

# Patrick K H Lee

## List of Publications by Year in descending order

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Version: 2024-02-01

82  
papers

4,867  
citations

109137

35  
h-index

98622

67  
g-index

89  
all docs

89  
docs citations

89  
times ranked

6766  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Microbial ecology of the atmosphere. FEMS Microbiology Reviews, 2022, 46, .  | 3.9  | 44        |
| 2  | Integrative Genome-Scale Metabolic Modeling Reveals Versatile Metabolic Strategies for Methane Utilization in Methylobacterium album BG8. MSystems, 2022, 7, e0007322.   | 1.7  | 2         |
| 3  | Fomite Transmission Follows Invasion Ecology Principles. MSystems, 2022, , e0021122.   | 1.7  | 1         |
| 4  | Microbial Communities in Full-Scale Wastewater Treatment Systems Exhibit Deterministic Assembly Processes and Functional Dependency over Time. Environmental Science & Technology, 2021, 55, 5312-5323.                                      | 4.6  | 30        |
| 5  | Characterization of the public transit air microbiome and resistome reveals geographical specificity. Microbiome, 2021, 9, 112.  | 4.9  | 26        |
| 6  | Diurnal variation in the human skin microbiome affects accuracy of forensic microbiome matching. Microbiome, 2021, 9, 129.   | 4.9  | 14        |
| 7  | A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.  | 13.5 | 164       |
| 8  | Quantification of Lactobacillus delbrueckii subsp. Bulgaricus and its applicability as a tracer for studying contamination spread on environmental surfaces. Building and Environment, 2021, 197, 107869.                                    | 3.0  | 3         |
| 9  | 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        |
| 10 | Dysbiosis of the Urinary Bladder Microbiome in Cats with Chronic Kidney Disease. MSystems, 2021, 6, e0051021.  | 1.7  | 7         |
| 11 | Surface touch network structure determines bacterial contamination spread on surfaces and occupant exposure. Journal of Hazardous Materials, 2021, 416, 126137.  | 6.5  | 6         |
| 12 | Multi-omics analysis to decipher the molecular link between chronic exposure to pollution and human skin dysfunction. Scientific Reports, 2021, 11, 18302.   | 1.6  | 16        |
| 13 | Profiling Airborne Microbiota in Mechanically Ventilated Buildings Across Seasons in Hong Kong Reveals Higher Metabolic Activity in Low-Abundance Bacteria. Environmental Science & Technology, 2021, 55, 249-259.                           | 4.6  | 11        |
| 14 | Metagenomic insights into the microbial communities of inert and oligotrophic outdoor pier surfaces of a coastal city. Microbiome, 2021, 9, 213.   | 4.9  | 6         |
| 15 | City-Scale Meta-Analysis of Indoor Airborne Microbiota Reveals that Taxonomic and Functional Compositions Vary with Building Types. Environmental Science & Technology, 2021, 55, 15051-15062.   | 4.6  | 5         |
| 16 | Cultivating environmentally responsible citizens in a local university in Hong Kong - evaluating the cognitive, attitudinal, and behavioral outcomes. International Research in Geographical and Environmental Education, 2020, 29, 301-315. | 0.8  | 6         |
| 17 | Catabolism and interactions of uncultured organisms shaped by eco-thermodynamics in methanogenic bioprocesses. Microbiome, 2020, 8, 111.   | 4.9  | 48        |
| 18 | Airborne Bacteria in Outdoor Air and Air of Mechanically Ventilated Buildings at City Scale in Hong Kong across Seasons. Environmental Science & Technology, 2020, 54, 11732-11743.  | 4.6  | 25        |

