

# Karoline Faust

## List of Publications by Year in descending order

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Version: 2024-02-01

59  
papers

23,705  
citations

109321

35  
h-index

123424

61  
g-index

70  
all docs

70  
docs citations

70  
times ranked

28766  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012, 486, 207-214.	27.8	9,614
2	Microbial interactions: from networks to models. <i>Nature Reviews Microbiology</i> , 2012, 10, 538-550.	28.6	2,693
3	A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.	27.8	2,249
4	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016, 352, 560-564.	12.6	1,716
5	Microbial Co-occurrence Relationships in the Human Microbiome. <i>PLoS Computational Biology</i> , 2012, 8, e1002606.	3.2	1,268
6	Determinants of community structure in the global plankton interactome. <i>Science</i> , 2015, 348, 1262073.	12.6	842
7	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016, 10, 1669-1681.	9.8	593
8	CoNet app: inference of biological association networks using Cytoscape. <i>F1000Research</i> , 2016, 5, 1519.	1.6	398
9	Computational approaches to predict bacteriophage-host relationships. <i>FEMS Microbiology Reviews</i> , 2016, 40, 258-272.	8.6	394
10	From hairballs to hypotheses—biological insights from microbial networks. <i>FEMS Microbiology Reviews</i> , 2018, 42, 761-780.	8.6	374
11	Metagenomics meets time series analysis: unraveling microbial community dynamics. <i>Current Opinion in Microbiology</i> , 2015, 25, 56-66.	5.1	345
12	CoNet app: inference of biological association networks using Cytoscape. <i>F1000Research</i> , 2016, 5, 1519.	1.6	331
13	Earth microbial co-occurrence network reveals interconnection pattern across microbiomes. <i>Microbiome</i> , 2020, 8, 82.	11.1	239
14	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , 2013, 7, 1678-1695.	9.8	185
15	Soil microbiome responses to the short-term effects of Amazonian deforestation. <i>Molecular Ecology</i> , 2015, 24, 2433-2448.	3.9	171
16	Millions of reads, thousands of taxa: microbial community structure and associations analyzed via marker genes. <i>FEMS Microbiology Reviews</i> , 2016, 40, 686-700.	8.6	159
17	Cross-biome comparison of microbial association networks. <i>Frontiers in Microbiology</i> , 2015, 6, 1200.	3.5	154
18	Microbial communities as dynamical systems. <i>Current Opinion in Microbiology</i> , 2018, 44, 41-49.	5.1	121

#	ARTICLE	IF	CITATIONS
19	Identifying genomic and metabolic features that can underlie early successional and opportunistic lifestyles of human gut symbionts. <i>Genome Research</i> , 2012, 22, 1974-1984.	5.5	120
20	Synthetic ecology of the human gut microbiota. <i>Nature Reviews Microbiology</i> , 2019, 17, 754-763.	28.6	117
21	Open challenges for microbial network construction and analysis. <i>ISME Journal</i> , 2021, 15, 3111-3118.	9.8	116
22	Multi-stability and the origin of microbial community types. <i>ISME Journal</i> , 2017, 11, 2159-2166.	9.8	104
23	Network Analysis Tools: from biological networks to clusters and pathways. <i>Nature Protocols</i> , 2008, 3, 1616-1629.	12.0	101
24	Temporal variability in quantitative human gut microbiome profiles and implications for clinical research. <i>Nature Communications</i> , 2021, 12, 6740.	12.8	89
25	NeAT: a toolbox for the analysis of biological networks, clusters, classes and pathways. <i>Nucleic Acids Research</i> , 2008, 36, W444-W451.	14.5	81
26	Signatures of ecological processes in microbial community time series. <i>Microbiome</i> , 2018, 6, 120.	11.1	81
27	Pathway discovery in metabolic networks by subgraph extraction. <i>Bioinformatics</i> , 2010, 26, 1211-1218.	4.1	74
28	Combined use of network inference tools identifies ecologically meaningful bacterial associations in a paddy soil. <i>Soil Biology and Biochemistry</i> , 2017, 105, 227-235.	8.8	72
29	Genetic correlation network prediction of forest soil microbial functional organization. <i>ISME Journal</i> , 2018, 12, 2492-2505.	9.8	63
30	Integrated culturing, modeling and transcriptomics uncovers complex interactions and emergent behavior in a three-species synthetic gut community. <i>ELife</i> , 2018, 7, .	6.0	62
31	Using metabolic networks to resolve ecological properties of microbiomes. <i>Current Opinion in Systems Biology</i> , 2018, 8, 73-80.	2.6	61
32	Can we predict keystones?. <i>Nature Reviews Microbiology</i> , 2019, 17, 193-193.	28.6	58
33	Metabolic Pathfinding Using RPAIR Annotation. <i>Journal of Molecular Biology</i> , 2009, 388, 390-414.	4.2	57
34	A web application for sample size and power calculation in case-control microbiome studies. <i>Bioinformatics</i> , 2016, 32, 2038-2040.	4.1	57
35	Fire modifies the phylogenetic structure of soil bacterial co-occurrence networks. <i>Environmental Microbiology</i> , 2017, 19, 317-327.	3.8	48
36	Successional Stages in Infant Gut Microbiota Maturation. <i>MBio</i> , 2021, 12, e0185721.	4.1	48

