

Erwin G Zoetendal

List of Publications by Year in descending order

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Version: 2024-02-01

77
papers

27,695
citations

76326

40
h-index

82547

72
g-index

79
all docs

79
docs citations

79
times ranked

29586
citing authors

#	ARTICLE	IF	CITATIONS
1	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	27.8	5,800
2	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	27.8	3,641
3	Duodenal Infusion of Donor Feces for Recurrent <i>Clostridium difficile</i> . <i>New England Journal of Medicine</i> , 2013, 368, 407-415.	27.0	3,157
4	Transfer of Intestinal Microbiota From Lean Donors Increases Insulin Sensitivity in Individuals With Metabolic Syndrome. <i>Gastroenterology</i> , 2012, 143, 913-916.e7.	1.3	2,287
5	The gut microbiota and host health: a new clinical frontier. <i>Gut</i> , 2016, 65, 330-339.	12.1	1,719
6	Temperature Gradient Gel Electrophoresis Analysis of 16S rRNA from Human Fecal Samples Reveals Stable and Host-Specific Communities of Active Bacteria. <i>Applied and Environmental Microbiology</i> , 1998, 64, 3854-3859.	3.1	1,186
7	Intestinal microbiota in functional bowel disorders: a Rome foundation report. <i>Gut</i> , 2013, 62, 159-176.	12.1	776
8	Findings From a Randomized Controlled Trial of Fecal Transplantation for Patients With Ulcerative Colitis. <i>Gastroenterology</i> , 2015, 149, 110-118.e4.	1.3	769
9	Fat, fibre and cancer risk in African Americans and rural Africans. <i>Nature Communications</i> , 2015, 6, 6342.	12.8	761
10	Improvement of Insulin Sensitivity after Lean Donor Feces in Metabolic Syndrome Is Driven by Baseline Intestinal Microbiota Composition. <i>Cell Metabolism</i> , 2017, 26, 611-619.e6.	16.2	689
11	Molecular Diversity of <i>Lactobacillus</i> spp. and Other Lactic Acid Bacteria in the Human Intestine as Determined by Specific Amplification of 16S Ribosomal DNA. <i>Applied and Environmental Microbiology</i> , 2002, 68, 114-123.	3.1	619
12	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	17.5	581
13	The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. <i>ISME Journal</i> , 2012, 6, 1415-1426.	9.8	544
14	Impact of oral vancomycin on gut microbiota, bile acid metabolism, and insulin sensitivity. <i>Journal of Hepatology</i> , 2014, 60, 824-831.	3.7	475
15	Mediterranean diet intervention alters the gut microbiome in older people reducing frailty and improving health status: the NU-AGE 1-year dietary intervention across five European countries. <i>Gut</i> , 2020, 69, 1218-1228.	12.1	465
16	Effects of Gut Microbiota Manipulation by Antibiotics on Host Metabolism in Obese Humans: A Randomized Double-Blind Placebo-Controlled Trial. <i>Cell Metabolism</i> , 2016, 24, 63-74.	16.2	278
17	Gut microbiome stability and resilience: elucidating the response to perturbations in order to modulate gut health. <i>Gut</i> , 2021, 70, 595-605.	12.1	265
18	High temporal and inter-individual variation detected in the human ileal microbiota. <i>Environmental Microbiology</i> , 2010, 12, 3213-3227.	3.8	254

