

Jeroen Raes

List of Publications by Year in descending order

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Version: 2024-02-01

249
papers

86,131
citations

2215

99
h-index

911

241
g-index

269
all docs

269
docs citations

269
times ranked

71670
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure, function and diversity of the healthy human microbiome. Nature, 2012, 486, 207-214.	27.8	9,614
2	A human gut microbial gene catalogue established by metagenomic sequencing. Nature, 2010, 464, 59-65.	27.8	9,342
3	Enterotypes of the human gut microbiome. Nature, 2011, 473, 174-180.	27.8	5,800
4	A metagenome-wide association study of gut microbiota in type 2 diabetes. Nature, 2012, 490, 55-60.	27.8	5,345
5	Richness of human gut microbiome correlates with metabolic markers. Nature, 2013, 500, 541-546.	27.8	3,641
6	Microbial interactions: from networks to models. Nature Reviews Microbiology, 2012, 10, 538-550.	28.6	2,693
7	A framework for human microbiome research. Nature, 2012, 486, 215-221.	27.8	2,249
8	Structure and function of the global ocean microbiome. Science, 2015, 348, 1261359.	12.6	2,137
9	Population-level analysis of gut microbiome variation. Science, 2016, 352, 560-564.	12.6	1,716
10	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. Nature, 2015, 528, 262-266.	27.8	1,627
11	Eukaryotic plankton diversity in the sunlit ocean. Science, 2015, 348, 1261605.	12.6	1,551
12	Human gut microbes impact host serum metabolome and insulin sensitivity. Nature, 2016, 535, 376-381.	27.8	1,506
13	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science, 2016, 352, 565-569.	12.6	1,398
14	Supplementation with Akkermansia muciniphila in overweight and obese human volunteers: a proof-of-concept exploratory study. Nature Medicine, 2019, 25, 1096-1103.	30.7	1,281
15	Microbial Co-occurrence Relationships in the Human Microbiome. PLoS Computational Biology, 2012, 8, e1002606.	3.2	1,268
16	The neuroactive potential of the human gut microbiota in quality of life and depression. Nature Microbiology, 2019, 4, 623-632.	13.3	1,206
17	How informative is the mouse for human gut microbiota research?. DMM Disease Models and Mechanisms, 2015, 8, 1-16.	2.4	990
18	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. Nature Biotechnology, 2014, 32, 822-828.	17.5	909

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19	Modeling gene and genome duplications in eukaryotes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 5454-5459.	7.1	850
20	Determinants of community structure in the global plankton interactome. Science, 2015, 348, 1262073.	12.6	842
21	Quantitative microbiome profiling links gut community variation to microbial load. Nature, 2017, 551, 507-511.	27.8	791
22	Duplication and Divergence: The Evolution of New Genes and Old Ideas. Annual Review of Genetics, 2004, 38, 615-643.	7.6	756
23	Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates. Gut, 2016, 65, 57-62.	12.1	737
24	Enterotypes in the landscape of gut microbial community composition. Nature Microbiology, 2018, 3, 8-16.	13.3	717
25	The resilience of the intestinal microbiota influences health and disease. Nature Reviews Microbiology, 2017, 15, 630-638.	28.6	696
26	Genome-Wide Characterization of the Lignification Toolbox in Arabidopsis Å. Plant Physiology, 2003, 133, 1051-1071.	4.8	689
27	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	21.4	676
28	Plankton networks driving carbon export in the oligotrophic ocean. Nature, 2016, 532, 465-470.	27.8	670
29	Regional variation limits applications of healthy gut microbiome reference ranges and disease models. Nature Medicine, 2018, 24, 1532-1535.	30.7	629
30	Patterns and ecological drivers of ocean viral communities. Science, 2015, 348, 1261498.	12.6	617
31	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MlxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	17.5	608
32	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. ISME Journal, 2016, 10, 1669-1681.	9.8	593
33	The Human Gut Microbiome: From Association to Modulation. Cell, 2018, 172, 1198-1215.	28.9	558
34	The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. ISME Journal, 2012, 6, 1415-1426.	9.8	544
35	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. Cell, 2019, 177, 1109-1123.e14.	28.9	541
36	Genome-Wide Analysis of Core Cell Cycle Genes in Arabidopsis. Plant Cell, 2002, 14, 903-916.	6.6	523

