

Jeroen Raes

List of Publications by Year in descending order

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246
papers

70,535
citations

1260

104
h-index

662

243
g-index

273
all docs

273
docs citations

273
times ranked

72099
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbiome confounders and quantitative profiling challenge predicted microbial targets in colorectal cancer development. <i>Nature Medicine</i> , 2024, 30, 1339-1348.	25.6	21
2	Examining the healthy human microbiome concept. <i>Nature Reviews Microbiology</i> , 2024, 23, 192-205.	27.5	8
3	Nifty new tools for microbiome treatment design. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2023, 20, 77-78.	14.7	8
4	Associations of HIV and iron status with gut microbiota composition, gut inflammation and gut integrity in South African school-age children: a two-way factorial case-control study. <i>Journal of Human Nutrition and Dietetics</i> , 2023, 36, 819-832.	2.7	9
5	The gut microbiota contributes to the pathogenesis of anorexia nervosa in humans and mice. <i>Nature Microbiology</i> , 2023, 8, 787-802.	12.8	62
6	Evidence of a causal and modifiable relationship between kidney function and circulating trimethylamine N-oxide. <i>Nature Communications</i> , 2023, 14, .	14.1	12
7	<i>Dysosmobacter welbionis</i> is a newly isolated human commensal bacterium preventing diet-induced obesity and metabolic disorders in mice. <i>Gut</i> , 2022, 71, 534-543.	14.8	118
8	FLEXiGUT: Rationale for exposomics associations with chronic low-grade gut inflammation. <i>Environment International</i> , 2022, 158, 106906.	10.3	10
9	Specific contributions of segmental transit times to gut microbiota composition. <i>Gut</i> , 2022, 71, 1443-1444.	14.8	6
10	Impairment of gut microbial biotin metabolism and host biotin status in severe obesity: effect of biotin and prebiotic supplementation on improved metabolism. <i>Gut</i> , 2022, 71, 2463-2480.	14.8	70
11	Exploring the relationship between the gut microbiome and mental health outcomes in a posttraumatic stress disorder cohort relative to trauma-exposed controls. <i>European Neuropsychopharmacology</i> , 2022, 56, 24-38.	0.9	44
12	OPO3 Standardized faecal microbiota transplantation with microbiome-guided donor selection in active UC patients: A randomized, placebo-controlled intervention study. <i>Journal of Crohn's and Colitis</i> , 2022, 16, i003-i004.	1.3	4
13	The effect of oral iron supplementation on the gut microbiota, gut inflammation, and iron status in iron-depleted South African school-age children with virally suppressed HIV and without HIV. <i>European Journal of Nutrition</i> , 2022, 61, 2067-2078.	3.6	4
14	P095 Anti-inflammatory effect of high acetate concentration on organoid-derived epithelial monolayer from patients with Ulcerative Colitis. <i>Journal of Crohn's and Colitis</i> , 2022, 16, i192-i195.	1.3	1
15	<i>Lactobacillus rhamnosus</i> CNCM I-3690 decreases subjective academic stress in healthy adults: a randomized placebo-controlled trial. <i>Gut Microbes</i> , 2022, 14, .	10.3	18
16	Fecal Microbiota Transplantation (FMT) as an Adjunctive Therapy for Depression—Case Report. <i>Frontiers in Psychiatry</i> , 2022, 13, .	2.7	78
17	The Effect of Å-Glucan Prebiotic on Kidney Function, Uremic Toxins and Gut Microbiome in Stage 3 to 5 Chronic Kidney Disease (CKD) Predialysis Participants: A Randomized Controlled Trial. <i>Nutrients</i> , 2022, 14, 805.	4.6	35
18	Microbiome and metabolome features of the cardiometabolic disease spectrum. <i>Nature Medicine</i> , 2022, 28, 303-314.	25.6	133

