

# Jeroen Raes

## List of Publications by Citations

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238  
papers

57,641  
citations

87  
h-index

240  
g-index

269  
ext. papers

74,896  
ext. citations

15.5  
avg. IF

8.26  
L-index

#	Paper	IF	Citations
238	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , <b>2010</b> , 464, 59-65	50.4	7044
237	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , <b>2012</b> , 486, 207-14	50.4	6938
236	Enterotypes of the human gut microbiome. <i>Nature</i> , <b>2011</b> , 473, 174-80	50.4	4240
235	A metagenome-wide association study of gut microbiota in type 2 diabetes. <i>Nature</i> , <b>2012</b> , 490, 55-60	50.4	3779
234	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , <b>2013</b> , 500, 541-6	50.4	2584
233	A framework for human microbiome research. <i>Nature</i> , <b>2012</b> , 486, 215-21	50.4	1722
232	Microbial interactions: from networks to models. <i>Nature Reviews Microbiology</i> , <b>2012</b> , 10, 538-50	22.2	1607
231	Ocean plankton. Structure and function of the global ocean microbiome. <i>Science</i> , <b>2015</b> , 348, 1261359	33.3	1261
230	Population-level analysis of gut microbiome variation. <i>Science</i> , <b>2016</b> , 352, 560-4	33.3	1120
229	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , <b>2015</b> , 528, 262-266	50.4	1107
228	Ocean plankton. Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , <b>2015</b> , 348, 1261605	33.3	990
227	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , <b>2016</b> , 535, 376-81	50.4	977
226	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , <b>2016</b> , 352, 565-9	33.3	929
225	Microbial co-occurrence relationships in the human microbiome. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002606	5	914
224	How informative is the mouse for human gut microbiota research?. <i>DMM Disease Models and Mechanisms</i> , <b>2015</b> , 8, 1-16	4.1	691
223	Modeling gene and genome duplications in eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 5454-9	11.5	670
222	The neuroactive potential of the human gut microbiota in quality of life and depression. <i>Nature Microbiology</i> , <b>2019</b> , 4, 623-632	26.6	651

221	Supplementation with <i>Akkermansia muciniphila</i> in overweight and obese human volunteers: a proof-of-concept exploratory study. <i>Nature Medicine</i> , <b>2019</b> , 25, 1096-1103	50.5	650
220	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 822-8	44.5	624
219	Duplication and divergence: the evolution of new genes and old ideas. <i>Annual Review of Genetics</i> , <b>2004</b> , 38, 615-43	14.5	620
218	Genome-wide characterization of the lignification toolbox in <i>Arabidopsis</i> . <i>Plant Physiology</i> , <b>2003</b> , 133, 1051-71	6.6	564
217	Ocean plankton. Determinants of community structure in the global plankton interactome. <i>Science</i> , <b>2015</b> , 348, 1262073	33.3	496
216	Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates. <i>Gut</i> , <b>2016</b> , 65, 57-62	19.2	488
215	Quantitative microbiome profiling links gut community variation to microbial load. <i>Nature</i> , <b>2017</b> , 551, 507-511	50.4	475
214	Genome-wide analysis of core cell cycle genes in <i>Arabidopsis</i> . <i>Plant Cell</i> , <b>2002</b> , 14, 903-16	11.6	450
213	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. <i>Nature Biotechnology</i> , <b>2011</b> , 29, 415-20	44.5	445
212	Ocean plankton. Patterns and ecological drivers of ocean viral communities. <i>Science</i> , <b>2015</b> , 348, 1261498	33.3	421
211	The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. <i>ISME Journal</i> , <b>2012</b> , 6, 1415-26	11.9	416
210	The resilience of the intestinal microbiota influences health and disease. <i>Nature Reviews Microbiology</i> , <b>2017</b> , 15, 630-638	22.2	398
209	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , <b>2016</b> , 532, 465-470	50.4	392
208	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , <b>2018</b> , 3, 8-16	26.6	387
207	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , <b>2016</b> , 10, 1669-81	11.9	365
206	Regional variation limits applications of healthy gut microbiome reference ranges and disease models. <i>Nature Medicine</i> , <b>2018</b> , 24, 1532-1535	50.5	348
205	The Human Gut Microbiome: From Association to Modulation. <i>Cell</i> , <b>2018</b> , 172, 1198-1215	56.2	344
204	Integrated metagenomics/metaproteomics reveals human host-microbiota signatures of Crohn's disease. <i>PLoS ONE</i> , <b>2012</b> , 7, e49138	3.7	320

