

Doyle V Ward

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

10,570
citations

147726

31
h-index

155592

55
g-index

60
all docs

60
docs citations

60
times ranked

18443
citing authors

#	ARTICLE	IF	CITATIONS
1	Epidemiological and clinical features of Panton-Valentine Leukocidin positive <i>Staphylococcus aureus</i> bacteremia: A case-control study. <i>PLoS ONE</i> , 2022, 17, e0265476.	1.1	4
2	Dietary manipulation of the gut microbiome in inflammatory bowel disease patients: Pilot study. <i>Gut Microbes</i> , 2022, 14, 2046244.	4.3	29
3	COVID-19 Variant Surveillance and Social Determinants in Central Massachusetts: Development Study. <i>JMIR Formative Research</i> , 2022, 6, e37858.	0.7	3
4	The epithelial-specific ER stress sensor ERN2/IRE1 β enables host-microbiota crosstalk to affect colon goblet cell development. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	19
5	Epithelial HNF4A shapes the intraepithelial lymphocyte compartment via direct regulation of immune signaling molecules. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	12
6	The high prevalence of <i>Clostridioides difficile</i> among nursing home elders associates with a dysbiotic microbiome. <i>Gut Microbes</i> , 2021, 13, 1-15.	4.3	10
7	Effect of Levodopa Initiation on the Gut Microbiota in Parkinson's Disease. <i>Frontiers in Neurology</i> , 2021, 12, 574529.	1.1	11
8	Dysbiosis exacerbates colitis by promoting ubiquitination and accumulation of the innate immune adaptor STING in myeloid cells. <i>Immunity</i> , 2021, 54, 1137-1153.e8.	6.6	46
9	The Nursing Home Older Adult Gut Microbiome Composition Shows Time-dependent Dysbiosis and Is Influenced by Medication Exposures, Age, Environment, and Frailty. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021, 76, 1930-1938.	1.7	7
10	Inflammation-type dysbiosis of the oral microbiome associates with the duration of COVID-19 symptoms and long COVID. <i>JCI Insight</i> , 2021, 6, .	2.3	92
11	Gut microbiota regulation of P-glycoprotein in the intestinal epithelium in maintenance of homeostasis. <i>Microbiome</i> , 2021, 9, 183.	4.9	54
12	The Urinary Microbiome of Older Adults Residing in a Nursing Home Varies with Duration of Residence and Shows Increases in Potential Pathogens. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021, , .	1.7	4
13	Upper Gastrointestinal Perforations: A Possible Danger of Antibiotic Overuse. <i>Journal of Gastrointestinal Surgery</i> , 2020, 24, 2730-2736.	0.9	1
14	Anaerobic Antibiotics and the Risk of Graft-versus-Host Disease after Allogeneic Hematopoietic Stem Cell Transplantation. <i>Biology of Blood and Marrow Transplantation</i> , 2020, 26, 2053-2060.	2.0	30
15	Dysbiosis in a canine model of human fistulizing Crohn's disease. <i>Gut Microbes</i> , 2020, 12, 1785246.	4.3	10
16	Associations between Diet, the Gut Microbiome, and Short-Chain Fatty Acid Production among Older Caribbean Latino Adults. <i>Journal of the Academy of Nutrition and Dietetics</i> , 2020, 120, 2047-2060.e6.	0.4	28
17	Accuracy of Infection Control Surveillance in Identifying Genomically Confirmed Cross Transmission Clusters. <i>Infection Control and Hospital Epidemiology</i> , 2020, 41, s439-s440.	1.0	0
18	174. Shotgun Metagenomics and Colonization by Antibiotic-resistant Bacteria in Pediatric Hematopoietic Stem Cell Transplant Recipients. <i>Open Forum Infectious Diseases</i> , 2020, 7, S216-S216.	0.4	2

