

# Orin C Shanks

## List of Publications by Year in descending order

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74  
papers

4,742  
citations

76326

40  
h-index

98798

67  
g-index

74  
all docs

74  
docs citations

74  
times ranked

3986  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Performance of NIST SRM <sup>®</sup> 2917 with 13 recreational water quality monitoring qPCR assays. <i>Water Research</i> , 2022, 212, 118114.	11.3	10
3	Effectiveness of two wastewater disinfection strategies for the removal of fecal indicator bacteria, bacteriophage, and enteric viral pathogens concentrated using dead-end hollow fiber ultrafiltration (D-HFUF). <i>Science of the Total Environment</i> , 2022, 831, 154861.	8.0	9
4	Identifying septic pollution exposure routes during a waterborne norovirus outbreak - A new application for human-associated microbial source tracking qPCR. <i>Journal of Microbiological Methods</i> , 2021, 180, 106091.	1.6	15
5	Metagenomic Sequencing and Quantitative Real-Time PCR for Fecal Pollution Assessment in an Urban Watershed. <i>Frontiers in Water</i> , 2021, 3, 626849.	2.3	15
6	Variable fecal source prioritization in recreational waters routinely monitored with viral and bacterial general indicators. <i>Water Research</i> , 2021, 192, 116845.	11.3	13
7	Variability in RT-qPCR assay parameters indicates unreliable SARS-CoV-2 RNA quantification for wastewater surveillance. <i>Water Research</i> , 2021, 203, 117516.	11.3	68
8	Microbial source tracking. , 2020, , 71-87.		1
9	Contamination Scenario Matters when Using Viral and Bacterial Human-Associated Genetic Markers as Indicators of a Health Risk in Untreated Sewage-Impacted Recreational Waters. <i>Environmental Science &amp; Technology</i> , 2020, 54, 13101-13109.	10.0	7
10	Fecal pollution source characterization at non-point source impacted beaches under dry and wet weather conditions. <i>Water Research</i> , 2020, 182, 116014.	11.3	32
11	Viral and Bacterial Fecal Indicators in Untreated Wastewater across the Contiguous United States Exhibit Geospatial Trends. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	24
12	Large-scale implementation of standardized quantitative real-time PCR fecal source identification procedures in the Tillamook Bay Watershed. <i>PLoS ONE</i> , 2019, 14, e0216827.	2.5	18
13	Extended persistence of general and cattle-associated fecal indicators in marine and freshwater environment. <i>Science of the Total Environment</i> , 2019, 650, 1292-1302.	8.0	29
14	Incidence of somatic and F+ coliphage in Great Lake Basin recreational waters. <i>Water Research</i> , 2018, 140, 200-210.	11.3	13
15	Global Distribution of Human-Associated Fecal Genetic Markers in Reference Samples from Six Continents. <i>Environmental Science &amp; Technology</i> , 2018, 52, 5076-5084.	10.0	73
16	A human fecal contamination score for ranking recreational sites using the HF183/BacR287 quantitative real-time PCR method. <i>Water Research</i> , 2018, 128, 148-156.	11.3	33
17	Evidence of Genetic Fecal Marker Interactions between Water Column and Periphyton in Artificial Streams. <i>ACS Omega</i> , 2018, 3, 10107-10113.	3.5	3
18	Comparison of somatic and F+ coliphage enumeration methods with large volume surface water samples. <i>Journal of Virological Methods</i> , 2018, 261, 63-66.	2.1	8