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37	CoNet app: inference of biological association networks using Cytoscape. F1000Research, 2016, 5, 1519.	1.6	398
38	Computational approaches to predict bacteriophage–host relationships. FEMS Microbiology Reviews, 2016, 40, 258-272.	8.6	394
39	Inflammation-associated enterotypes, host genotype, cage and inter-individual effects drive gut microbiota variation in common laboratory mice. Genome Biology, 2013, 14, R4.	9.6	381
40	Integrated Metagenomics/Metaproteomics Reveals Human Host-Microbiota Signatures of Crohn's Disease. PLoS ONE, 2012, 7, e49138.	2.5	374
41	Prebiotic inulin-type fructans induce specific changes in the human gut microbiota. Gut, 2017, 66, 1968-1974.	12.1	370
42	A Holistic Approach to Marine Eco-Systems Biology. PLoS Biology, 2011, 9, e1001177.	5.6	353
43	Metagenomics meets time series analysis: unraveling microbial community dynamics. Current Opinion in Microbiology, 2015, 25, 56-66.	5.1	345
44	Molecular eco-systems biology: towards an understanding of community function. Nature Reviews Microbiology, 2008, 6, 693-699.	28.6	339
45	CoNet app: inference of biological association networks using Cytoscape. F1000Research, 2016, 5, 1519.	1.6	331
46	Open science resources for the discovery and analysis of Tara Oceans data. Scientific Data, 2015, 2, 150023.	5.3	330
47	Primary sclerosing cholangitis is characterised by intestinal dysbiosis independent from IBD. Gut, 2016, 65, 1681-1689.	12.1	312
48	Heterogeneity of the gut microbiome in mice: guidelines for optimizing experimental design. FEMS Microbiology Reviews, 2016, 40, 117-132.	8.6	303
49	A metagenomic insight into our gut's microbiome. Gut, 2013, 62, 146-158.	12.1	302
50	Quantitative Phylogenetic Assessment of Microbial Communities in Diverse Environments. Science, 2007, 315, 1126-1130.	12.6	300
51	A global ocean atlas of eukaryotic genes. Nature Communications, 2018, 9, 373.	12.8	297
52	Metagenomic <scp>16S rDNA l</scp>llumina tags are a powerful alternative to amplicon sequencing to explore diversity and structure of microbial communities. Environmental Microbiology, 2014, 16, 2659-2671.	3.8	291
53	Intestinal Microbiota And Diet in IBS: Causes, Consequences, or Epiphenomena?. American Journal of Gastroenterology, 2015, 110, 278-287.	0.4	283
54	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. Nature, 2020, 581, 310-315.	27.8	283

