

# 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	Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. <i>Genome Research</i> , 2011, 21, 494-504.	2.4	3,015
2	Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. <i>Genome Biology</i> , 2012, 13, R79.	13.9	2,258
3	A Catalog of Reference Genomes from the Human Microbiome. <i>Science</i> , 2010, 328, 994-999.	6.0	621
4	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	9.4	608
5	Recovery of ethanol-induced <i>Akkermansia muciniphila</i> depletion ameliorates alcoholic liver disease. <i>Gut</i> , 2018, 67, 891-901.	6.1	458
6	Strain-level microbial epidemiology and population genomics from shotgun metagenomics. <i>Nature Methods</i> , 2016, 13, 435-438.	9.0	328
7	Tracking insertion mutants within libraries by deep sequencing and a genome-wide screen for <i>Haemophilus</i> genes required in the lung. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16422-16427.	3.3	324
8	Early Empiric Antibiotic Use in Preterm Infants Is Associated with Lower Bacterial Diversity and Higher Relative Abundance of Enterobacter. <i>Journal of Pediatrics</i> , 2014, 165, 23-29.	0.9	306
9	Alzheimer's Disease Microbiome Is Associated with Dysregulation of the Anti-Inflammatory P-Glycoprotein Pathway. <i>MBio</i> , 2019, 10, .	1.8	269
10	Non-Invasive Mapping of the Gastrointestinal Microbiota Identifies Children with Inflammatory Bowel Disease. <i>PLoS ONE</i> , 2012, 7, e39242.	1.1	252
11	Whole Genome Characterization of the Mechanisms of Daptomycin Resistance in Clinical and Laboratory Derived Isolates of <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2012, 7, e28316.	1.1	202
12	The Success of <i>Acinetobacter</i> Species; Genetic, Metabolic and Virulence Attributes. <i>PLoS ONE</i> , 2012, 7, e46984.	1.1	165
13	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
14	Peptide linkage mapping of the <i>Agrobacterium tumefaciens</i> vir-encoded type IV secretion system reveals protein subassemblies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11493-11500.	3.3	131
15	Comparative Phylogenomics and Evolution of the <i>Brucellae</i> Reveal a Path to Virulence. <i>Journal of Bacteriology</i> , 2014, 196, 920-930.	1.0	122
16	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
17	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
18	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

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19	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
20	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
21	<i>Agrobacterium tumefaciens</i> VirB8 structure reveals potential protein-protein interaction sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2582-2587.	3.3	71
22	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
23	Distinct microbiome in pouchitis compared to healthy pouches in ulcerative colitis and familial adenomatous polyposis. <i>Inflammatory Bowel Diseases</i> , 2011, 17, 1092-1100.	0.9	67
24	Prophages of the genus <i>Bifidobacterium</i> as modulating agents of the infant gut microbiota. <i>Environmental Microbiology</i> , 2016, 18, 2196-2213.	1.8	66
25	Center Variation in Intestinal Microbiota Prior to Late-Onset Sepsis in Preterm Infants. <i>PLoS ONE</i> , 2015, 10, e0130604.	1.1	61
26	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
27	Gut microbiota regulation of P-glycoprotein in the intestinal epithelium in maintenance of homeostasis. <i>Microbiome</i> , 2021, 9, 183.	4.9	54
28	VirB1* Promotes T-Pilus Formation in the <i>vir</i> -Type IV Secretion System of <i>Agrobacterium tumefaciens</i> . <i>Journal of Bacteriology</i> , 2007, 189, 6551-6563.	1.0	53
29	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
30	<i>Agrobacterium</i> VirE2 gets the VIP1 treatment in plant nuclear import. <i>Trends in Plant Science</i> , 2002, 7, 1-3.	4.3	38
31	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
32	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. <i>PLoS ONE</i> , 2014, 9, e99979.	1.1	34
33	16S rRNA Gene Survey of Microbial Communities in Winogradsky Columns. <i>PLoS ONE</i> , 2014, 9, e104134.	1.1	32
34	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
35	Dietary manipulation of the gut microbiome in inflammatory bowel disease patients: Pilot study. <i>Gut Microbes</i> , 2022, 14, 2046244.	4.3	29
36	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

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37	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
38	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
39	The epithelial-specific ER stress sensor ERN2/IRE1 $\beta$ enables host-microbiota crosstalk to affect colon goblet cell development. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	19
40	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
41	Effect of Levodopa Initiation on the Gut Microbiota in Parkinson's Disease. <i>Frontiers in Neurology</i> , 2021, 12, 574529.	1.1	11
42	Dysbiosis in a canine model of human fistulizing Crohn's disease. <i>Gut Microbes</i> , 2020, 12, 1785246.	4.3	10
43	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
44	Cognitive and Microbiome Impacts of Experimental <i>Ancylostoma ceylanicum</i> Hookworm Infections in Hamsters. <i>Scientific Reports</i> , 2019, 9, 7868.	1.6	9
45	Inter-kingdom DNA transfer decoded. <i>Nature Biotechnology</i> , 2002, 20, 129-131.	9.4	7
46	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
47	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
48	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
49	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
50	COVID-19 Variant Surveillance and Social Determinants in Central Massachusetts: Development Study. <i>JMIR Formative Research</i> , 2022, 6, e37858.	0.7	3
51	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
52	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
53	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
54	Upper Gastrointestinal Perforations: A Possible Danger of Antibiotic Overuse. <i>Journal of Gastrointestinal Surgery</i> , 2020, 24, 2730-2736.	0.9	1

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55	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
56	2602. Genetic Basis of <i>Staphylococcus aureus</i> Virulence. <i>Open Forum Infectious Diseases</i> , 2019, 6, S904-S904.	0.4	0
57	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