

Christopher Yost

List of Publications by Year in descending order

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Version: 2024-02-01

78
papers

2,550
citations

172207

29
h-index

205818

48
g-index

82
all docs

82
docs citations

82
times ranked

3139
citing authors

#	ARTICLE	IF	CITATIONS
1	Metagenomic and Metatranscriptomic Analyses Reveal that Biobed Systems can Enrich for Antibiotic Resistance and Genetic Mobility Genes. <i>Letters in Applied Microbiology</i> , 2022, , .	1.0	0
2	An epigenetic switch activates bacterial quorum sensing and horizontal transfer of an integrative and conjugative element. <i>Nucleic Acids Research</i> , 2022, 50, 975-988.	6.5	17
3	Alternative, environmentally conscious approaches for removing antibiotics from wastewater treatment systems. <i>Chemosphere</i> , 2021, 263, 128177.	4.2	63
4	A bacteriophage infecting <i>Mesorhizobium</i> species has a prolate capsid and shows similarities to a family of <i>Caulobacter crescentus</i> phages. <i>Canadian Journal of Microbiology</i> , 2021, 67, 147-160.	0.8	3
5	Complete Genome Sequence of a <i>Pseudomonas simiae</i> Strain with Biocontrol Potential against <i>Aphanomyces</i> Root Rot. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
6	Fate and distribution of determinants of antimicrobial resistance in lateral flow sand filters used for treatment of domestic wastewater. <i>Science of the Total Environment</i> , 2021, 767, 145481.	3.9	4
7	Comparative genomic analyses of β -lactamase (<i>bla</i> _{CMY-42})-encoding plasmids isolated from wastewater treatment plants in Canada. <i>Canadian Journal of Microbiology</i> , 2021, 67, 737-748.	0.8	3
8	Metagenomic and metatranscriptomic analysis reveals enrichment for xenobiotic-degrading bacterial specialists and xenobiotic-degrading genes in a Canadian Prairie cell biobed system. <i>Environmental Microbiology Reports</i> , 2021, 13, 720-727.	1.0	11
9	A Meta-Analysis to Determine the State of Biological Control of <i>Aphanomyces</i> Root Rot. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 777042.	1.6	3
10	Introduction. <i>Canadian Journal of Microbiology</i> , 2020, 66, v-v.	0.8	0
11	Setting a baseline for global urban virome surveillance in sewage. <i>Scientific Reports</i> , 2020, 10, 13748.	1.6	39
12	Isolation and Characterization of ν B_PagP-SK1, a T7-Like Phage Infecting <i>Pantoea agglomerans</i> . <i>Phage</i> , 2020, 1, 45-56.	0.8	7
13	Genome Sequences of ν B_RleM_RL38JI and ν B_RleM_RL2RES, Two Virulent <i>Rhizobium leguminosarum</i> Transducing Phages. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
14	Transcriptomics reveal core activities of the plant growth-promoting bacterium <i>Delftia acidovorans</i> RAY209 during interaction with canola and soybean roots. <i>Microbial Genomics</i> , 2020, 6, .	1.0	5
15	Lateral flow sand filters are effective for removal of antibiotic resistance genes from domestic wastewater. <i>Water Research</i> , 2019, 162, 482-491.	5.3	22
16	Spatial analysis of a hydrocarbon waste-remediating landfarm demonstrates influence of management practices on bacterial and fungal community structure. <i>Microbial Biotechnology</i> , 2019, 12, 1199-1209.	2.0	11
17	Draft Whole-Genome Sequence of <i>Deinococcus</i> sp. UR1, a Putative Novel Species Isolated from an External Stainless Steel Surface in the Canadian Prairies. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
18	Sources of Antibiotic Resistance Genes in a Rural River System. <i>Journal of Environmental Quality</i> , 2018, 47, 997-1005.	1.0	24

