Curtis Huttenhower

List of Publications by Year in Descending Order

247 papers	**57,075** citations
101 h-index	**238** g-index
276 ext. papers	**81,677** ext. citations
15.7 avg, IF	**7.59** L-index

#	Paper	IF	Citations
247	Strain-level fitness in the gut microbiome is an emergent property of glycans and a single metabolite.. *Cell*, **2022**, 185, 513-529.e21	56.2	3
246	Dietary lignans, plasma enterolactone levels, and metabolic risk in men: exploring the role of the gut microbiome.. *BMC Microbiology*, **2022**, 22, 82	4.5	2
245	Human gut bacteria produce ⴈ17-modulating bile´acid metabolites.. *Nature*, **2022**,	50.4	20
244	Association of midlife antibiotic use with subsequent cognitive function in women.. *PLoS ONE*, **2022**, 17, e0264649	3.7	1
243	Strain identification and quantitative analysis in microbial communities.. *Journal of Molecular Biology*, **2022**, 167582	6.5	3
242	Dietary fiber and probiotics influence the gut microbiome and melanoma immunotherapy response.. *Science*, **2021**, 374, 1632-1640	33.3	52
241	Density-based binning of gene clusters to infer function or evolutionary history using GeneGrouper. *Bioinformatics*, **2021**,	7.2	1
240	The Gut Microbiome Modifies the Association between a Mediterranean Diet and Diabetes in US Hispanic / Latino Population. *Journal of Clinical Endocrinology and Metabolism*, **2021**,	5.6	3
239	Association Between the Sulfur Microbial Diet and Risk of Colorectal Cancer. *JAMA Network Open*, **2021**, 4, e2134308	10.4	4
238	Multivariable association discovery in population-scale meta-omics studies. *PLoS Computational Biology*, **2021**, 17, e1009442	5	72
237	Reporting guidelines for human microbiome research: the STORMS checklist. *Nature Medicine*, **2021**, 27, 1885-1892	50.5	19
236	Of mice and men and women: Sexual dimorphism of the gut microbiome.. *International Journal of Womenls Dermatology*, **2021**, 7, 533-538	2	0
235	The oral microbiome in relation to pancreatic cancer risk in African Americans. *British Journal of Cancer*, **2021**,	8.7	2
234	Overview of the Microbiome Among Nurses study (Micro-N) as an example of prospective characterization of the microbiome within cohort studies. *Nature Protocols*, **2021**, 16, 2724-2731	18.8	2
233	A framework for microbiome science in public health. *Nature Medicine*, **2021**, 27, 766-774	50.5	14
232	Interplay between diet and gut microbiome, and circulating concentrations of trimethylamine N-oxide: findings from a longitudinal cohort of US men. *Gut*, **2021**,	19.2	10
231	A polymorphism in the promoter of FRAS1 is a candidate SNP associated with metastatic prostate cancer. *Prostate*, **2021**, 81, 683-693	4.2	1

