

# Kyle J Bibby

## List of Publications by Year in descending order

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116  
papers

11,206  
citations

38742

50  
h-index

34986

98  
g-index

126  
all docs

126  
docs citations

126  
times ranked

11043  
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative risk assessment of COVID-19 aerosol transmission indoors: a mechanistic stochastic web application. <i>Environmental Technology (United Kingdom)</i> , 2023, 44, 1201-1212.	2.2	8
2	Contribution of SARS-CoV-2 RNA shedding routes to RNA loads in wastewater. <i>Science of the Total Environment</i> , 2022, 806, 150376.	8.0	60
3	Minimizing errors in RT-PCR detection and quantification of SARS-CoV-2 RNA for wastewater surveillance. <i>Science of the Total Environment</i> , 2022, 805, 149877.	8.0	153
4	Sodium hypochlorite disinfection of SARS-CoV-2 spiked in water and municipal wastewater. <i>Science of the Total Environment</i> , 2022, 807, 150766.	8.0	29
5	Inferring SARS-CoV-2 RNA shedding into wastewater relative to the time of infection. <i>Epidemiology and Infection</i> , 2022, 150, e21.	2.1	17
6	Comparison of RT-qPCR and RT-dPCR Platforms for the Trace Detection of SARS-CoV-2 RNA in Wastewater. <i>ACS ES&amp;T Water</i> , 2022, 2, 1871-1880.	4.6	51
7	Impact of Disaster Research on the Development of Early Career Researchers: Lessons Learned from the Wastewater Monitoring Pandemic Response Efforts. <i>Environmental Science &amp; Technology</i> , 2022, 56, 4724-4727.	10.0	1
8	Quantitative microbial risk assessment of outdoor aerosolized pathogens in cities with poor sanitation. <i>Science of the Total Environment</i> , 2022, 827, 154233.	8.0	8
9	Persistence of viable MS2 and Phi6 bacteriophages on carpet and dust. <i>Indoor Air</i> , 2022, 32, .	4.3	6
10	Wastewater-based epidemiological surveillance to monitor the prevalence of SARS-CoV-2 in developing countries with onsite sanitation facilities. <i>Environmental Pollution</i> , 2022, 311, 119679.	7.5	42
11	Intraday variability of indicator and pathogenic viruses in 1-h and 24-h composite wastewater samples: Implications for wastewater-based epidemiology. <i>Environmental Research</i> , 2021, 193, 110531.	7.5	72
12	SARS-CoV-2 RNA monitoring in wastewater as a potential early warning system for COVID-19 transmission in the community: A temporal case study. <i>Science of the Total Environment</i> , 2021, 761, 144216.	8.0	218
13	Using C-Doping to Identify Photocatalytic Properties of Graphitic Carbon Nitride That Govern Antibacterial Efficacy. <i>ACS ES&amp;T Water</i> , 2021, 1, 269-280.	4.6	23
14	Implications of SARS-CoV-2 on current and future operation and management of wastewater systems. <i>Water Environment Research</i> , 2021, 93, 502-515.	2.7	18
15	Standardizing data reporting in the research community to enhance the utility of open data for SARS-CoV-2 wastewater surveillance. <i>Environmental Science: Water Research and Technology</i> , 2021, 7, 1545-1551.	2.4	34
16	Building-level wastewater surveillance using tampon swabs and RT-LAMP for rapid SARS-CoV-2 RNA detection. <i>Environmental Science: Water Research and Technology</i> , 2021, 8, 173-183.	2.4	31
17	Indoor Dust as a Matrix for Surveillance of COVID-19. <i>MSystems</i> , 2021, 6, .	3.8	35
18	Letter to the Editor regarding Mathavarajah et al. (2020) Pandemic danger to the deep: The risk of marine mammals contracting SARS-CoV-2 from wastewater. <i>Science of the Total Environment</i> , 2021, 773, 144855.	8.0	9