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19	The virota and its transkingdom interactions in the healthy infant gut. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.7	32
20	Sputum Bacterial Metacommunities in Distinguishing Heterogeneity in Respiratory Health and Disease. Frontiers in Microbiology, 2022, 13, .	3.9	1
21	Fast quantification of gut bacterial species in cocultures using flow cytometry and supervised classification. ISME Communications, 2022, 2, .	5.6	6
22	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. Cell Genomics, 2022, 2, 100123.	7.1	85
23	MO590: A Home-Based Exercise and Physical Activity Intervention After Kidney Transplantation: Impact of Exercise Intensity. The Phoenix-Kidney Study Protocol. Nephrology Dialysis Transplantation, 2022, 37, .	0.8	2
24	Effect of cryopreservation medium conditions on growth and isolation of gut anaerobes from human faecal samples. Microbiome, 2022, 10, .	11.5	13
25	Clinical, gut microbial and neural effects of a probiotic add-on therapy in depressed patients: a randomized controlled trial. Translational Psychiatry, 2022, 12, .	5.7	100
26	High Serum Vitamin D Concentrations, Induced via Diet, Trigger Immune and Intestinal Microbiota Alterations Leading to Type 1 Diabetes Protection in NOD Mice. Frontiers in Immunology, 2022, 13, .	5.0	8
27	Microbiota, not host origin drives <i>ex vivo</i> intestinal epithelial responses. Gut Microbes, 2022, 14, .	10.3	15
28	Single-cell approaches in human microbiome research. Cell, 2022, 185, 2725-2738.	35.1	56
29	Bidirectional Interactions between Arboviruses and the Bacterial and Viral Microbiota in <i>Aedes aegypti</i> and <i>Culex quinquefasciatus</i> . MBio, 2022, 13, .	4.5	15
30	Long-term life history predicts current gut microbiome in a population-based cohort study. Nature Aging, 2022, 2, 885-895.	8.5	16
31	Gut microbiome studies in CKD: opportunities, pitfalls and therapeutic potential. Nature Reviews Nephrology, 2022, 19, 87-101.	13.6	35
32	Fecal Microbiota Transplantation Reduces Symptoms in Some Patients With Irritable Bowel Syndrome With Predominant Abdominal Bloating: Short- and Long-term Results From a Placebo-Controlled Randomized Trial. Gastroenterology, 2021, 160, 145-157.e8.	1.0	132
33	Interactions between soil compositions and the wheat root microbiome under drought stress: From an <i>in silico</i> to <i>in planta</i> perspective. Computational and Structural Biotechnology Journal, 2021, 19, 4235-4247.	4.2	13
34	Local immune response to food antigens drives meal-induced abdominal pain. Nature, 2021, 590, 151-156.	40.1	187
35	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	16.3	950
36	Short chain fatty acids and its producing organisms: An overlooked therapy for IBD?. EBioMedicine, 2021, 66, 103293.	10.0	399

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37	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021, 4, .	4.5	121
38	P676 The small intestinal microbiome in Crohn's disease is characterised by increased luminal diversity and stable mucosa-associated communities. <i>Journal of Crohn's and Colitis</i> , 2021, 15, S597-S598.	1.3	0
39	Human and preclinical studies of the host's gut microbiome co-metabolite hippurate as a marker and mediator of metabolic health. <i>Gut</i> , 2021, 70, 2105-2114.	14.8	74
40	P082 Assessment of anti-inflammatory effect of high acetate administration in UC patient-derived epithelial monolayer cultures. <i>Journal of Crohn's and Colitis</i> , 2021, 15, S182-S183.	1.3	0
41	Novel insights into the genetically obese (ob/ob) and diabetic (db/db) mice: two sides of the same coin. <i>Microbiome</i> , 2021, 9, .	11.5	138
42	Benchmarking microbiome transformations favors experimental quantitative approaches to address compositionality and sampling depth biases. <i>Nature Communications</i> , 2021, 12, .	14.1	36
43	Wheat bran with reduced particle size increases serum SCFAs in obese subjects without improving health parameters compared with a maltodextrin placebo. <i>American Journal of Clinical Nutrition</i> , 2021, 114, 1328-1341.	5.1	6
44	Nutrient load acts as a driver of gut microbiota load, community composition and metabolic functionality in the simulator of the human intestinal microbial ecosystem. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	3.0	6
45	Monocyte-driven atypical cytokine storm and aberrant neutrophil activation as key mediators of COVID-19 disease severity. <i>Nature Communications</i> , 2021, 12, .	14.1	171
46	Unstable regulatory T cells, enriched for na ⁺ ve and Nrp1 ^{neg} cells, are purged after fate challenge. <i>Science Immunology</i> , 2021, 6, .	14.0	17
47	Null-model-based network comparison reveals core associations. <i>ISME Communications</i> , 2021, 1, .	5.6	21
48	Macroscale patterns of oceanic zooplankton composition and size structure. <i>Scientific Reports</i> , 2021, 11, .	3.7	29
49	Effect of obesity on gastrointestinal transit, pressure and pH using a wireless motility capsule. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2021, 167, 1-8.	4.2	21
50	<i>Treponema peruense</i> sp. nov., a commensal spirochaete isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	6
51	Clinical practices underlie COVID-19 patient respiratory microbiome composition and its interactions with the host. <i>Nature Communications</i> , 2021, 12, .	14.1	58
52	Gut Microbiome Profiling Uncovers a Lower Abundance of <i>Butyricoccus</i> in Advanced Stages of Chronic Kidney Disease. <i>Journal of Personalized Medicine</i> , 2021, 11, 1118.	2.7	15
53	Disentangling environmental effects in microbial association networks. <i>Microbiome</i> , 2021, 9, .	11.5	20
54	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. <i>Nature Microbiology</i> , 2021, 6, 1561-1574.	12.8	64