203	Inflammation-associated enterotypes, host genotype, cage and inter-individual effects drive gut microbiota variation in common laboratory mice. <i>Genome Biology</i> , <b>2013</b> , 14, R4	18.3	293
202	Molecular eco-systems biology: towards an understanding of community function. <i>Nature Reviews Microbiology</i> , <b>2008</b> , 6, 693-9	22.2	284
201	A holistic approach to marine eco-systems biology. <i>PLoS Biology</i> , <b>2011</b> , 9, e1001177	9.7	265
200	Quantitative phylogenetic assessment of microbial communities in diverse environments. <i>Science</i> , <b>2007</b> , 315, 1126-30	33.3	259
199	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , <b>2019</b> , 177, 1109-1123.e14	56.2	256
198	Prebiotic inulin-type fructans induce specific changes in the human gut microbiota. <i>Gut</i> , <b>2017</b> , 66, 1968-1974	19.4	236
197	Metagenomics meets time series analysis: unraveling microbial community dynamics. <i>Current Opinion in Microbiology</i> , <b>2015</b> , 25, 56-66	7.9	236
196	Computational approaches to predict bacteriophage-host relationships. <i>FEMS Microbiology Reviews</i> , <b>2016</b> , 40, 258-72	15.1	235
195	A metagenomic insight into our gut's microbiome. <i>Gut</i> , <b>2013</b> , 62, 146-58	19.2	234
194	CoNet app: inference of biological association networks using Cytoscape. <i>F1000Research</i> , <b>2016</b> , 5, 1519	3.6	231
193	Intestinal microbiota and diet in IBS: causes, consequences, or epiphenomena?. <i>American Journal of Gastroenterology</i> , <b>2015</b> , 110, 278-87	0.7	225
192	Prediction of effective genome size in metagenomic samples. <i>Genome Biology</i> , <b>2007</b> , 8, R10	18.3	219
191	Heterogeneity of the gut microbiome in mice: guidelines for optimizing experimental design. <i>FEMS Microbiology Reviews</i> , <b>2016</b> , 40, 117-32	15.1	217
190	Primary sclerosing cholangitis is characterised by intestinal dysbiosis independent from IBD. <i>Gut</i> , <b>2016</b> , 65, 1681-9	19.2	212
189	Nonsense-mediated mRNA decay factors act in concert to regulate common mRNA targets. <i>Rna</i> , <b>2005</b> , 11, 1530-44	5.8	206
188	Metagenomic 16S rDNA Illumina tags are a powerful alternative to amplicon sequencing to explore diversity and structure of microbial communities. <i>Environmental Microbiology</i> , <b>2014</b> , 16, 2659-71	5.2	200
187	Open science resources for the discovery and analysis of Tara Oceans data. <i>Scientific Data</i> , <b>2015</b> , 2, 150083	3	198
186	Meeting report: the terabase metagenomics workshop and the vision of an Earth microbiome project. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 243-8		187

185	LotuS: an efficient and user-friendly OTU processing pipeline. <i>Microbiome</i> , <b>2014</b> , 2, 30	16.6	186
184	Donor Species Richness Determines Faecal Microbiota Transplantation Success in Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , <b>2016</b> , 10, 387-94	1.5	183
183	CoNet app: inference of biological association networks using Cytoscape. <i>F1000Research</i> , <b>2016</b> , 5, 1519	3.6	183
182	Towards microbial fermentation metabolites as markers for health benefits of prebiotics. <i>Nutrition Research Reviews</i> , <b>2015</b> , 28, 42-66	7	173
181	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , <b>2018</b> , 9, 373	17.4	168
180	Assessment of metagenomic assembly using simulated next generation sequencing data. <i>PLoS ONE</i> , <b>2012</b> , 7, e31386	3.7	157
179	Brief Report: Dialister as a Microbial Marker of Disease Activity in Spondyloarthritis. <i>Arthritis and Rheumatology</i> , <b>2017</b> , 69, 114-121	9.5	150
178	Quantifying environmental adaptation of metabolic pathways in metagenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 1374-9	11.5	148
177	Species-function relationships shape ecological properties of the human gut microbiome. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16088	26.6	145
176	And then there were many: MADS goes genomic. <i>Trends in Plant Science</i> , <b>2003</b> , 8, 475-83	13.1	145
175	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , <b>2013</b> , 7, 1678-95	11.9	142
174	Nonrandom divergence of gene expression following gene and genome duplications in the flowering plant <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , <b>2006</b> , 7, R13	18.3	134
173	Toward molecular trait-based ecology through integration of biogeochemical, geographical and metagenomic data. <i>Molecular Systems Biology</i> , <b>2011</b> , 7, 473	12.2	129
172	Get the most out of your metagenome: computational analysis of environmental sequence data. <i>Current Opinion in Microbiology</i> , <b>2007</b> , 10, 490-8	7.9	127
171	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , <b>2016</b> , 17, 189	18.3	124
170	Transcriptome analysis during cell division in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 14825-30	11.5	120
169	Millimeter-scale genetic gradients and community-level molecular convergence in a hypersaline microbial mat. <i>Molecular Systems Biology</i> , <b>2008</b> , 4, 198	12.2	118
168	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , <b>2019</b> , 179, 1068-1083.e21	56.2	113