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19	Biogeochemistry of the Antrim Shale Natural Gas Reservoir. ACS Earth and Space Chemistry, 2021, 5, 1752-1761.	2.7	8
20	Assessing and managing SARS-CoV-2 occupational health risk to workers handling residuals and biosolids. Science of the Total Environment, 2021, 774, 145732.	8.0	17
21	Wastewater Surveillance during Mass COVID-19 Vaccination on a College Campus. Environmental Science and Technology Letters, 2021, 8, 792-798.	8.7	45
22	Within- and between-Day Variability of SARS-CoV-2 RNA in Municipal Wastewater during Periods of Varying COVID-19 Prevalence and Positivity. ACS ES&T Water, 2021, 1, 2097-2108.	4.6	45
23	SARS-CoV-2 Wastewater Surveillance for Public Health Action. Emerging Infectious Diseases, 2021, 27, 1-8.	4.3	73
24	Variability in RT-qPCR assay parameters indicates unreliable SARS-CoV-2 RNA quantification for wastewater surveillance. Water Research, 2021, 203, 117516.	11.3	68
25	Making waves: Plausible lead time for wastewater based epidemiology as an early warning system for COVID-19. Water Research, 2021, 202, 117438.	11.3	85
26	Differentiating between the possibility and probability of SARS-CoV-2 transmission associated with wastewater: empirical evidence is needed to substantiate risk. FEMS Microbes, 2021, 2, .	2.1	24
27	Viruses in the Built Environment (VIBE) meeting report. Microbiome, 2020, 8, 1.	11.1	345
28	COVID-19 surveillance in Southeastern Virginia using wastewater-based epidemiology. Water Research, 2020, 186, 116296.	11.3	373
29	Decay of SARS-CoV-2 and surrogate murine hepatitis virus RNA in untreated wastewater to inform application in wastewater-based epidemiology. Environmental Research, 2020, 191, 110092.	7.5	285
30	Frontier review on the propensity and repercussion of SARS-CoV-2 migration to aquatic environment. Journal of Hazardous Materials Letters, 2020, 1, 100001.	3.6	49
31	Surveillance of SARS-CoV-2 RNA in wastewater: Methods optimization and quality control are crucial for generating reliable public health information. Current Opinion in Environmental Science and Health, 2020, 17, 82-93.	4.1	126
32	Persistence of SARS-CoV-2 in Water and Wastewater. Environmental Science and Technology Letters, 2020, 7, 937-942.	8.7	318
33	CrAssphage abundance and correlation with molecular viral markers in Italian wastewater. Water Research, 2020, 184, 116161.	11.3	41
34	Detection of SARS-CoV-2 RNA in commercial passenger aircraft and cruise ship wastewater: a surveillance tool for assessing the presence of COVID-19 infected travellers. Journal of Travel Medicine, 2020, 27, .	3.0	146
35	Rethinking wastewater risks and monitoring in light of the COVID-19 pandemic. Nature Sustainability, 2020, 3, 981-990.	23.7	195
36	Persistence of emerging viral fecal indicators in large-scale freshwater mesocosms. Water Research X, 2020, 9, 100067.	6.1	24

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37	Wastewater-Based Epidemiology: Global Collaborative to Maximize Contributions in the Fight Against COVID-19. <i>Environmental Science &amp; Technology</i> , 2020, 54, 7754-7757.	10.0	337
38	Comparison of virus concentration methods for the RT-qPCR-based recovery of murine hepatitis virus, a surrogate for SARS-CoV-2 from untreated wastewater. <i>Science of the Total Environment</i> , 2020, 739, 139960.	8.0	405
39	Editorial Perspectives: will SARS-CoV-2 reset public health requirements in the water industry? Integrating lessons of the past and emerging research. <i>Environmental Science: Water Research and Technology</i> , 2020, 6, 1761-1764.	2.4	8
40	Bacterial community structure correlates with <i>Legionella pneumophila</i> colonization of New York City high rise building premises plumbing systems. <i>Environmental Science: Water Research and Technology</i> , 2020, 6, 1324-1335.	2.4	6
41	Cross-assembly phage and pepper mild mottle virus as viral water quality monitoring tools—potential, research gaps, and way forward. <i>Current Opinion in Environmental Science and Health</i> , 2020, 16, 54-61.	4.1	40
42	Comparative fate of CrAssphage with culturable and molecular fecal pollution indicators during activated sludge wastewater treatment. <i>Environment International</i> , 2020, 136, 105452.	10.0	52
43	SARS-CoV-2 in wastewater: State of the knowledge and research needs. <i>Science of the Total Environment</i> , 2020, 739, 139076.	8.0	599
44	First confirmed detection of SARS-CoV-2 in untreated wastewater in Australia: A proof of concept for the wastewater surveillance of COVID-19 in the community. <i>Science of the Total Environment</i> , 2020, 728, 138764.	8.0	1,393
45	Insights into microbial community structure and function from a shallow, simulated CO <sub>2</sub> leakage aquifer demonstrate microbial selection and adaptation. <i>Environmental Microbiology Reports</i> , 2019, 11, 338-351.	2.4	14
46	The Effects of Sample Storage Conditions on the Microbial Community Composition in Hydraulic Fracturing Produced Water. <i>Geomicrobiology Journal</i> , 2019, 36, 630-638.	2.0	10
47	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	13.3	184
48	Quantitative Microbial Risk Assessment of Swimming in Sewage Impacted Waters Using CrAssphage and Pepper Mild Mottle Virus in a Customizable Model. <i>Environmental Science and Technology Letters</i> , 2019, 6, 571-577.	8.7	41
49	Characterization and biological removal of organic compounds from hydraulic fracturing produced water. <i>Environmental Sciences: Processes and Impacts</i> , 2019, 21, 279-290.	3.5	24
50	Upregulation of peroxide scavenging enzymes and multidrug efflux proteins highlight an active sodium hypochlorite response in <i>Pseudomonas fluorescens</i> biofilms. <i>Biofouling</i> , 2019, 35, 329-339.	2.2	7
51	Co-Occurrence of crAssphage with Antibiotic Resistance Genes in an Impacted Urban Watershed. <i>Environmental Science and Technology Letters</i> , 2019, 6, 216-221.	8.7	46
52	Glutaraldehyde inhibits biological treatment of organic additives in hydraulic fracturing produced water. <i>Science of the Total Environment</i> , 2019, 666, 1161-1168.	8.0	16
53	Metagenomics and the development of viral water quality tools. <i>Npj Clean Water</i> , 2019, 2, .	8.0	51
54	Seasonal dynamics of DNA and RNA viral bioaerosol communities in a daycare center. <i>Microbiome</i> , 2019, 7, 53.	11.1	30

