, 4, 92-96.	1.3	11
46	The human microbiome in evolution. <i>BMC Biology</i> , 2017, 15, 127.	1.7	243
47	Microbial Communities of Lycaenid Butterflies Do Not Correlate with Larval Diet. <i>Frontiers in Microbiology</i> , 2016, 7, 1920.	1.5	75
48	Dissecting host-associated communities with DNA barcodes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150328.	1.8	23
49	Gut microbiota of dung beetles correspond to dietary specializations of adults and larvae. <i>Molecular Ecology</i> , 2016, 25, 6092-6106.	2.0	79
50	<i>Cephalotococcus</i> gen. nov., a new genus of <i>Verrucomicrobia</i> containing two novel species isolated from <i>Cephalotes</i> ant guts. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 3034-3040.	0.8	48
51	The uptake and excretion of partially oxidized sulfur expands the repertoire of energy resources metabolized by hydrothermal vent symbioses. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20142811.	1.2	41
52	Sporadic pollen consumption among tropical ants. <i>Insectes Sociaux</i> , 2015, 62, 379-382.	0.7	4
53	Baleen whales host a unique gut microbiome with similarities to both carnivores and herbivores. <i>Nature Communications</i> , 2015, 6, 8285.	5.8	184
54	DNA extraction protocols cause differences in 16S rRNA amplicon sequencing efficiency but not in community profile composition or structure. <i>MicrobiologyOpen</i> , 2014, 3, 910-921.	1.2	89

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55	Stability and phylogenetic correlation in gut microbiota: lessons from ants and apes. <i>Molecular Ecology</i> , 2014, 23, 1268-1283.	2.0	276
56	Animals in a bacterial world, a new imperative for the life sciences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3229-3236.	3.3	2,181
57	Metatranscriptomics reveal differences in <i>in situ</i> energy and nitrogen metabolism among hydrothermal vent snail symbionts. <i>ISME Journal</i> , 2013, 7, 1556-1567.	4.4	73
58	Evidence for the role of endosymbionts in regional-scale habitat partitioning by hydrothermal vent symbioses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3241-50.	3.3	94
59	Populations of <i>Symbiodinium muscatinei</i> Show Strong Biogeographic Structuring in the Intertidal Anemone <i>Anthopleura elegantissima</i> . <i>Biological Bulletin</i> , 2011, 220, 199-208.	0.7	18
60	Program note: Cladescan, a program for automated phylogenetic sensitivity analysis. <i>Cladistics</i> , 2010, 26, 114-116.	1.5	24
61	Transcriptomic responses to heat stress in invasive and native blue mussels (genus <i>Mytilus</i> ): molecular correlates of invasive success. <i>Journal of Experimental Biology</i> , 2010, 213, 3548-3558.	0.8	220
62	The tip of the tail: molecular identification of seahorses for sale in apothecary shops and curio stores in California. <i>Conservation Genetics</i> , 2008, 9, 65-71.	0.8	33
63	Heat-Shock Protein 70 (Hsp70) Expression in Four Limpets of the Genus <i>Lottia</i> : Interspecific Variation in Constitutive and Inducible Synthesis Correlates With <i>in situ</i> Exposure to Heat Stress. <i>Biological Bulletin</i> , 2008, 215, 173-181.	0.7	152