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19	Removal of antibiotic resistance genes in two tertiary level municipal wastewater treatment plants. <i>Science of the Total Environment</i> , 2018, 643, 292-300.	3.9	86
20	Fate of antibiotic resistance genes in two Arctic tundra wetlands impacted by municipal wastewater. <i>Science of the Total Environment</i> , 2018, 642, 1415-1428.	3.9	27
21	Identifying the core bacterial and fungal communities within four agricultural biobeds used for the treatment of pesticide rinsates. <i>Journal of Applied Microbiology</i> , 2018, 125, 1333-1342.	1.4	15
22	Antimicrobial resistance gene surveillance in the receiving waters of an upgraded wastewater treatment plant. <i>Facets</i> , 2018, 3, 128-138.	1.1	19
23	Editorial foreword to Dr. Gregor Reid's review paper: The development of probiotics for women's health. <i>Canadian Journal of Microbiology</i> , 2017, 63, iii-iii.	0.8	0
24	Antibiotic resistance genes in municipal wastewater treatment systems and receiving waters in Arctic Canada. <i>Science of the Total Environment</i> , 2017, 598, 1085-1094.	3.9	71
25	An uncharacterized gene coding a conserved lytic transglycosylase domain (RL4716) is required for proper cell envelope function in <i>Rhizobium leguminosarum</i> . <i>FEMS Microbiology Letters</i> , 2017, 364, .	0.7	3
26	Complete Genome Sequence of <i>Delftia acidovorans</i> RAY209, a Plant Growth-Promoting Rhizobacterium for Canola and Soybean. <i>Genome Announcements</i> , 2017, 5, .	0.8	14
27	The Use of Transposon Insertion Sequencing to Interrogate the Core Functional Genome of the Legume Symbiont <i>Rhizobium leguminosarum</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1873.	1.5	29
28	Temporal variation in the prevalence and species richness of <i>Campylobacter</i> spp. in a prairie watershed impacted by urban and agricultural mixed inputs. <i>Canadian Journal of Microbiology</i> , 2016, 62, 402-410.	0.8	3
29	Does it take a community to raise a plant? A summary of the Canadian Crop Microbiome Workshop. <i>Canadian Journal of Microbiology</i> , 2016, 62, 980-982.	0.8	3
30	Characterization of the temperate phage vB_RleM_PPF1 and its site-specific integration into the <i>Rhizobium leguminosarum</i> F1 genome. <i>Molecular Genetics and Genomics</i> , 2016, 291, 349-362.	1.0	7
31	Fecal Contamination in the Surface Waters of a Rural- and an Urban-Source Watershed. <i>Journal of Environmental Quality</i> , 2015, 44, 1556-1567.	1.0	20
32	Draft Genome Sequence of <i>Rheinheimera</i> sp. KL1, Isolated from a Freshwater Lake in Southern Saskatchewan, Canada. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
33	Oxidative stress and metabolic perturbations in <i>Escherichia coli</i> exposed to sublethal levels of 2,4-dichlorophenoxyacetic acid. <i>Chemosphere</i> , 2015, 135, 453-461.	4.2	59
34	Genomic and phenotypic characterization of <i>Rhizobium gallicum</i> phage vB_RglS_P106B. <i>Microbiology (United Kingdom)</i> , 2015, 161, 611-620.	0.7	12
35	Comparison of the Prevalences and Diversities of <i>Listeria</i> Species and <i>Listeria monocytogenes</i> in an Urban and a Rural Agricultural Watershed. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3812-3822.	1.4	53
36	Draft Genome Sequence and Annotation of Phyllosphere-Persisting <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Livingstone Strain CKY-S4, Isolated from an Urban Lake in Regina, Canada. <i>Genome Announcements</i> , 2015, 3, .	0.8	1

