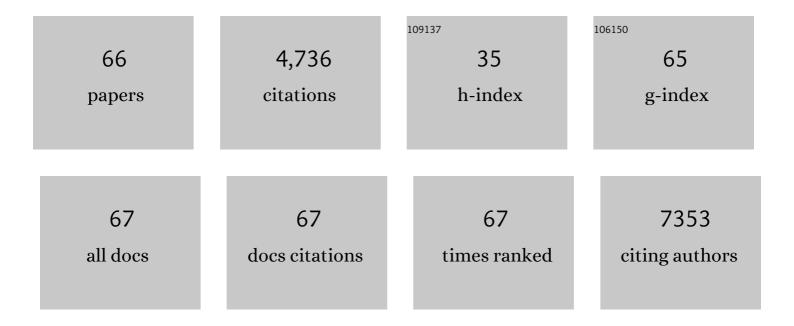
JérÃ'me Hamelin

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8905131/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Screening and Application of Ligninolytic Microbial Consortia to Enhance Aerobic Degradation of Solid Digestate. Microorganisms, 2022, 10, 277.	1.6	2
2	Mapping the biological activities of filamentous oxygenic photogranules. Biotechnology and Bioengineering, 2021, 118, 601-611.	1.7	7
3	Wastewater treatment using oxygenic photogranule-based process has lower environmental impact than conventional activated sludge process. Bioresource Technology, 2021, 319, 124204.	4.8	30
4	Engineered methanotrophic syntrophy in photogranule communities removes dissolved methane. Water Research X, 2021, 12, 100106.	2.8	19
5	Growth Progression of Oxygenic Photogranules and Its Impact on Bioactivity for Aeration-Free Wastewater Treatment. Environmental Science & Technology, 2020, 54, 486-496.	4.6	58
6	Novel Outlook in Microbial Ecology: Nonmutualistic Interspecies Electron Transfer. Trends in Microbiology, 2020, 28, 245-253.	3.5	14
7	Absolute quantitation of microbes using 16S rRNA gene metabarcoding: A rapid normalization of relative abundances by quantitative PCR targeting a 16S rRNA gene spikeâ€in standard. MicrobiologyOpen, 2020, 9, e977.	1.2	43
8	Simple Time-lapse Imaging for Quantifying the Hydrostatic Production of Oxygenic Photogranules. Bio-protocol, 2020, 10, e3784.	0.2	3
9	The use of green macroalgae (Ulva lactuca and Codium tomentosum) that have a high methane potential, as a source of biogas in Senegal. Journal of Applied Bioscience, 2019, 132, 13404.	0.7	5
10	The Oxygenic Photogranule Process for Aeration-Free Wastewater Treatment. Environmental Science & Technology, 2018, 52, 3503-3511.	4.6	109
11	CO2 addition to increase biomass production and control microalgae species in high rate algal ponds treating wastewater. Journal of CO2 Utilization, 2018, 28, 292-298.	3.3	39
12	Multiplexed chemostat system for quantification of biodiversity and ecosystem functioning in anaerobic digestion. PLoS ONE, 2018, 13, e0193748.	1.1	2
13	Correlating methane production to microbiota in anaerobic digesters fed synthetic wastewater. Water Research, 2017, 110, 161-169.	5.3	49
14	A Single Community Dominates Structure and Function of a Mixture of Multiple Methanogenic Communities. Current Biology, 2017, 27, 3390-3395.e4.	1.8	65
15	Biogranules applied in environmental engineering. International Journal of Hydrogen Energy, 2017, 42, 27801-27811.	3.8	38
16	World Scientists' Warning to Humanity: A Second Notice. BioScience, 2017, 67, 1026-1028.	2.2	817
17	The importance of filamentous cyanobacteria in the development of oxygenic photogranules. Scientific Reports, 2017, 7, 17944.	1.6	78
18	Challenges in microbial ecology: building predictive understanding of community function and dynamics. ISME Journal, 2016, 10, 2557-2568.	4.4	570

