Doris Vandeputte

List of Publications by Citations

Source: https://exaly.com/author-pdf/8626517/doris-vandeputte-publications-by-citations.pdf
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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	A human gut microbial gene catalogue established by metagenomic sequencing. *Nature*, **2010**, 464, 59-65	50.4	7044
46	Enterotypes of the human gut microbiome. *Nature*, **2011**, 473, 174-80	50.4	4240
45	Richness of human gut microbiome correlates with metabolic markers. *Nature*, **2013**, 500, 541-6	50.4	2584
44	Population-level analysis of gut microbiome variation. *Science*, **2016**, 352, 560-4	33.3	1120
43	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. *Nature*, **2015**, 528, 262-266	50.4	1107
42	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. *Science*, **2016**, 352, 565-9	33.3	929
41	The neuroactive potential of the human gut microbiota in quality of life and depression. *Nature Microbiology*, **2019**, 4, 623-632	26.6	651
40	Ocean plankton. Determinants of community structure in the global plankton interactome. *Science*, **2015**, 348, 1262073	33.3	496
39	Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates. *Gut*, **2016**, 65, 57-62	19.2	488
38	Quantitative microbiome profiling links gut community variation to microbial load. *Nature*, **2017**, 551, 507-511	50.4	475
37	Enterotypes in the landscape of gut microbial community composition. *Nature Microbiology*, **2018**, 3, 8-16	26.6	387
36	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. *ISME Journal*, **2016**, 10, 1669-81	11.9	365
35	The Human Gut Microbiome: From Association to Modulation. *Cell*, **2018**, 172, 1198-1215	56.2	344
34	Prebiotic inulin-type fructans induce specific changes in the human gut microbiota. *Gut*, **2017**, 66, 1968-1974	19.2	236
33	CoNet app: inference of biological association networks using Cytoscape. *F1000Research*, **2016**, 5, 1519	3.6	231
32	LotuS: an efficient and user-friendly OTU processing pipeline. *Microbiome*, **2014**, 2, 30	16.6	186
31	Brief Report: Dialister as a Microbial Marker of Disease Activity in Spondyloarthritis. *Arthritis and Rheumatology*, **2017**, 69, 114-121	9.5	150

30	Species-function relationships shape ecological properties of the human gut microbiome. *Nature Microbiology*, **2016**, 1, 16088	26.6	145
29	Get the most out of your metagenome: computational analysis of environmental sequence data. *Current Opinion in Microbiology*, **2007**, 10, 490-8	7.9	127
28	Metabolic Functions of Gut Microbes Associate With Efficacy of Tumor Necrosis Factor Antagonists in Patients With Inflammatory Bowel Diseases. *Gastroenterology*, **2019**, 157, 1279-1292.e11	13.3	101
27	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. *Nature*, **2020**, 581, 310-315	50.4	100
26	Microbiology Meets Big Data: The Case of Gut Microbiota-Derived Trimethylamine. *Annual Review of Microbiology*, **2015**, 69, 305-21	17.5	94
25	Practical considerations for large-scale gut microbiome studies. *FEMS Microbiology Reviews*, **2017**, 41, S154-S167	15.1	93
24	Large-scale association analyses identify host factors influencing human gut microbiome composition. *Nature Genetics*, **2021**, 53, 156-165	36.3	80
23	Population-level analysis of subtype prevalence and variation in the human gut microbiota. *Gut*, **2019**, 68, 1180-1189	19.2	79
22	Quantitative microbiome profiling disentangles inflammation- and bile duct obstruction-associated microbiota alterations across PSC/IBD diagnoses. *Nature Microbiology*, **2019**, 4, 1826-1831	26.6	71
21	Multi-stability and the origin of microbial community types. *ISME Journal*, **2017**, 11, 2159-2166	11.9	57
20	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. *Nature Microbiology*, **2020**, 5, 1079-1087	26.6	55
19	Combined use of network inference tools identifies ecologically meaningful bacterial associations in a paddy soil. *Soil Biology and Biochemistry*, **2017**, 105, 227-235	7.5	50
18	Richness and ecosystem development across faecal snapshots of the gut microbiota. *Nature Microbiology*, **2018**, 3, 526-528	26.6	48
17	Assessment of faecal microbial transfer in irritable bowel syndrome with severe bloating. *Gut*, **2017** , 66, 980-982	19.2	42
16	Towards biome-specific analysis of meta-omics data. *ISME Journal*, **2016**, 10, 1025-8	11.9	40
15	Gut microbiome variation is associated to Multiple Sclerosis phenotypic subtypes. *Annals of Clinical and Translational Neurology*, **2020**, 7, 406-419	5.3	28
14	Meta-omics in Inflammatory Bowel Disease Research: Applications, Challenges, and Guidelines. *Journal of Crohn's and Colitis*, **2016**, 10, 735-46	1.5	23
13	Prebiotic Wheat Bran Fractions Induce Specific Microbiota Changes. *Frontiers in Microbiology*, **2018**, 9, 31	5.7	22

12	The human microbiome in health and disease: hype or hope. *Acta Clinica Belgica*, **2019**, 74, 53-64	1.8	20
11	Human and preclinical studies of the host-gut microbiome co-metabolite hippurate as a marker and mediator of metabolic health. *Gut*, **2021**, 70, 2105-2114	19.2	13
10	Temporal variability in quantitative human gut microbiome profiles and implications for clinical research. *Nature Communications*, **2021**, 12, 6740	17.4	10
9	Large-scale association analyses identify host factors influencing human gut microbiome composition		9
8	Water activity does not shape the microbiota in the human colon. *Gut*, **2017**, 66, 1865-1866	19.2	8
7	Personalized Nutrition Through The Gut Microbiota: Current Insights And Future Perspectives. *Nutrition Reviews*, **2020**, 78, 66-74	6.4	7
6	Effects of Low and High FODMAP Diets on Human Gastrointestinal Microbiota Composition in Adults with Intestinal Diseases: A Systematic Review. *Microorganisms*, **2020**, 8,	4.9	6
5	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	8.2	5
4	Variation and transmission of the human gut microbiota across multiple familial generations.. *Nature Microbiology*, **2021**,	26.6	4
3	GWAS of stool frequency provides insights into gastrointestinal motility and irritable bowel syndrome.. *Cell Genomics*, **2021**, 1, None		2
2	A framework for comparing microbial networks reveals core associations		1
1	Null-model-based network comparison reveals core associations. *ISME Communications*, **2021**, 1,		1