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37	A previously uncharacterized tetratricopeptide-repeat-containing protein is involved in cell envelope function in <i>Rhizobium leguminosarum</i> . <i>Microbiology (United Kingdom)</i> , 2015, 161, 148-157.	0.7	6
38	Effect of Hillslope Position and Manure Application Rates on the Persistence of Fecal Source Tracking Indicators in an Agricultural Soil. <i>Journal of Environmental Quality</i> , 2014, 43, 450-458.	1.0	5
39	Characterization and comparative analysis of antibiotic resistance plasmids isolated from a wastewater treatment plant. <i>Frontiers in Microbiology</i> , 2014, 5, 558.	1.5	37
40	Homoserine catabolism by <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> 3841 requires a plasmid-borne gene cluster that also affects competitiveness for nodulation. <i>Environmental Microbiology</i> , 2014, 16, 205-217.	1.8	24
41	Construction of a mariner-based transposon vector for use in insertion sequence mutagenesis in selected members of the Rhizobiaceae. <i>BMC Microbiology</i> , 2014, 14, 298.	1.3	30
42	Characterizing spatial structure of sediment <i>E. coli</i> populations to inform sampling design. <i>Environmental Monitoring and Assessment</i> , 2014, 186, 277-291.	1.3	13
43	Reach specificity in sediment <i>E. coli</i> population turnover and interaction with waterborne populations. <i>Science of the Total Environment</i> , 2014, 496, 402-413.	3.9	15
44	Legume seed exudates and <i>Physcomitrella patens</i> extracts influence swarming behavior in <i>Rhizobium leguminosarum</i> . <i>Canadian Journal of Microbiology</i> , 2014, 60, 15-24.	0.8	22
45	Baseline and storm event monitoring of Bacteroidales marker concentrations and enteric pathogen presence in a rural Canadian watershed. <i>Water Research</i> , 2014, 60, 278-288.	5.3	22
46	Point-of-use water disinfection using UV light-emitting diodes to reduce bacterial contamination. <i>Environmental Science and Pollution Research</i> , 2013, 20, 5441-5448.	2.7	44
47	Evaluation of statistical models for predicting <i>Escherichia coli</i> particle attachment in fluvial systems. <i>Water Research</i> , 2013, 47, 6701-6711.	5.3	12
48	Mutation of the Sensor Kinase <i>chvG</i> in <i>Rhizobium leguminosarum</i> Negatively Impacts Cellular Metabolism, Outer Membrane Stability, and Symbiosis. <i>Journal of Bacteriology</i> , 2012, 194, 768-777.	1.0	42
49	Changes in the Gut Microbiome of the Sea Lamprey during Metamorphosis. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7638-7644.	1.4	33
50	Persistence of host-associated Bacteroidales gene markers and their quantitative detection in an urban and agricultural mixed prairie watershed. <i>Water Research</i> , 2012, 46, 2891-2904.	5.3	72
51	Genetic analysis reveals links between lipid A structure and expression of the outer membrane protein gene, <i>ropB</i> , in <i>Rhizobium leguminosarum</i> . <i>FEMS Microbiology Letters</i> , 2012, 335, 130-139.	0.7	10
52	Evaluation of two quantitative PCR assays using Bacteroidales and mitochondrial DNA markers for tracking dog fecal contamination in waterbodies. <i>Journal of Microbiological Methods</i> , 2012, 91, 459-467.	0.7	22
53	Characterization of a mobile and multiple resistance plasmid isolated from swine manure and its detection in soil after manure application. <i>Journal of Applied Microbiology</i> , 2012, 112, 1123-1133.	1.4	30
54	Atomic force microscopy of a <i>ctpA</i> mutant in <i>Rhizobium leguminosarum</i> reveals surface defects linking CtpA function to biofilm formation. <i>Microbiology (United Kingdom)</i> , 2011, 157, 3049-3058.	0.7	32