230	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. *ELife*, **2021**, 10,	8.9	114
229	Dietary fiber intake, the gut microbiome, and chronic systemic inflammation in a cohort of adult men. *Genome Medicine*, **2021**, 13, 102	14.4	10
228	Plant-Based Diet Index and Metabolic Risk in Men: Exploring the Role of the Gut Microbiome. *Journal of Nutrition*, **2021**, 151, 2780-2789	4.1	2
227	Statistical approaches for differential expression analysis in metatranscriptomics. *Bioinformatics*, **2021**, 37, i34-i41	7.2	2
226	Metatranscriptomics for the Human Microbiome and Microbial Community Functional Profiling. *Annual Review of Biomedical Data Science*, **2021**, 4, 279-311	5.6	7
225	The human gut microbiota in people with amyotrophic lateral sclerosis. *Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration*, **2021**, 22, 186-194	3.6	16
224	A Phase 1b Safety Study of SER-287, a Spore-Based Microbiome Therapeutic, for Active Mild to Moderate Ulcerative Colitis. *Gastroenterology*, **2021**, 160, 115-127.e30	13.3	25
223	Microbiome Biomarkers: One Step Closer in NAFLD Cirrhosis. *Hepatology*, **2021**, 73, 2063-2066	11.2	2
222	Identification of Natural CRISPR Systems and Targets in the Human Microbiome. *Cell Host and Microbe*, **2021**, 29, 94-106.e4	23.4	3
221	Whole microbial community viability is not quantitatively reflected by propidium monoazide sequencing approach. *Microbiome*, **2021**, 9, 17	16.6	10
220	Association of with Specific T-cell Subsets in the Colorectal Carcinoma Microenvironment. *Clinical Cancer Research*, **2021**, 27, 2816-2826	12.9	12
219	The gut microbiome modulates the protective association between a Mediterranean diet and cardiometabolic disease risk. *Nature Medicine*, **2021**, 27, 333-343	50.5	63
218	The colorectal cancer-associated faecal microbiome of developing countries resembles that of developed countries. *Genome Medicine*, **2021**, 13, 27	14.4	5
217	Triclosan Tolerance Is Driven by a Conserved Mechanism in Diverse Species. *Applied and Environmental Microbiology*, **2021**, 87,	4.8	3
216	Microbiome Analysis of More Than 2,000 NHS Bowel Cancer Screening Programme Samples Shows the Potential to Improve Screening Accuracy. *Clinical Cancer Research*, **2021**, 27, 2246-2254	12.9	1
215	The Sulfur Microbial Diet Is Associated With Increased Risk of Early-Onset Colorectal Cancer Precursors. *Gastroenterology*, **2021**, 161, 1423-1432.e4	13.3	6
214	The Sulfur Microbial Diet and Risk of Colorectal Cancer by Molecular Subtypes and Intratumoral Microbial Species in Adult Men. *Clinical and Translational Gastroenterology*, **2021**, 12, e00338	4.2	1
213	A statistical model for describing and simulating microbial community profiles. *PLoS Computational Biology*, **2021**, 17, e1008913	5	5

212 A bacterial bile acid metabolite modulates T activity through the nuclear hormone receptor NR4A1. *Cell Host and Microbe*, **2021**, 29, 1366-1377.e9 — 23.4 — 22

211 Microbiome connections with host metabolism and habitual diet from 1,098 deeply phenotyped individuals. *Nature Medicine*, **2021**, 27, 321-332 — 50.5 — 124

210 Determinants of Staphylococcus aureus carriage in the developing infant nasal microbiome. *Genome Biology*, **2020**, 21, 301 — 18.3 — 4

209 Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. *Nature Communications*, **2020**, 11, 2500 — 17.4 — 99

208 PICRUSt2 for prediction of metagenome functions. *Nature Biotechnology*, **2020**, 38, 685-688 — 44.5 — 696

207 The Gut Microbiome Modifies the Protective Effects of a Mediterranean Diet Against Cardiometabolic Disease Risk. *Current Developments in Nutrition*, **2020**, 4, 1597-1597 — 0.4 — 1

206 Analysis of 1321 Eubacterium rectale genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. *Genome Biology*, **2020**, 21, 138 — 18.3 — 27

205 Global chemical effects of the microbiome include new bile-acid conjugations. *Nature*, **2020**, 579, 123-129 — 50.4 — 129

204 Mobilizable antibiotic resistance genes are present in dust microbial communities. *PLoS Pathogens*, **2020**, 16, e1008211 — 7.6 — 16

203 Growth effects of N-acylethanolamines on gut bacteria reflect altered bacterial abundances in inflammatory bowel disease. *Nature Microbiology*, **2020**, 5, 486-497 — 26.6 — 25

202 Association Between Sulfur-Metabolizing Bacterial Communities in Stool and Risk of Distal Colorectal Cancer in Men. *Gastroenterology*, **2020**, 158, 1313-1325 — 13.3 — 50

