

# Falk Hildebrand

## List of Publications by Year in Descending Order

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**Version:** 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

64 papers	11,284 citations	32 h-index	77 g-index
77 ext. papers	15,301 ext. citations	13.6 avg, IF	5.74 L-index

#	Paper	IF	Citations
64	Enrichment of gut microbiome strains for cultivation-free genome sequencing using droplet microfluidics.. <i>Cell Reports Methods</i> , <b>2022</b> , 2, None		2
63	Benchmark of Data Processing Methods and Machine Learning Models for Gut Microbiome-Based Diagnosis of Inflammatory Bowel Disease.. <i>Frontiers in Genetics</i> , <b>2022</b> , 13, 784397	4.5	3
62	Structure and function of the soil microbiome underlying NO emissions from global wetlands.. <i>Nature Communications</i> , <b>2022</b> , 13, 1430	17.4	0
61	Towards the biogeography of prokaryotic genes.. <i>Nature</i> , <b>2021</b> ,	50.4	8
60	Much ado about nothing? Off-target amplification can lead to false-positive bacterial brain microbiome detection in healthy and Parkinson's disease individuals. <i>Microbiome</i> , <b>2021</b> , 9, 75	16.6	6
59	Systematic analysis of gut microbiome reveals the role of bacterial folate and homocysteine metabolism in Parkinson's disease. <i>Cell Reports</i> , <b>2021</b> , 34, 108807	10.6	13
58	Meta-analysis of the Parkinson's disease gut microbiome suggests alterations linked to intestinal inflammation. <i>Npj Parkinsons Disease</i> , <b>2021</b> , 7, 27	9.7	97
57	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , <b>2021</b> , 9, e10941	3.1	21
56	Metagenomic assessment of the global diversity and distribution of bacteria and fungi. <i>Environmental Microbiology</i> , <b>2021</b> , 23, 316-326	5.2	9
55	Dispersal strategies shape persistence and evolution of human gut bacteria. <i>Cell Host and Microbe</i> , <b>2021</b> , 29, 1167-1176.e9	23.4	15
54	Ultra-resolution Metagenomics: When Enough Is Not Enough. <i>MSystems</i> , <b>2021</b> , e0088121	7.6	2
53	Intestinal Microbiome-Macrophage Crosstalk Contributes to Cholestatic Liver Disease by Promoting Intestinal Permeability in Mice. <i>Hepatology</i> , <b>2020</b> , 72, 2090-2108	11.2	27
52	From bag-of-genes to bag-of-genomes: metabolic modelling of communities in the era of metagenome-assembled genomes. <i>Computational and Structural Biotechnology Journal</i> , <b>2020</b> , 18, 1722-1734	6.8	22
51	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , <b>2020</b> , 14, 1247-1259	11.9	23
50	Plant nutrient-acquisition strategies drive topsoil microbiome structure and function. <i>New Phytologist</i> , <b>2020</b> , 227, 1189-1199	9.8	33
49	Metage2Metabo, microbiota-scale metabolic complementarity for the identification of key species. <i>ELife</i> , <b>2020</b> , 9,	8.9	10
48	Towards standardisation of naming novel prokaryotic taxa in the age of high-throughput microbiology. <i>Gut</i> , <b>2020</b> , 69, 1358-1359	19.2	2

47	Antibiotics-induced monodominance of a novel gut bacterial order. <i>Gut</i> , <b>2019</b> , 68, 1781-1790	19.2	33
46	Ice-Age Climate Adaptations Trap the Alpine Marmot in a State of Low Genetic Diversity. <i>Current Biology</i> , <b>2019</b> , 29, 1712-1720.e7	6.3	14
45	Newly designed 16S rRNA metabarcoding primers amplify diverse and novel archaeal taxa from the environment. <i>Environmental Microbiology Reports</i> , <b>2019</b> , 11, 487-494	3.7	44
44	Plasmid DNA contaminant in molecular reagents. <i>Scientific Reports</i> , <b>2019</b> , 9, 1652	4.9	9
43	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
42	Host genetic variation strongly influences the microbiome structure and function in fungal fruiting-bodies. <i>Environmental Microbiology</i> , <b>2018</b> , 20, 1641-1650	5.2	12
41	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , <b>2018</b> , 3, 8-16	26.6	387
40	Toxic Cyanobacteria in Svalbard: Chemical Diversity of Microcystins Detected Using a Liquid Chromatography Mass Spectrometry Precursor Ion Screening Method. <i>Toxins</i> , <b>2018</b> , 10,	4.9	16
39	Structure and function of the global topsoil microbiome. <i>Nature</i> , <b>2018</b> , 560, 233-237	50.4	654
38	Gut microbiota composition is associated with environmental landscape in honey bees. <i>Ecology and Evolution</i> , <b>2018</b> , 8, 441-451	2.8	59
37	A computational framework to integrate high-throughput 'omics' datasets for the identification of potential mechanistic links. <i>Nature Protocols</i> , <b>2018</b> , 13, 2781-2800	18.8	44
36	The gut microbiome is associated with behavioural task in honey bees. <i>Insectes Sociaux</i> , <b>2018</b> , 65, 419-429.5	4.5	44
35	RTK: efficient rarefaction analysis of large datasets. <i>Bioinformatics</i> , <b>2017</b> , 33, 2594-2595	7.2	43
34	Functional implications of microbial and viral gut metagenome changes in early stage L-DOPA-naïve Parkinson's disease patients. <i>Genome Medicine</i> , <b>2017</b> , 9, 39	14.4	274
33	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , <b>2017</b> , 13, 960	12.2	69
32	Pole-to-Pole Connections: Similarities between Arctic and Antarctic Microbiomes and Their Vulnerability to Environmental Change. <i>Frontiers in Ecology and Evolution</i> , <b>2017</b> , 5,	3.7	27
31	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , <b>2016</b> , 535, 376-81	50.4	977
30	Species-function relationships shape ecological properties of the human gut microbiome. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16088	26.6	145