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55	Prediction of effective genome size in metagenomic samples. <i>Genome Biology</i> , 2007, 8, R10.	9.6	281
56	Short chain fatty acids and its producing organisms: An overlooked therapy for IBD?. <i>EBioMedicine</i> , 2021, 66, 103293.	6.1	281
57	Species–function relationships shape ecological properties of the human gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16088.	13.3	279
58	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	28.9	271
59	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	28.9	268
60	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	256
61	Towards microbial fermentation metabolites as markers for health benefits of prebiotics. <i>Nutrition Research Reviews</i> , 2015, 28, 42-66.	4.1	251
62	LotuS: an efficient and user-friendly OTU processing pipeline. <i>Microbiome</i> , 2014, 2, 30.	11.1	233
63	Brief Report: <i>Dialister</i> as a Microbial Marker of Disease Activity in Spondyloarthritis. <i>Arthritis and Rheumatology</i> , 2017, 69, 114-121.	5.6	233
64	Meeting Report: The Terabase Metagenomics Workshop and the Vision of an Earth Microbiome Project. <i>Standards in Genomic Sciences</i> , 2010, 3, 243-248.	1.5	228
65	Nonsense-mediated mRNA decay factors act in concert to regulate common mRNA targets. <i>Rna</i> , 2005, 11, 1530-1544.	3.5	226
66	Toward molecular trait-based ecology through integration of biogeochemical, geographical and metagenomic data. <i>Molecular Systems Biology</i> , 2011, 7, 473.	7.2	218
67	Assessment of Metagenomic Assembly Using Simulated Next Generation Sequencing Data. <i>PLoS ONE</i> , 2012, 7, e31386.	2.5	214
68	Microglia Require CD4 ⁺ Cells to Complete the Fetal-to-Adult Transition. <i>Cell</i> , 2020, 182, 625-640.e24.	28.9	191
69	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , 2013, 7, 1678-1695.	9.8	185
70	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016, 17, 189.	8.8	183
71	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.	1.3	180
72	And then there were many: MADS goes genomic. <i>Trends in Plant Science</i> , 2003, 8, 475-483.	8.8	179

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73	Quantifying environmental adaptation of metabolic pathways in metagenomics. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1374-1379.	7.1	177
74	Soil microbiome responses to the short-term effects of Amazonian deforestation. Molecular Ecology, 2015, 24, 2433-2448.	3.9	171
75	Monocyte-driven atypical cytokine storm and aberrant neutrophil activation as key mediators of COVID-19 disease severity. Nature Communications, 2021, 12, 4117.	12.8	170
76	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
77	Get the most out of your metagenome: computational analysis of environmental sequence data. Current Opinion in Microbiology, 2007, 10, 490-498.	5.1	169
78	Nonrandom divergence of gene expression following gene and genome duplications in the flowering plant <i>Arabidopsis thaliana</i> . Genome Biology, 2006, 7, R13.	9.6	163
79	Environmental characteristics of Agulhas rings affect interocean plankton transport. Science, 2015, 348, 1261-1267.	12.6	158
80	Cross-biome comparison of microbial association networks. Frontiers in Microbiology, 2015, 6, 1200.	3.5	154
81	Local immune response to food antigens drives meal-induced abdominal pain. Nature, 2021, 590, 151-156.	27.8	153
82	Quantitative microbiome profiling disentangles inflammation- and bile duct obstruction-associated microbiota alterations across PSC/IBD diagnoses. Nature Microbiology, 2019, 4, 1826-1831.	13.3	149
83	Population-level analysis of <i>Blastocystis</i> subtype prevalence and variation in the human gut microbiota. Gut, 2019, 68, 1180-1189.	12.1	149
84	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. Scientific Data, 2017, 4, 170093.	5.3	147
85	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. Nature Microbiology, 2020, 5, 1079-1087.	13.3	144
86	Practical considerations for large-scale gut microbiome studies. FEMS Microbiology Reviews, 2017, 41, S154-S167.	8.6	142
87	Nlrp6- and ASC-Dependent Inflammasomes Do Not Shape the Commensal Gut Microbiota Composition. Immunity, 2017, 47, 339-348.e4.	14.3	141
88	Transcriptome analysis during cell division in plants. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14825-14830.	7.1	140
89	Millimeter-scale genetic gradients and community-level molecular convergence in a hypersaline microbial mat. Molecular Systems Biology, 2008, 4, 198.	7.2	139
90	Microbiology Meets Big Data: The Case of Gut Microbiota-Derived Trimethylamine. Annual Review of Microbiology, 2015, 69, 305-321.	7.3	133

