

Falk Hildebrand

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

18,095
citations

76196

40
h-index

91712

69
g-index

77
all docs

77
docs citations

77
times ranked

26651
citing authors

#	ARTICLE	IF	CITATIONS
1	Enrichment of gut microbiome strains for cultivation-free genome sequencing using droplet microfluidics. <i>Cell Reports Methods</i> , 2022, 2, 100137.	1.4	14
2	Towards the biogeography of prokaryotic genes. <i>Nature</i> , 2022, 601, 252-256.	13.7	85
3	Benchmark of Data Processing Methods and Machine Learning Models for Gut Microbiome-Based Diagnosis of Inflammatory Bowel Disease. <i>Frontiers in Genetics</i> , 2022, 13, 784397.	1.1	14
4	Landscape of mobile genetic elements and their antibiotic resistance cargo in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2022, 50, 3155-3168.	6.5	34
5	Structure and function of the soil microbiome underlying N ₂ O emissions from global wetlands. <i>Nature Communications</i> , 2022, 13, 1430.	5.8	72
6	Glacier melt-down changes habitat characteristics and unique microbial community composition and physiology in alpine lake sediments. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	3
7	Metagenomic assessment of the global diversity and distribution of bacteria and fungi. <i>Environmental Microbiology</i> , 2021, 23, 316-326.	1.8	42
8	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> , 2021, 9, 75.	4.9	31
9	Systematic analysis of gut microbiome reveals the role of bacterial folate and homocysteine metabolism in Parkinson's disease. <i>Cell Reports</i> , 2021, 34, 108807.	2.9	77
10	Meta-analysis of the Parkinson's disease gut microbiome suggests alterations linked to intestinal inflammation. <i>Npj Parkinson's Disease</i> , 2021, 7, 27.	2.5	315
11	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , 2021, 9, e10941.	0.9	79
12	mTAGs: taxonomic profiling using degenerate consensus reference sequences of ribosomal RNA genes. <i>Bioinformatics</i> , 2021, 38, 270-272.	1.8	5
13	Dispersal strategies shape persistence and evolution of human gut bacteria. <i>Cell Host and Microbe</i> , 2021, 29, 1167-1176.e9.	5.1	66
14	Ultra-resolution Metagenomics: When Enough Is Not Enough. <i>MSystems</i> , 2021, 6, e0088121.	1.7	8
15	Lifelong sex-dependent trajectories of the human gut microbiota. <i>Nature Aging</i> , 2021, 1, 22-23.	5.3	3
16	Towards standardisation of naming novel prokaryotic taxa in the age of high-throughput microbiology. <i>Gut</i> , 2020, 69, 1358.1-1359.	6.1	14
17	Absence of BSEP (ABCB11) protects MDR2 (ABCB4) KO mice from cholestatic liver and bile duct injury through modulating hepatic and intestinal inflammatory signaling. <i>Journal of Hepatology</i> , 2020, 73, S195-S196.	1.8	0
18	Intestinal Microbiome-Macrophage Crosstalk Contributes to Cholestatic Liver Disease by Promoting Intestinal Permeability in Mice. <i>Hepatology</i> , 2020, 72, 2090-2108.	3.6	47

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19	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> , 2020, 18, 1722-1734.	1.9	52
20	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , 2020, 14, 1247-1259.	4.4	74
21	Plant nutrient acquisition strategies drive topsoil microbiome structure and function. <i>New Phytologist</i> , 2020, 227, 1189-1199.	3.5	96
22	Metage2Metabo, microbiota-scale metabolic complementarity for the identification of key species. <i>ELife</i> , 2020, 9, .	2.8	44
23	Newly designed 16S rRNA metabarcoding primers amplify diverse and novel archaeal taxa from the environment. <i>Environmental Microbiology Reports</i> , 2019, 11, 487-494.	1.0	91
24	Antibiotics-induced monodominance of a novel gut bacterial order. <i>Gut</i> , 2019, 68, 1781-1790.	6.1	73
25	Ice-Age Climate Adaptations Trap the Alpine Marmot in a State of Low Genetic Diversity. <i>Current Biology</i> , 2019, 29, 1712-1720.e7.	1.8	27
26	Plasmid DNA contaminant in molecular reagents. <i>Scientific Reports</i> , 2019, 9, 1652.	1.6	20
27	Population-level analysis of <i>Blastocystis</i> subtype prevalence and variation in the human gut microbiota. <i>Gut</i> , 2019, 68, 1180-1189.	6.1	149
28	Host genetic variation strongly influences the microbiome structure and function in fungal fruiting bodies. <i>Environmental Microbiology</i> , 2018, 20, 1641-1650.	1.8	23
29	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	5.9	717
30	Gut microbiota composition is associated with environmental landscape in honey bees. <i>Ecology and Evolution</i> , 2018, 8, 441-451.	0.8	106
31	A computational framework to integrate high-throughput omics datasets for the identification of potential mechanistic links. <i>Nature Protocols</i> , 2018, 13, 2781-2800.	5.5	82
32	The gut microbiome is associated with behavioural task in honey bees. <i>Insectes Sociaux</i> , 2018, 65, 419-429.	0.7	90
33	Toxic Cyanobacteria in Svalbard: Chemical Diversity of Microcystins Detected Using a Liquid Chromatography Mass Spectrometry Precursor Ion Screening Method. <i>Toxins</i> , 2018, 10, 147.	1.5	31
34	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018, 560, 233-237.	18.7	1,370
35	RTK: efficient rarefaction analysis of large datasets. <i>Bioinformatics</i> , 2017, 33, 2594-2595.	1.8	100
36	Functional implications of microbial and viral gut metagenome changes in early stage L-DOPA-naïve Parkinson's disease patients. <i>Genome Medicine</i> , 2017, 9, 39.	3.6	420