29	Gut Microbiota Linked to Sexual Preference and HIV Infection. <i>EBioMedicine</i> , <b>2016</b> , 5, 135-46	8.8	230
28	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , <b>2016</b> , 352, 586-9	33.3	326
27	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
26	Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi. <i>MycoKeys</i> , <b>2015</b> , 10, 1-43	2.4	275
25	FUNGAL BIOGEOGRAPHY. Response to Comment on "Global diversity and geography of soil fungi". <i>Science</i> , <b>2015</b> , 349, 936	33.3	28
24	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
23	Ocean plankton. Structure and function of the global ocean microbiome. <i>Science</i> , <b>2015</b> , 348, 1261359	33.3	1261
22	Genome Sequence of Muroid <i>Pseudomonas aeruginosa</i> Strain FRD1. <i>Genome Announcements</i> , <b>2015</b> , 3,		3
21	The deletion of TonB-dependent receptor genes is part of the genome reduction process that occurs during adaptation of <i>Pseudomonas aeruginosa</i> to the cystic fibrosis lung. <i>Pathogens and Disease</i> , <b>2014</b> , 71, 26-38	4.2	25
20	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
19	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
18	Correction: LotuS: an efficient and user-friendly OTU processing pipeline. <i>Microbiome</i> , <b>2014</b> , 2, 37	16.6	6
17	Diversity of toxin and non-toxin containing cyanobacterial mats of meltwater ponds on the Antarctic Peninsula: a pyrosequencing approach. <i>Antarctic Science</i> , <b>2014</b> , 26, 521-532	1.7	52
16	LotuS: an efficient and user-friendly OTU processing pipeline. <i>Microbiome</i> , <b>2014</b> , 2, 30	16.6	186
15	The skin microbiome of caspase-14-deficient mice shows mild dysbiosis. <i>Experimental Dermatology</i> , <b>2014</b> , 23, 561-7	4	11
14	Draft genome sequence analysis of a <i>Pseudomonas putida</i> W15Oct28 strain with antagonistic activity to Gram-positive and <i>Pseudomonas</i> sp. pathogens. <i>PLoS ONE</i> , <b>2014</b> , 9, e110038	3.7	18
13	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
12	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

11	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , <b>2013</b> , 500, 541-6	50.4	2584
10	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
9	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
8	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
7	Global regulation of gene expression by OxyR in an important human opportunistic pathogen. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 4320-33	20.1	135
6	Unresolved orthology and peculiar coding sequence properties of lamprey genes: the KCNA gene family as test case. <i>BMC Genomics</i> , <b>2011</b> , 12, 325	4.5	52
5	Caspase deficiency alters the murine gut microbiome. <i>Cell Death and Disease</i> , <b>2011</b> , 2, e220	9.8	54
4	Evidence of selection upon genomic GC-content in bacteria. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001107	6	261
3	Origin, spread and demography of the Mycobacterium tuberculosis complex. <i>PLoS Pathogens</i> , <b>2008</b> , 4, e1000160	7.6	320
2	Meta-analysis of the gut microbiome of Parkinson's disease patients suggests alterations linked to intestinal inflammation		3
1	Enrichment of Gut Microbiome Strains for Cultivation-Free Genome Sequencing Using Droplet Microfluidics. <i>SSRN Electronic Journal</i> ,	1	1