201 Structure of the Mucosal and Stool Microbiome in Lynch Syndrome. *Cell Host and Microbe*, **2020**, 27, 585-600.e4 — 21.4 — 20

200 Delivery Mode Affects Stability of Early Infant Gut Microbiota. *Cell Reports Medicine*, **2020**, 1, 100156 — 18 — 32

199 Association of autophagy status with amount of Fusobacterium nucleatum in colorectal cancer. *Journal of Pathology*, **2020**, 250, 397-408 — 9.4 — 16

198 Strain-level epidemiology of microbial communities and the human microbiome. *Genome Medicine*, **2020**, 12, 71 — 14.4 — 25

197 The interleukin-33 receptor contributes to pulmonary responses to ozone in male mice: role of the microbiome. *Respiratory Research*, **2019**, 20, 197 — 7.3 — 11

196 OP19 Corticosteroid response rectal gene signature and associated microbial variation in treatment naïve ulcerative colitis. *Journal of Crohnls and Colitis*, **2019**, 13, S013-S014 — 1.5

195 Comparative genomics and genome biology of. *Emerging Microbes and Infections*, **2019**, 8, 827-840 — 18.9 — 4

194	Naturally acquired immunity against immature gametocytes. *Science Translational Medicine*, **2019**, 11,	17.5	24
193	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. *Nature*, **2019**, 569, 655-662	50.4	761
192	Bacteroides-Derived Sphingolipids Are Critical for Maintaining Intestinal Homeostasis and Symbiosis. *Cell Host and Microbe*, **2019**, 25, 668-680.e7	23.4	112
191	Establishing What Constitutes a Healthy Human Gut Microbiome: State of the Science, Regulatory Considerations, and Future Directions. *Journal of Nutrition*, **2019**, 149, 1882-1895	4.1	91
190	Obese Individuals with and without Type 2 Diabetes Show Different Gut Microbial Functional Capacity and Composition. *Cell Host and Microbe*, **2019**, 26, 252-264.e10	23.4	120
189	Predictive metabolomic profiling of microbial communities using amplicon or metagenomic sequences. *Nature Communications*, **2019**, 10, 3136	17.4	89
188	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, **2019**, 37, 852-857	44.5	4050
187	The Prevotella copri Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. *Cell Host and Microbe*, **2019**, 26, 666-679.e7	23.4	141
186	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. *Nature Communications*, **2019**, 10, 5477	17.4	89
185	Genomic variation and strain-specific functional adaptation in the human gut microbiome during early life. *Nature Microbiology*, **2019**, 4, 470-479	26.6	97
184	Ulcerative colitis mucosal transcriptomes reveal mitochondriopathy and personalized mechanisms underlying disease severity and treatment response. *Nature Communications*, **2019**, 10, 38	17.4	98
183	Low Tristetraprolin Expression Is Associated with Lethal Prostate Cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2019**, 28, 584-590	4	4
182	Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. *Cell*, **2019**, 176, 649-662.e20	56.2	588
181	HMP16SData: Efficient Access to the Human Microbiome Project Through Bioconductor. *American Journal of Epidemiology*, **2019**, 188, 1023-1026	3.8	21
180	Gut microbiome structure and metabolic activity in inflammatory bowel disease. *Nature Microbiology*, **2019**, 4, 293-305	26.6	512
179	Sex Differences in Pulmonary Responses to Ozone in Mice. Role of the Microbiome. *American Journal of Respiratory Cell and Molecular Biology*, **2019**, 60, 198-208	5.7	28
178	A screen of Crohn's disease-associated microbial metabolites identifies ascorbate as a novel metabolic inhibitor of activated human T cells. *Mucosal Immunology*, **2019**, 12, 457-467	9.2	31
177	Long-term use of antibiotics and risk of colorectal adenoma. *Gut*, **2018**, 67, 672-678	19.2	93