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37	Roles of bacteriophages, plasmids and CRISPR immunity in microbial community dynamics revealed using time-series integrated meta-omics. <i>Nature Microbiology</i> , 2021, 6, 123-135.	13.3	47
38	Gut microbiota dynamics and uraemic toxins: one size does not fit all. <i>Gut</i> , 2019, 68, 2257.1-2260.	12.1	37
39	Microbial Consortium Design Benefits from Metabolic Modeling. <i>Trends in Biotechnology</i> , 2019, 37, 123-125.	9.3	36
40	New species of prunoid radiolarians from the Antarctic Neogene. <i>Journal of Micropalaeontology</i> , 2005, 24, 97-121.	3.6	32
41	Speciesâ€orting and massâ€transfer paradigms control managed natural metacommunities. <i>Environmental Microbiology</i> , 2016, 18, 4862-4877.	3.8	31
42	Prediction of metabolic pathways from genome-scale metabolic networks. <i>BioSystems</i> , 2011, 105, 109-121.	2.0	30
43	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> , 2022, 119, e2114619119.	7.1	30
44	Bistability in a system of two species interacting through mutualism as well as competition: Chemostat vs. Lotka-Volterra equations. <i>PLoS ONE</i> , 2018, 13, e0197462.	2.5	27
45	Structure of association networks in food bacterial communities. <i>Food Microbiology</i> , 2018, 73, 49-60.	4.2	22
46	Disentangling environmental effects in microbial association networks. <i>Microbiome</i> , 2021, 9, 232.	11.1	21
47	Rules of the game for microbiota. <i>Nature</i> , 2016, 534, 182-183.	27.8	17
48	Consumer Safety Considerations of Skin and Oral Microbiome Perturbation. <i>Clinical Microbiology Reviews</i> , 2019, 32, .	13.6	15
49	Towards a Better Understanding of Microbial Community Dynamics through High-Throughput Cultivation and Data Integration. <i>MSystems</i> , 2019, 4, .	3.8	12
50	Gut Microbiome Profiling Uncovers a Lower Abundance of <i>Butyricoccus</i> in Advanced Stages of Chronic Kidney Disease. <i>Journal of Personalized Medicine</i> , 2021, 11, 1118.	2.5	11
51	In response to â€Can sugars be produced from fatty acids? A test case for pathway analysis toolsâ€ <sup>TM</sup> . <i>Bioinformatics</i> , 2009, 25, 3202-3205.	4.1	9
52	Null-model-based network comparison reveals core associations. <i>ISME Communications</i> , 2021, 1, .	4.2	9
53	Quantifying the impact of ecological memory on the dynamics of interacting communities. <i>PLoS Computational Biology</i> , 2022, 18, e1009396.	3.2	9
54	Predicting Metabolic Pathways by Sub-network Extraction. <i>Methods in Molecular Biology</i> , 2012, 804, 107-130.	0.9	8

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55	manta: a Clustering Algorithm for Weighted Ecological Networks. MSystems, 2020, 5, .	3.8	7
56	Fast and flexible analysis of linked microbiome data with mako. Nature Methods, 2022, 19, 51-54.	19.0	7
57	Fast quantification of gut bacterial species in cocultures using flow cytometry and supervised classification. ISME Communications, 2022, 2, .	4.2	6
58	Regime transition Shapes the Composition, Assembly Processes, and Co-occurrence Pattern of Bacterioplankton Community in a Large Eutrophic Freshwater Lake. Microbial Ecology, 2022, 84, 336-350.	2.8	4
59	The Dynamic of a River Model Bacterial Community in Two Different Media Reveals a Divergent Succession and an Enhanced Growth of Most Strains Compared to Monocultures. Microbial Ecology, 2019, 78, 313-323.	2.8	3