

Brian B Oakley

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

24,323
citations

196777

29
h-index

139680

61
g-index

67
all docs

67
docs citations

67
times ranked

33883
citing authors

#	ARTICLE	IF	CITATIONS
1	Considerations and best practices in animal science 16S ribosomal RNA gene sequencing microbiome studies. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	36
2	Assessment of bacterial and fungal populations in urine from clinically healthy dogs using next-generation sequencing. <i>Journal of Veterinary Internal Medicine</i> , 2021, 35, 1416-1426.	0.6	14
3	Data analysis workflow for the detection of canine vector-borne pathogens using 16S rRNA Next-Generation Sequencing. <i>BMC Veterinary Research</i> , 2021, 17, 262.	0.7	2
4	Emerging Pathogenic Gammaproteobacteria <i>Wohlfahrtiimonas chitiniclastica</i> and <i>Ignatzschineria</i> Species in a Turkey Vulture (<i>Cathartes aura</i>). , 2021, 35, 280-289.		1
5	Evaluation of a commercial microbial enrichment kit used prior DNA extraction to improve the molecular detection of vector-borne pathogens from naturally infected dogs. <i>Journal of Microbiological Methods</i> , 2021, 188, 106163.	0.7	3
6	Draft Genome Sequences of Two <i>Paenibacillus</i> Isolates from Goose and Chicken Gastrointestinal Material. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
7	Draft Genome Sequences of Two <i>Clostridium</i> Isolates from the Poultry Gastrointestinal Tract. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
8	Draft Genome Sequences of Two Potentially Novel <i>Bacillus</i> Isolates from Backyard and Commercial Chicken Gastrointestinal Tracts. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
9	Broiler chickens and early life programming: Microbiome transplant-induced cecal community dynamics and phenotypic effects. <i>PLoS ONE</i> , 2020, 15, e0242108.	1.1	16
10	Characterization of LysBC17, a Lytic Endopeptidase from <i>Bacillus cereus</i> . <i>Antibiotics</i> , 2019, 8, 155.	1.5	9
11	Comparison of mycotoxin concentrations in grain versus grain-free dry and wet commercial dog foods. <i>Toxicology Communications</i> , 2019, 3, 61-66.	0.3	9
12	Chicken Gut Microbiota: Importance and Detection Technology. <i>Frontiers in Veterinary Science</i> , 2018, 5, 254.	0.9	274
13	Microbial-derived products as potential new antimicrobials. <i>Veterinary Research</i> , 2018, 49, 66.	1.1	53
14	Characterization of two glycosyl hydrolases, putative prophage endolysins, that target <i>Clostridium perfringens</i> . <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	16
15	The cecal microbiome of commercial broiler chickens varies significantly by season. <i>Poultry Science</i> , 2018, 97, 3635-3644.	1.5	26
16	Assessing Cat Flea Microbiomes in Northern and Southern California by 16S rRNA Next-Generation Sequencing. <i>Vector-Borne and Zoonotic Diseases</i> , 2018, 18, 491-499.	0.6	19
17	<i>Bartonella rochalimae</i> Detection by a Sensitive and Specific PCR Platform. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 99, 840-843.	0.6	6
18	Molecular Characterization of Tandem Repeat Protein 36 Gene of <i>Ehrlichia canis</i> Detected in Naturally Infected Dogs from Peru. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 99, 297-302.	0.6	11