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55	Temporal variability in quantitative human gut microbiome profiles and implications for clinical research. <i>Nature Communications</i> , 2021, 12, .	14.1	113
56	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	25.6	225
57	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021, 600, 500-505.	40.1	124
58	Successional Stages in Infant Gut Microbiota Maturation. <i>MBio</i> , 2021, 12, .	4.5	65
59	Variation and transmission of the human gut microbiota across multiple familial generations. <i>Nature Microbiology</i> , 2021, 7, 87-96.	12.8	43
60	GWAS of stool frequency provides insights into gastrointestinal motility and irritable bowel syndrome. <i>Cell Genomics</i> , 2021, 1, 100069.	7.1	17
61	Duodenal Dysbiosis and Relation to the Efficacy of Proton Pump Inhibitors in Functional Dyspepsia. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13609.	4.5	26
62	Red Wine Consumption Associated With Increased Gut Microbiota α -Diversity in 3 Independent Cohorts. <i>Gastroenterology</i> , 2020, 158, 270-272.e2.	1.0	61
63	Microglia Require CD4 ⁺ T Cells to Complete the Fetal-to-Adult Transition. <i>Cell</i> , 2020, 182, 625-640.e24.	35.1	214
64	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. <i>Nature Communications</i> , 2020, 11, .	14.1	134
65	Increased IL-10-producing regulatory T cells are characteristic of severe cases of COVID-19. <i>Clinical and Translational Immunology</i> , 2020, 9, .	3.7	64
66	Depression and suicidality: A link to premature T helper cell aging and increased Th17 cells. <i>Brain, Behavior, and Immunity</i> , 2020, 87, 603-609.	4.3	69
67	In vitro ecology: a discovery engine for microbiome therapies. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2020, 17, 711-712.	14.7	8
68	Dietary Emulsifiers Alter Composition and Activity of the Human Gut Microbiota in vitro, Irrespective of Chemical or Natural Emulsifier Origin. <i>Frontiers in Microbiology</i> , 2020, 11, .	3.9	39
69	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020, 581, 310-315.	40.1	300
70	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. <i>Nature Microbiology</i> , 2020, 5, 1079-1087.	12.8	139
71	Gut microbiome variation is associated to Multiple Sclerosis phenotypic subtypes. <i>Annals of Clinical and Translational Neurology</i> , 2020, 7, 406-419.	3.8	69
72	OP20 The gut microbiota during biological therapy for inflammatory bowel disease. <i>Journal of Crohn's and Colitis</i> , 2020, 14, S016-S018.	1.3	0