176	bioBakery: a metaSomic analysis environment. *Bioinformatics*, **2018**, 34, 1235-1237	7.2	108
175	Enterotypes in the landscape of gut microbial community composition. *Nature Microbiology*, **2018**, 3, 8-16	26.6	387
174	Metatranscriptome of human faecal microbial communities in a cohort of adult men. *Nature Microbiology*, **2018**, 3, 356-366	26.6	103
173	Stability of the human faecal microbiome in a cohort of adult men. *Nature Microbiology*, **2018**, 3, 347-355	26.6	104
172	Dynamics of metatranscription in the inflammatory bowel disease gut microbiome. *Nature Microbiology*, **2018**, 3, 337-346	26.6	249
171	Interplay of host genetics and gut microbiota underlying the onset and clinical presentation of inflammatory bowel disease. *Gut*, **2018**, 67, 108-119	19.2	368
170	The Role of Gut Microbiome in the Pathogenesis of Prostate Cancer: A Prospective, Pilot Study. *Urology*, **2018**, 111, 122-128	1.6	81
169	Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome. *Cell Host and Microbe*, **2018**, 24, 133-145.e5	23.4	435
168	Strain-Level Analysis of Mother-to-Child Bacterial Transmission during the First Few Months of Life. *Cell Host and Microbe*, **2018**, 24, 146-154.e4	23.4	189
167	Host genetic variation and its microbiome interactions within the Human Microbiome Project. *Genome Medicine*, **2018**, 10, 6	14.4	86
166	Bone Marrow Is a Major Parasite Reservoir in Plasmodium vivax Infection. *MBio*, **2018**, 9,	7.8	93
165	Bifidobacterium Genus in Colorectal Carcinoma Tissue in relation to Tumor Characteristics and Patient Survival. *FASEB Journal*, **2018**, 32, 407.3	0.9	
164	Antimicrobial Chemicals Associate with Microbial Function and Antibiotic Resistance Indoors. *MSystems*, **2018**, 3,	7.6	46
163	Continuity of transcriptomes among colorectal cancer subtypes based on meta-analysis. *Genome Biology*, **2018**, 19, 142	18.3	12
162	The Amount of Bifidobacterium Genus in Colorectal Carcinoma Tissue in Relation to Tumor Characteristics and Clinical Outcome. *American Journal of Pathology*, **2018**, 188, 2839-2852	5.8	31
161	Compositional and Temporal Changes in the Gut Microbiome of Pediatric Ulcerative Colitis Patients Are Linked to Disease Course. *Cell Host and Microbe*, **2018**, 24, 600-610.e4	23.4	93
160	Temporal development of the gut microbiome in early childhood from the TEDDY study. *Nature*, **2018**, 562, 583-588	50.4	619
159	The human gut microbiome in early-onset type 1 diabetes from the TEDDY study. *Nature*, **2018**, 562, 589-594	50.4	323

