F-M Kerckhof

List of Publications by Year
in descending order

53 papers	3,112 citations	201575 27 h-index	168321 53 g-index
59 all docs	59 docs citations	59 times ranked	5527 citing authors

#	Article	IF	Citations
1	Butyrate-producing Clostridium cluster XIVa species specifically colonize mucins in an in vitro gut model. ISME Journal, 2013, 7, 949-961.	4.4	501
2	Absolute quantification of microbial taxon abundances. ISME Journal, 2017, 11, 584-587.	4.4	273
3	Conceptualizing functional traits and ecological characteristics of methaneâ€oxidizing bacteria as life strategies. Environmental Microbiology Reports, 2013, 5, 335-345.	1.0	225
4	Chronic cigarette smoke exposure induces microbial and inflammatory shifts and mucin changes in the murine gut. Environmental Microbiology, 2016, 18, 1352-1363.	1.8	149
5	Gut microbiota generation of protein-bound uremic toxins and related metabolites is not altered at different stages of chronic kidney disease. Kidney International, 2020, 97, 1230-1242.	2.6	125
6	Microbial Odor Profile of Polyester and Cotton Clothes after a Fitness Session. Applied and Environmental Microbiology, 2014, 80, 6611-6619.	1.4	102
7	Biotic Interactions in Microbial Communities as Modulators of Biogeochemical Processes: Methanotrophy as a Model System. Frontiers in Microbiology, 2016, 7, 1285.	1.5	95
8	Microbiological, chemical and sensory spoilage analysis of raw Atlantic cod (Gadus morhua) stored under modified atmospheres. Food Microbiology, 2018, 70, 232-244.	2.1	90
9	Interâ€individual differences determine the outcome of wheat bran colonization by the human gut microbiome. Environmental Microbiology, 2017, 19, 3251-3267.	1.8	88
10	New Methyloceanibacter diversity from North Sea sediments includes methanotroph containing solely the soluble methane monooxygenase. Environmental Microbiology, 2016, 18, 4523-4536.	1.8	81
11	Conversion of Biogas to Bioproducts by Algae and Methane Oxidizing Bacteria. Environmental Science & Technology, 2012, 46, 13425-13431.	4.6	78
12	Characterization of Staphylococcus and Corynebacterium Clusters in the Human Axillary Region. PLoS ONE, 2013, 8, e70538.	1.1	74
13	Optimized Cryopreservation of Mixed Microbial Communities for Conserved Functionality and Diversity. PLoS ONE, 2014, 9, e99517.	1.1	74
14	Reconciliation between operational taxonomic units and species boundaries. FEMS Microbiology Ecology, 2017, 93, .	1.3	71
15	Chronic rhinosinusitis with nasal polyps is characterized by dysbacteriosis of the nasal microbiota. Scientific Reports, 2018, 8, 7926.	1.6	67
16	Bacterial Exchange in Household Washing Machines. Frontiers in Microbiology, 2015, 6, 1381.	1.5	64
17	Community structure, population dynamics and diversity of fungi in a full-scale membrane bioreactor (MBR) for urban wastewater treatment. Water Research, 2016, 105, 507-519.	5.3	60
18	Exploration and prediction of interactions between methanotrophs and heterotrophs. Research in Microbiology, 2013, 164, 1045-1054.	1.0	57

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19	Effect of Operational Parameters in the Continuous Anaerobic Fermentation of Cheese Whey on Titers, Yields, Productivities, and Microbial Community Structures. ACS Sustainable Chemistry and Engineering, 2017, 5, 1400-1407.	3.2	55
20	Oxygen-reducing microbial cathodes monitoring toxic shocks in tap water. Biosensors and Bioelectronics, 2019, 132, 115-121.	5.3	53
21	Mucin degradation niche as a driver of microbiome composition and Akkermansia muciniphila abundance in a dynamic gut model is donor independent. FEMS Microbiology Ecology, 2018, 94, .	1.3	51
22	Flow cytometric fingerprinting for microbial strain discrimination and physiological characterization. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2018, 93, 201-212.	1.1	43
23	Label-free Raman characterization of bacteria calls for standardized procedures. Journal of Microbiological Methods, 2018, 151, 69-75.	0.7	38
24	Exploring methane-oxidizing communities for the co-metabolic degradation of organic micropollutants. Applied Microbiology and Biotechnology, 2015, 99, 3609-3618.	1.7	35
25	Microbial Protein out of Thin Air: Fixation of Nitrogen Gas by an Autotrophic Hydrogen-Oxidizing Bacterial Enrichment. Environmental Science & Technology, 2020, 54, 3609-3617.	4.6	35
26	Pinpointing wastewater and process parameters controlling the AOB to NOB activity ratio in sewage treatment plants. Water Research, 2018, 138, 37-46.	5.3	34
27	Future prospects for dissecting inter-individual variability in the absorption, distribution and elimination of plant bioactives of relevance for cardiometabolic endpoints. European Journal of Nutrition, 2019, 58, 21-36.	1.8	34
28	Microbial protein production from methane via electrochemical biogas upgrading. Chemical Engineering Journal, 2020, 391, 123625.	6.6	31
29	Strain-Specific Transfer of Antibiotic Resistance from an Environmental Plasmid to Foodborne Pathogens. Journal of Biomedicine and Biotechnology, 2012, 2012, 1-8.	3.0	29
30	Characterization of spoilage markers in modified atmosphere packaged iceberg lettuce. International Journal of Food Microbiology, 2018, 279, 1-13.	2.1	29
31	Cocultivating aerobic heterotrophs and purple bacteria for microbial protein in sequential photo- and chemotrophic reactors. Bioresource Technology, 2021, 319, 124192.	4.8	28
32	Bacterial mock communities as standards for reproducible cytometric microbiome analysis. Nature Protocols, 2020, 15, 2788-2812.	5.5	26
33	Gut Microbiota of Migrating Wild Rabbit Fish (Siganus guttatus) Larvae Have Low Spatial and Temporal Variability. Microbial Ecology, 2020, 79, 539-551.	1.4	25
34	Enriched hydrogen-oxidizing microbiomes show a high diversity of co-existing hydrogen-oxidizing bacteria. Applied Microbiology and Biotechnology, 2019, 103, 8241-8253.	1.7	24
35	Development of an oral mucosa model to study host-microbiome interactions during wound healing. Applied Microbiology and Biotechnology, 2014, 98, 6831-6846.	1.7	21
36	PhenoGMM: Gaussian Mixture Modeling of Cytometry Data Quantifies Changes in Microbial Community Structure. MSphere, 2021, 6, .	1.3	21

