

Patrick K H Lee

List of Publications by Year in descending order

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82
papers

4,867
citations

109137

35
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98622

67
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89
all docs

89
docs citations

89
times ranked

6766
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanisms of Antibacterial Activity of MgO: Non-ROS Mediated Toxicity of MgO Nanoparticles Towards <i>Escherichia coli</i> . <i>Small</i> , 2014, 10, 1171-1183.	5.2	418
2	Toxicity of Metal Oxide Nanoparticles: Mechanisms, Characterization, and Avoiding Experimental Artefacts. <i>Small</i> , 2015, 11, 26-44.	5.2	308
3	Microbiota fingerprints lose individually identifying features over time. <i>Microbiome</i> , 2017, 5, 1.	4.9	300
4	Influence of Vitamin B12 and Cocultures on the Growth of <i>Dehalococcoides</i> Isolates in Defined Medium. <i>Applied and Environmental Microbiology</i> , 2007, 73, 2847-2853.	1.4	182
5	An Internal Reference Technique for Accurately Quantifying Specific mRNAs by Real-Time PCR with Application to the <i>tceA</i> Reductive Dehalogenase Gene. <i>Applied and Environmental Microbiology</i> , 2005, 71, 3866-3871.	1.4	168
6	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	13.5	164
7	Quantifying Genes and Transcripts To Assess the In Situ Physiology of <i>Dehalococcoides</i> spp. in a Trichloroethene-Contaminated Groundwater Site. <i>Applied and Environmental Microbiology</i> , 2008, 74, 2728-2739.	1.4	155
8	Indoor-Air Microbiome in an Urban Subway Network: Diversity and Dynamics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6760-6770.	1.4	141
9	Sustainable syntrophic growth of <i>Dehalococcoides ethenogenes</i> strain 195 with <i>Desulfovibrio vulgaris</i> Hildenborough and <i>Methanobacterium congolense</i> : global transcriptomic and proteomic analyses. <i>ISME Journal</i> , 2012, 6, 410-421.	4.4	137
10	Interfacial electron transfer and bioelectrocatalysis of carbonized plant material as effective anode of microbial fuel cell. <i>Electrochimica Acta</i> , 2015, 157, 314-323.	2.6	134
11	Discrimination of Multiple <i>Dehalococcoides</i> Strains in a Trichloroethene Enrichment by Quantification of Their Reductive Dehalogenase Genes. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5877-5883.	1.4	132
12	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. <i>Nature Medicine</i> , 2020, 26, 941-951.	15.2	130
13	Toxicity of ZnO and TiO ₂ to <i>Escherichia coli</i> cells. <i>Scientific Reports</i> , 2016, 6, 35243.	1.6	127
14	Insights into the pan-microbiome: skin microbial communities of Chinese individuals differ from other racial groups. <i>Scientific Reports</i> , 2015, 5, 11845.	1.6	112
15	Metagenomic Reconstruction of Key Anaerobic Digestion Pathways in Municipal Sludge and Industrial Wastewater Biogas-Producing Systems. <i>Frontiers in Microbiology</i> , 2016, 7, 778.	1.5	103
16	Reductive Dehalogenase Gene Expression as a Biomarker for Physiological Activity of <i>Dehalococcoides</i> spp. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6161-6168.	1.4	100
17	The roles of the outdoors and occupants in contributing to a potential pan-microbiome of the built environment: a review. <i>Microbiome</i> , 2016, 4, 21.	4.9	99
18	Pyrosequencing of <i>mcrA</i> and Archaeal 16S rRNA Genes Reveals Diversity and Substrate Preferences of Methanogen Communities in Anaerobic Digesters. <i>Applied and Environmental Microbiology</i> , 2015, 81, 604-613.	1.4	98