158	Daylight exposure modulates bacterial communities associated with household dust. *Microbiome*, **2018**, 6, 175	16.6	40
157	Species-level functional profiling of metagenomes and metatranscriptomes. *Nature Methods*, **2018**, 15, 962-968	21.6	608
156	Multiomics Analyses to Deliver the Most Effective Treatment to Every Patient With Inflammatory Bowel Disease. *Gastroenterology*, **2018**, 155, e1-e4	13.3	18
155	in Colorectal Cancer Relates to Immune Response Differentially by Tumor Microsatellite Instability Status. *Cancer Immunology Research*, **2018**, 6, 1327-1336	12.5	78
154	American Gut: an Open Platform for Citizen Science Microbiome Research. *MSystems*, **2018**, 3,	7.6	336
153	gametocytes display homing and vascular transmigration in the host bone marrow. *Science Advances*, **2018**, 4, eaat3775	14.3	41
152	Lactobacillus-Deficient Cervicovaginal Bacterial Communities Are Associated with Increased HIV Acquisition in Young South African Women. *Immunity*, **2017**, 46, 29-37	32.3	320
151	Prediction of complicated disease course for children newly diagnosed with Crohn's disease: a multicentre inception cohort study. *Lancet, The*, **2017**, 389, 1710-1718	40	315
150	Microbial strain-level population structure and genetic diversity from metagenomes. *Genome Research*, **2017**, 27, 626-638	9.7	337
149	A prominent glycyl radical enzyme in human gut microbiomes metabolizes -4-hydroxy-l-proline. *Science*, **2017**, 355,	33.3	85
148	ASPirin Intervention for the REDuction of colorectal cancer risk (ASPIRED): a study protocol for a randomized controlled trial. *Trials*, **2017**, 18, 50	2.8	30
147	QseC inhibition as an antivirulence approach for colitis-associated bacteria. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 142-147	11.5	36
146	Accessible, curated metagenomic data through ExperimentHub. *Nature Methods*, **2017**, 14, 1023-1024	21.6	136
145	Assessment of variation in microbial community amplicon sequencing by the Microbiome Quality Control (MBQC) project consortium. *Nature Biotechnology*, **2017**, 35, 1077-1086	44.5	240
144	Experimental design and quantitative analysis of microbial community multiomics. *Genome Biology*, **2017**, 18, 228	18.3	87
143	A novel Ruminococcus gnavus clade enriched in inflammatory bowel disease patients. *Genome Medicine*, **2017**, 9, 103	14.4	254
142	Schrödinger's microbes: Tools for distinguishing the living from the dead in microbial ecosystems. *Microbiome*, **2017**, 5, 86	16.6	214
141	Strains, functions and dynamics in the expanded Human Microbiome Project. *Nature*, **2017**, 550, 61-66	50.4	595

140	Potential role of intratumor bacteria in mediating tumor resistance to the chemotherapeutic drug gemcitabine. *Science*, **2017**, 357, 1156-1160	33.3	577
139	Fluoride Depletes Acidogenic Taxa in Oral but Not Gut Microbial Communities in Mice. *MSystems*, **2017**, 2,	7.6	11
138	Indoleacrylic Acid Produced by Commensal Peptostreptococcus Species Suppresses Inflammation. *Cell Host and Microbe*, **2017**, 22, 25-37.e6	23.4	287
137	Alterations in oral bacterial communities are associated with risk factors for oral and oropharyngeal cancer. *Scientific Reports*, **2017**, 7, 17686	4.9	63
136	Association of Dietary Patterns With Risk of Colorectal Cancer Subtypes Classified by Fusobacterium nucleatum in Tumor Tissue. *JAMA Oncology*, **2017**, 3, 921-927	13.4	177
135	A Bayesian method for detecting pairwise associations in compositional data. *PLoS Computational Biology*, **2017**, 13, e1005852	5	21
134	Fusobacterium nucleatum in colorectal carcinoma tissue and patient prognosis. *Gut*, **2016**, 65, 1973-1980	19.2	454
133	Uncovering oral Neisseria tropism and persistence using metagenomic sequencing. *Nature Microbiology*, **2016**, 1, 16070	26.6	46
132	Natural history of the infant gut microbiome and impact of antibiotic treatment on bacterial strain diversity and stability. *Science Translational Medicine*, **2016**, 8, 343ra81	17.5	514
131	Fusobacterium nucleatum in Colorectal Carcinoma Tissue According to Tumor Location. *Clinical and Translational Gastroenterology*, **2016**, 7, e200	4.2	156
130	Infected erythrocyte-derived extracellular vesicles alter vascular function via regulatory Ago2-miRNA complexes in malaria. *Nature Communications*, **2016**, 7, 12727	17.4	130
129	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. *Cell*, **2016**, 167, 1125-1136.e8	56.9	457
128	Sub-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes. *Genome Medicine*, **2016**, 8, 17	14.4	127
127	Intestinal microbiome analyses identify melanoma patients at risk for checkpoint-blockade-induced colitis. *Nature Communications*, **2016**, 7, 10391	17.4	524
126	Fecal Microbiome in Epidemiologic Studies-Letter. *Cancer Epidemiology Biomarkers and Prevention*, **2016**, 25, 869	4	3
125	Computational Reconstruction of NFB Pathway Interaction Mechanisms during Prostate Cancer. *PLoS Computational Biology*, **2016**, 12, e1004820	5	17
124	Paneth cell defects in Crohns disease patients promote dysbiosis. *JCI Insight*, **2016**, 1, e86907	9.9	54
123	A conserved bacterial protein induces pancreatic beta cell expansion during zebrafish development. *ELife*, **2016**, 5,	8.9	64