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55	Mutation of a Broadly Conserved Operon (RL3499-RL3502) from <i>Rhizobium leguminosarum</i> Biovar <i>viciae</i> Causes Defects in Cell Morphology and Envelope Integrity. <i>Journal of Bacteriology</i> , 2011, 193, 2684-2694.	1.0	24
56	Identification of a novel ABC transporter required for desiccation tolerance, and biofilm formation in <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> 3841. <i>FEMS Microbiology Ecology</i> , 2010, 71, 327-340.	1.3	97
57	Characterization of swarming motility in <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> . <i>FEMS Microbiology Letters</i> , 2010, 307, 165-174.	0.7	29
58	Characterization of a Gene Family of Outer Membrane Proteins (<i>ropB</i>) in <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> VF39SM and the Role of the Sensor Kinase ChvG in Their Regulation. <i>Journal of Bacteriology</i> , 2010, 192, 975-983.	1.0	28
59	Quantitative Real-Time PCR Assays for Sensitive Detection of Canada Goose-Specific Fecal Pollution in Water Sources. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4886-4889.	1.4	35
60	<i>Rhizobium leguminosarum</i> biovar <i>viciae</i> 3841, deficient in 27-hydroxyoctacosanoate-modified lipopolysaccharide, is impaired in desiccation tolerance, biofilm formation and motility. <i>Microbiology (United Kingdom)</i> , 2009, 155, 3055-3069.	0.7	66
61	Assessment of the microbial quality of irrigation water in a prairie watershed. <i>Journal of Applied Microbiology</i> , 2009, 106, 442-454.	1.4	13
62	Evaluation of host-specific Bacteroidales 16S rRNA gene markers as a complementary tool for detecting fecal pollution in a prairie watershed. <i>Water Research</i> , 2009, 43, 4838-4849.	5.3	75
63	The major chemotaxis gene cluster of <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> is essential for competitive nodulation. <i>Molecular Microbiology</i> , 2007, 63, 348-362.	1.2	106
64	Mutagenesis of the carboxy terminal protease CtpA decreases desiccation tolerance in <i>Rhizobium leguminosarum</i> . <i>FEMS Microbiology Letters</i> , 2007, 272, 65-74.	0.7	28
65	Characterization of genes involved in erythritol catabolism in <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> . <i>Microbiology (United Kingdom)</i> , 2006, 152, 2061-2074.	0.7	61
66	LORE1, an active low-copy-number TY3-gypsy retrotransposon family in the model legume <i>Lotus japonicus</i> . <i>Plant Journal</i> , 2005, 44, 372-381.	2.8	56
67	<i>Rhizobium leguminosarum</i> methyl-accepting chemotaxis protein genes are down-regulated in the pea nodule. <i>Archives of Microbiology</i> , 2004, 182, 505-513.	1.0	32
68	Characterization of the nodulation plasmid encoded chemoreceptor gene <i>mcpG</i> from <i>Rhizobium leguminosarum</i> . <i>BMC Microbiology</i> , 2003, 3, 1.	1.3	24
69	Origin of Contamination and Genetic Diversity of <i>Escherichia coli</i> in Beef Cattle. <i>Applied and Environmental Microbiology</i> , 2003, 69, 2794-2799.	1.4	95
70	The <i>glcB</i> locus of <i>Rhizobium leguminosarum</i> VF39 encodes an arabinose-inducible malate synthase. <i>Canadian Journal of Microbiology</i> , 2002, 48, 922-932.	0.8	12
71	Molecular typing techniques to characterize the development of a lactic acid bacteria community on vacuum-packaged beef. <i>International Journal of Food Microbiology</i> , 2002, 72, 97-105.	2.1	37
72	Evaluation of the ability of lysozyme and nisin to control meat spoilage bacteria. <i>International Journal of Food Microbiology</i> , 2001, 70, 111-119.	2.1	93

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73	The use of multiplex PCR reactions to characterize populations of lactic acid bacteria associated with meat spoilage. <i>Letters in Applied Microbiology</i> , 2000, 31, 129-133.	1.0	77
74	Megaplasmid pRme2011a of <i>Sinorhizobium meliloti</i> Is Not Required for Viability. <i>Journal of Bacteriology</i> , 2000, 182, 3582-3586.	1.0	87
75	<i>Rhizobium leguminosarum</i> contains a group of genes that appear to code for methyl-accepting chemotaxis proteins. <i>Microbiology (United Kingdom)</i> , 1998, 144, 1945-1956.	0.7	65
76	Plasmid-Encoded Catabolic Genes in <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> : Evidence for a Plant-Inducible Rhamnose Locus Involved in Competition for Nodulation. <i>Molecular Plant-Microbe Interactions</i> , 1998, 11, 1175-1185.	1.4	76
77	<i>Rhizobium leguminosarum</i> as a plant growth-promoting rhizobacterium: direct growth promotion of canola and lettuce. <i>Canadian Journal of Microbiology</i> , 1996, 42, 279-283.	0.8	209
78	Animals and Humans as Sources of Fecal Indicator Bacteria. , 0, , 67-91.		9