167	Nonsense-mediated mRNA decay: Target genes and functional diversification of effectors. <i>Trends in Biochemical Sciences</i> , <b>2006</b> , 31, 639-46	10.3	113
166	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> , <b>2005</b> , 77, 205-18	11	112
165	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , <b>2019</b> , 179, 1084-1097.e21	56.2	108
164	Nlrp6- and ASC-Dependent Inflammasomes Do Not Shape the Commensal Gut Microbiota Composition. <i>Immunity</i> , <b>2017</b> , 47, 339-348.e4	32.3	108
163	The automatic detection of homologous regions (ADHoRe) and its application to microcolinearity between Arabidopsis and rice. <i>Genome Research</i> , <b>2002</b> , 12, 1792-801	9.7	105
162	Soil microbiome responses to the short-term effects of Amazonian deforestation. <i>Molecular Ecology</i> , <b>2015</b> , 24, 2433-48	5.7	103
161	Cross-biome comparison of microbial association networks. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 1200	5.7	102
160	Metabolic Functions of Gut Microbes Associate With Efficacy of Tumor Necrosis Factor Antagonists in Patients With Inflammatory Bowel Diseases. <i>Gastroenterology</i> , <b>2019</b> , 157, 1279-1292.e11	13.3	101
159	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , <b>2020</b> , 581, 310-315.4	15.4	100
158	Ocean plankton. Environmental characteristics of Agulhas rings affect interocean plankton transport. <i>Science</i> , <b>2015</b> , 348, 1261447	33.3	100
157	Identifying genomic and metabolic features that can underlie early successional and opportunistic lifestyles of human gut symbionts. <i>Genome Research</i> , <b>2012</b> , 22, 1974-84	9.7	97
156	Microbiology Meets Big Data: The Case of Gut Microbiota-Derived Trimethylamine. <i>Annual Review of Microbiology</i> , <b>2015</b> , 69, 305-21	17.5	94
155	Practical considerations for large-scale gut microbiome studies. <i>FEMS Microbiology Reviews</i> , <b>2017</b> , 41, S154-S167	15.1	93
154	Induction of bone loss by pathobiont-mediated Nod1 signaling in the oral cavity. <i>Cell Host and Microbe</i> , <b>2013</b> , 13, 595-601	23.4	93
153	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , <b>2017</b> , 4, 170093	8.2	89
152	Genomewide structural annotation and evolutionary analysis of the type I MADS-box genes in plants. <i>Journal of Molecular Evolution</i> , <b>2003</b> , 56, 573-86	3.1	89
151	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , <b>2021</b> , 53, 156-165	36.3	80
150	Commensal microbiota influence systemic autoimmune responses. <i>EMBO Journal</i> , <b>2015</b> , 34, 466-74	13	79