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19	Modular Metabolic Engineering for Biobased Chemical Production. Trends in Biotechnology, 2019, 37, 152-166.	4.9	94
20	Operation-driven heterogeneity and overlooked feed-associated populations in global anaerobic digester microbiome. Water Research, 2017, 124, 77-84.	5.3	82
21	Transcriptional Expression of the tceA Gene in a Dehalococcoides-Containing Microbial Enrichment. Applied and Environmental Microbiology, 2005, 71, 7145-7151.	1.4	80
22	Skin fungal community and its correlation with bacterial community of urban Chinese individuals. Microbiome, 2016, 4, 46.	4.9	79
23	Stable Carbon Isotope Fractionation of Chloroethenes by Dehalorespiring Isolates. Environmental Science & Technology, 2007, 41, 4277-4285.	4.6	61
24	Metagenomic analysis of a stable trichloroethene-degrading microbial community. ISME Journal, 2012, 6, 1702-1714.	4.4	58
25	Changes of the human skin microbiota upon chronic exposure to polycyclic aromatic hydrocarbon pollutants. Microbiome, 2020, 8, 100.	4.9	58
26	Comparative genomics of two newly isolated <i>Dehalococcoides</i> strains and an enrichment using a genus microarray. ISME Journal, 2011, 5, 1014-1024.	4.4	54
27	Characterization of four TCE-dechlorinating microbial enrichments grown with different cobalamin stress and methanogenic conditions. Applied Microbiology and Biotechnology, 2013, 97, 6439-6450.	1.7	54
28	Comparative Genomics of <i>Dehalococcoides ethenogenes</i> 195 and an Enrichment Culture Containing Unsequenced <i>Dehalococcoides</i> Strains. Applied and Environmental Microbiology, 2008, 74, 3533-3540.	1.4	53
29	Individual and household attributes influence the dynamics of the personal skin microbiota and its association network. Microbiome, 2018, 6, 26.	4.9	48
30	Catabolism and interactions of uncultured organisms shaped by eco-thermodynamics in methanogenic bioprocesses. Microbiome, 2020, 8, 111.	4.9	48
31	Indoor air bacterial communities in Hong Kong households assemble independently of occupant skin microbiomes. Environmental Microbiology, 2016, 18, 1754-1763.	1.8	47
32	Microbial ecology of the atmosphere. FEMS Microbiology Reviews, 2022, 46, .	3.9	44
33	Effect of composites based nickel foam anode in microbial fuel cell using <i>Acetobacter acetii</i> and <i>Gluconobacter roseus</i> as biocatalysts. Bioresource Technology, 2016, 217, 113-120.	4.8	43
34	Tribo-charge enhanced hybrid air filter masks for efficient particulate matter capture with greatly extended service life. Nano Energy, 2021, 85, 106015.	8.2	43
35	Isolation of two new <i>Dehalococcoides mccartyi</i> strains with dissimilar dechlorination functions and their characterization by comparative genomics via microarray analysis. Environmental Microbiology, 2013, 15, 2293-2305.	1.8	41
36	Effects of sludge inoculum and organic feedstock on active microbial communities and methane yield during anaerobic digestion. Frontiers in Microbiology, 2015, 6, 1114.	1.5	40

