

# Derrick E Fouts

## List of Publications by Year in descending order

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76  
papers

15,343  
citations

61984

43  
h-index

76900

74  
g-index

79  
all docs

79  
docs citations

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times ranked

18103  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cross-Genus “Boot-Up” of Synthetic Bacteriophage in <i>Staphylococcus aureus</i> by Using a New and Efficient DNA Transformation Method. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0148621.	3.1	6
2	Machine Learning Applied to Omics Datasets Predicts Mortality in Patients with Alcoholic Hepatitis. <i>Metabolites</i> , 2022, 12, 41.	2.9	6
3	The fecal mycobiome in non-alcoholic fatty liver disease. <i>Journal of Hepatology</i> , 2022, 76, 788-799.	3.7	66
4	Clinical challenges treating <i>Stenotrophomonas maltophilia</i> infections: an update. <i>JAC-Antimicrobial Resistance</i> , 2022, 4, dlac040.	2.1	39
5	Identification and Characterization of vB_PreP_EPr2, a Lytic Bacteriophage of Pan-Drug Resistant <i>Providencia rettgeri</i> . <i>Viruses</i> , 2022, 14, 708.	3.3	5
6	Imipenem/Relebactam Resistance in Clinical Isolates of Extensively Drug Resistant <i>Pseudomonas aeruginosa</i> : Inhibitor-Resistant $\beta$ -Lactamases and Their Increasing Importance. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, e0179021.	3.2	8
7	A comprehensive and contemporary “snapshot” of $\beta$ -lactamases in carbapenem resistant <i>Acinetobacter baumannii</i> . <i>Diagnostic Microbiology and Infectious Disease</i> , 2021, 99, 115242.	1.8	16
8	Genomic and clinical characterisation of multidrug-resistant carbapenemase-producing ST231 and ST16 <i>Klebsiella pneumoniae</i> isolates colonising patients at Siriraj hospital, Bangkok, Thailand from 2015 to 2017. <i>BMC Infectious Diseases</i> , 2021, 21, 142.	2.9	18
9	In Vitro Activity of a Novel Siderophore-Cephalosporin LCB10-0200 (GT-1), and LCB10-0200/Avibactam, against Carbapenem-Resistant <i>Escherichia coli</i> , <i>Klebsiella pneumoniae</i> , <i>Acinetobacter baumannii</i> , and <i>Pseudomonas aeruginosa</i> Strains at a Tertiary Hospital in Korea. <i>Pharmaceuticals</i> , 2021, 14, 370.	3.8	5
10	Dynamic Changes of the Fungal Microbiome in Alcohol Use Disorder. <i>Frontiers in Physiology</i> , 2021, 12, 699253.	2.8	45
11	Intestinal virome and therapeutic potential of bacteriophages in liver disease. <i>Journal of Hepatology</i> , 2021, 75, 1465-1475.	3.7	28
12	Intestinal Fungal Dysbiosis and Systemic Immune Response to Fungi in Patients With Alcoholic Hepatitis. <i>Hepatology</i> , 2020, 71, 522-538.	7.3	151
13	Changes in the fecal bacterial microbiota associated with disease severity in alcoholic hepatitis patients. <i>Gut Microbes</i> , 2020, 12, 1785251.	9.8	60
14	AbGRI4, a novel antibiotic resistance island in multiply antibiotic-resistant <i>Acinetobacter baumannii</i> clinical isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2760-2768.	3.0	18
15	Complete Genome Sequence of Broad-Host-Range <i>Staphylococcus aureus</i> Myophage ESa1. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
16	Newly Named <i>Klebsiella aerogenes</i> (formerly <i>Enterobacter aerogenes</i> ) Is Associated with Poor Clinical Outcomes Relative to Other <i>Enterobacter</i> Species in Patients with Bloodstream Infection. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	29
17	Intestinal Virome Signature Associated With Severity of Nonalcoholic Fatty Liver Disease. <i>Gastroenterology</i> , 2020, 159, 1839-1852.	1.3	103
18	Intestinal Virome in Patients With Alcoholic Hepatitis. <i>Hepatology</i> , 2020, 72, 2182-2196.	7.3	74