149	Population-level analysis of subtype prevalence and variation in the human gut microbiota. <i>Gut</i> , <b>2019</b> , 68, 1180-1189	19.2	79
148	A20 controls intestinal homeostasis through cell-specific activities. <i>Nature Communications</i> , <b>2014</b> , 5, 5103-4	7.4	78
147	SmashCommunity: a metagenomic annotation and analysis tool. <i>Bioinformatics</i> , <b>2010</b> , 26, 2977-8	7.2	77
146	Microglia Require CD4 <sup>+</sup> T Cells to Complete the Fetal-to-Adult Transition. <i>Cell</i> , <b>2020</b> , 182, 625-640.e24	56.2	77
145	The Gut Microbiome and Mental Health: Implications for Anxiety- and Trauma-Related Disorders. <i>OMICS A Journal of Integrative Biology</i> , <b>2018</b> , 22, 90-107	3.8	76
144	The TORNADO1 and TORNADO2 genes function in several patterning processes during early leaf development in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , <b>2006</b> , 18, 852-66	11.6	74
143	Linking gut microbiota, metabolic syndrome and economic status based on a population-level analysis. <i>Microbiome</i> , <b>2018</b> , 6, 172	16.6	72
142	Quantitative microbiome profiling disentangles inflammation- and bile duct obstruction-associated microbiota alterations across PSC/IBD diagnoses. <i>Nature Microbiology</i> , <b>2019</b> , 4, 1826-1831	26.6	71
141	A low-gluten diet induces changes in the intestinal microbiome of healthy Danish adults. <i>Nature Communications</i> , <b>2018</b> , 9, 4630	17.4	69
140	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> , <b>2007</b> , 104, 13913-8	11.5	66
139	Synthetic ecology of the human gut microbiota. <i>Nature Reviews Microbiology</i> , <b>2019</b> , 17, 754-763	22.2	64
138	Universally distributed single-copy genes indicate a constant rate of horizontal transfer. <i>PLoS ONE</i> , <b>2011</b> , 6, e22099	3.7	61
137	Faecal Metaproteomic Analysis Reveals a Personalized and Stable Functional Microbiome and Limited Effects of a Probiotic Intervention in Adults. <i>PLoS ONE</i> , <b>2016</b> , 11, e0153294	3.7	59
136	Multi-stability and the origin of microbial community types. <i>ISME Journal</i> , <b>2017</b> , 11, 2159-2166	11.9	57
135	The Probiotic Reduces Feed Conversion and Protects from Potentially Harmful Intestinal Microorganisms and Necrotic Enteritis in Broilers. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 1416	5.7	56
134	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. <i>Nature Microbiology</i> , <b>2020</b> , 5, 1079-1087	26.6	55
133	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , <b>2018</b> , 9, 310	17.4	55
132	Gut microbiota affects sensitivity to acute DSS-induced colitis independently of host genotype. <i>Inflammatory Bowel Diseases</i> , <b>2013</b> , 19, 2560-7	4.5	54

131	Caspase deficiency alters the murine gut microbiome. <i>Cell Death and Disease</i> , <b>2011</b> , 2, e220	9.8	54
130	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , <b>2018</b> , 6, 101	16.6	53
129	Monocyte-driven atypical cytokine storm and aberrant neutrophil activation as key mediators of COVID-19 disease severity. <i>Nature Communications</i> , <b>2021</b> , 12, 4117	17.4	53
128	Local immune response to food antigens drives meal-induced abdominal pain. <i>Nature</i> , <b>2021</b> , 590, 151-156	10.4	53
127	Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton. <i>Nature Communications</i> , <b>2016</b> , 7, 11071	17.4	51
126	Combined use of network inference tools identifies ecologically meaningful bacterial associations in a paddy soil. <i>Soil Biology and Biochemistry</i> , <b>2017</b> , 105, 227-235	7.5	50
125	Discovering functional novelty in metagenomes: examples from light-mediated processes. <i>Journal of Bacteriology</i> , <b>2009</b> , 191, 32-41	3.5	50
124	Investigating ancient duplication events in the Arabidopsis genome. <i>Journal of Structural and Functional Genomics</i> , <b>2003</b> , 3, 117-129		49
123	Richness and ecosystem development across faecal snapshots of the gut microbiota. <i>Nature Microbiology</i> , <b>2018</b> , 3, 526-528	26.6	48
122	Butyrate Producers as Potential Next-Generation Probiotics: Safety Assessment of the Administration of to Healthy Volunteers. <i>MSystems</i> , <b>2018</b> , 3,	7.6	45
121	Functional divergence of proteins through frameshift mutations. <i>Trends in Genetics</i> , <b>2005</b> , 21, 428-31	8.5	43
120	Assessment of faecal microbial transfer in irritable bowel syndrome with severe bloating. <i>Gut</i> , <b>2017</b> , 66, 980-982	19.2	42
119	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , <b>2019</b> , 33, 391-419	5.9	42
118	Short chain fatty acids and its producing organisms: An overlooked therapy for IBD?. <i>EBioMedicine</i> , <b>2021</b> , 66, 103293	8.8	41
117	Reconciliation between operational taxonomic units and species boundaries. <i>FEMS Microbiology Ecology</i> , <b>2017</b> , 93,	4.3	40
116	Towards biome-specific analysis of meta-omics data. <i>ISME Journal</i> , <b>2016</b> , 10, 1025-8	11.9	40
115	A web application for sample size and power calculation in case-control microbiome studies. <i>Bioinformatics</i> , <b>2016</b> , 32, 2038-40	7.2	38
114	Interindividual differences in response to treatment with butyrate-producing <i>Butyricoccus pullicaecorum</i> 25-3T studied in an in vitro gut model. <i>FEMS Microbiology Ecology</i> , <b>2015</b> , 91,	4.3	37