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37	Superior resolution characterisation of microbial diversity in anaerobic digesters using full-length 16S rRNA gene amplicon sequencing. <i>Water Research</i> , 2020, 178, 115815.	5.3	40
38	Phylogenetic Microarray Analysis of a Microbial Community Performing Reductive Dechlorination at a TCE-Contaminated Site. <i>Environmental Science & Technology</i> , 2012, 46, 1044-1054.	4.6	36
39	Neutral Processes Drive Seasonal Assembly of the Skin Mycobiome. <i>MSystems</i> , 2019, 4, .	1.7	33
40	Evidence for Nitrogen Fixation by <i>Dehalococcoides ethenogenes</i> Strain 195. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7551-7555.	1.4	30
41	Microbial Communities in Full-Scale Wastewater Treatment Systems Exhibit Deterministic Assembly Processes and Functional Dependency over Time. <i>Environmental Science & Technology</i> , 2021, 55, 5312-5323.	4.6	30
42	Substrate induced emergence of different active bacterial and archaeal assemblages during biomethane production. <i>Bioresource Technology</i> , 2013, 148, 517-524.	4.8	29
43	Genome-centric metatranscriptomes and ecological roles of the active microbial populations during cellulosic biomass anaerobic digestion. <i>Biotechnology for Biofuels</i> , 2018, 11, 117.	6.2	29
44	Long-Term Enrichment on Cellulose or Xylan Causes Functional and Taxonomic Convergence of Microbial Communities from Anaerobic Digesters. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1519-1529.	1.4	28
45	Smart Food Waste Recycling Bin (S-FRB) to turn food waste into green energy resources. <i>Journal of Environmental Management</i> , 2019, 234, 290-296.	3.8	28
46	Effect of CH ₄ /O ₂ ratio on fatty acid profile and polyhydroxybutyrate content in a heterotrophic-methanotrophic consortium. <i>Chemosphere</i> , 2015, 141, 235-242.	4.2	27
47	Designing and Engineering <i>Methylobacterium extorquens</i> AM1 for Itaconic Acid Production. <i>Frontiers in Microbiology</i> , 2019, 10, 1027.	1.5	27
48	Characterization of the public transit air microbiome and resistome reveals geographical specificity. <i>Microbiome</i> , 2021, 9, 112.	4.9	26
49	Airborne Bacteria in Outdoor Air and Air of Mechanically Ventilated Buildings at City Scale in Hong Kong across Seasons. <i>Environmental Science & Technology</i> , 2020, 54, 11732-11743.	4.6	25
50	Global Transcriptomic and Proteomic Responses of <i>Dehalococcoides ethenogenes</i> Strain 195 to Fixed Nitrogen Limitation. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1424-1436.	1.4	24
51	Resource recovery from wastewater: application of meta-omics to phosphorus and carbon management. <i>Current Opinion in Biotechnology</i> , 2015, 33, 260-267.	3.3	24
52	City-scale distribution and dispersal routes of mycobiome in residences. <i>Microbiome</i> , 2017, 5, 131.	4.9	24
53	Effects of cellulose concentrations on the syntrophic interactions between <i>Clostridium cellulovorans</i> 743B and <i>Rhodospseudomonas palustris</i> CGA009 in coculture fermentation for biohydrogen production. <i>International Journal of Hydrogen Energy</i> , 2015, 40, 11800-11808.	3.8	23
54	Transcriptomic Responses of the Interactions between <i>Clostridium cellulovorans</i> 743B and <i>Rhodospseudomonas palustris</i> CGA009 in a Cellulose-Grown Coculture for Enhanced Hydrogen Production. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4546-4559.	1.4	22