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19	ARGONAUT II Study of the <i>In Vitro</i> Activity of Plazomicin against Carbapenemase-Producing <i>Klebsiella pneumoniae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	11
20	Complete Genome Sequence of <i>Staphylococcus aureus</i> Phage SA75, Isolated from Goat Feces. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
21	Large-scale comparative analysis of microbial pan-genomes using PanOCT. <i>Bioinformatics</i> , 2019, 35, 1049-1050.	4.1	27
22	Population Structure, Molecular Epidemiology, and $\beta$ -Lactamase Diversity among <i>Stenotrophomonas maltophilia</i> Isolates in the United States. <i>MBio</i> , 2019, 10, .	4.1	52
23	Closed Genome Sequences of Clinical <i>Neisseria gonorrhoeae</i> Strains Obtained from Combined Oxford Nanopore and Illumina Sequencing. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0
24	Emergence of New Delhi Metallo- $\beta$ -Lactamase (NDM-5) in <i>Klebsiella quasipneumoniae</i> from Neonates in a Nigerian Hospital. <i>MSphere</i> , 2019, 4, .	2.9	37
25	Bacteriophage $\phi$ Ef11 ORF28 Endolysin, a Multifunctional Lytic Enzyme with Properties Distinct from All Other Identified <i>Enterococcus faecalis</i> Phage Endolysins. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	24
26	Rapid Replacement of <i>Acinetobacter baumannii</i> Strains Accompanied by Changes in Lipooligosaccharide Loci and Resistance Gene Repertoire. <i>MBio</i> , 2019, 10, .	4.1	28
27	Bacteriophage targeting of gut bacterium attenuates alcoholic liver disease. <i>Nature</i> , 2019, 575, 505-511.	27.8	493
28	OMeta: an ontology-based, data-driven metadata tracking system. <i>BMC Bioinformatics</i> , 2019, 20, 8.	2.6	17
29	ARGONAUT-I: Activity of Cefiderocol (S-649266), a Siderophore Cephalosporin, against Gram-Negative Bacteria, Including Carbapenem-Resistant Nonfermenters and <i>Enterobacteriaceae</i> with Defined Extended-Spectrum $\beta$ -Lactamases and Carbapenemases. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	81
30	GGRaSP: a R-package for selecting representative genomes using Gaussian mixture models. <i>Bioinformatics</i> , 2018, 34, 3032-3034.	4.1	16
31	<i>Enterobacter hormaechei</i> subsp. <i>hoffmannii</i> subsp. nov., <i>Enterobacter hormaechei</i> subsp. <i>xiangfangensis</i> comb. nov., <i>Enterobacter roggenkampii</i> sp. nov., and <i>Enterobacter muelleri</i> is a later heterotypic synonym of <i>Enterobacter asburiae</i> based on computational analysis of sequenced <i>Enterobacter</i> genomes. <i>F1000Research</i> , 2018, 7, 521.	1.6	68
32	PanACEA: a bioinformatics tool for the exploration and visualization of bacterial pan-chromosomes. <i>BMC Bioinformatics</i> , 2018, 19, 246.	2.6	9
33	Genomic Comparison Among Global Isolates of <i>L. interrogans</i> Serovars <i>Copenhageni</i> and <i>Icterohaemorrhagiae</i> Identified Natural Genetic Variation Caused by an Indel. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 193.	3.9	39
34	Multidrug resistant pathogens respond differently to the presence of co-pathogen, commensal, probiotic and host cells. <i>Scientific Reports</i> , 2018, 8, 8656.	3.3	19
35	<i>Enterobacter hormaechei</i> subsp. <i>hoffmannii</i> subsp. nov., <i>Enterobacter hormaechei</i> subsp. <i>xiangfangensis</i> comb. nov., <i>Enterobacter roggenkampii</i> sp. nov., and <i>Enterobacter muelleri</i> is a later heterotypic synonym of <i>Enterobacter asburiae</i> based on computational analysis of sequenced <i>Enterobacter</i> genomes. <i>F1000Research</i> , 2018, 7, 521.	1.6	56
36	LOCUST: a custom sequence locus typer for classifying microbial isolates. <i>Bioinformatics</i> , 2017, 33, 1725-1726.	4.1	16