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19	Environmental reservoirs of pathogenic mycobacteria across the Ethiopian biogeographical landscape. <i>PLoS ONE</i> , 2017, 12, e0173811.	1.1	34
20	Rapid Microbiome Changes in Freshly Deposited Cow Feces under Field Conditions. <i>Frontiers in Microbiology</i> , 2016, 7, 500.	1.5	49
21	Spatial and Temporal Changes in the Broiler Chicken Cecal and Fecal Microbiomes and Correlations of Bacterial Taxa with Cytokine Gene Expression. <i>Frontiers in Veterinary Science</i> , 2016, 3, 11.	0.9	169
22	Characterizing relationships among fecal indicator bacteria, microbial source tracking markers, and associated waterborne pathogen occurrence in stream water and sediments in a mixed land use watershed. <i>Water Research</i> , 2016, 101, 498-509.	5.3	122
23	Genome Sequence of a Urease-Positive <i>Campylobacter lari</i> Strain. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
24	Comparative Analysis of the Intestinal Bacterial and RNA Viral Communities from Sentinel Birds Placed on Selected Broiler Chicken Farms. <i>PLoS ONE</i> , 2015, 10, e0117210.	1.1	33
25	Detection of <i>Campylobacter</i> in 100 commercial flocksâ€“Evaluation of plating media and filtration method. <i>Journal of Applied Poultry Research</i> , 2015, 24, 240-245.	0.6	3
26	A Thermophilic Phage Endolysin Fusion to a <i>Clostridium perfringens</i> -Specific Cell Wall Binding Domain Creates an Anti- <i>Clostridium</i> Antimicrobial with Improved Thermostability. <i>Viruses</i> , 2015, 7, 3019-3034.	1.5	46
27	Sampling by Sponge Wipe or Skin Excision for Recovery of Inoculated <i>Salmonella</i> and <i>Campylobacter</i> from Defeathered Broiler Carcassesâ€“. <i>Journal of Food Protection</i> , 2014, 77, 824-827.	0.8	4
28	The chicken gastrointestinal microbiome. <i>FEMS Microbiology Letters</i> , 2014, 360, 100-112.	0.7	521
29	Successional changes in the chicken cecal microbiome during 42 days of growth are independent of organic acid feed additives. <i>BMC Veterinary Research</i> , 2014, 10, 282.	0.7	143
30	Metabolic Flexibility as a Major Predictor of Spatial Distribution in Microbial Communities. <i>PLoS ONE</i> , 2014, 9, e85105.	1.1	42
31	Can Probiotics Improve the Environmental Microbiome and Resistome of Commercial Poultry Production?. <i>International Journal of Environmental Research and Public Health</i> , 2013, 10, 4534-4559.	1.2	44
32	Construction, expression, purification and antigenicity of recombinant <i>Campylobacter jejuni</i> flagellar proteins. <i>Microbiological Research</i> , 2013, 168, 192-198.	2.5	18
33	The Poultry-Associated Microbiome: Network Analysis and Farm-to-Fork Characterizations. <i>PLoS ONE</i> , 2013, 8, e57190.	1.1	104
34	Prospecting Environmental Mycobacteria: Combined Molecular Approaches Reveal Unprecedented Diversity. <i>PLoS ONE</i> , 2013, 8, e68648.	1.1	34
35	Isolation of Shiga Toxinâ€“Producing <i>Escherichia coli</i> Serogroups O26, O45, O103, O111, O121, and O145 from Ground Beef Using Modified Rainbow Agar and Postâ€“Immunomagnetic Separation Acid Treatment. <i>Journal of Food Protection</i> , 2012, 75, 1548-1554.	0.8	36
36	Contrasting patterns of niche partitioning between two anaerobic terminal oxidizers of organic matter. <i>ISME Journal</i> , 2012, 6, 905-914.	4.4	20