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91	Linking gut microbiota, metabolic syndrome and economic status based on a population-level analysis. <i>Microbiome</i> , 2018, 6, 172.	11.1	131
92	The Automatic Detection of Homologous Regions (ADHoRe) and Its Application to Microcolinearity Between Arabidopsis and Rice. <i>Genome Research</i> , 2002, 12, 1792-1801.	5.5	127
93	Nonsense-mediated mRNA decay: target genes and functional diversification of effectors. <i>Trends in Biochemical Sciences</i> , 2006, 31, 639-646.	7.5	125
94	A low-gluten diet induces changes in the intestinal microbiome of healthy Danish adults. <i>Nature Communications</i> , 2018, 9, 4630.	12.8	124
95	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. <i>Nature Communications</i> , 2020, 11, 5881.	12.8	122
96	Identifying genomic and metabolic features that can underlie early successional and opportunistic lifestyles of human gut symbionts. <i>Genome Research</i> , 2012, 22, 1974-1984.	5.5	120
97	Synthetic ecology of the human gut microbiota. <i>Nature Reviews Microbiology</i> , 2019, 17, 754-763.	28.6	117
98	Deletions Involving Long-Range Conserved Nongenic Sequences Upstream and Downstream of FOXL2 as a Novel Disease-Causing Mechanism in Blepharophimosis Syndrome. <i>American Journal of Human Genetics</i> , 2005, 77, 205-218.	6.2	116
99	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.	2.0	110
100	Genomewide Structural Annotation and Evolutionary Analysis of the Type I MADS-Box Genes in Plants. <i>Journal of Molecular Evolution</i> , 2003, 56, 573-586.	1.8	109
101	A20 controls intestinal homeostasis through cell-specific activities. <i>Nature Communications</i> , 2014, 5, 5103.	12.8	109
102	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018, 6, 101.	11.1	109
103	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. <i>Gastroenterology</i> , 2021, 160, 145-157.e8.	1.3	109
104	Induction of Bone Loss by Pathobiont-Mediated Nod1 Signaling in the Oral Cavity. <i>Cell Host and Microbe</i> , 2013, 13, 595-601.	11.0	108
105	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021, 4, 604.	4.4	107
106	Multi-stability and the origin of microbial community types. <i>ISME Journal</i> , 2017, 11, 2159-2166.	9.8	104
107	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021, 600, 500-505.	27.8	102
108	Microbiome and metabolome features of the cardiometabolic disease spectrum. <i>Nature Medicine</i> , 2022, 28, 303-314.	30.7	102

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109	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018, 9, 310.	12.8	101
110	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, 1416.	3.5	99
111	Butyrate Producers as Potential Next-Generation Probiotics: Safety Assessment of the Administration of <i>Butyricicoccus pullicaecorum</i> to Healthy Volunteers. <i>MSystems</i> , 2018, 3, .	3.8	99
112	Universally Distributed Single-Copy Genes Indicate a Constant Rate of Horizontal Transfer. <i>PLoS ONE</i> , 2011, 6, e22099.	2.5	99
113	The TORNADO1 and TORNADO2 Genes Function in Several Patterning Processes during Early Leaf Development in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2006, 18, 852-866.	6.6	96
114	<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.	12.1	95
115	Commensal microbiota influence systemic autoimmune responses. <i>EMBO Journal</i> , 2015, 34, 466-474.	7.8	93
116	Novel insights into the genetically obese (ob/ob) and diabetic (db/db) mice: two sides of the same coin. <i>Microbiome</i> , 2021, 9, 147.	11.1	92
117	SmashCommunity: a metagenomic annotation and analysis tool. <i>Bioinformatics</i> , 2010, 26, 2977-2978.	4.1	89
118	Temporal variability in quantitative human gut microbiome profiles and implications for clinical research. <i>Nature Communications</i> , 2021, 12, 6740.	12.8	89
119	Richness and ecosystem development across faecal snapshots of the gut microbiota. <i>Nature Microbiology</i> , 2018, 3, 526-528.	13.3	81
120	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	4.9	76
121	Quantitative assessment of protein function prediction from metagenomics shotgun sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13913-13918.	7.1	72
122	Towards biome-specific analysis of meta-omics data. <i>ISME Journal</i> , 2016, 10, 1025-1028.	9.8	72
123	Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton. <i>Nature Communications</i> , 2016, 7, 11071.	12.8	72
124	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.	8.8	72
125	Reconciliation between operational taxonomic units and species boundaries. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	71
126	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	70