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19	Vertebrate bacterial gut diversity: size also matters. BMC Ecology, 2016, 16, 12.	3.0	46
20	Anaerobic digester bioaugmentation influences quasi steady state performance and microbial community. Water Research, 2016, 104, 128-136.	5.3	54
21	Nutritional stress induces exchange of cell material and energetic coupling between bacterial species. Nature Communications, 2015, 6, 6283.	5.8	136
22	Adaptation of acidogenic sludge to increasing glycerol concentrations for biohydrogen production. Applied Microbiology and Biotechnology, 2015, 99, 8295-8308.	1.7	23
23	Bioaerosol emissions from open microalgal processes and their potential environmental impacts: what can be learned from natural and anthropogenic aquatic environments?. Current Opinion in Biotechnology, 2015, 33, 279-286.	3.3	11
24	How to use molecular biology tools for the study of the anaerobic digestion process?. Reviews in Environmental Science and Biotechnology, 2015, 14, 555-593.	3.9	60
25	Similar PAH Fate in Anaerobic Digesters Inoculated with Three Microbial Communities Accumulating Either Volatile Fatty Acids or Methane. PLoS ONE, 2015, 10, e0125552.	1.1	18
26	Spatial distribution of microbial communities in the shallow submarine alkaline hydrothermal field of the <scp>P</scp> rony <scp>B</scp> ay, <scp>N</scp> ew <scp>C</scp> aledonia. Environmental Microbiology Reports, 2014, 6, 665-674.	1.0	64
27	Biofilm development during the startâ€up period of anaerobic biofilm reactors: the biofilm <i>Archaea</i> community is highly dependent on the support material. Microbial Biotechnology, 2014, 7, 257-264.	2.0	47
28	New urban wastewater treatment with autotrophic membrane bioreactor at low chemical oxygen demand/N substrate ratio. Water Science and Technology, 2014, 69, 960-965.	1.2	7
29	Substrate milling pretreatment as a key parameter for Solid-State Anaerobic Digestion optimization. Bioresource Technology, 2014, 173, 185-192.	4.8	59
30	Only Simpson Diversity can be Estimated Accurately from Microbial Community Fingerprints. Microbial Ecology, 2014, 68, 169-172.	1.4	23
31	Total solid content drives hydrogen production through microbial selection during thermophilic fermentation. Bioresource Technology, 2014, 166, 610-615.	4.8	38
32	Specific inhibition of biohydrogen-producing Clostridium sp. after dilute-acid pretreatment ofÂsunflower stalks. International Journal of Hydrogen Energy, 2013, 38, 12273-12282.	3.8	68
33	Total solids content: a key parameter of metabolic pathways in dry anaerobic digestion. Biotechnology for Biofuels, 2013, 6, 164.	6.2	128
34	Two-Stage Alkaline–Enzymatic Pretreatments To Enhance Biohydrogen Production from Sunflower Stalks. Environmental Science & Technology, 2013, 47, 12591-12599.	4.6	40
35	Sub-dominant bacteria as keystone species in microbial communities producing bio-hydrogen. International Journal of Hydrogen Energy, 2013, 38, 4975-4985.	3.8	79
36	Distribution and hydrophobic properties of Extracellular Polymeric Substances in biofilms in relation towards cohesion. Journal of Biotechnology, 2013, 165, 85-92.	1.9	23