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37	Pyrosequencing-based validation of a simple cell-suspension polymerase chain reaction assay for <i>Campylobacter</i> with application of high-processivity polymerase and novel internal amplification controls for rapid and specific detection. <i>Diagnostic Microbiology and Infectious Disease</i> , 2012, 72, 131-138.	0.8	8
38	Molecular Characterization of Podoviral Bacteriophages Virulent for <i>Clostridium perfringens</i> and Their Comparison with Members of the Picovirinae. <i>PLoS ONE</i> , 2012, 7, e38283.	1.1	37
39	Genotypic Distribution of a Specialist Model Microorganism, <i>Methanosaeta</i> , along an Estuarine Gradient: Does Metabolic Restriction Limit Niche Differentiation Potential?. <i>Microbial Ecology</i> , 2012, 63, 856-864.	1.4	5
40	Complete genome sequence of the podoviral bacteriophage $\hat{\imath}$ CP24R, which is virulent for <i>Clostridium perfringens</i> . <i>Archives of Virology</i> , 2012, 157, 769-772.	0.9	18
41	Application of high-throughput sequencing to measure the performance of commonly used selective cultivation methods for the foodborne pathogen <i>Campylobacter</i> . <i>FEMS Microbiology Ecology</i> , 2012, 79, 327-336.	1.3	30
42	Free-living and aggregate-associated Planctomycetes in the Black Sea. <i>FEMS Microbiology Ecology</i> , 2012, 80, 402-416.	1.3	96
43	Recombinant Expression of a Putative Amidase Cloned from the Genome of <i>Listeria monocytogenes</i> that Lyses the Bacterium and its Monolayer in Conjunction with a Protease. <i>Probiotics and Antimicrobial Proteins</i> , 2012, 4, 1-10.	1.9	15
44	The genome sequence and proteome of bacteriophage $\hat{\imath}$ CPV1 virulent for <i>Clostridium perfringens</i> . <i>Virus Research</i> , 2011, 155, 433-439.	1.1	26
45	ThermoPhyl: a software tool for selecting phylogenetically optimized conventional and quantitative-PCR taxon-targeted assays for use with complex samples. <i>FEMS Microbiology Ecology</i> , 2011, 77, 17-27.	1.3	6
46	Chicken intestine microbiota following the administration of lupulone, a hop-based antimicrobial. <i>FEMS Microbiology Ecology</i> , 2011, 77, 395-403.	1.3	43
47	Ovine pedomics: the first study of the ovine foot 16S rRNA-based microbiome. <i>ISME Journal</i> , 2011, 5, 1426-1437.	4.4	46
48	Comparative genomics of four closely related <i>Clostridium perfringens</i> bacteriophages reveals variable evolution among core genes with therapeutic potential. <i>BMC Genomics</i> , 2011, 12, 282.	1.2	23
49	Evolutionary divergence and biogeography of sympatric niche-differentiated bacterial populations. <i>ISME Journal</i> , 2010, 4, 488-497.	4.4	61
50	Improving the isolation of anaerobes on solid media: The example of the fastidious <i>Methanosaeta</i> . <i>Journal of Microbiological Methods</i> , 2010, 80, 203-205.	0.7	12
51	Spatial variability in microclimate in a mixed-conifer forest before and after thinning and burning treatments. <i>Forest Ecology and Management</i> , 2010, 259, 904-915.	1.4	154
52	Systems Biology for Ecology. <i>Advances in Ecological Research</i> , 2010, 43, 87-149.	1.4	29
53	Diazotrophic endophytes of native black cottonwood and willow. <i>Symbiosis</i> , 2009, 47, 23-33.	1.2	210
54	Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7537-7541.	1.4	18,390

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55	Diversity of Human Vaginal Bacterial Communities and Associations with Clinically Defined Bacterial Vaginosis. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4898-4909.	1.4	230
56	Targeted PCR for Detection of Vaginal Bacteria Associated with Bacterial Vaginosis. <i>Journal of Clinical Microbiology</i> , 2007, 45, 3270-3276.	1.8	328
57	Analysis of nitrite reductase (<i>nirK</i> and <i>nirS</i>) genes and cultivation reveal depauperate community of denitrifying bacteria in the Black Sea suboxic zone. <i>Environmental Microbiology</i> , 2007, 9, 118-130.	1.8	85
58	Facilitative and competitive effects of a N-fixing shrub on white fir saplings. <i>Forest Ecology and Management</i> , 2006, 233, 100-107.	1.4	26
59	Diversity and Distribution of Planctomycetes and Related Bacteria in the Suboxic Zone of the Black Sea. <i>Applied and Environmental Microbiology</i> , 2006, 72, 3079-3083.	1.4	79
60	Influence of light and soil moisture on Sierran mixed-conifer understory communities. <i>Plant Ecology</i> , 2005, 177, 13-24.	0.7	242
61	Ubiquity and diversity of ammonia-oxidizing archaea in water columns and sediments of the ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 14683-14688.	3.3	2,072
62	Diversity and Distribution of Frankia Strains Symbiotic with <i>Ceanothus</i> in California. <i>Applied and Environmental Microbiology</i> , 2004, 70, 6444-6452.	1.4	28
63	The effects of fire on soil nitrogen associated with patches of the actinorhizal shrub <i>Ceanothus cordulatus</i> . <i>Plant and Soil</i> , 2003, 254, 35-46.	1.8	20
64	Bitter cherry (<i>Prunus emarginata</i>) distribution, successional dynamics, and implications for the role of the seed bank. <i>Canadian Journal of Botany</i> , 1998, 76, 1725-1732.	1.2	7
65	Cecal Microbial Hydrogen Cycling Potential Is Linked to Feed Efficiency Phenotypes in Chickens. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2