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55	Critical issues in application of molecular methods to environmental virology. <i>Journal of Virological Methods</i> , 2019, 266, 11-24.	2.1	35
56	Microbial communities in Bakken region produced water. <i>FEMS Microbiology Letters</i> , 2018, 365, .	1.8	27
57	Intestinal epithelial Toll-like receptor 4 prevents metabolic syndrome by regulating interactions between microbes and intestinal epithelial cells in mice. <i>Mucosal Immunology</i> , 2018, 11, 727-740.	6.0	34
58	Environmental sources of community-acquired legionnairesâ€™ disease: A review. <i>International Journal of Hygiene and Environmental Health</i> , 2018, 221, 764-774.	4.3	48
59	Correlation of crAssphage qPCR Markers with Culturable and Molecular Indicators of Human Fecal Pollution in an Impacted Urban Watershed. <i>Environmental Science &amp; Technology</i> , 2018, 52, 7505-7512.	10.0	79
60	Efficient Low-pH Iron Removal by a Microbial Iron Oxide Mound Ecosystem at Scalp Level Run. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	20
61	Research Needs for Wastewater Handling in Virus Outbreak Response. <i>Environmental Science &amp; Technology</i> , 2017, 51, 2534-2535.	10.0	12
62	Predominance and Metabolic Potential of Halanaerobium spp. in Produced Water from Hydraulically Fractured Marcellus Shale Wells. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	64
63	Free chlorine and monochloramine inactivation kinetics of <i>Aspergillus</i> and <i>Penicillium</i> in drinking water. <i>Water Research</i> , 2017, 120, 265-271.	11.3	48
64	Centralized Drinking Water Treatment Operations Shape Bacterial and Fungal Community Structure. <i>Environmental Science &amp; Technology</i> , 2017, 51, 7648-7657.	10.0	35
65	Communicating the promise, risks, and ethics of large-scale, open space microbiome and metagenome research. <i>Microbiome</i> , 2017, 5, 132.	11.1	26
66	Quantitative CrAssphage PCR Assays for Human Fecal Pollution Measurement. <i>Environmental Science &amp; Technology</i> , 2017, 51, 9146-9154.	10.0	236
67	Bioreactors for low-pH iron (<sc>ii</sc>) oxidation remove considerable amounts of total iron. <i>RSC Advances</i> , 2017, 7, 35962-35972.	3.6	25
68	Evaluation of Phi6 Persistence and Suitability as an Enveloped Virus Surrogate. <i>Environmental Science &amp; Technology</i> , 2017, 51, 8692-8700.	10.0	157
69	Disinfection of Ebola Virus in Sterilized Municipal Wastewater. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005299.	3.0	20
70	Draft Genome Sequence of <i>Pseudomonas</i> sp. BDAL1 Reconstructed from a Bakken Shale Hydraulic Fracturing-Produced Water Storage Tank Metagenome. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
71	Risks from <i>Ebolavirus</i> Discharge from Hospitals to Sewer Workers. <i>Water Environment Research</i> , 2017, 89, 357-368.	2.7	25
72	Seasonal Dynamics of the Airborne Bacterial Community and Selected Viruses in a Childrenâ€™s Daycare Center. <i>PLoS ONE</i> , 2016, 11, e0151004.	2.5	46