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19	The Intestinal Microenvironment and Functional Gastrointestinal Disorders. <i>Gastroenterology</i> , 2016, 150, 1305-1318.e8.	1.3	243
20	Long-term monitoring of the human intestinal microbiota composition. <i>Environmental Microbiology</i> , 2013, 15, 1146-1159.	3.8	195
21	Fecal Microbiota in Pediatric Inflammatory Bowel Disease and Its Relation to Inflammation. <i>American Journal of Gastroenterology</i> , 2015, 110, 921-930.	0.4	193
22	Reset of a critically disturbed microbial ecosystem: faecal transplant in recurrent <i>Clostridium difficile</i> infection. <i>ISME Journal</i> , 2014, 8, 1621-1633.	9.8	172
23	Isolation of DNA from bacterial samples of the human gastrointestinal tract. <i>Nature Protocols</i> , 2006, 1, 870-873.	12.0	171
24	Effect of Vegan Fecal Microbiota Transplantation on Carnitine and Choline Derived Trimethylamine N-Oxide Production and Vascular Inflammation in Patients With Metabolic Syndrome. <i>Journal of the American Heart Association</i> , 2018, 7, .	3.7	164
25	Microbial shifts and signatures of long-term remission in ulcerative colitis after faecal microbiota transplantation. <i>ISME Journal</i> , 2017, 11, 1877-1889.	9.8	157
26	Supplementation of Diet With Galacto-oligosaccharides Increases Bifidobacteria, but Not Insulin Sensitivity, in Obese Prediabetic Individuals. <i>Gastroenterology</i> , 2017, 153, 87-97.e3.	1.3	150
27	Age-dependent changes in GI physiology and microbiota: time to reconsider?. <i>Gut</i> , 2018, 67, 2213-2222.	12.1	148
28	Microarray Analysis and Barcoded Pyrosequencing Provide Consistent Microbial Profiles Depending on the Source of Human Intestinal Samples. <i>Applied and Environmental Microbiology</i> , 2011, 77, 2071-2080.	3.1	141
29	NG-Tax, a highly accurate and validated pipeline for analysis of 16S rRNA amplicons from complex biomes. <i>F1000Research</i> , 2016, 5, 1791.	1.6	140
30	The Intestinal LABs. <i>Antonie Van Leeuwenhoek</i> , 2002, 82, 341-352.	1.7	133
31	Diversity of human small intestinal <i>Streptococcus</i> and <i>Veillonella</i> populations. <i>FEMS Microbiology Ecology</i> , 2013, 85, 376-388.	2.7	121
32	Immunomodulatory Properties of <i>Streptococcus</i> and <i>Veillonella</i> Isolates from the Human Small Intestine Microbiota. <i>PLoS ONE</i> , 2014, 9, e114277.	2.5	118
33	Quantification of Uncultured <i>Ruminococcus obeum</i> -Like Bacteria in Human Fecal Samples by Fluorescent In Situ Hybridization and Flow Cytometry Using 16S rRNA-Targeted Probes. <i>Applied and Environmental Microbiology</i> , 2002, 68, 4225-4232.	3.1	115
34	A comprehensive metatranscriptome analysis pipeline and its validation using human small intestine microbiota datasets. <i>BMC Genomics</i> , 2013, 14, 530.	2.8	111
35	The Mucosa-associated Microbiota of PSC Patients is Characterized by Low Diversity and Low Abundance of Uncultured Clostridiales II. <i>Journal of Crohn's and Colitis</i> , 2015, 9, 342-348.	1.3	106
36	Isolation of RNA from bacterial samples of the human gastrointestinal tract. <i>Nature Protocols</i> , 2006, 1, 954-959.	12.0	82