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127	Microbial communities of the house fly <i>Musca domestica</i> vary with geographical location and habitat. <i>Microbiome</i> , 2019, 7, 147.	11.1	70
128	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022, 2, 100123.	6.5	70
129	Tapping into the maize root microbiome to identify bacteria that promote growth under chilling conditions. <i>Microbiome</i> , 2020, 8, 54.	11.1	63
130	Integrated culturing, modeling and transcriptomics uncovers complex interactions and emergent behavior in a three-species synthetic gut community. <i>ELife</i> , 2018, 7, .	6.0	62
131	Functional divergence of proteins through frameshift mutations. <i>Trends in Genetics</i> , 2005, 21, 428-431.	6.7	61
132	Caspase deficiency alters the murine gut microbiome. <i>Cell Death and Disease</i> , 2011, 2, e220-e220.	6.3	61
133	Gut Microbiota Affects Sensitivity to Acute DSS-induced Colitis Independently of Host Genotype. <i>Inflammatory Bowel Diseases</i> , 2013, 19, 2560-2567.	1.9	61
134	Increased IL-10-producing regulatory T cells are characteristic of severe cases of COVID-19. <i>Clinical and Translational Immunology</i> , 2020, 9, e1204.	3.8	59
135	Gut microbiome variation is associated to Multiple Sclerosis phenotypic subtypes. <i>Annals of Clinical and Translational Neurology</i> , 2020, 7, 406-419.	3.7	59
136	CATCH, an Ensemble Classifier for Chimera Detection in 16S rRNA Sequencing Studies. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1573-1584.	3.1	58
137	Red Wine Consumption Associated With Increased Gut Microbiota α -Diversity in 3 Independent Cohorts. <i>Gastroenterology</i> , 2020, 158, 270-272.e2.	1.3	58
138	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.	12.1	58
139	A web application for sample size and power calculation in case-control microbiome studies. <i>Bioinformatics</i> , 2016, 32, 2038-2040.	4.1	57
140	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.	4.1	57
141	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. <i>Nature Microbiology</i> , 2021, 6, 1561-1574.	13.3	57
142	Assessment of faecal microbial transfer in irritable bowel syndrome with severe bloating. <i>Gut</i> , 2017, 66, 980-982.	12.1	56
143	Discovering Functional Novelty in Metagenomes: Examples from Light-Mediated Processes. <i>Journal of Bacteriology</i> , 2009, 191, 32-41.	2.2	54
144	Molecular characterization of Arabidopsis PHO80-like proteins, a novel class of CDKA;1-interacting cyclins. <i>Cellular and Molecular Life Sciences</i> , 2004, 61, 1485-97.	5.4	53