122	PWE-102 Elucidating The Role of Non JEJUNI/Coli-Campylobacter in The Development of Colorectal Cancer Utilising Comparative Genomics to Study Their Pathogenic Potential. *Gut*, **2016**, 65, A188.2-A189	19.2	
121	Urban Transit System Microbial Communities Differ by Surface Type and Interaction with Humans and the Environment. *MSystems*, **2016**, 1,	7.6	73
120	The Chthonomonas calidirosea Genome Is Highly Conserved across Geographic Locations and Distinct Chemical and Microbial Environments in New Zealand's Taupō Volcanic Zone. *Applied and Environmental Microbiology*, **2016**, 82, 3572-81	4.8	5
119	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. *Cell*, **2016**, 165, 842-53	56.2	584
118	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. *Science*, **2016**, 352, 565-9	33.3	929
117	The healthy human microbiome. *Genome Medicine*, **2016**, 8, 51	14.4	789
116	Antimicrobial Chemicals Are Associated with Elevated Antibiotic Resistance Genes in the Indoor Dust Microbiome. *Environmental Science & Technology*, **2016**, 50, 9807-15	10.3	93
115	CellMapper: rapid and accurate inference of gene expression in difficult-to-isolate cell types. *Genome Biology*, **2016**, 17, 201	18.3	13
114	Transcriptional profiling defines dynamics of parasite tissue sequestration during malaria infection. *Genome Medicine*, **2015**, 7, 19	14.4	63
113	Biogeography of the intestinal mucosal and lumenal microbiome in the rhesus macaque. *Cell Host and Microbe*, **2015**, 17, 385-391	23.4	185
112	Sequencing and beyond: integrating molecular 'omics' for microbial community profiling. *Nature Reviews Microbiology*, **2015**, 13, 360-72	22.2	394
111	Identifying personal microbiomes using metagenomic codes. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, E2930-8	11.5	270
110	Associations between host gene expression, the mucosal microbiome, and clinical outcome in the pelvic pouch of patients with inflammatory bowel disease. *Genome Biology*, **2015**, 16, 67	18.3	119
109	MetaPhlAn2 for enhanced metagenomic taxonomic profiling. *Nature Methods*, **2015**, 12, 902-3	21.6	1107
108	Complete genome sequence of the thermophilic Acidobacteria, Pyrinomonas methylaliphatogenes type strain K22(T). *Standards in Genomic Sciences*, **2015**, 10, 101		13
107	Cross-biome comparison of microbial association networks. *Frontiers in Microbiology*, **2015**, 6, 1200	5.7	102
106	Cervicovaginal bacteria are a major modulator of host inflammatory responses in the female genital tract. *Immunity*, **2015**, 42, 965-76	32.3	343
105	Fusobacterium nucleatum and T Cells in Colorectal Carcinoma. *JAMA Oncology*, **2015**, 1, 653-61	13.4	336