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19	Quantitative CrAssphage PCR Assays for Human Fecal Pollution Measurement. <i>Environmental Science &amp; Technology</i> , 2017, 51, 9146-9154.	10.0	236
20	Differential decomposition of bacterial and viral fecal indicators in common human pollution types. <i>Water Research</i> , 2016, 105, 591-601.	11.3	32
21	Occurrence of Host-Associated Fecal Markers on Child Hands, Household Soil, and Drinking Water in Rural Bangladeshi Households. <i>Environmental Science and Technology Letters</i> , 2016, 3, 393-398.	8.7	69
22	Data Acceptance Criteria for Standardized Human-Associated Fecal Source Identification Quantitative Real-Time PCR Methods. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2773-2782.	3.1	51
23	Identification of Specialists and Abundance-Occupancy Relationships among Intestinal Bacteria of <i>Aves</i> , Mammalia, and Actinopterygii. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1496-1503.	3.1	3
24	Occurrence of Host-Associated Fecal Markers on Child Hands, Household Soil, and Drinking Water in Rural Bangladeshi Households. <i>Environmental Science and Technology Letters</i> , 2016, 3, 393-398.	8.7	26
25	Overview of Microbial Source Tracking Methods Targeting Human Fecal Pollution Sources. , 2015, , 3.4.3-1-3.4.3-8.		1
26	Human-Associated Fecal Quantitative Polymerase Chain Reaction Measurements and Simulated Risk of Gastrointestinal Illness in Recreational Waters Contaminated with Raw Sewage. <i>Environmental Science and Technology Letters</i> , 2015, 2, 270-275.	8.7	99
27	Comparison of Sewage and Animal Fecal Microbiomes by Using Oligotyping Reveals Potential Human Fecal Indicators in Multiple Taxonomic Groups. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7023-7033.	3.1	57
28	Changes in bacterial and eukaryotic communities during sewage decomposition in Mississippi river water. <i>Water Research</i> , 2015, 69, 30-39.	11.3	49
29	Biotic Interactions and Sunlight Affect Persistence of Fecal Indicator Bacteria and Microbial Source Tracking Genetic Markers in the Upper Mississippi River. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3952-3961.	3.1	63
30	Factors affecting the presence of human-associated and fecal indicator real-time quantitative PCR genetic markers in urban-impacted recreational beaches. <i>Water Research</i> , 2014, 64, 196-208.	11.3	47
31	Improved HF183 Quantitative Real-Time PCR Assay for Characterization of Human Fecal Pollution in Ambient Surface Water Samples. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3086-3094.	3.1	221
32	Age-Related Shifts in the Density and Distribution of Genetic Marker Water Quality Indicators in Cow and Calf Feces. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1588-1594.	3.1	10
33	Detection limits and cost comparisons of human- and gull-associated conventional and quantitative PCR assays in artificial and environmental waters. <i>Journal of Environmental Management</i> , 2014, 136, 112-120.	7.8	21
34	New Performance Metrics for Quantitative Polymerase Chain Reaction-Based Microbial Source Tracking Methods. <i>Environmental Science and Technology Letters</i> , 2014, 1, 20-25.	8.7	12
35	Development of Rapid Canine Fecal Source Identification PCR-Based Assays. <i>Environmental Science &amp; Technology</i> , 2014, 48, 11453-11461.	10.0	35
36	Human Fecal Source Identification with Real-Time Quantitative PCR. <i>Methods in Molecular Biology</i> , 2014, 1096, 85-99.	0.9	5

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37	Marine and Freshwater Fecal Indicators and Source Identification. , 2014, , 1-33.		0
38	Sewage reflects the distribution of human faecal <i>achnospiraceae</i> . Environmental Microbiology, 2013, 15, 2213-2227.	3.8	88
39	Performance of forty-one microbial source tracking methods: A twenty-seven lab evaluation study. Water Research, 2013, 47, 6812-6828.	11.3	253
40	Recommendations following a multi-laboratory comparison of microbial source tracking methods. Water Research, 2013, 47, 6829-6838.	11.3	53
41	Evaluation of the repeatability and reproducibility of a suite of qPCR-based microbial source tracking methods. Water Research, 2013, 47, 6839-6848.	11.3	56
42	Enterococcus and Escherichia coli fecal source apportionment with microbial source tracking genetic markers – Is it feasible?. Water Research, 2013, 47, 6849-6861.	11.3	39
43	Comparison of PCR and quantitative real-time PCR methods for the characterization of ruminant and cattle fecal pollution sources. Water Research, 2013, 47, 6921-6928.	11.3	45
44	Performance of human fecal anaerobe-associated PCR-based assays in a multi-laboratory method evaluation study. Water Research, 2013, 47, 6897-6908.	11.3	117
45	Characterization of fecal concentrations in human and other animal sources by physical, culture-based, and quantitative real-time PCR methods. Water Research, 2013, 47, 6873-6882.	11.3	52
46	Performance evaluation of canine-associated Bacteroidales assays in a multi-laboratory comparison study. Water Research, 2013, 47, 6909-6920.	11.3	48
47	Comparison of the Microbial Community Structures of Untreated Wastewaters from Different Geographic Locales. Applied and Environmental Microbiology, 2013, 79, 2906-2913.	3.1	142
48	Differential Decay of Enterococci and Escherichia coli Originating from Two Fecal Pollution Sources. Applied and Environmental Microbiology, 2013, 79, 2488-2492.	3.1	45
49	Marine and Freshwater Fecal Indicators and Source Identification. , 2013, , 199-235.		3
50	Dramatic Improvements in Beach Water Quality Following Gull Removal. Environmental Science & Technology, 2012, 46, 10206-10213.	10.0	80
51	Interlaboratory Comparison of Real-Time PCR Protocols for Quantification of General Fecal Indicator Bacteria. Environmental Science & Technology, 2012, 46, 945-953.	10.0	72
52	Distribution of Genetic Marker Concentrations for Fecal Indicator Bacteria in Sewage and Animal Feces. Applied and Environmental Microbiology, 2012, 78, 4225-4232.	3.1	33
53	Community Structures of Fecal Bacteria in Cattle from Different Animal Feeding Operations. Applied and Environmental Microbiology, 2011, 77, 2992-3001.	3.1	342
54	Combining Land Use Information and Small Stream Sampling with PCR-Based Methods for Better Characterization of Diffuse Sources of Human Fecal Pollution. Environmental Science & Technology, 2011, 45, 5652-5659.	10.0	53