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37	Barcoded pyrosequencing analysis of the microbial community in a simulator of the human gastrointestinal tract showed a colon region-specific microbiota modulation for two plant-derived polysaccharide blends. Antonie Van Leeuwenhoek, 2013, 103, 409-420.	0.7	19
38	Efficient molasses fermentation under high salinity by inocula of marine and terrestrial origin. Biotechnology for Biofuels, 2017, 10, 23.	6.2	19
39	Cytometric fingerprints of gut microbiota predict Crohnâ€™s disease state. ISME Journal, 2021, 15, 354-358.	4.4	19
40	From Biogas and Hydrogen to Microbial Protein Through Co-Cultivation of Methane and Hydrogen Oxidizing Bacteria. Frontiers in Bioengineering and Biotechnology, 2021, 9, 733753.	2.0	17
41	Discriminating Bacterial Phenotypes at the Population and Singleâ€Cell Level: A Comparison of Flow Cytometry and Raman Spectroscopy Fingerprinting. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 97, 713-726.	1.1	16
42	A unified framework for unconstrained and constrained ordination of microbiome read count data. PLoS ONE, 2019, 14, e0205474.	1.1	14
43	Reduced TCA cycle rates at high hydrostatic pressure hinder hydrocarbon degradation and obligate oil degraders in natural, deep-sea microbial communities. ISME Journal, 2019, 13, 1004-1018.	4.4	14
44	Bacillus cereus NVH 0500/00 Can Adhere to Mucin but Cannot Produce Enterotoxins during Gastrointestinal Simulation. Applied and Environmental Microbiology, 2016, 82, 289-296.	1.4	12
45	Initial evenness determines diversity and cell density dynamics in synthetic microbial ecosystems. Scientific Reports, 2018, 8, 340.	1.6	12
46	Bacillus cereusAdhesion to Simulated Intestinal Mucus Is Determined by Its Growth on Mucin, Rather Than Intestinal Environmental Parameters. Foodborne Pathogens and Disease, 2015, 12, 904-913.	0.8	10
47	A prebiotic-enhanced lipid-based nutrient supplement (LNSp) increases Bifidobacterium relative abundance and enhances short-chain fatty acid production in simulated colonic microbiota from undernourished infants. FEMS Microbiology Ecology, 2020, 96, .	1.3	10
48	In vitro Increased Respiratory Activity of Selected Oral Bacteria May Explain Competitive and Collaborative Interactions in the Oral Microbiome. Frontiers in Cellular and Infection Microbiology, 2017, 7, 235.	1.8	9
49	Determining stoichiometry and kinetics of two thermophilic nitrifying communities as a crucial step in the development of thermophilic nitrogen removal. Water Research, 2019, 156, 34-45.	5.3	8
50	Root-Associated Bacterial Community Shifts in Hydroponic Lettuce Cultured with Urine-Derived Fertilizer. Microorganisms, 2021, 9, 1326.	1.6	8
51	Low microbial biomass within the reproductive tract of mid-lactation dairy cows: A study approach. Journal of Dairy Science, 2021, 104, 6159-6174.	1.4	6
52	Learning Singleâ€Cell Distances from Cytometry Data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2019, 95, 782-791.	1.1	4
53	Electrochemical and phylogenetic comparisons of oxygen-reducing electroautotrophic communities. Biosensors and Bioelectronics, 2021, 171, 112700.	5.3	2