104	The microbiome quality control project: baseline study design and future directions. *Genome Biology*, **2015**, 16, 276	18.3	140
103	The dynamics of the human infant gut microbiome in development and in progression toward type 1 diabetes. *Cell Host and Microbe*, **2015**, 17, 260-73	23.4	639
102	Genomic Sequencing and Other Tools for Studying Microbial Communities. *Microbe Magazine*, **2015**, 10, 419-425		3
101	High-Specificity Targeted Functional Profiling in Microbial Communities with ShortBRED. *PLoS Computational Biology*, **2015**, 11, e1004557	5	146
100	Compact graphical representation of phylogenetic data and metadata with GraPhlAn. *PeerJ*, **2015**, 3, e1029	3.1	415
99	A reproducible approach to high-throughput biological data acquisition and integration. *PeerJ*, **2015**, 3, e791	3.1	11
98	Gene-targeted metagenomic analysis of glucan-branching enzyme gene profiles among human and animal fecal microbiota. *ISME Journal*, **2014**, 8, 493-503	11.9	23
97	Functional and phylogenetic assembly of microbial communities in the human microbiome. *Trends in Microbiology*, **2014**, 22, 261-6	12.4	129
96	Metaʼomic analytic techniques for studying the intestinal microbiome. *Gastroenterology*, **2014**, 146, 1437-1448.e16	13.3	
95	The treatment-naive microbiome in new-onset Crohnʼs disease. *Cell Host and Microbe*, **2014**, 15, 382-392	23.4	1836
94	Relating the metatranscriptome and metagenome of the human gut. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, E2329-38	11.5	410
93	Comparative meta-analysis of prognostic gene signatures for late-stage ovarian cancer. *Journal of the National Cancer Institute*, **2014**, 106,	9.7	77
92	Determining microbial products and identifying molecular targets in the human microbiome. *Cell Metabolism*, **2014**, 20, 731-741	24.6	68
91	Gut microbiome composition and function in experimental colitis during active disease and treatment-induced remission. *ISME Journal*, **2014**, 8, 1403-17	11.9	275
90	Inflammatory bowel disease as a model for translating the microbiome. *Immunity*, **2014**, 40, 843-54	32.3	237
89	Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. *Microbiome*, **2014**, 2,	16.6	18
88	Advancing the microbiome research community. *Cell*, **2014**, 159, 227-30	56.2	50
87	MetaRef: a pan-genomic database for comparative and community microbial genomics. *Nucleic Acids Research*, **2014**, 42, D617-24	20.1	46

86	Complex host genetics influence the microbiome in inflammatory bowel disease. *Genome Medicine*, **2014**, 6, 107	14.4	253
85	Reprograming of gut microbiome energy metabolism by the FUT2 Crohns disease risk polymorphism. *ISME Journal*, **2014**, 8, 2193-206	11.9	140
84	Cross-study validation for the assessment of prediction algorithms. *Bioinformatics*, **2014**, 30, i105-12	7.2	44
83	MS-o-menos: a simple sign averaging method for discrimination in genomic data analysis. *Bioinformatics*, **2014**, 30, 3062-9	7.2	29
82	Skin microbiome imbalance in patients with STAT1/STAT3 defects impairs innate host defense responses. *Journal of Innate Immunity*, **2014**, 6, 253-62	6.9	67
81	Risk prediction for late-stage ovarian cancer by meta-analysis of 1525 patient samples. *Journal of the National Cancer Institute*, **2014**, 106,	9.7	123
80	Pediatric Crohn disease patients exhibit specific ileal transcriptome and microbiome signature. *Journal of Clinical Investigation*, **2014**, 124, 3617-33	15.9	320
79	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. *Nature Biotechnology*, **2013**, 31, 814-21	44.5	5270
78	PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. *Nature Communications*, **2013**, 4, 2304	17.4	511
77	Functional profiling of the gut microbiome in disease-associated inflammation. *Genome Medicine*, **2013**, 5, 65	14.4	39
76	Two-stage microbial community experimental design. *ISME Journal*, **2013**, 7, 2330-9	11.9	16
75	Integrative analysis of the microbiome and metabolome of the human intestinal mucosal surface reveals exquisite inter-relationships. *Microbiome*, **2013**, 1, 17	16.6	175
74	Early microbial and metabolomic signatures predict later onset of necrotizing enterocolitis in preterm infants. *Microbiome*, **2013**, 1, 13	16.6	213
73	Tryptophan biosynthesis protects mycobacteria from CD4 T-cell-mediated killing. *Cell*, **2013**, 155, 1296-308	38.2	222
72	Sixty years of genome biology. *Genome Biology*, **2013**, 14, 113	18.3	4
71	Biodiversity and functional genomics in the human microbiome. *Trends in Genetics*, **2013**, 29, 51-8	8.5	167
70	Translating the human microbiome. *Nature Biotechnology*, **2013**, 31, 304-8	44.5	25
69	Computational metaSomics for microbial community studies. *Molecular Systems Biology*, **2013**, 9, 666	12.2	216