113	Molecular characterization of Arabidopsis PHO80-like proteins, a novel class of CDKA;1-interacting cyclins. <i>Cellular and Molecular Life Sciences</i> , <b>2004</b> , 61, 1485-97	10.3	37
112	Tapping into the maize root microbiome to identify bacteria that promote growth under chilling conditions. <i>Microbiome</i> , <b>2020</b> , 8, 54	16.6	37
111	CATCh, an ensemble classifier for chimera detection in 16S rRNA sequencing studies. <i>Applied and Environmental Microbiology</i> , <b>2015</b> , 81, 1573-84	4.8	35
110	From reads to operational taxonomic units: an ensemble processing pipeline for MiSeq amplicon sequencing data. <i>GigaScience</i> , <b>2017</b> , 6, 1-10	7.6	35
109	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> , <b>2012</b> , 13, 514	4.5	35
108	Protein function space: viewing the limits or limited by our view?. <i>Current Opinion in Structural Biology</i> , <b>2007</b> , 17, 362-9	8.1	34
107	Integrated culturing, modeling and transcriptomics uncovers complex interactions and emergent behavior in a three-species synthetic gut community. <i>ELife</i> , <b>2018</b> , 7,	8.9	34
106	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> , <b>2021</b> , 160, 145-157.e8	13.3	34
105	Low eukaryotic viral richness is associated with faecal microbiota transplantation success in patients with UC. <i>Gut</i> , <b>2018</b> , 67, 1558-1559	19.2	33
104	Microbial communities of the house fly <i>Musca domestica</i> vary with geographical location and habitat. <i>Microbiome</i> , <b>2019</b> , 7, 147	16.6	33
103	Investigating ancient duplication events in the Arabidopsis genome. <i>Journal of Structural and Functional Genomics</i> , <b>2003</b> , 3, 117-29		32
102	Fire modifies the phylogenetic structure of soil bacterial co-occurrence networks. <i>Environmental Microbiology</i> , <b>2017</b> , 19, 317-327	5.2	31
101	Red Wine Consumption Associated With Increased Gut Microbiota Diversity in 3 Independent Cohorts. <i>Gastroenterology</i> , <b>2020</b> , 158, 270-272.e2	13.3	31
100	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. <i>Nature Communications</i> , <b>2020</b> , 11, 5881	17.4	29
99	Gut microbiome variation is associated to Multiple Sclerosis phenotypic subtypes. <i>Annals of Clinical and Translational Neurology</i> , <b>2020</b> , 7, 406-419	5.3	28
98	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> , <b>2019</b> , 180, 165-176	6.5	28
97	Gene duplication, the evolution of novel gene functions, and detecting functional divergence of duplicates in silico. <i>Applied Bioinformatics</i> , <b>2003</b> , 2, 91-101		28
96	IPED: a highly efficient denoising tool for Illumina MiSeq Paired-end 16S rRNA gene amplicon sequencing data. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 192	3.6	25