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|----|--|------|-----------|
| 19 | Interplay between Position-Dependent Codon Usage Bias and Hydrogen Bonding at the 5' End of ORFomes. <i>MSystems</i> , 2020, 5, .  | 1.7  | 6         |
| 20 | Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. <i>Nature Medicine</i> , 2020, 26, 941-951.   | 15.2 | 130       |
| 21 | 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        |
| 22 | Changes of the human skin microbiota upon chronic exposure to polycyclic aromatic hydrocarbon pollutants. <i>Microbiome</i> , 2020, 8, 100.  | 4.9  | 58        |
| 23 | 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        |
| 24 | Modular Metabolic Engineering for Biobased Chemical Production. <i>Trends in Biotechnology</i> , 2019, 37, 152-166.  | 4.9  | 94        |
| 25 | 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         |
| 26 | Rare Taxa Exhibit Disproportionate Cell-Level Metabolic Activity in Enriched Anaerobic Digestion Microbial Communities. <i>MSystems</i> , 2019, 4, .   | 1.7  | 22        |
| 27 | Designing and Engineering <i>Methylobacterium extorquens</i> AM1 for Itaconic Acid Production. <i>Frontiers in Microbiology</i> , 2019, 10, 1027.  | 1.5  | 27        |
| 28 | Neutral Processes Drive Seasonal Assembly of the Skin Mycobiome. <i>MSystems</i> , 2019, 4, .  | 1.7  | 33        |
| 29 | Single-Bacteria Isolation and Selective Extraction Based on Microfluidic Emulsion and Sequential Micro-Sieves. , 2019, , .   |      | 0         |
| 30 | 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        |
| 31 | Indoor Microbiome and Airborne Pathogens. , 2019, , 96-106.  |      | 3         |
| 32 | 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        |
| 33 | Airborne bacterial assemblage in a zero carbon building: A case study. <i>Indoor Air</i> , 2018, 28, 40-50.  | 2.0  | 11        |
| 34 | 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        |
| 35 | Individual and household attributes influence the dynamics of the personal skin microbiota and its association network. <i>Microbiome</i> , 2018, 6, 26.   | 4.9  | 48        |
| 36 | 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        |

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|----|---|-----|-----------|
| 37 | Physiological and molecular characterizations of the interactions in two cellulose-to-methane cocultures. <i>Biotechnology for Biofuels</i> , 2017, 10, 37.   | 6.2 | 9         |
| 38 | Microbiota fingerprints lose individually identifying features over time. <i>Microbiome</i> , 2017, 5, 1.   | 4.9 | 300       |
| 39 | Operation-driven heterogeneity and overlooked feed-associated populations in global anaerobic digester microbiome. <i>Water Research</i> , 2017, 124, 77-84.  | 5.3 | 82        |
| 40 | City-scale distribution and dispersal routes of mycobiome in residences. <i>Microbiome</i> , 2017, 5, 131.  | 4.9 | 24        |
| 41 | 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       |
| 42 | Effect of composites based nickel foam anode in microbial fuel cell using <i>Acetobacter acetii</i> and <i>Gluconobacter roseus</i> as a biocatalysts. <i>Bioresource Technology</i> , 2016, 217, 113-120.  | 4.8 | 43        |
| 43 | 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        |
| 44 | 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         |
| 45 | Toxicity of ZnO and TiO <sub>2</sub> to <i>Escherichia coli</i> cells. <i>Scientific Reports</i> , 2016, 6, 35243.  | 1.6 | 127       |
| 46 | Skin fungal community and its correlation with bacterial community of urban Chinese individuals. <i>Microbiome</i> , 2016, 4, 46.   | 4.9 | 79        |
| 47 | 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        |
| 48 | Indoor air bacterial communities in <scp>H</scp>ong <scp>K</scp>ong households assemble independently of occupant skin microbiomes. <i>Environmental Microbiology</i> , 2016, 18, 1754-1763.  | 1.8 | 47        |
| 49 | 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        |
| 50 | 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        |
| 51 | 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        |
| 52 | Effects of sludge inoculum and organic feedstock on active microbial communities and methane yield during anaerobic digestion. <i>Frontiers in Microbiology</i> , 2015, 6, 1114.  | 1.5 | 40        |
| 53 | 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        |
| 54 | 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        |