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145	Metformin induces weight loss associated with gut microbiota alteration in non-diabetic obese women: a randomized double-blind clinical trial. <i>European Journal of Endocrinology</i> , 2019, 180, 165-176.	3.7	53
146	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.	12.1	53
147	Investigating ancient duplication events in the Arabidopsis genome. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 117-129.	1.2	52
148	Interindividual differences in response to treatment with butyrate-producing <i>Butyricoccus pullicaecorum</i> 25â€³T studied in an in vitro gut model. <i>FEMS Microbiology Ecology</i> , 2015, 91, .	2.7	50
149	Clinical, gut microbial and neural effects of a probiotic add-on therapy in depressed patients: a randomized controlled trial. <i>Translational Psychiatry</i> , 2022, 12, .	4.8	49
150	Fire modifies the phylogenetic structure of soil bacterial co-occurrence networks. <i>Environmental Microbiology</i> , 2017, 19, 317-327.	3.8	48
151	Successional Stages in Infant Gut Microbiota Maturation. <i>MBio</i> , 2021, 12, e0185721.	4.1	48
152	From reads to operational taxonomic units: an ensemble processing pipeline for MiSeq amplicon sequencing data. <i>GigaScience</i> , 2017, 6, 1-10.	6.4	47
153	Low eukaryotic viral richness is associated with faecal microbiota transplantation success in patients with UC. <i>Gut</i> , 2018, 67, 1558-1559.	12.1	46
154	Prebiotic Wheat Bran Fractions Induce Specific Microbiota Changes. <i>Frontiers in Microbiology</i> , 2018, 9, 31.	3.5	45
155	A comparative analysis of the intestinal metagenomes present in guinea pigs (<i>Cavia porcellus</i>) and humans (<i>Homo sapiens</i>). <i>BMC Genomics</i> , 2012, 13, 514.	2.8	43
156	Clinical practices underlie COVID-19 patient respiratory microbiome composition and its interactions with the host. <i>Nature Communications</i> , 2021, 12, 6243.	12.8	42
157	Protein function space: viewing the limits or limited by our view?. <i>Current Opinion in Structural Biology</i> , 2007, 17, 362-369.	5.7	37
158	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	37
159	Design of synthetic microbial consortia for gut microbiota modulation. <i>Current Opinion in Pharmacology</i> , 2019, 49, 52-59.	3.5	37
160	Gut microbiota dynamics and uraemic toxins: one size does not fit all. <i>Gut</i> , 2019, 68, 2257.1-2260.	12.1	37
161	Fecal Microbiota Transplantation (FMT) as an Adjunctive Therapy for Depressionâ€”Case Report. <i>Frontiers in Psychiatry</i> , 2022, 13, 815422.	2.6	37
162	A Molecular Study of Microbe Transfer between Distant Environments. <i>PLoS ONE</i> , 2008, 3, e2607.	2.5	36

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163	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	35
164	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.	5.1	34
165	The human microbiome in health and disease: hype or hope. <i>Acta Clinica Belgica</i> , 2019, 74, 53-64.	1.2	34
166	Dietary Emulsifiers Alter Composition and Activity of the Human Gut Microbiota <i>in vitro</i> , Irrespective of Chemical or Natural Emulsifier Origin. <i>Frontiers in Microbiology</i> , 2020, 11, 577474.	3.5	33
167	Investigating ancient duplication events in the Arabidopsis genome. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 117-29.	1.2	32
168	Variation and transmission of the human gut microbiota across multiple familial generations. <i>Nature Microbiology</i> , 2022, 7, 87-96.	13.3	32
169	An Improved Statistical Method for Detecting Heterotachy in Nucleotide Sequences. <i>Molecular Biology and Evolution</i> , 2006, 23, 1397-1405.	8.9	31
170	Speciesâ€sorting and massâ€transfer paradigms control managed natural metacommunities. <i>Environmental Microbiology</i> , 2016, 18, 4862-4877.	3.8	31
171	Translating the human microbiome. <i>Nature Biotechnology</i> , 2013, 31, 304-308.	17.5	30
172	IPED: a highly efficient denoising tool for Illumina MiSeq Paired-end 16S rRNAâ€gene amplicon sequencing data. <i>BMC Bioinformatics</i> , 2016, 17, 192.	2.6	30
173	Benchmarking microbiome transformations favors experimental quantitative approaches to address compositionality and sampling depth biases. <i>Nature Communications</i> , 2021, 12, 3562.	12.8	30
174	The virota and its transkingdom interactions in the healthy infant gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2114619119.	7.1	30
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