95	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> , <b>2018</b> , 44, 1-8	7.9	25
94	Translating the human microbiome. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 304-8	44.5	25
93	Prediction and identification of sequences coding for orphan enzymes using genomic and metagenomic neighbours. <i>Molecular Systems Biology</i> , <b>2012</b> , 8, 581	12.2	25
92	An improved statistical method for detecting heterotachy in nucleotide sequences. <i>Molecular Biology and Evolution</i> , <b>2006</b> , 23, 1397-405	8.3	24
91	Increased IL-10-producing regulatory T cells are characteristic of severe cases of COVID-19. <i>Clinical and Translational Immunology</i> , <b>2020</b> , 9, e1204	6.8	24
90	Meta-omics in Inflammatory Bowel Disease Research: Applications, Challenges, and Guidelines. <i>Journal of Crohn's and Colitis</i> , <b>2016</b> , 10, 735-46	1.5	23
89	Species-sorting and mass-transfer paradigms control managed natural metacommunities. <i>Environmental Microbiology</i> , <b>2016</b> , 18, 4862-4877	5.2	23
88	Prebiotic Wheat Bran Fractions Induce Specific Microbiota Changes. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 31	5.7	22
87	Introducing insoluble wheat bran as a gut microbiota niche in an in vitro 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> , <b>2018</b> , 20, 3406-3426	5.2	22
86	Gut microbiota dynamics and uraemic toxins: one size does not fit all. <i>Gut</i> , <b>2019</b> , 68, 2257-2260	19.2	22
85	Relationship between genome and epigenome--challenges and requirements for future research. <i>BMC Genomics</i> , <b>2014</b> , 15, 487	4.5	21
84	SmashCell: a software framework for the analysis of single-cell amplified genome sequences. <i>Bioinformatics</i> , <b>2010</b> , 26, 2979-80	7.2	21
83	In silico analyses of pericycle cell populations reinforce their relation with associated vasculature in Arabidopsis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2012</b> , 367, 1479-88	5.8	21
82	A nitrile hydratase in the eukaryote <i>Monosiga brevicollis</i> . <i>PLoS ONE</i> , <b>2008</b> , 3, e3976	3.7	21
81	The human microbiome in health and disease: hype or hope. <i>Acta Clinica Belgica</i> , <b>2019</b> , 74, 53-64	1.8	20
80	Design of synthetic microbial consortia for gut microbiota modulation. <i>Current Opinion in Pharmacology</i> , <b>2019</b> , 49, 52-59	5.1	20
79	Addition of acacia gum to a FOS/inulin blend improves its fermentation profile in the Simulator of the Human Intestinal Microbial Ecosystem (SHIME <sup>®</sup> ). <i>Journal of Functional Foods</i> , <b>2015</b> , 16, 211-222	5.1	19
78	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , <b>2021</b> , 27, 1885-1892	50.5	19

77	Depression and suicidality: A link to premature T helper cell aging and increased Th17 cells. <i>Brain, Behavior, and Immunity</i> , <b>2020</b> , 87, 603-609	16.6	19
76	Multiomics Analyses to Deliver the Most Effective Treatment to Every Patient With Inflammatory Bowel Disease. <i>Gastroenterology</i> , <b>2018</b> , 155, e1-e4	13.3	18
75	Metabolic Architecture of the Deep Ocean Microbiome		17
74	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , <b>2021</b> , 4, 604	6.7	17
73	is a newly isolated human commensal bacterium preventing diet-induced obesity and metabolic disorders in mice. <i>Gut</i> , <b>2021</b> ,	19.2	17
72	Microbiome-based companion diagnostics: no longer science fiction?. <i>Gut</i> , <b>2016</b> , 65, 896-7	19.2	16
71	The chemical interactome space between the human host and the genetically defined gut metabotypes. <i>ISME Journal</i> , <b>2013</b> , 7, 730-42	11.9	16
70	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> , <b>2017</b> , 9,	6.7	16
69	A molecular study of microbe transfer between distant environments. <i>PLoS ONE</i> , <b>2008</b> , 3, e2607	3.7	16
68	GeneFarm, structural and functional annotation of Arabidopsis gene and protein families by a network of experts. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D641-6	20.1	15
67	Novel insights into the genetically obese (ob/ob) and diabetic (db/db) mice: two sides of the same coin. <i>Microbiome</i> , <b>2021</b> , 9, 147	16.6	15
66	A combinatorial approach to the structure elucidation of a pyoverdine siderophore produced by a <i>Pseudomonas putida</i> isolate and the use of pyoverdine as a taxonomic marker for typing <i>P. putida</i> subspecies. <i>BioMetals</i> , <b>2013</b> , 26, 561-75	3.4	14
65	NoDe: a fast error-correction algorithm for pyrosequencing amplicon reads. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 88	3.6	13
64	Human and preclinical studies of the host-gut microbiome co-metabolite hippurate as a marker and mediator of metabolic health. <i>Gut</i> , <b>2021</b> , 70, 2105-2114	19.2	13
63	The skin microbiome of caspase-14-deficient mice shows mild dysbiosis. <i>Experimental Dermatology</i> , <b>2014</b> , 23, 561-7	4	11
62	Small-Scale Gene Duplications <b>2005</b> , 289-327		11
61	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , <b>2021</b> ,	50.4	11
60	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> , <b>2018</b> , 8, e018166	3	11