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37	HSV-1 clinical isolates with unique in vivo and in vitro phenotypes and insight into genomic differences. <i>Journal of NeuroVirology</i> , 2017, 23, 171-185.	2.1	4
38	Intestinal fungi contribute to development of alcoholic liver disease. <i>Journal of Clinical Investigation</i> , 2017, 127, 2829-2841.	8.2	336
39	What Makes a Bacterial Species Pathogenic?:Comparative Genomic Analysis of the Genus <i>Leptospira</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004403.	3.0	253
40	Comprehensive Genome Analysis of Carbapenemase-Producing <i>Enterobacter</i> spp.: New Insights into Phylogeny, Population Structure, and Resistance Mechanisms. <i>MBio</i> , 2016, 7, .	4.1	154
41	Structural proteins of <i>Enterococcus faecalis</i> bacteriophage $\Phi$ Ef11. <i>Bacteriophage</i> , 2016, 6, e1251381.	1.9	6
42	Intestinal REG3 Lectins Protect against Alcoholic Steatohepatitis by Reducing Mucosa-Associated Microbiota and Preventing Bacterial Translocation. <i>Cell Host and Microbe</i> , 2016, 19, 227-239.	11.0	284
43	A novel method of consensus pan-chromosome assembly and large-scale comparative analysis reveal the highly flexible pan-genome of <i>Acinetobacter baumannii</i> . <i>Genome Biology</i> , 2015, 16, 143.	9.6	122
44	Supplementation of Saturated Long-Chain Fatty Acids Maintains Intestinal Eubiosis and Reduces Ethanol-induced Liver Injury in Mice. <i>Gastroenterology</i> , 2015, 148, 203-214.e16.	1.3	266
45	NeatFreq: reference-free data reduction and coverage normalization for De Novo sequence assembly. <i>BMC Bioinformatics</i> , 2014, 15, 357.	2.6	17
46	Leptospiral Pathogenomics. <i>Pathogens</i> , 2014, 3, 280-308.	2.8	94
47	Sequencing viral genomes from a single isolated plaque. <i>Virology Journal</i> , 2013, 10, 181.	3.4	16
48	Pathogenomic Inference of Virulence-Associated Genes in <i>Leptospira interrogans</i> . <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2468.	3.0	50
49	Whole Genome Analysis of <i>Leptospira licerasiae</i> Provides Insight into Leptospiral Evolution and Pathogenicity. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1853.	3.0	60
50	PanOCT: automated clustering of orthologs using conserved gene neighborhood for pan-genomic analysis of bacterial strains and closely related species. <i>Nucleic Acids Research</i> , 2012, 40, e172-e172.	14.5	227
51	Bacterial translocation and changes in the intestinal microbiome in mouse models of liver disease. <i>Journal of Hepatology</i> , 2012, 56, 1283-1292.	3.7	289
52	Integrated next-generation sequencing of 16S rDNA and metaproteomics differentiate the healthy urine microbiome from asymptomatic bacteriuria in neuropathic bladder associated with spinal cord injury. <i>Journal of Translational Medicine</i> , 2012, 10, 174.	4.4	388
53	Next Generation Sequencing to Define Prokaryotic and Fungal Diversity in the Bovine Rumen. <i>PLoS ONE</i> , 2012, 7, e48289.	2.5	234
54	The annotated complete DNA sequence of <i>Enterococcus faecalis</i> bacteriophage $\Phi$ Ef11 and its comparison with all available phage and predicted prophage genomes. <i>FEMS Microbiology Letters</i> , 2011, 317, 9-26.	1.8	31