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73	Pulmonary Th17 Antifungal Immunity Is Regulated by the Gut Microbiome. <i>Journal of Immunology</i> , 2016, 197, 97-107.	0.8	108
74	Geochemical and Temporal Influences on the Enrichment of Acidophilic Iron-Oxidizing Bacterial Communities. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3611-3621.	3.1	46
75	Draft Genome Sequence of <i>Methanohalophilus mahii</i> Strain DAL1 Reconstructed from a Hydraulic Fracturing-Produced Water Metagenome. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
76	Ten questions concerning the microbiomes of buildings. <i>Building and Environment</i> , 2016, 109, 224-234.	6.9	143
77	Metatranscriptome analysis of active microbial communities in produced water samples from the Marcellus Shale. <i>Microbial Ecology</i> , 2016, 72, 571-581.	2.8	41
78	Intestinal Interleukin-17 Receptor Signaling Mediates Reciprocal Control of the Gut Microbiota and Autoimmune Inflammation. <i>Immunity</i> , 2016, 44, 659-671.	14.3	256
79	Impacts of Pristine and Transformed Ag and Cu Engineered Nanomaterials on Surficial Sediment Microbial Communities Appear Short-Lived. <i>Environmental Science &amp; Technology</i> , 2016, 50, 2641-2651.	10.0	63
80	Response to Comment on "Ebola Virus Persistence in the Environment: State of the Knowledge and Research Needs". <i>Environmental Science and Technology Letters</i> , 2015, 2, 50-51.	8.7	3
81	Fungal diversity and presence of potentially pathogenic fungi in a hospital hot water system treated with on-site monochloramine. <i>Water Research</i> , 2015, 71, 197-206.	11.3	35
82	Microbial Mats as a Biological Treatment Approach for Saline Wastewaters: The Case of Produced Water from Hydraulic Fracturing. <i>Environmental Science &amp; Technology</i> , 2015, 49, 6172-6180.	10.0	54
83	Efflux as a Glutaraldehyde Resistance Mechanism in <i>Pseudomonas fluorescens</i> and <i>Pseudomonas aeruginosa</i> Biofilms. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 3433-3440.	3.2	64
84	Arsenic induces structural and compositional colonic microbiome change and promotes host nitrogen and amino acid metabolism. <i>Toxicology and Applied Pharmacology</i> , 2015, 289, 397-408.	2.8	89
85	From commensalism to mutualism: integrating the microbial ecology, building science, and indoor air communities to advance research on the indoor microbiome. <i>Indoor Air</i> , 2015, 25, 1-3.	4.3	7
86	Persistence of Ebola Virus in Sterilized Wastewater. <i>Environmental Science and Technology Letters</i> , 2015, 2, 245-249.	8.7	71
87	Ebola Virus Persistence in the Environment: State of the Knowledge and Research Needs. <i>Environmental Science and Technology Letters</i> , 2015, 2, 2-6.	8.7	58
88	The Functional Potential of Microbial Communities in Hydraulic Fracturing Source Water and Produced Water from Natural Gas Extraction Characterized by Metagenomic Sequencing. <i>PLoS ONE</i> , 2014, 9, e107682.	2.5	51
89	Identification accuracy and diversity reproducibility associated with internal transcribed spacer-based fungal taxonomic library preparation. <i>Environmental Microbiology</i> , 2014, 16, 2764-2776.	3.8	14
90	Challenges of studying viral aerosol metagenomics and communities in comparison with bacterial and fungal aerosols. <i>FEMS Microbiology Letters</i> , 2014, 357, 1-9.	1.8	51