59	Host-microbe interaction: Rules of the game for microbiota. <i>Nature</i> , <b>2016</b> , 534, 182-3	50.4	10
58	Temporal variability in quantitative human gut microbiome profiles and implications for clinical research. <i>Nature Communications</i> , <b>2021</b> , 12, 6740	17.4	10
57	Worldwide trends in scientific publications on association of gut microbiota with obesity. <i>Iranian Journal of Basic Medical Sciences</i> , <b>2019</b> , 22, 65-71	1.8	10
56	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. <i>Nature Microbiology</i> , <b>2021</b> , 6, 1561-1574	26.6	9
55	Clinical practices underlie COVID-19 patient respiratory microbiome composition and its interactions with the host. <i>Nature Communications</i> , <b>2021</b> , 12, 6243	17.4	9
54	Large-scale association analyses identify host factors influencing human gut microbiome composition		9
53	Duodenal Dysbiosis and Relation to the Efficacy of Proton Pump Inhibitors in Functional Dyspepsia.. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	9
52	Dietary Emulsifiers Alter Composition and Activity of the Human Gut Microbiota , Irrespective of Chemical or Natural Emulsifier Origin. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 577474	5.7	8
51	Water activity does not shape the microbiota in the human colon. <i>Gut</i> , <b>2017</b> , 66, 1865-1866	19.2	8
50	Benchmarking microbiome transformations favors experimental quantitative approaches to address compositionality and sampling depth biases. <i>Nature Communications</i> , <b>2021</b> , 12, 3562	17.4	8
49	Analysis of the draft genome of <i>Pseudomonas fluorescens</i> ATCC17400 indicates a capacity to take up iron from a wide range of sources, including different exogenous pyoverdines. <i>BioMetals</i> , <b>2014</b> , 27, 633-44	3.4	7
48	Isolation of wheat bran-colonizing and metabolizing species from the human fecal microbiota. <i>PeerJ</i> , <b>2019</b> , 7, e6293	3.1	7
47	Successional Stages in Infant Gut Microbiota Maturation.. <i>MBio</i> , <b>2021</b> , e0185721	7.8	7
46	Correction: LotuS: an efficient and user-friendly OTU processing pipeline. <i>Microbiome</i> , <b>2014</b> , 2, 37	16.6	6
45	The Genomic Sequence of the Oral Pathobiont Strain NI1060 Reveals Unique Strategies for Bacterial Competition and Pathogenicity. <i>PLoS ONE</i> , <b>2016</b> , 11, e0158866	3.7	6
44	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , <b>2022</b> , 2, 100123		6
43	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> , <b>2022</b> ,	19.2	5
42	Investigating ancient duplication events in the Arabidopsis genome <b>2003</b> , 117-129		5

41	Ecogenomics and biogeochemical impacts of uncultivated globally abundant ocean viruses		5
40	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> , <b>2018</b> , 4, 18	8.2	5
39	Zinc inhibits lethal inflammatory shock by preventing microbe-induced interferon signature in intestinal epithelium. <i>EMBO Molecular Medicine</i> , <b>2020</b> , 12, e11917	12	4
38	Microbiome and metabolome features of the cardiometabolic disease spectrum.. <i>Nature Medicine</i> , <b>2022</b> ,	50.5	4
37	Variation and transmission of the human gut microbiota across multiple familial generations.. <i>Nature Microbiology</i> , <b>2021</b> ,	26.6	4
36	Therapeutic Manipulation of the Gut Microbiota Through Diet to Reduce Intestinal Inflammation: Results from the FIT Trial. <i>Gastroenterology</i> , <b>2017</b> , 152, S1	13.3	3
35	Author response: Integrated culturing, modeling and transcriptomics uncovers complex interactions and emergent behavior in a three-species synthetic gut community <b>2018</b> ,		3
34	In vitro ecology: a discovery engine for microbiome therapies. <i>Nature Reviews Gastroenterology and Hepatology</i> , <b>2020</b> , 17, 711-712	24.2	3
33	Microbiology: Crowdsourcing Earth's microbes. <i>Nature</i> , <b>2017</b> ,	50.4	2
32	The gut microbiome - a new target for understanding, diagnosing and treating disease. <i>Archives of Public Health</i> , <b>2014</b> , 72,	2.6	2
31	CNCM I-3690 decreases subjective academic stress in healthy adults: a randomized placebo-controlled trial.. <i>Gut Microbes</i> , <b>2022</b> , 14, 2031695	8.8	2
30	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> , <b>2021</b> , 56, 24-38	1.2	2
29	Successional Stages in Infant Gut Microbiota Maturation		2
28	Unstable regulatory T cells, enriched for naïve and Nrp1 cells, are purged after fate challenge. <i>Science Immunology</i> , <b>2021</b> , 6,	28	2
27	Macroscale patterns of oceanic zooplankton composition and size structure. <i>Scientific Reports</i> , <b>2021</b> , 11, 15714	4.9	2
26	Effect of obesity on gastrointestinal transit, pressure and pH using a wireless motility capsule. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , <b>2021</b> , 167, 1-8	5.7	2
25	Fecal Microbiota Transplantation (FMT) as an Adjunctive Therapy for Depression-Case Report.. <i>Frontiers in Psychiatry</i> , <b>2022</b> , 13, 815422	5	2
24	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> , <b>2022</b> , 119, e2114619119	11.5	2