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|----|---|-----|-----------|
| 55 | 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        |
| 56 | 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       |
| 57 | 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 &amp; Technology</i> , 2015, 49, 1585-1593. | 4.6 | 14        |
| 58 | 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       |
| 59 | Effect of CH <sub>4</sub> /O <sub>2</sub> ratio on fatty acid profile and polyhydroxybutyrate content in a heterotrophic-methanotrophic consortium. <i>Chemosphere</i> , 2015, 141, 235-242.  | 4.2 | 27        |
| 60 | Toxicity of Metal Oxide Nanoparticles: Mechanisms, Characterization, and Avoiding Experimental Artefacts. <i>Small</i> , 2015, 11, 26-44.   | 5.2 | 308       |
| 61 | Indoor-Air Microbiome in an Urban Subway Network: Diversity and Dynamics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6760-6770.  | 1.4 | 141       |
| 62 | 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       |
| 63 | Characterization of four TCE-dechlorinating microbial enrichments grown with different cobalamin stress and methanogenic conditions. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 6439-6450.   | 1.7 | 54        |
| 64 | Effects of Varying Growth Conditions on Stable Carbon Isotope Fractionation of Trichloroethene (TCE) by <i>tceA</i> -containing <i>Dehalococcoides mccartyi</i> strains. <i>Environmental Science &amp; Technology</i> , 2013, 47, 12342-12350.                 | 4.6 | 18        |
| 65 | Global gene expression of <i>Dehalococcoides</i> within a robust dynamic TCE-dechlorinating community under conditions of periodic substrate supply. <i>Biotechnology and Bioengineering</i> , 2013, 110, 1333-1341.  | 1.7 | 17        |
| 66 | Substrate induced emergence of different active bacterial and archaeal assemblages during biomethane production. <i>Bioresource Technology</i> , 2013, 148, 517-524.  | 4.8 | 29        |
| 67 | Isolation of two new <i>D</i> - <i>Dehalococcoides mccartyi</i> strains with dissimilar dechlorination functions and their characterization by comparative genomics via microarray analysis. <i>Environmental Microbiology</i> , 2013, 15, 2293-2305.           | 1.8 | 41        |
| 68 | 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        |
| 69 | Phylogenetic Microarray Analysis of a Microbial Community Performing Reductive Dechlorination at a TCE-Contaminated Site. <i>Environmental Science &amp; Technology</i> , 2012, 46, 1044-1054.  | 4.6 | 36        |
| 70 | 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       |
| 71 | Metagenomic analysis of a stable trichloroethene-degrading microbial community. <i>ISME Journal</i> , 2012, 6, 1702-1714.   | 4.4 | 58        |
| 72 | Comparative genomics of two newly isolated <i>Dehalococcoides</i> strains and an enrichment using a genus microarray. <i>ISME Journal</i> , 2011, 5, 1014-1024.   | 4.4 | 54        |

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|----|---|-----|-----------|
| 73 | Evidence for Nitrogen Fixation by <i>Dehalococcoides ethenogenes</i> Strain 195. Applied and Environmental Microbiology, 2009, 75, 7551-7555.   | 1.4 | 30        |
| 74 | Influence of trace erythromycin and erythromycin-H <sub>2</sub> O on carbon and nutrients removal and on resistance selection in sequencing batch reactors (SBRs). Applied Microbiology and Biotechnology, 2009, 85, 185-195. | 1.7 | 21        |
| 75 | 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        |
| 76 | Quantifying Genes and Transcripts To Assess the In Situ Physiology of <i>Dehalococcoides</i> spp. in a Trichloroethene-Contaminated Groundwater Site. Applied and Environmental Microbiology, 2008, 74, 2728-2739.            | 1.4 | 155       |
| 77 | Influence of Vitamin B12 and Cocultures on the Growth of <i>Dehalococcoides</i> Isolates in Defined Medium. Applied and Environmental Microbiology, 2007, 73, 2847-2853.  | 1.4 | 182       |
| 78 | Stable Carbon Isotope Fractionation of Chloroethenes by Dehalorespiring Isolates. Environmental Science & Technology, 2007, 41, 4277-4285.  | 4.6 | 61        |
| 79 | Reductive Dehalogenase Gene Expression as a Biomarker for Physiological Activity of <i>Dehalococcoides</i> spp. Applied and Environmental Microbiology, 2006, 72, 6161-6168.  | 1.4 | 100       |
| 80 | Discrimination of Multiple <i>Dehalococcoides</i> Strains in a Trichloroethene Enrichment by Quantification of Their Reductive Dehalogenase Genes. Applied and Environmental Microbiology, 2006, 72, 5877-5883.               | 1.4 | 132       |
| 81 | An Internal Reference Technique for Accurately Quantifying Specific mRNAs by Real-Time PCR with Application to the <i>tceA</i> Reductive Dehalogenase Gene. Applied and Environmental Microbiology, 2005, 71, 3866-3871.      | 1.4 | 168       |
| 82 | Transcriptional Expression of the <i>tceA</i> Gene in a <i>Dehalococcoides</i> -Containing Microbial Enrichment. Applied and Environmental Microbiology, 2005, 71, 7145-7151.   | 1.4 | 80        |