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55	Rare Taxa Exhibit Disproportionate Cell-Level Metabolic Activity in Enriched Anaerobic Digestion Microbial Communities. <i>MSystems</i> , 2019, 4, .	1.7	22
56	Influence of trace erythromycin and erythromycin-H ₂ O on carbon and nutrients removal and on resistance selection in sequencing batch reactors (SBRs). <i>Applied Microbiology and Biotechnology</i> , 2009, 85, 185-195.	1.7	21
57	A comparison of methods used to unveil the genetic and metabolic pool in the built environment. <i>Microbiome</i> , 2018, 6, 71.	4.9	19
58	Effects of Varying Growth Conditions on Stable Carbon Isotope Fractionation of Trichloroethene (TCE) by <i>A</i> -containing <i>Dehalococcoides mccartyi</i> strains. <i>Environmental Science & Technology</i> , 2013, 47, 12342-12350.	4.6	18
59	A comparative genomics and reductive dehalogenase gene transcription study of two chloroethene-respiring bacteria, <i>Dehalococcoides mccartyi</i> strains MB and 11a. <i>Scientific Reports</i> , 2015, 5, 15204.	1.6	18
60	Global gene expression of <i>Dehalococcoides</i> within a robust dynamic TCEâ€˜dechlorinating community under conditions of periodic substrate supply. <i>Biotechnology and Bioengineering</i> , 2013, 110, 1333-1341.	1.7	17
61	Antibiotic resistance gene sharing networks and the effect of dietary nutritional content on the canine and feline gut resistome. <i>Animal Microbiome</i> , 2020, 2, 4.	1.5	17
62	Multi-omics analysis to decipher the molecular link between chronic exposure to pollution and human skin dysfunction. <i>Scientific Reports</i> , 2021, 11, 18302.	1.6	16
63	Physiological and Metagenomic Characterizations of the Synergistic Relationships between Ammonia- and Nitrite-Oxidizing Bacteria in Freshwater Nitrification. <i>Frontiers in Microbiology</i> , 2018, 9, 280.	1.5	15
64	Development of a Fluorescence-Activated Cell Sorting Method Coupled with Whole Genome Amplification To Analyze Minority and Trace <i>Dehalococcoides</i> Genomes in Microbial Communities. <i>Environmental Science & Technology</i> , 2015, 49, 1585-1593.	4.6	14
65	Diurnal variation in the human skin microbiome affects accuracy of forensic microbiome matching. <i>Microbiome</i> , 2021, 9, 129.	4.9	14
66	Airborne bacterial assemblage in a zero carbon building: A case study. <i>Indoor Air</i> , 2018, 28, 40-50.	2.0	11
67	Profiling Airborne Microbiota in Mechanically Ventilated Buildings Across Seasons in Hong Kong Reveals Higher Metabolic Activity in Low-Abundance Bacteria. <i>Environmental Science & Technology</i> , 2021, 55, 249-259.	4.6	11
68	Development and laboratory evaluation of a compact swirling aerosol sampler (SAS) for collection of atmospheric bioaerosols. <i>Atmospheric Pollution Research</i> , 2015, 6, 556-561.	1.8	10
69	Physiological and molecular characterizations of the interactions in two cellulose-to-methane cocultures. <i>Biotechnology for Biofuels</i> , 2017, 10, 37.	6.2	9
70	Genomic Evidence for Simultaneous Optimization of Transcription and Translation through Codon Variants in the <i>pmoCAB</i> Operon of Type Ia Methanotrophs. <i>MSystems</i> , 2019, 4, .	1.7	7
71	Dysbiosis of the Urinary Bladder Microbiome in Cats with Chronic Kidney Disease. <i>MSystems</i> , 2021, 6, e0051021.	1.7	7
72	Cultivating environmentally responsible citizens in a local university in Hong Kong - evaluating the cognitive, attitudinal, and behavioral outcomes. <i>International Research in Geographical and Environmental Education</i> , 2020, 29, 301-315.	0.8	6

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73	Interplay between Position-Dependent Codon Usage Bias and Hydrogen Bonding at the 5' End of ORFs. <i>MSystems</i> , 2020, 5, .	1.7	6
74	Surface touch network structure determines bacterial contamination spread on surfaces and occupant exposure. <i>Journal of Hazardous Materials</i> , 2021, 416, 126137.	6.5	6
75	Metagenomic insights into the microbial communities of inert and oligotrophic outdoor pier surfaces of a coastal city. <i>Microbiome</i> , 2021, 9, 213.	4.9	6
76	City-Scale Meta-Analysis of Indoor Airborne Microbiota Reveals that Taxonomic and Functional Compositions Vary with Building Types. <i>Environmental Science & Technology</i> , 2021, 55, 15051-15062.	4.6	5
77	Recent Advances of Anaerobic Digestion for Energy Recovery. <i>Environmental Footprints and Eco-design of Products and Processes</i> , 2016, , 87-126.	0.7	3
78	Quantification of <i>Lactobacillus delbrueckii</i> subsp. <i>Bulgaricus</i> and its applicability as a tracer for studying contamination spread on environmental surfaces. <i>Building and Environment</i> , 2021, 197, 107869.	3.0	3
79	Indoor Microbiome and Airborne Pathogens. , 2019, , 96-106.		3
80	Integrative Genome-Scale Metabolic Modeling Reveals Versatile Metabolic Strategies for Methane Utilization in <i>Methylobacterium album</i> BG8. <i>MSystems</i> , 2022, 7, e0007322.	1.7	2
81	Fomite Transmission Follows Invasion Ecology Principles. <i>MSystems</i> , 2022, , e0021122.	1.7	1
82	Single-Bacteria Isolation and Selective Extraction Based on Microfluidic Emulsion and Sequential Micro-Sieves. , 2019, , .		0