

Doris Vandeputte

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

47
papers

22,387
citations

32
h-index

51
g-index

51
ext. papers

28,905
ext. citations

21.4
avg, IF

6.21
L-index

#	Paper	IF	Citations
47	Temporal variability in quantitative human gut microbiome profiles and implications for clinical research. <i>Nature Communications</i> , 2021 , 12, 6740	17.4	10
46	Human and preclinical studies of the host-gut microbiome co-metabolite hippurate as a marker and mediator of metabolic health. <i>Gut</i> , 2021 , 70, 2105-2114	19.2	13
45	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021 , 53, 156-165	36.3	80
44	Null-model-based network comparison reveals core associations. <i>ISME Communications</i> , 2021 , 1,		1
43	Variation and transmission of the human gut microbiota across multiple familial generations.. <i>Nature Microbiology</i> , 2021 ,	26.6	4
42	GWAS of stool frequency provides insights into gastrointestinal motility and irritable bowel syndrome.. <i>Cell Genomics</i> , 2021 , 1, None		2
41	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020 , 581, 310-315	50.4	100
40	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. <i>Nature Microbiology</i> , 2020 , 5, 1079-1087	26.6	55
39	Gut microbiome variation is associated to Multiple Sclerosis phenotypic subtypes. <i>Annals of Clinical and Translational Neurology</i> , 2020 , 7, 406-419	5.3	28
38	Personalized Nutrition Through The Gut Microbiota: Current Insights And Future Perspectives. <i>Nutrition Reviews</i> , 2020 , 78, 66-74	6.4	7
37	Effects of Low and High FODMAP Diets on Human Gastrointestinal Microbiota Composition in Adults with Intestinal Diseases: A Systematic Review. <i>Microorganisms</i> , 2020 , 8,	4.9	6
36	Metabolic Functions of Gut Microbes Associate With Efficacy of Tumor Necrosis Factor Antagonists in Patients With Inflammatory Bowel Diseases. <i>Gastroenterology</i> , 2019 , 157, 1279-1292.e11	13.3	101
35	Quantitative microbiome profiling disentangles inflammation- and bile duct obstruction-associated microbiota alterations across PSC/IBD diagnoses. <i>Nature Microbiology</i> , 2019 , 4, 1826-1831	26.6	71
34	The human microbiome in health and disease: hype or hope. <i>Acta Clinica Belgica</i> , 2019 , 74, 53-64	1.8	20
33	The neuroactive potential of the human gut microbiota in quality of life and depression. <i>Nature Microbiology</i> , 2019 , 4, 623-632	26.6	651
32	Population-level analysis of subtype prevalence and variation in the human gut microbiota. <i>Gut</i> , 2019 , 68, 1180-1189	19.2	79
31	The Human Gut Microbiome: From Association to Modulation. <i>Cell</i> , 2018 , 172, 1198-1215	56.2	344

30	Richness and ecosystem development across faecal snapshots of the gut microbiota. <i>Nature Microbiology</i> , 2018 , 3, 526-528	26.6	48
29	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018 , 3, 8-16	26.6	387
28	Prebiotic Wheat Bran Fractions Induce Specific Microbiota Changes. <i>Frontiers in Microbiology</i> , 2018 , 9, 31	5.7	22
27	Comparisons of gut microbiota profiles in wild-type and gelatinase B/matrix metalloproteinase-9-deficient mice in acute DSS-induced colitis. <i>Npj Biofilms and Microbiomes</i> , 2018 , 4, 18	8.2	5
26	Prebiotic inulin-type fructans induce specific changes in the human gut microbiota. <i>Gut</i> , 2017 , 66, 1968-1974	19.4	236
25	Assessment of faecal microbial transfer in irritable bowel syndrome with severe bloating. <i>Gut</i> , 2017 , 66, 980-982	19.2	42
24	Multi-stability and the origin of microbial community types. <i>ISME Journal</i> , 2017 , 11, 2159-2166	11.9	57
23	Combined use of network inference tools identifies ecologically meaningful bacterial associations in a paddy soil. <i>Soil Biology and Biochemistry</i> , 2017 , 105, 227-235	7.5	50
22	Water activity does not shape the microbiota in the human colon. <i>Gut</i> , 2017 , 66, 1865-1866	19.2	8
21	Quantitative microbiome profiling links gut community variation to microbial load. <i>Nature</i> , 2017 , 551, 507-511	50.4	475
20	Brief Report: Dialister as a Microbial Marker of Disease Activity in Spondyloarthritis. <i>Arthritis and Rheumatology</i> , 2017 , 69, 114-121	9.5	150
19	Practical considerations for large-scale gut microbiome studies. <i>FEMS Microbiology Reviews</i> , 2017 , 41, S154-S167	15.1	93
18	Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates. <i>Gut</i> , 2016 , 65, 57-62	19.2	488
17	Species-function relationships shape ecological properties of the human gut microbiome. <i>Nature Microbiology</i> , 2016 , 1, 16088	26.6	145
16	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016 , 10, 1669-81	11.9	365
15	Meta-omics in Inflammatory Bowel Disease Research: Applications, Challenges, and Guidelines. <i>Journal of Crohn's and Colitis</i> , 2016 , 10, 735-46	1.5	23
14	CoNet app: inference of biological association networks using Cytoscape. <i>F1000Research</i> , 2016 , 5, 1519	3.6	231
13	Towards biome-specific analysis of meta-omics data. <i>ISME Journal</i> , 2016 , 10, 1025-8	11.9	40

12	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016 , 352, 565-9	33.3	929
11	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016 , 352, 560-4	33.3	1120
10	Microbiology Meets Big Data: The Case of Gut Microbiota-Derived Trimethylamine. <i>Annual Review of Microbiology</i> , 2015 , 69, 305-21	17.5	94
9	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015 , 528, 262-266	50.4	1107
8	Ocean plankton. Determinants of community structure in the global plankton interactome. <i>Science</i> , 2015 , 348, 1262073	33.3	496
7	LotuS: an efficient and user-friendly OTU processing pipeline. <i>Microbiome</i> , 2014 , 2, 30	16.6	186
6	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013 , 500, 541-6	50.4	2584
5	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011 , 473, 174-80	50.4	4240
4	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010 , 464, 59-65	50.4	7044
3	Get the most out of your metagenome: computational analysis of environmental sequence data. <i>Current Opinion in Microbiology</i> , 2007 , 10, 490-8	7.9	127
2	Large-scale association analyses identify host factors influencing human gut microbiome composition		9
1	A framework for comparing microbial networks reveals core associations		1