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55	Differential decay of human faecal <i>Bacteroides</i> in marine and freshwater. <i>Environmental Microbiology</i> , 2011, 13, 3235-3249.	3.8	102
56	Decay of Bacterial Pathogens, Fecal Indicators, and Real-Time Quantitative PCR Genetic Markers in Manure-Amended Soils. <i>Applied and Environmental Microbiology</i> , 2011, 77, 4839-4848.	3.1	95
57	Evaluation of genetic markers from the 16S rRNA gene V2 region for use in quantitative detection of selected Bacteroidales species and human fecal waste by qPCR. <i>Systematic and Applied Microbiology</i> , 2010, 33, 348-357.	2.8	188
58	Performance Assessment PCR-Based Assays Targeting <i>Bacteroidales</i> Genetic Markers of Bovine Fecal Pollution. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1359-1366.	3.1	81
59	Improved strategies and optimization of calibration models for real-time PCR absolute quantification. <i>Water Research</i> , 2010, 44, 4726-4735.	11.3	86
60	Performance of PCR-Based Assays Targeting <i>Bacteroidales</i> Genetic Markers of Human Fecal Pollution in Sewage and Fecal Samples. <i>Environmental Science &amp; Technology</i> , 2010, 44, 6281-6288.	10.0	106
61	Quantitative PCR for Genetic Markers of Human Fecal Pollution. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5507-5513.	3.1	135
62	A Bayesian method for calculating real-time quantitative PCR calibration curves using absolute plasmid DNA standards. <i>BMC Bioinformatics</i> , 2008, 9, 120.	2.6	77
63	Quantitative PCR for Detection and Enumeration of Genetic Markers of Bovine Fecal Pollution. <i>Applied and Environmental Microbiology</i> , 2008, 74, 745-752.	3.1	183
64	Temporal Assessment of the Impact of Exposure to Cow Feces in Two Watersheds by Multiple Host-Specific PCR Assays. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6839-6847.	3.1	23
65	Identification of Bacterial DNA Markers for the Detection of Human Fecal Pollution in Water. <i>Applied and Environmental Microbiology</i> , 2007, 73, 2416-2422.	3.1	61
66	Identification of chicken-specific fecal microbial sequences using a metagenomic approach. <i>Water Research</i> , 2007, 41, 3561-3574.	11.3	73
67	Animal DNA in PCR reagents plagues ancient DNA research. <i>Journal of Archaeological Science</i> , 2007, 34, 1361-1366.	2.4	142
68	Competitive Metagenomic DNA Hybridization Identifies Host-Specific Microbial Genetic Markers in Cow Fecal Samples. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4054-4060.	3.1	77
69	Use of competitive DNA hybridization to identify differences in the genomes of bacteria. <i>Journal of Microbiological Methods</i> , 2006, 66, 321-330.	1.6	19
70	Basin-Wide Analysis of the Dynamics of Fecal Contamination and Fecal Source Identification in Tillamook Bay, Oregon. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5537-5546.	3.1	89
71	DNA from ancient stone tools and bones excavated at Bugas-Holding, Wyoming. <i>Journal of Archaeological Science</i> , 2005, 32, 27-38.	2.4	29
72	DNA AND PROTEIN RECOVERY FROM WASHED EXPERIMENTAL STONE TOOLS*. <i>Archaeometry</i> , 2004, 46, 663-672.	1.3	20

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73	Recovery of Protein and DNA Trapped in Stone Tool Microcracks. <i>Journal of Archaeological Science</i> , 2001, 28, 965-972.	2.4	42
74	Protein Analysis of Bugas-Holding Tools: New Trends in Immunological Studies. <i>Journal of Archaeological Science</i> , 1999, 26, 1183-1191.	2.4	32