

# Falk Hildebrand

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/2432117/falk-hildebrand-publications-by-citations.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , <b>2013</b> , 500, 541-6	50.4	2584
63	Ocean plankton. Structure and function of the global ocean microbiome. <i>Science</i> , <b>2015</b> , 348, 1261-1359	33.3	1261
62	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
61	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , <b>2016</b> , 535, 376-81	50.4	977
60	Structure and function of the global topsoil microbiome. <i>Nature</i> , <b>2018</b> , 560, 233-237	50.4	654
59	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
58	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , <b>2018</b> , 3, 8-16	26.6	387
57	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , <b>2016</b> , 352, 586-9	33.3	326
56	Origin, spread and demography of the <i>Mycobacterium tuberculosis</i> complex. <i>PLoS Pathogens</i> , <b>2008</b> , 4, e1000160	7.6	320
55	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
54	Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi. <i>Mycology</i> , <b>2015</b> , 10, 1-43	2.4	275
53	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
52	Evidence of selection upon genomic GC-content in bacteria. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001107	6	261
51	Gut Microbiota Linked to Sexual Preference and HIV Infection. <i>EBioMedicine</i> , <b>2016</b> , 5, 135-46	8.8	230
50	LotuS: an efficient and user-friendly OTU processing pipeline. <i>Microbiome</i> , <b>2014</b> , 2, 30	16.6	186
49	Species-function relationships shape ecological properties of the human gut microbiome. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16088	26.6	145
48	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

47	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
46	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
45	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , <b>2017</b> , 13, 960	12.2	69
44	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
43	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
42	Caspase deficiency alters the murine gut microbiome. <i>Cell Death and Disease</i> , <b>2011</b> , 2, e220	9.8	54
41	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
40	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
39	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
38	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
37	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
36	RTK: efficient rarefaction analysis of large datasets. <i>Bioinformatics</i> , <b>2017</b> , 33, 2594-2595	7.2	43
35	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
34	Antibiotics-induced monodominance of a novel gut bacterial order. <i>Gut</i> , <b>2019</b> , 68, 1781-1790	19.2	33
33	Plant nutrient-acquisition strategies drive topsoil microbiome structure and function. <i>New Phytologist</i> , <b>2020</b> , 227, 1189-1199	9.8	33
32	FUNGAL BIOGEOGRAPHY. Response to Comment on "Global diversity and geography of soil fungi". <i>Science</i> , <b>2015</b> , 349, 936	33.3	28
31	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
30	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

29	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
28	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
27	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
26	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , <b>2021</b> , 9, e10941	3.1	21
25	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
24	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
23	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
22	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
21	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
20	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
19	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
18	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
17	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
16	The skin microbiome of caspase-14-deficient mice shows mild dysbiosis. <i>Experimental Dermatology</i> , <b>2014</b> , 23, 561-7	4	11
15	Metage2Metabo, microbiota-scale metabolic complementarity for the identification of key species. <i>ELife</i> , <b>2020</b> , 9,	8.9	10
14	Plasmid DNA contaminant in molecular reagents. <i>Scientific Reports</i> , <b>2019</b> , 9, 1652	4.9	9
13	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
12	Towards the biogeography of prokaryotic genes.. <i>Nature</i> , <b>2021</b> ,	50.4	8

11	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
10	Correction: LotuS: an efficient and user-friendly OTU processing pipeline. <i>Microbiome</i> , <b>2014</b> , 2, 37	16.6	6
9	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
8	Genome Sequence of Muroid <i>Pseudomonas aeruginosa</i> Strain FRD1. <i>Genome Announcements</i> , <b>2015</b> , 3,		3
7	Meta-analysis of the gut microbiome of Parkinson's disease patients suggests alterations linked to intestinal inflammation		3
6	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
5	Enrichment of gut microbiome strains for cultivation-free genome sequencing using droplet microfluidics.. <i>Cell Reports Methods</i> , <b>2022</b> , 2, None		2
4	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
3	Ultra-resolution Metagenomics: When Enough Is Not Enough. <i>MSystems</i> , <b>2021</b> , e0088121	7.6	2
2	Enrichment of Gut Microbiome Strains for&nbsp;Cultivation-Free Genome Sequencing&nbsp;Using Droplet Microfluidics. <i>SSRN Electronic Journal</i> ,	1	1
1	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