

Doris Vandeputte

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

33,384
citations

101496

36
h-index

206029

48
g-index

51
all docs

51
docs citations

51
times ranked

35474
citing authors

#	ARTICLE	IF	CITATIONS
1	Variation and transmission of the human gut microbiota across multiple familial generations. <i>Nature Microbiology</i> , 2022, 7, 87-96.	5.9	32
2	Effect of cryopreservation medium conditions on growth and isolation of gut anaerobes from human faecal samples. <i>Microbiome</i> , 2022, 10, .	4.9	6
3	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	9.4	676
4	Human and preclinical studies of the hostâ€™ gut microbiome co-metabolite hippurate as a marker and mediator of metabolic health. <i>Gut</i> , 2021, 70, 2105-2114.	6.1	58
5	Null-model-based network comparison reveals core associations. <i>ISME Communications</i> , 2021, 1, .	1.7	9
6	Temporal variability in quantitative human gut microbiome profiles and implications for clinical research. <i>Nature Communications</i> , 2021, 12, 6740.	5.8	89
7	GWAS of stool frequency provides insights into gastrointestinal motility and irritable bowel syndrome. <i>Cell Genomics</i> , 2021, 1, 100069.	3.0	15
8	Personalized Nutrition Through The Gut Microbiota: Current Insights And Future Perspectives. <i>Nutrition Reviews</i> , 2020, 78, 66-74.	2.6	20
9	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, 1638.	1.6	41
10	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020, 581, 310-315.	13.7	283
11	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. <i>Nature Microbiology</i> , 2020, 5, 1079-1087.	5.9	144
12	Gut microbiome variation is associated to Multiple Sclerosis phenotypic subtypes. <i>Annals of Clinical and Translational Neurology</i> , 2020, 7, 406-419.	1.7	59
13	Tracking humans and microbes. <i>Nature</i> , 2019, 569, 632-633.	13.7	14
14	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.	0.6	180
15	Quantitative microbiome profiling disentangles inflammation- and bile duct obstruction-associated microbiota alterations across PSC/IBD diagnoses. <i>Nature Microbiology</i> , 2019, 4, 1826-1831.	5.9	149
16	The human microbiome in health and disease: hype or hope. <i>Acta Clinica Belgica</i> , 2019, 74, 53-64.	0.5	34
17	The neuroactive potential of the human gut microbiota in quality of life and depression. <i>Nature Microbiology</i> , 2019, 4, 623-632.	5.9	1,206
18	Population-level analysis of <i>Blastocystis</i> subtype prevalence and variation in the human gut microbiota. <i>Gut</i> , 2019, 68, 1180-1189.	6.1	149

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19	Practical guidelines for gut microbiome analysis in microbiota-gut-brain axis research. Behavioral and Brain Sciences, 2019, 42, .	0.4	1
20	The Human Gut Microbiome: From Association to Modulation. Cell, 2018, 172, 1198-1215.	13.5	558
21	Richness and ecosystem development across faecal snapshots of the gut microbiota. Nature Microbiology, 2018, 3, 526-528.	5.9	81
22	Enterotypes in the landscape of gut microbial community composition. Nature Microbiology, 2018, 3, 8-16.	5.9	717
23	Comparisons of gut microbiota profiles in wild-type and gelatinase B/matrix metalloproteinase-9-deficient mice in acute DSS-induced colitis. Npj Biofilms and Microbiomes, 2018, 4, 18.	2.9	10
24	Prebiotic Wheat Bran Fractions Induce Specific Microbiota Changes. Frontiers in Microbiology, 2018, 9, 31.	1.5	45
25	Prebiotic inulin-type fructans induce specific changes in the human gut microbiota. Gut, 2017, 66, 1968-1974.	6.1	370
26	Assessment of faecal microbial transfer in irritable bowel syndrome with severe bloating. Gut, 2017, 66, 980-982.	6.1	56
27	Multi-stability and the origin of microbial community types. ISME Journal, 2017, 11, 2159-2166.	4.4	104
28	Combined use of network inference tools identifies ecologically meaningful bacterial associations in a paddy soil. Soil Biology and Biochemistry, 2017, 105, 227-235.	4.2	72
29	Matrix Metalloproteinase/MMP-9 Gene Knockout does not Influence Changes in Gut Microbiota in a Model of Acute Dextran Sodium Sulphate/DSS-Induced Colitis. Gastroenterology, 2017, 152, S623.	0.6	1
30	Water activity does not shape the microbiota in the human colon. Gut, 2017, 66, 1865-1866.	6.1	9
31	Quantitative microbiome profiling links gut community variation to microbial load. Nature, 2017, 551, 507-511.	13.7	791
32	Brief Report: <i>Dialister</i> as a Microbial Marker of Disease Activity in Spondyloarthritis. Arthritis and Rheumatology, 2017, 69, 114-121.	2.9	233
33	Practical considerations for large-scale gut microbiome studies. FEMS Microbiology Reviews, 2017, 41, S154-S167.	3.9	142
34	Towards biome-specific analysis of meta-omics data. ISME Journal, 2016, 10, 1025-1028.	4.4	72
35	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science, 2016, 352, 565-569.	6.0	1,398
36	Population-level analysis of gut microbiome variation. Science, 2016, 352, 560-564.	6.0	1,716

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37	Speciesâ€“function relationships shape ecological properties of the human gut microbiome. Nature Microbiology, 2016, 1, 16088.	5.9	279
38	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. ISME Journal, 2016, 10, 1669-1681.	4.4	593
39	Meta-omics in Inflammatory Bowel Disease Research: Applications, Challenges, and Guidelines. Journal of Crohn's and Colitis, 2016, 10, 735-746.	0.6	37
40	Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates. Gut, 2016, 65, 57-62.	6.1	737
41	CoNet app: inference of biological association networks using Cytoscape. F1000Research, 2016, 5, 1519.	0.8	398
42	Determinants of community structure in the global plankton interactome. Science, 2015, 348, 1262073.	6.0	842
43	Microbiology Meets Big Data: The Case of Gut Microbiotaâ€“Derived Trimethylamine. Annual Review of Microbiology, 2015, 69, 305-321.	2.9	133
44	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. Nature, 2015, 528, 262-266.	13.7	1,627
45	LotuS: an efficient and user-friendly OTU processing pipeline. Microbiome, 2014, 2, 30.	4.9	233
46	Richness of human gut microbiome correlates with metabolic markers. Nature, 2013, 500, 541-546.	13.7	3,641
47	Enterotypes of the human gut microbiome. Nature, 2011, 473, 174-180.	13.7	5,800
48	A human gut microbial gene catalogue established by metagenomic sequencing. Nature, 2010, 464, 59-65.	13.7	9,342
49	Get the most out of your metagenome: computational analysis of environmental sequence data. Current Opinion in Microbiology, 2007, 10, 490-498.	2.3	169