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37	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , 2017, 13, 960.	3.2	115
38	Pole-to-Pole Connections: Similarities between Arctic and Antarctic Microbiomes and Their Vulnerability to Environmental Change. <i>Frontiers in Ecology and Evolution</i> , 2017, 5, .	1.1	51
39	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , 2016, 352, 586-589.	6.0	461
40	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016, 535, 376-381.	13.7	1,506
41	Speciesâ€“function relationships shape ecological properties of the human gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16088.	5.9	279
42	Gut Microbiota Linked to Sexual Preference and HIV Infection. <i>EBioMedicine</i> , 2016, 5, 135-146.	2.7	328
43	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	6.0	2,137
44	Genome Sequence of Mucoid <i>Pseudomonas aeruginosa</i> Strain FRD1. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
45	Addition of acacia gum to a FOS/inulin blend improves its fermentation profile in the Simulator of the Human Intestinal Microbial Ecosystem (SHIMEÂ®). <i>Journal of Functional Foods</i> , 2015, 16, 211-222.	1.6	21
46	Response to Comment on â€œGlobal diversity and geography of soil fungiâ€“. <i>Science</i> , 2015, 349, 936-936.	6.0	43
47	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	13.7	1,627
48	Diversity of toxin and non-toxin containing cyanobacterial mats of meltwater ponds on the Antarctic Peninsula: a pyrosequencing approach. <i>Antarctic Science</i> , 2014, 26, 521-532.	0.5	63
49	LotuS: an efficient and user-friendly OTU processing pipeline. <i>Microbiome</i> , 2014, 2, 30.	4.9	233
50	The skin microbiome of caspaseâ€“4â€“deficient mice shows mild dysbiosis. <i>Experimental Dermatology</i> , 2014, 23, 561-567.	1.4	15
51	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> , 2014, 71, 26-38.	0.8	32
52	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> , 2014, 27, 633-644.	1.8	10
53	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	9.4	909
54	Draft Genome Sequence Analysis of a <i>Pseudomonas putida</i> W15Oct28 Strain with Antagonistic Activity to Gram-Positive and <i>Pseudomonas</i> sp. <i>Pathogens</i> . <i>PLoS ONE</i> , 2014, 9, e110038.	1.1	25

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55	Inflammation-associated enterotypes, host genotype, cage and inter-individual effects drive gut microbiota variation in common laboratory mice. <i>Genome Biology</i> , 2013, 14, R4.	13.9	381
56	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> , 2013, 26, 561-575.	1.8	18
57	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	13.7	3,641
58	The chemical interactome space between the human host and the genetically defined gut metabotypes. <i>ISME Journal</i> , 2013, 7, 730-742.	4.4	21
59	Gut Microbiota Affects Sensitivity to Acute DSS-induced Colitis Independently of Host Genotype. <i>Inflammatory Bowel Diseases</i> , 2013, 19, 2560-2567.	0.9	61
60	Global regulation of gene expression by OxyR in an important human opportunistic pathogen. <i>Nucleic Acids Research</i> , 2012, 40, 4320-4333.	6.5	189
61	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.	1.2	43
62	Unresolved orthology and peculiar coding sequence properties of lamprey genes: the KCNA gene family as test case. <i>BMC Genomics</i> , 2011, 12, 325.	1.2	70
63	Caspase deficiency alters the murine gut microbiome. <i>Cell Death and Disease</i> , 2011, 2, e220-e220.	2.7	61
64	Evidence of Selection upon Genomic GC-Content in Bacteria. <i>PLoS Genetics</i> , 2010, 6, e1001107.	1.5	355
65	Origin, Spread and Demography of the Mycobacterium tuberculosis Complex. <i>PLoS Pathogens</i> , 2008, 4, e1000160.	2.1	378
66	Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi. <i>MycKeys</i> , 0, 10, 1-43.	0.8	409
67	Enrichment of Gut Microbiome Strains for Cultivation-Free Genome Sequencing Using Droplet Microfluidics. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2