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37	Robust estimation of microbial diversity in theory and in practice. ISME Journal, 2013, 7, 1092-1101.	4.4	321
38	Microbial community signature of high-solid content methanogenic ecosystems. Bioresource Technology, 2013, 133, 256-262.	4.8	42
39	Homogeneity and Synchronous Dynamics of Microbial Communities in Particulate Biofilms: from Major Populations to Minor Groups. Microbes and Environments, 2012, 27, 142-148.	0.7	5
40	Improvement of RNA-SIP by pyrosequencing to identify putative 4-n-nonylphenol degraders in activated sludge. Water Research, 2012, 46, 601-610.	5.3	26
41	Carbon conversion efficiency and population dynamics of a marine algae–bacteria consortium growing on simplified synthetic digestate: First step in a bioprocess coupling algal production and anaerobic digestion. Bioresource Technology, 2012, 119, 79-87.	4.8	46
42	<i>In situ</i> proteo-metabolomics reveals metabolite secretion by the acid mine drainage bio-indicator, <i>Euglena mutabilis</i> . ISME Journal, 2012, 6, 1391-1402.	4.4	37
43	Spatial variability of the functional stability of microbial respiration process: a microcosm study using tropical forest soil. Journal of Soils and Sediments, 2012, 12, 1030-1039.	1.5	8
44	Inhibition of fermentative hydrogen production by lignocellulose-derived compounds in mixed cultures. International Journal of Hydrogen Energy, 2012, 37, 3150-3159.	3.8	167
45	Changes in hydrogenase genetic diversity and proteomic patterns in mixed-culture dark fermentation of mono-, di- and tri-saccharides. International Journal of Hydrogen Energy, 2011, 36, 11654-11665.	3.8	41
46	Influence of support material properties on the potential selection of Archaea during initial adhesion of a methanogenic consortium. Bioresource Technology, 2011, 102, 4054-4060.	4.8	53
47	Functional versus phylogenetic fingerprint analyses for monitoring hydrogen-producing bacterial populations in dark fermentation cultures. International Journal of Hydrogen Energy, 2011, 36, 3870-3879.	3.8	32
48	Development and Application of an Enzymatic and Cell Flotation Treatment for the Recovery of Viable Microbial Cells from Environmental Matrices Such as Anaerobic Sludge. Applied and Environmental Microbiology, 2011, 77, 8487-8493.	1.4	22
49	Distribution of Pseudomonas populations harboring phID or hcnAB biocontrol genes is related to depth in vineyard soils. Soil Biology and Biochemistry, 2010, 42, 466-472.	4.2	7
50	Development and application of a functional CE-SSCP fingerprinting method based on [Fe–Fe]-hydrogenase genes for monitoring hydrogen-producing Clostridium in mixed cultures. International Journal of Hydrogen Energy, 2010, 35, 13158-13167.	3.8	30
51	Selective microbial aerosolization in biogas demonstrated by quantitative PCR. Bioresource Technology, 2010, 101, 7252-7257.	4.8	21
52	Spatial and temporal variations of the bacterial community in the bovine digestive tract. Journal of Applied Microbiology, 2009, 107, 1642-1650.	1.4	34
53	Structural divergence of bacterial communities from functionally similar laboratory-scale vermicomposts assessed by PCR-CE-SSCP. Journal of Applied Microbiology, 2008, 105, 2123-2132.	1.4	23
54	DNA reassociation kinetics and diversity indices: richness is not rich enough. Oikos, 2008, 117, 177-181.	1.2	6

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55	Differences between Bacterial Communities in the Gut of a Soil-Feeding Termite (Cubitermes) Tj ETQq1 1 0.7843	14 rgBT /(1.4	Overlock 1
56	How elevated pCO2 modifies total and metabolically active bacterial communities in the rhizosphere of two perennial grasses grown under field conditions. FEMS Microbiology Ecology, 2006, 55, 339-350.	1.3	55
57	Phenotypic structure of Pseudomonas populations is altered under elevated pCO2 in the rhizosphere of perennial grasses. Soil Biology and Biochemistry, 2006, 38, 1193-1201.	4.2	30
58	Nitrogen fertiliser rate affects the frequency of nitrate-dissimilating Pseudomonas spp. in the rhizosphere of Lolium perenne grown under elevated pCO2 (Swiss FACE). Soil Biology and Biochemistry, 2005, 37, 1962-1965.	4.2	9
59	Frequency and Diversity of Nitrate Reductase Genes among Nitrate-Dissimilating Pseudomonas in the Rhizosphere of Perennial Grasses Grown in Field Conditions. Microbial Ecology, 2005, 49, 63-72.	1.4	39
60	Soil Microbial Community Changes in Wooded Mountain Pastures due to Simulated Effects of Cattle Grazing. Plant and Soil, 2005, 278, 327-340.	1.8	64
61	Examination of Gould's modified S1 (mS1) selective medium and Angle's non-selective medium for describing the diversity of Pseudomonas spp. in soil and root environments. FEMS Microbiology Ecology, 2003, 45, 97-104.	1.3	18
62	Specific PCR Amplification for the Genus Pseudomonas Targeting the 3′ Half of 16S rDNA and the Whole 16S–23S rDNA Spacer. Systematic and Applied Microbiology, 2002, 25, 220-227.	1.2	42
63	nifH gene diversity in the bacterial community associated with the rhizosphere of Molinia coerulea, an oligonitrophilic perennial grass. Environmental Microbiology, 2002, 4, 477-481.	1.8	72
64	Statistical analysis of denaturing gel electrophoresis (DGE) fingerprinting patterns. Environmental Microbiology, 2002, 4, 634-643.	1.8	469
65	Co-evolution between Frankia populations and host plants in the family Casuarinaceae and consequent patterns of global dispersal. Environmental Microbiology, 1999, 1, 525-533.	1.8	71

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