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73	Tapping into the maize root microbiome to identify bacteria that promote growth under chilling conditions. <i>Microbiome</i> , 2020, 8, .	11.5	79
74	Zinc inhibits lethal inflammatory shock by preventing microbe-induced interferon signature in intestinal epithelium. <i>EMBO Molecular Medicine</i> , 2020, 12, .	7.2	16
75	Design of synthetic microbial consortia for gut microbiota modulation. <i>Current Opinion in Pharmacology</i> , 2019, 49, 52-59.	4.1	42
76	Supplementation with <i>Akkermansia muciniphila</i> in overweight and obese human volunteers: a proof-of-concept exploratory study. <i>Nature Medicine</i> , 2019, 25, 1096-1103.	25.6	1,457
77	Microbial communities of the house fly <i>Musca domestica</i> vary with geographical location and habitat. <i>Microbiome</i> , 2019, 7, .	11.5	78
78	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	35.1	236
79	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	35.1	269
80	Expanding the scope and scale of microbiome research. <i>Genome Biology</i> , 2019, 20, .	8.4	1
81	Tracking humans and microbes. <i>Nature</i> , 2019, 569, 632-633.	40.1	13
82	Synthetic ecology of the human gut microbiota. <i>Nature Reviews Microbiology</i> , 2019, 17, 754-763.	27.5	116
83	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.	1.0	184
84	Quantitative microbiome profiling disentangles inflammation- and bile duct obstruction-associated microbiota alterations across PSC/IBD diagnoses. <i>Nature Microbiology</i> , 2019, 4, 1826-1831.	12.8	156
85	Early-Career Scientists Shaping the World. <i>MSystems</i> , 2019, 4, .	4.6	0
86	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	35.1	487
87	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	5.4	67
88	The human microbiome in health and disease: hype or hope. <i>Acta Clinica Belgica</i> , 2019, 74, 53-64.	1.5	38
89	P836 The predictive role of gut microbiota in treatment response to vedolizumab and ustekinumab in inflammatory bowel disease. <i>Journal of Crohn's and Colitis</i> , 2019, 13, S542-S542.	1.3	1
90	The neuroactive potential of the human gut microbiota in quality of life and depression. <i>Nature Microbiology</i> , 2019, 4, 623-632.	12.8	1,253

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91	Population-level analysis of <i>Blastocystis</i> subtype prevalence and variation in the human gut microbiota. <i>Gut</i> , 2019, 68, 1180-1189.	14.8	154
92	Gut microbiota dynamics and uraemic toxins: one size does not fit all. <i>Gut</i> , 2019, 68, 2257.1-2260.	14.8	38
93	Practical guidelines for gut microbiome analysis in microbiota-gut-brain axis research. <i>Behavioral and Brain Sciences</i> , 2019, 42, .	0.9	3
94	The Human Gut Microbiome: From Association to Modulation. <i>Cell</i> , 2018, 172, 1198-1215.	35.1	572
95	Richness and ecosystem development across faecal snapshots of the gut microbiota. <i>Nature Microbiology</i> , 2018, 3, 526-528.	12.8	83
96	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, .	14.1	234
97	Low eukaryotic viral richness is associated with faecal microbiota transplantation success in patients with UC. <i>Gut</i> , 2018, 67, 1558-1559.	14.8	45
98	The Gut Microbiome and Mental Health: Implications for Anxiety- and Trauma-Related Disorders. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 90-107.	1.9	116
99	Impact of red and processed meat and fibre intake on treatment outcomes among patients with chronic inflammatory diseases: protocol for a prospective cohort study of prognostic factors and personalised medicine. <i>BMJ Open</i> , 2018, 8, e018166.	2.0	19
100	Butyrate Producers as Potential Next-Generation Probiotics: Safety Assessment of the Administration of <i>Butyricoccus pullicaecorum</i> to Healthy Volunteers. <i>MSystems</i> , 2018, 3, .	4.6	97
101	A low-gluten diet induces changes in the intestinal microbiome of healthy Danish adults. <i>Nature Communications</i> , 2018, 9, .	14.1	129
102	Linking gut microbiota, metabolic syndrome and economic status based on a population-level analysis. <i>Microbiome</i> , 2018, 6, .	11.5	134
103	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, .	8.4	8
104	Prebiotic Wheat Bran Fractions Induce Specific Microbiota Changes. <i>Frontiers in Microbiology</i> , 2018, 9, .	3.9	37
105	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018, 6, .	11.5	119
106	Editorial overview: It's the ecology, stupid: microbiome research in the post-stamp collecting age. <i>Current Opinion in Microbiology</i> , 2018, 44, iv-v.	7.7	2
107	Regional variation limits applications of healthy gut microbiome reference ranges and disease models. <i>Nature Medicine</i> , 2018, 24, 1532-1535.	25.6	598
108	Introducing insoluble wheat bran as a gut microbiota niche in an <i>in vitro</i> dynamic gut model stimulates propionate and butyrate production and induces colon region specific shifts in the luminal and mucosal microbial community. <i>Environmental Microbiology</i> , 2018, 20, 3406-3426.	3.8	32