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19	The influence of payor status on outcomes associated with surgical repair of upper gastrointestinal perforations due to peptic ulcer disease in the United States. <i>American Journal of Surgery</i> , 2019, 217, 121-125.	0.9	2
20	Gut Colonization Preceding Mucosal Barrier Injury Bloodstream Infection in Pediatric Hematopoietic Stem Cell Transplantation Recipients. <i>Biology of Blood and Marrow Transplantation</i> , 2019, 25, 2274-2280.	2.0	36
21	Cognitive and Microbiome Impacts of Experimental <i>Ancylostoma ceylanicum</i> Hookworm Infections in Hamsters. <i>Scientific Reports</i> , 2019, 9, 7868.	1.6	9
22	Alzheimer's Disease Microbiome Is Associated with Dysregulation of the Anti-Inflammatory P-Glycoprotein Pathway. <i>MBio</i> , 2019, 10, .	1.8	269
23	Integration of genomic and clinical data augments surveillance of healthcare-acquired infections. <i>Infection Control and Hospital Epidemiology</i> , 2019, 40, 649-655.	1.0	21
24	ANTIBIOTIC EXPOSURE IN LONG-TERM CARE FACILITIES IS ASSOCIATED WITH URINARY MICROBIOME PERTURBATIONS. <i>Innovation in Aging</i> , 2019, 3, S86-S86.	0.0	0
25	2602. Genetic Basis of <i>Staphylococcus aureus</i> Virulence. <i>Open Forum Infectious Diseases</i> , 2019, 6, S904-S904.	0.4	0
26	Recovery of ethanol-induced <i>Akkermansia muciniphila</i> depletion ameliorates alcoholic liver disease. <i>Gut</i> , 2018, 67, 891-901.	6.1	458
27	Variability of indoor fungal microbiome of green and non-green low-income homes in Cincinnati, Ohio. <i>Science of the Total Environment</i> , 2018, 610-611, 212-218.	3.9	21
28	The nursing home elder microbiome stability and associations with age, frailty, nutrition and physical location. <i>Journal of Medical Microbiology</i> , 2018, 67, 40-51.	0.7	69
29	Alcohol-related changes in the intestinal microbiome influence neutrophil infiltration, inflammation and steatosis in early alcoholic hepatitis in mice. <i>PLoS ONE</i> , 2017, 12, e0174544.	1.1	88
30	Intestinal organoids model human responses to infection by commensal and Shiga toxin producing <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2017, 12, e0178966.	1.1	107
31	Prophages of the genus <i>Bacteriophage</i> as modulating agents of the infant gut microbiota. <i>Environmental Microbiology</i> , 2016, 18, 2196-2213.	1.8	66
32	Metagenomic Sequencing with Strain-Level Resolution Implicates Uropathogenic <i>E. coli</i> in Necrotizing Enterocolitis and Mortality in Preterm Infants. <i>Cell Reports</i> , 2016, 14, 2912-2924.	2.9	143
33	Strain-level microbial epidemiology and population genomics from shotgun metagenomics. <i>Nature Methods</i> , 2016, 13, 435-438.	9.0	328
34	Center Variation in Intestinal Microbiota Prior to Late-Onset Sepsis in Preterm Infants. <i>PLoS ONE</i> , 2015, 10, e0130604.	1.1	61
35	16S Community Profiling Identifies Proton Pump Inhibitor Related Differences in Gastric, Lung, and Oropharyngeal Microflora. <i>Journal of Pediatrics</i> , 2015, 166, 917-923.	0.9	78
36	A Pilot Study of Donor Enteral Human Milk to Modulate the Gut Microbiome in Children Receiving Stem Cell Transplant. <i>Biology of Blood and Marrow Transplantation</i> , 2015, 21, S218-S219.	2.0	1

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37	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. PLoS ONE, 2014, 9, e99979.	1.1	34
38	Early Empiric Antibiotic Use in Preterm Infants Is Associated with Lower Bacterial Diversity and Higher Relative Abundance of Enterobacter. Journal of Pediatrics, 2014, 165, 23-29.	0.9	306
39	Comparative Phylogenomics and Evolution of the Brucellae Reveal a Path to Virulence. Journal of Bacteriology, 2014, 196, 920-930.	1.0	122
40	16S rRNA Gene Survey of Microbial Communities in Winogradsky Columns. PLoS ONE, 2014, 9, e104134.	1.1	32
41	Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. Genome Biology, 2012, 13, R79.	13.9	2,258
42	Non-Invasive Mapping of the Gastrointestinal Microbiota Identifies Children with Inflammatory Bowel Disease. PLoS ONE, 2012, 7, e39242.	1.1	252
43	The Success of Acinetobacter Species; Genetic, Metabolic and Virulence Attributes. PLoS ONE, 2012, 7, e46984.	1.1	165
44	Whole Genome Characterization of the Mechanisms of Daptomycin Resistance in Clinical and Laboratory Derived Isolates of Staphylococcus aureus. PLoS ONE, 2012, 7, e28316.	1.1	202
45	Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. Genome Research, 2011, 21, 494-504.	2.4	3,015
46	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. Nature Biotechnology, 2011, 29, 415-420.	9.4	608
47	Distinct microbiome in pouchitis compared to healthy pouches in ulcerative colitis and familial adenomatous polyposis. Inflammatory Bowel Diseases, 2011, 17, 1092-1100.	0.9	67
48	A Catalog of Reference Genomes from the Human Microbiome. Science, 2010, 328, 994-999.	6.0	621
49	Tracking insertion mutants within libraries by deep sequencing and a genome-wide screen for <i>Haemophilus</i> genes required in the lung. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16422-16427.	3.3	324
50	VirB1* Promotes T-Pilus Formation in the <i>vir</i> -Type IV Secretion System of <i>Agrobacterium tumefaciens</i> . Journal of Bacteriology, 2007, 189, 6551-6563.	1.0	53
51	<i>Agrobacterium tumefaciens</i> VirB8 structure reveals potential protein-protein interaction sites. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2582-2587.	3.3	71
52	Peptide linkage mapping of the <i>Agrobacterium tumefaciens</i> vir-encoded type IV secretion system reveals protein subassemblies. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11493-11500.	3.3	131
53	<i>Agrobacterium</i> VirE2 gets the VIP1 treatment in plant nuclear import. Trends in Plant Science, 2002, 7, 1-3.	4.3	38
54	Inter-kingdom DNA transfer decoded. Nature Biotechnology, 2002, 20, 129-131.	9.4	7

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55	Cell Cycle Expression and Transcriptional Regulation of DNA Topoisomerase IV Genes in <i>Caulobacter</i> . <i>Journal of Bacteriology</i> , 1999, 181, 3321-3329.	1.0	5
56	Assembly of the VirB transport complex for DNA transfer from <i>Agrobacterium tumefaciens</i> to plant cells. <i>Current Opinion in Microbiology</i> , 1998, 1, 649-655.	2.3	60
57	Requirement of topoisomerase IV parC and parE genes for cell cycle progression and developmental regulation in <i>Caulobacter crescentus</i> . <i>Molecular Microbiology</i> , 1997, 26, 897-910.	1.2	73