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37	Effect of diet on the intestinal microbiota and its activity. <i>Current Opinion in Gastroenterology</i> , 2014, 30, 189-195.	2.3	74
38	Distal colonic transit is linked to gut microbiota diversity and microbial fermentation in humans with slow colonic transit. <i>American Journal of Physiology - Renal Physiology</i> , 2020, 318, G361-G369.	3.4	66
39	Microbiome Analysis of Stool Samples from African Americans with Colon Polyps. <i>PLoS ONE</i> , 2013, 8, e81352.	2.5	61
40	Comparative Genomics Analysis of <i>Streptococcus</i> Isolates from the Human Small Intestine Reveals their Adaptation to a Highly Dynamic Ecosystem. <i>PLoS ONE</i> , 2013, 8, e83418.	2.5	57
41	Effect of wheat bran derived prebiotic supplementation on gastrointestinal transit, gut microbiota, and metabolic health: a randomized controlled trial in healthy adults with a slow gut transit. <i>Gut Microbes</i> , 2020, 12, 1704141.	9.8	46
42	Associations between Pro- and Anti-Inflammatory Gastro-Intestinal Microbiota, Diet, and Cognitive Functioning in Dutch Healthy Older Adults: The NU-AGE Study. <i>Nutrients</i> , 2020, 12, 3471.	4.1	42
43	Bacterial folate biosynthesis and colorectal cancer risk: more than just a gut feeling. <i>Critical Reviews in Food Science and Nutrition</i> , 2020, 60, 244-256.	10.3	39
44	Sugar Beet Pectin Supplementation Did Not Alter Profiles of Fecal Microbiota and Exhaled Breath in Healthy Young Adults and Healthy Elderly. <i>Nutrients</i> , 2019, 11, 2193.	4.1	35
45	Effect of galactooligosaccharides and <i>Bifidobacterium animalis</i> Bb-12 on growth of <i>Lactobacillus amylovorus</i> DSM 16698, microbial community structure, and metabolite production in an <i>in vitro</i> colonic model set up with human or pig microbiota. <i>FEMS Microbiology Ecology</i> , 2013, 84, 110-123.	2.7	33
46	Galacto-oligosaccharides supplementation in prefrail older and healthy adults increased faecal bifidobacteria, but did not impact immune function and oxidative stress. <i>Clinical Nutrition</i> , 2021, 40, 3019-3031.	5.0	25
47	Fermentation of Chicory Fructo-oligosaccharides and Native Inulin by Infant Fecal Microbiota Attenuates Pro-inflammatory Responses in Immature Dendritic Cells in an Infant Age-Dependent and Fructan-Specific Way. <i>Molecular Nutrition and Food Research</i> , 2020, 64, e2000068.	3.3	23
48	Fermentation Kinetics of Selected Dietary Fibers by Human Small Intestinal Microbiota Depend on the Type of Fiber and Subject. <i>Molecular Nutrition and Food Research</i> , 2020, 64, e2000455.	3.3	22
49	Microbiome-based stratification to guide dietary interventions to improve human health. <i>Nutrition Research</i> , 2020, 82, 1-10.	2.9	21
50	Individual and cohort-specific gut microbiota patterns associated with tissue-specific insulin sensitivity in overweight and obese males. <i>Scientific Reports</i> , 2020, 10, 7523.	3.3	21
51	Endo-1,3(4)- β -Glucanase-Treatment of Oat β -Glucan Enhances Fermentability by Infant Fecal Microbiota, Stimulates Dectin-1 Activation and Attenuates Inflammatory Responses in Immature Dendritic Cells. <i>Nutrients</i> , 2020, 12, 1660.	4.1	19
52	A Microbiomic Analysis in African Americans with Colonic Lesions Reveals <i>Streptococcus</i> sp.VT162 as a Marker of Neoplastic Transformation. <i>Genes</i> , 2017, 8, 314.	2.4	16
53	Microbial communities in a dynamic <i>in vitro</i> model for the human ileum resemble the human ileal microbiota. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	16
54	High throughput cultivation-based screening on porous aluminum oxide chips allows targeted isolation of antibiotic resistant human gut bacteria. <i>PLoS ONE</i> , 2019, 14, e0210970.	2.5	15