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109	Go with the flow or solitary confinement: a look inside the single-cell toolbox for isolation of rare and uncultured microbes. <i>Current Opinion in Microbiology</i> , 2018, 44, 1-8.	7.7	35
110	Author response: Integrated culturing, modeling and transcriptomics uncovers complex interactions and emergent behavior in a three-species synthetic gut community. , 2018, , .		3
111	Prebiotic inulin-type fructans induce specific changes in the human gut microbiota. <i>Gut</i> , 2017, 66, 1968-1974.	14.8	386
112	Assessment of faecal microbial transfer in irritable bowel syndrome with severe bloating. <i>Gut</i> , 2017, 66, 980-982.	14.8	56
113	Multi-stability and the origin of microbial community types. <i>ISME Journal</i> , 2017, 11, 2159-2166.	9.1	83
114	Therapeutic Manipulation of the Gut Microbiota Through Diet to Reduce Intestinal Inflammation: Results from the FIT Trial. <i>Gastroenterology</i> , 2017, 152, S1.	1.0	5
115	The resilience of the intestinal microbiota influences health and disease. <i>Nature Reviews Microbiology</i> , 2017, 15, 630-638.	27.5	727
116	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.	10.3	63
117	Crowdsourcing Earth's microbes. <i>Nature</i> , 2017, 551, 446-447.	40.1	2
118	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.	1.0	1
119	Profiling of the Fecal Microbiota and Metabolome in Patients with Inflammatory Bowel Disease and their Unaffected Relatives. <i>Gastroenterology</i> , 2017, 152, S991.	1.0	0
120	P774 Metagenomics and metabolomics of patients with inflammatory bowel disease and their unaffected relatives. <i>Journal of Crohn's and Colitis</i> , 2017, 11, S476-S477.	1.3	1
121	Water activity does not shape the microbiota in the human colon. <i>Gut</i> , 2017, 66, 1865-1866.	14.8	8
122	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, .	6.4	117
123	Nlrp6- and ASC-Dependent Inflammasomes Do Not Shape the Commensal Gut Microbiota Composition. <i>Immunity</i> , 2017, 47, 339-348.e4.	22.7	143
124	Quantitative microbiome profiling links gut community variation to microbial load. <i>Nature</i> , 2017, 551, 507-511.	40.1	723
125	Brief Report: <i>Dialister</i> as a Microbial Marker of Disease Activity in Spondyloarthritis. <i>Arthritis and Rheumatology</i> , 2017, 69, 114-121.	6.2	235
126	Fire modifies the phylogenetic structure of soil bacterial co-occurrence networks. <i>Environmental Microbiology</i> , 2017, 19, 317-327.	3.8	51