68	A guide to enterotypes across the human body: meta-analysis of microbial community structures in human microbiome datasets. *PLoS Computational Biology*, **2013**, 9, e1002863	5	359
67	Simultaneous quantification of multiple bacteria by the BactoChip microarray designed to target species-specific marker genes. *PLoS ONE*, **2013**, 8, e55764	3.7	14
66	Inferring developmental stage composition from gene expression in human malaria. *PLoS Computational Biology*, **2013**, 9, e1003392	5	40
65	curatedOvarianData: clinically annotated data for the ovarian cancer transcriptome. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013, bat013	5	123
64	Expansion of intestinal Prevotella copri correlates with enhanced susceptibility to arthritis. *ELife*, **2013**, 2, e01202	8.9	1092
63	Passing messages between biological networks to refine predicted interactions. *PLoS ONE*, **2013**, 8, e64832	3.7	108
62	Author response: Expansion of intestinal Prevotella copri correlates with enhanced susceptibility to arthritis **2013**,		8
61	Early intestinal colonization phenotypes predict necrotizing enterocolitis in preterm infants. *FASEB Journal*, **2013**, 27, 357.1	0.9	
60	Expression profiling of archival tumors for long-term health studies. *Clinical Cancer Research*, **2012**, 18, 6136-46	12.9	25
59	Composition of the adult digestive tract bacterial microbiome based on seven mouth surfaces, tonsils, throat and stool samples. *Genome Biology*, **2012**, 13, R42	18.3	572
58	Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. *Genome Biology*, **2012**, 13, R79	18.3	1668
57	Assessment of colorectal cancer molecular features along bowel subsites challenges the conception of distinct dichotomy of proximal versus distal colorectum. *Gut*, **2012**, 61, 847-54	19.2	429
56	The Human Microbiome Project: a community resource for the healthy human microbiome. *PLoS Biology*, **2012**, 10, e1001377	9.7	268
55	Metagenomic microbial community profiling using unique clade-specific marker genes. *Nature Methods*, **2012**, 9, 811-4	21.6	1120
54	Colorectal cancer: a tale of two sides or a continuum?. *Gut*, **2012**, 61, 794-7	19.2	192
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List of Publications

14   BAYESIAN DATA INTEGRATION: A FUNCTIONAL PERSPECTIVE **2006,**   9

13   Bayesian data integration: a functional perspective. *Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference*, **2006**, 341-51   6

12   QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science   36

11   Accessible, curated metagenomic data through ExperimentHub   3

10   Gut microbes and their genes are associated with brain development and cognitive function in healthy children   1

9   Population Structure Discovery in Meta-Analyzed Microbial Communities and Inflammatory Bowel Disease   3

8   Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3   22

7   HMP16SData: Efficient Access to the Human Microbiome Project through Bioconductor   1

6   The Prevotella copri complex comprises four distinct clades that are underrepresented in Westernised populations   6

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4   Density-based binning of gene clusters to infer function or evolutionary history using GeneGrouper   1

3   Human gut bacteria produce TH17-modulating bile acid metabolites   3

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