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55	Temperature and Denaturing Gradient Gel Electrophoresis Analysis of 16S rRNA from Human Faecal Samples. <i>Bioscience and Microflora</i> , 2000, 19, 93-98.	0.5	15
56	Impact of a fermented soy beverage supplemented with acerola by-product on the gut microbiota from lean and obese subjects using an in vitro model of the human colon. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 3771-3785.	3.6	13
57	Structure-specific Fermentation of Galacto-oligosaccharides, Isomalto-oligosaccharides and Isomalto/malto-polysaccharides by Infant Fecal Microbiota and Impact on Dendritic Cell Cytokine Responses. <i>Molecular Nutrition and Food Research</i> , 2021, 65, e2001077.	3.3	13
58	Stimulation of Gastric Transit Function Driven by Hydrolyzed Casein Increases Small Intestinal Carbohydrate Availability and Its Microbial Metabolism. <i>Molecular Nutrition and Food Research</i> , 2020, 64, e2000250.	3.3	11
59	Increasing dietary fibre intake in healthy adults using personalised dietary advice compared with general advice: a single-blind randomised controlled trial. <i>Public Health Nutrition</i> , 2021, 24, 1117-1128.	2.2	10
60	Fecal Microbiota Signatures Are Not Consistently Related to Symptom Severity in Irritable Bowel Syndrome. <i>Digestive Diseases and Sciences</i> , 2022, 67, 5137-5148.	2.3	10
61	Endothelial dysfunction: what is the role of the microbiota?. <i>Gut</i> , 2018, 67, 201-202.	12.1	9
62	Draft Genome Sequence of <i>Veillonella parvula</i> HSIVP1, Isolated from the Human Small Intestine. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
63	Development and validation of the FiberScreen: A short questionnaire to screen fibre intake in adults. <i>Journal of Human Nutrition and Dietetics</i> , 2021, 34, 969-980.	2.5	8
64	Faecal Microbiota in Patients with Neurogenic Bowel Dysfunction and Spinal Cord Injury or Multiple Sclerosis – A Systematic Review. <i>Journal of Clinical Medicine</i> , 2021, 10, 1598.	2.4	7
65	Chicory inulin enhances fermentation of 2-fucosyllactose by infant fecal microbiota and differentially influences immature dendritic cell and T-cell cytokine responses under normal and Th2-polarizing conditions. <i>Food and Function</i> , 2021, 12, 9018-9029.	4.6	6
66	In vitro metabolic capacity of carbohydrate degradation by intestinal microbiota of adults and pre-frail elderly. <i>ISME Communications</i> , 2021, 1, .	4.2	6
67	Combining galacto-oligosaccharides and 2-fucosyllactose alters their fermentation kinetics by infant fecal microbiota and influences AhR-receptor dependent cytokine responses in immature dendritic cells. <i>Food and Function</i> , 2022, 13, 6510-6521.	4.6	5
68	Draft Genome Sequence of <i>Enterococcus</i> sp. Strain HSIEG1, Isolated from the Human Small Intestine. <i>Genome Announcements</i> , 2013, 1, .	0.8	3
69	Reply. <i>Gastroenterology</i> , 2016, 150, 286-287.	1.3	1
70	Molecular ecology of the yet uncultured bacterial Ct85-cluster in the mammalian gut. <i>Anaerobe</i> , 2020, 62, 102104.	2.1	1
71	A novel technique capable of taking "protected" biopsies for reliable assessment of the distribution of microbiota along the colonic mucosa. <i>Journal of Microbiological Methods</i> , 2021, 185, 106204.	1.6	1
72	The Human Intestinal Microbiota and Its Impact on Health. , 0, , 11-32.		1

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73	â€œWe Are What We Eatâ€ How Diet Impacts the Gut Microbiota in Adulthood. , 2019, , 259-283.		1
74	A high-fibre personalised dietary advice given via a web tool reduces constipation complaints in adults. Journal of Nutritional Science, 2022, 11, e31.	1.9	1
75	Fecal carriage of <i>vanB</i> antibiotic resistance gene affects adipose tissue function under vancomycin use. Gut Microbes, 2022, 14, .	9.8	1
76	PS14 - 68. Differential effects of antibiotics on bile acid metabolism, intestinal microbiota composition and insulin resistance in obese humans; a randomised controlled trial. Nederlands Tijdschrift Voor Diabetologie, 2012, 10, 147-147.	0.0	0
77	PS14 - 70. Intestinal microbiota translocation is associated with inflamed visceral adipose tissue. Nederlands Tijdschrift Voor Diabetologie, 2012, 10, 148-148.	0.0	0