23	GWAS of stool frequency provides insights into gastrointestinal motility and irritable bowel syndrome.. <i>Cell Genomics</i> , <b>2021</b> , 1, None		2
22	P767 The FIT trial: anti-inflammatory dietary intervention effects on the intestinal microbiota. <i>Journal of Crohn's and Colitis</i> , <b>2017</b> , 11, S473-S473	1.5	1
21	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> , <b>2017</b> , 11, S116-S117	1.5	1
20	P004 Microbiota, not host origin drives ex vivo epithelial response in ulcerative colitis patients and non-IBD controls. <i>Journal of Crohn's and Colitis</i> , <b>2022</b> , 16, i136-i136	1.5	1
19	Disentangling environmental effects in microbial association networks. <i>Microbiome</i> , <b>2021</b> , 9, 232	16.6	1
18	Specific contributions of segmental transit times to gut microbiota composition. <i>Gut</i> , <b>2021</b> ,	19.2	1
17	Microbiome Determinants and Physiological Effects of the Benzoate-Hippurate Microbial-Host Co-Metabolic Pathway		1
16	Dietary emulsifiers alter composition and activity of the human gut microbiota in vitro, irrespective of chemical or natural emulsifier origin		1
15	A framework for comparing microbial networks reveals core associations		1
14	Clinical practices underlie COVID-19 patient respiratory microbiome composition and its interactions with the host		1
13	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> , <b>2021</b> , 114, 1328-1341	7	1
12	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> , <b>2019</b> , 13, S542-S542	1.5	1
11	Interactions between soil compositions and the wheat root microbiome under drought stress: From an to perspective. <i>Computational and Structural Biotechnology Journal</i> , <b>2021</b> , 19, 4235-4247	6.8	1
10	Null-model-based network comparison reveals core associations. <i>ISME Communications</i> , <b>2021</b> , 1,		1
9	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> , <b>2022</b> , 1	5.2	0
8	FLEXiGUT: Rationale for exposomics associations with chronic low-grade gut inflammation. <i>Environment International</i> , <b>2021</b> , 158, 106906	12.9	0
7	OP20 The gut microbiota during biological therapy for inflammatory bowel disease. <i>Journal of Crohn's and Colitis</i> , <b>2020</b> , 14, S016-S018	1.5	
6	An implementation approach for local area networks. <i>Computer Networks</i> , <b>1987</b> , 14, 365-372		

- 5 OP03 Standardized faecal microbiota transplantation with microbiome-guided donor selection in active UC patients: A randomized, placebo-controlled intervention study. *Journal of Crohn's and Colitis*, **2022**, 16, i003-i004 1.5
- 4 P095 Anti-inflammatory effect of high acetate concentration on organoid-derived epithelial monolayer from patients with Ulcerative Colitis. *Journal of Crohn's and Colitis*, **2022**, 16, i192-i195 1.5
- 3 P676 The small intestinal microbiome in Crohn's disease is characterised by increased luminal diversity and stable mucosa-associated communities. *Journal of Crohn's and Colitis*, **2021**, 15, S597-S598 1.5
- 2 P082 Assessment of anti-inflammatory effect of high acetate administration in UC patient-derived epithelial monolayer cultures. *Journal of Crohn's and Colitis*, **2021**, 15, S182-S183 1.5
- 1 Sputum Bacterial Metacomunities in Distinguishing Heterogeneity in Respiratory Health and Disease.. *Frontiers in Microbiology*, **2022**, 13, 719541 5.7