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127	P767 The FIT trial: anti-inflammatory dietary intervention effects on the intestinal microbiota. <i>Journal of Crohn's and Colitis</i> , 2017, 11, S473-S473.	1.3	1
128	Reconciliation between operational taxonomic units and species boundaries. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	3.0	54
129	P078 Gut microbiome profiling of MMP-9 deficient mice and their wild-type littermates in a model of acute DSS-induced colitis. <i>Journal of Crohn's and Colitis</i> , 2017, 11, S116-S117.	1.3	1
130	From reads to operational taxonomic units: an ensemble processing pipeline for MiSeq amplicon sequencing data. <i>GigaScience</i> , 2017, 6, .	3.4	47
131	Practical considerations for large-scale gut microbiome studies. <i>FEMS Microbiology Reviews</i> , 2017, 41, S154-S167.	11.0	146
132	A Proposal for a Study on Treatment Selection and Lifestyle Recommendations in Chronic Inflammatory Diseases: A Danish Multidisciplinary Collaboration on Prognostic Factors and Personalised Medicine. <i>Nutrients</i> , 2017, 9, 499.	4.6	26
133	P776 Dysbiosis in Nlrp6/Asc-deficient mice does not result from inflammasome deficiency. <i>Journal of Crohn's and Colitis</i> , 2017, 11, S477-S478.	1.3	0
134	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2017, 3, 8-16.	12.8	699
135	The Probiotic <i>Butyricicoccus pullicaecorum</i> Reduces Feed Conversion and Protects from Potentially Harmful Intestinal Microorganisms and Necrotic Enteritis in Broilers. <i>Frontiers in Microbiology</i> , 2016, 7, .	3.9	101
136	Faecal Metaproteomic Analysis Reveals a Personalized and Stable Functional Microbiome and Limited Effects of a Probiotic Intervention in Adults. <i>PLoS ONE</i> , 2016, 11, e0153294.	2.5	62
137	The Genomic Sequence of the Oral Pathobiont Strain NI1060 Reveals Unique Strategies for Bacterial Competition and Pathogenicity. <i>PLoS ONE</i> , 2016, 11, e0158866.	2.5	7
138	Speciesâ€sorting and massâ€transfer paradigms control managed natural metacommunities. <i>Environmental Microbiology</i> , 2016, 18, 4862-4877.	3.8	25
139	Primary sclerosing cholangitis is characterised by intestinal dysbiosis independent from IBD. <i>Gut</i> , 2016, 65, 1681-1689.	14.8	323
140	Tu1713 Host-Microbiome Interactions in Primary Sclerosing Cholangitis. <i>Gastroenterology</i> , 2016, 150, S927-S928.	1.0	0
141	Su1909 Genetic Risk for Crohn's Disease has Little Impact on Intestinal Microbiota Composition. <i>Gastroenterology</i> , 2016, 150, S585-S586.	1.0	0
142	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016, 352, 560-564.	38.2	1,635
143	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016, 17, .	8.4	186
144	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016, 535, 376-381.	40.1	1,500

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145	Species–function relationships shape ecological properties of the human gut microbiome. <i>Nature Microbiology</i> , 2016, 1, .	12.8	277
146	Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton. <i>Nature Communications</i> , 2016, 7, .	14.1	59
147	Rules of the game for microbiota. <i>Nature</i> , 2016, 534, 182-183.	40.1	16
148	IPED: a highly efficient denoising tool for Illumina MiSeq Paired-end 16S rRNA gene amplicon sequencing data. <i>BMC Bioinformatics</i> , 2016, 17, .	3.3	26
149	Microbiome-based companion diagnostics: no longer science fiction?. <i>Gut</i> , 2016, 65, 896-897.	14.8	18
150	Computational approaches to predict bacteriophage–host relationships. <i>FEMS Microbiology Reviews</i> , 2016, 40, 258-272.	11.0	310
151	A web application for sample size and power calculation in case-control microbiome studies. <i>Bioinformatics</i> , 2016, 32, 2038-2040.	5.0	54
152	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016, 10, 1669-1681.	9.1	525
153	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016, 532, 465-470.	40.1	554
154	Meta-omics in Inflammatory Bowel Disease Research: Applications, Challenges, and Guidelines. <i>Journal of Crohn's and Colitis</i> , 2016, 10, 735-746.	1.3	35
155	Donor Species Richness Determines Faecal Microbiota Transplantation Success in Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , 2016, 10, 387-394.	1.3	253
156	Heterogeneity of the gut microbiome in mice: guidelines for optimizing experimental design. <i>FEMS Microbiology Reviews</i> , 2016, 40, 117-132.	11.0	274
157	Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates. <i>Gut</i> , 2016, 65, 57-62.	14.8	714
158	CoNet app: inference of biological association networks using Cytoscape. <i>F1000Research</i> , 2016, 5, 1519.	0.6	361
159	CoNet app: inference of biological association networks using Cytoscape. <i>F1000Research</i> , 2016, 5, 1519.	0.6	278
160	Towards microbial fermentation metabolites as markers for health benefits of prebiotics. <i>Nutrition Research Reviews</i> , 2015, 28, 42-66.	5.6	271
161	Open science resources for the discovery and analysis of Tara Oceans data. <i>Scientific Data</i> , 2015, 2, .	6.4	283
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