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91	Fungal High-throughput Taxonomic Identification tool for use with Next-Generation Sequencing (FHITINGS). <i>Journal of Basic Microbiology</i> , 2014, 54, 315-321.	3.3	60
92	Improved Bacteriophage Genome Data is Necessary for Integrating Viral and Bacterial Ecology. <i>Microbial Ecology</i> , 2014, 67, 242-244.	2.8	23
93	Produced Water Exposure Alters Bacterial Response to Biocides. <i>Environmental Science &amp; Technology</i> , 2014, 48, 13001-13009.	10.0	68
94	Clustering of fungal community internal transcribed spacer sequence data obscures taxonomic diversity. <i>Environmental Microbiology</i> , 2014, 16, 2491-2500.	3.8	24
95	Thermodynamic Controls on the Kinetics of Microbial Low-pH Fe(II) Oxidation. <i>Environmental Science &amp; Technology</i> , 2014, 48, 9246-9254.	10.0	22
96	<i>Lactobacillus rhamnosus</i> HN001 decreases the severity of necrotizing enterocolitis in neonatal mice and preterm piglets: evidence in mice for a role of TLR9. <i>American Journal of Physiology - Renal Physiology</i> , 2014, 306, G1021-G1032.	3.4	103
97	Metagenomic Evaluation of the Highly Abundant Human Gut Bacteriophage CrAssphage for Source Tracking of Human Fecal Pollution. <i>Environmental Science and Technology Letters</i> , 2014, 1, 405-409.	8.7	80
98	Shift in the Microbial Ecology of a Hospital Hot Water System following the Introduction of an On-Site Monochloramine Disinfection System. <i>PLoS ONE</i> , 2014, 9, e102679.	2.5	62
99	Identification of Viral Pathogen Diversity in Sewage Sludge by Metagenome Analysis. <i>Environmental Science &amp; Technology</i> , 2013, 47, 1945-1951.	10.0	301
100	Prevalence of respiratory adenovirus species B and C in sewage sludge. <i>Environmental Sciences: Processes and Impacts</i> , 2013, 15, 336-338.	3.5	23
101	Metagenomic identification of viral pathogens. <i>Trends in Biotechnology</i> , 2013, 31, 275-279.	9.3	69
102	Suppression of methanogenesis in cellulose-fed microbial fuel cells in relation to performance, metabolite formation, and microbial population. <i>Bioresource Technology</i> , 2013, 129, 281-288.	9.6	77
103	Suggested Reporting Parameters for Investigations of Wastewater from Unconventional Shale Gas Extraction. <i>Environmental Science &amp; Technology</i> , 2013, 47, 13220-13221.	10.0	24
104	Microbial Community Changes in Hydraulic Fracturing Fluids and Produced Water from Shale Gas Extraction. <i>Environmental Science &amp; Technology</i> , 2013, 47, 13141-13150.	10.0	149
105	Convergent development of anodic bacterial communities in microbial fuel cells. <i>ISME Journal</i> , 2012, 6, 2002-2013.	9.8	190
106	Particle-size distributions and seasonal diversity of allergenic and pathogenic fungi in outdoor air. <i>ISME Journal</i> , 2012, 6, 1801-1811.	9.8	211
107	Application of enteric viruses for fecal pollution source tracking in environmental waters. <i>Environment International</i> , 2012, 45, 151-164.	10.0	105
108	Human Occupancy as a Source of Indoor Airborne Bacteria. <i>PLoS ONE</i> , 2012, 7, e34867.	2.5	404

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109	Toward a Consensus View on the Infectious Risks Associated with Land Application of Sewage Sludge. Environmental Science & Technology, 2011, 45, 5459-5469.	10.0	100
110	Viral metagenome analysis to guide human pathogen monitoring in environmental samples. Letters in Applied Microbiology, 2011, 52, 386-392.	2.2	90
111	New Directions: A revolution in DNA sequencing now allows for the meaningful integration of biology with aerosol science. Atmospheric Environment, 2011, 45, 1896-1897.	4.1	36
112	Transcriptome sequencing and annotation of the microalgae <i>Dunaliella tertiolecta</i> : Pathway description and gene discovery for production of next-generation biofuels. BMC Genomics, 2011, 12, 148.	2.8	258
113	Nitrogen Removal from Wastewater Using a Hybrid Membrane-Biofilm Process: Pilot-Scale Studies. Water Environment Research, 2010, 82, 195-201.	2.7	16
114	Next-Generation DNA Sequencing Identifies Pathogens in Biosolids. Proceedings of the Water Environment Federation, 2010, 2010, 5606-5613.	0.0	0
115	Pyrosequencing of the 16S rRNA gene to reveal bacterial pathogen diversity in biosolids. Water Research, 2010, 44, 4252-4260.	11.3	137
116	The Hybrid Membrane Biofilm Process for TN Removal from Wastewater: Bench and Pilot Scale Studies. , 2008, , .		0