

Doris Vandeputte

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

33,384
citations

101384

36
h-index

205818

48
g-index

51
all docs

51
docs citations

51
times ranked

35474
citing authors

#	ARTICLE	IF	CITATIONS
1	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	13.7	9,342
2	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	13.7	5,800
3	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	13.7	3,641
4	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016, 352, 560-564.	6.0	1,716
5	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	13.7	1,627
6	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016, 352, 565-569.	6.0	1,398
7	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
8	Determinants of community structure in the global plankton interactome. <i>Science</i> , 2015, 348, 1262073.	6.0	842
9	Quantitative microbiome profiling links gut community variation to microbial load. <i>Nature</i> , 2017, 551, 507-511.	13.7	791
10	Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates. <i>Gut</i> , 2016, 65, 57-62.	6.1	737
11	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	5.9	717
12	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	9.4	676
13	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016, 10, 1669-1681.	4.4	593
14	The Human Gut Microbiome: From Association to Modulation. <i>Cell</i> , 2018, 172, 1198-1215.	13.5	558
15	CoNet app: inference of biological association networks using Cytoscape. <i>F1000Research</i> , 2016, 5, 1519.	0.8	398
16	Prebiotic inulin-type fructans induce specific changes in the human gut microbiota. <i>Gut</i> , 2017, 66, 1968-1974.	6.1	370
17	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020, 581, 310-315.	13.7	283
18	Speciesâ€‘function relationships shape ecological properties of the human gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16088.	5.9	279

#	ARTICLE	IF	CITATIONS
19	LotuS: an efficient and user-friendly OTU processing pipeline. <i>Microbiome</i> , 2014, 2, 30.	4.9	233
20	Brief Report: <i>Dialister</i> as a Microbial Marker of Disease Activity in Spondyloarthritis. <i>Arthritis and Rheumatology</i> , 2017, 69, 114-121.	2.9	233
21	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
22	Get the most out of your metagenome: computational analysis of environmental sequence data. <i>Current Opinion in Microbiology</i> , 2007, 10, 490-498.	2.3	169
23	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
24	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
25	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
26	Practical considerations for large-scale gut microbiome studies. <i>FEMS Microbiology Reviews</i> , 2017, 41, S154-S167.	3.9	142
27	Microbiology Meets Big Data: The Case of Gut Microbiota-Derived Trimethylamine. <i>Annual Review of Microbiology</i> , 2015, 69, 305-321.	2.9	133
28	Multi-stability and the origin of microbial community types. <i>ISME Journal</i> , 2017, 11, 2159-2166.	4.4	104
29	Temporal variability in quantitative human gut microbiome profiles and implications for clinical research. <i>Nature Communications</i> , 2021, 12, 6740.	5.8	89
30	Richness and ecosystem development across faecal snapshots of the gut microbiota. <i>Nature Microbiology</i> , 2018, 3, 526-528.	5.9	81
31	Towards biome-specific analysis of meta-omics data. <i>ISME Journal</i> , 2016, 10, 1025-1028.	4.4	72
32	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.	4.2	72
33	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
34	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.	6.1	58
35	Assessment of faecal microbial transfer in irritable bowel syndrome with severe bloating. <i>Gut</i> , 2017, 66, 980-982.	6.1	56
36	Prebiotic Wheat Bran Fractions Induce Specific Microbiota Changes. <i>Frontiers in Microbiology</i> , 2018, 9, 31.	1.5	45

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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, 1638.	1.6	41
38	Meta-omics in Inflammatory Bowel Disease Research: Applications, Challenges, and Guidelines. <i>Journal of Crohn's and Colitis</i> , 2016, 10, 735-746.	0.6	37
39	The human microbiome in health and disease: hype or hope. <i>Acta Clinica Belgica</i> , 2019, 74, 53-64.	0.5	34
40	Variation and transmission of the human gut microbiota across multiple familial generations. <i>Nature Microbiology</i> , 2022, 7, 87-96.	5.9	32
41	Personalized Nutrition Through The Gut Microbiota: Current Insights And Future Perspectives. <i>Nutrition Reviews</i> , 2020, 78, 66-74.	2.6	20
42	GWAS of stool frequency provides insights into gastrointestinal motility and irritable bowel syndrome. <i>Cell Genomics</i> , 2021, 1, 100069.	3.0	15
43	Tracking humans and microbes. <i>Nature</i> , 2019, 569, 632-633.	13.7	14
44	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.	2.9	10
45	Water activity does not shape the microbiota in the human colon. <i>Gut</i> , 2017, 66, 1865-1866.	6.1	9
46	Null-model-based network comparison reveals core associations. <i>ISME Communications</i> , 2021, 1, .	1.7	9
47	Effect of cryopreservation medium conditions on growth and isolation of gut anaerobes from human faecal samples. <i>Microbiome</i> , 2022, 10, .	4.9	6
48	Matrix Metalloproteinase/MMP-9 Gene Knockout does not Influence Changes in Gut Microbiota in a Model of Acute Dextran Sodium Sulphate/DSS-Induced Colitis. <i>Gastroenterology</i> , 2017, 152, S623.	0.6	1
49	Practical guidelines for gut microbiome analysis in microbiota-gut-brain axis research. <i>Behavioral and Brain Sciences</i> , 2019, 42, .	0.4	1