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55	Clostridium perfringens bacteriophages $\hat{1}$ CP39O and $\hat{1}$ CP26F: genomic organization and proteomic analysis of the virions. Archives of Virology, 2011, 156, 25-35.	2.1	32
56	Comparative genomic analysis of Vibrio parahaemolyticus: serotype conversion and virulence. BMC Genomics, 2011, 12, 294.	2.8	82
57	Enteric dysbiosis associated with a mouse model of alcoholic liver disease. Hepatology, 2011, 53, 96-105.	7.3	636
58	Comparative Genome Analysis of Prevotella ruminicola and Prevotella bryantii: Insights into Their Environmental Niche. Microbial Ecology, 2010, 60, 721-729.	2.8	293
59	Comparative ICE Genomics: Insights into the Evolution of the SXT/R391 Family of ICEs. PLoS Genetics, 2009, 5, e1000786.	3.5	247
60	Complete Genome Sequence of the N2-Fixing Broad Host Range Endophyte Klebsiella pneumoniae 342 and Virulence Predictions Verified in Mice. PLoS Genetics, 2008, 4, e1000141.	3.5	253
61	Phage_Finder: Automated identification and classification of prophage regions in complete bacterial genome sequences. Nucleic Acids Research, 2006, 34, 5839-5851.	14.5	283
62	Comparative genomics of Neisseria meningitidis: core genome, islands of horizontal transfer and pathogen-specific genes. Microbiology (United Kingdom), 2006, 152, 3733-3749.	1.8	102
63	Sequencing Bacillus anthracis Typing Phages Gamma and Cherry Reveals a Common Ancestry. Journal of Bacteriology, 2006, 188, 3402-3408.	2.2	49
64	Genome Sequence of the PCE-Dechlorinating Bacterium <i>Dehalococcoides ethenogenes</i> . Science, 2005, 307, 105-108.	12.6	402
65	Insights on Evolution of Virulence and Resistance from the Complete Genome Analysis of an Early Methicillin-Resistant <i>Staphylococcus aureus</i> Strain and a Biofilm-Producing Methicillin-Resistant <i>Staphylococcus epidermidis</i> Strain. Journal of Bacteriology, 2005, 187, 2426-2438.	2.2	940
66	Major Structural Differences and Novel Potential Virulence Mechanisms from the Genomes of Multiple Campylobacter Species. PLoS Biology, 2005, 3, e15.	5.6	483
67	Comparison of the genome of the oral pathogen <i>Treponema denticola</i> with other spirochete genomes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 5646-5651.	7.1	251
68	Genomic Insights into Methanotrophy: The Complete Genome Sequence of Methylococcus capsulatus (Bath). PLoS Biology, 2004, 2, e303.	5.6	275
69	The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough. Nature Biotechnology, 2004, 22, 554-559.	17.5	559
70	The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXO1. Nucleic Acids Research, 2004, 32, 977-988.	14.5	273
71	Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen Listeria monocytogenes reveal new insights into the core genome components of this species. Nucleic Acids Research, 2004, 32, 2386-2395.	14.5	460
72	Environmental Genome Shotgun Sequencing of the Sargasso Sea. Science, 2004, 304, 66-74.	12.6	3,776

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73	The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria. <i>Nature</i> , 2003, 423, 81-86.	27.8	760
74	Complete Genome Sequence of the Oral Pathogenic Bacterium <i>Porphyromonas gingivalis</i> Strain W83. <i>Journal of Bacteriology</i> , 2003, 185, 5591-5601.	2.2	362
75	A <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000 Hrp (Type III Secretion) Deletion Mutant Expressing the Hrp System of Bean Pathogen <i>P. syringae</i> pv. <i>syringae</i> 61 Retains Normal Host Specificity for Tomato. <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 43-52.	2.6	41
76	Genomewide identification of <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000 promoters controlled by the HrpL alternative sigma factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 2275-2280.	7.1	280