

# Derrick E Fouts

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9251686/publications.pdf>

Version: 2024-02-01

76  
papers

15,343  
citations

61945

43  
h-index

76872

74  
g-index

79  
all docs

79  
docs citations

79  
times ranked

18103  
citing authors

#	ARTICLE	IF	CITATIONS
1	Environmental Genome Shotgun Sequencing of the Sargasso Sea. <i>Science</i> , 2004, 304, 66-74.	6.0	3,776
2	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. <i>Journal of Bacteriology</i> , 2005, 187, 2426-2438.	1.0	940
3	The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria. <i>Nature</i> , 2003, 423, 81-86.	13.7	760
4	Enteric dysbiosis associated with a mouse model of alcoholic liver disease. <i>Hepatology</i> , 2011, 53, 96-105.	3.6	636
5	The genome sequence of the anaerobic, sulfate-reducing bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Nature Biotechnology</i> , 2004, 22, 554-559.	9.4	559
6	Bacteriophage targeting of gut bacterium attenuates alcoholic liver disease. <i>Nature</i> , 2019, 575, 505-511.	13.7	493
7	Major Structural Differences and Novel Potential Virulence Mechanisms from the Genomes of Multiple <i>Campylobacter</i> Species. <i>PLoS Biology</i> , 2005, 3, e15.	2.6	483
8	Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen <i>Listeria monocytogenes</i> reveal new insights into the core genome components of this species. <i>Nucleic Acids Research</i> , 2004, 32, 2386-2395.	6.5	460
9	Genome Sequence of the PCE-Dechlorinating Bacterium <i>Dehalococcoides ethenogenes</i> . <i>Science</i> , 2005, 307, 105-108.	6.0	402
10	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.	1.8	388
11	Complete Genome Sequence of the Oral Pathogenic Bacterium <i>Porphyromonas gingivalis</i> Strain W83. <i>Journal of Bacteriology</i> , 2003, 185, 5591-5601.	1.0	362
12	Intestinal fungi contribute to development of alcoholic liver disease. <i>Journal of Clinical Investigation</i> , 2017, 127, 2829-2841.	3.9	336
13	Comparative Genome Analysis of <i>Prevotella ruminicola</i> and <i>Prevotella bryantii</i> : Insights into Their Environmental Niche. <i>Microbial Ecology</i> , 2010, 60, 721-729.	1.4	293
14	Bacterial translocation and changes in the intestinal microbiome in mouse models of liver disease. <i>Journal of Hepatology</i> , 2012, 56, 1283-1292.	1.8	289
15	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.	5.1	284
16	Phage_Finder: Automated identification and classification of prophage regions in complete bacterial genome sequences. <i>Nucleic Acids Research</i> , 2006, 34, 5839-5851.	6.5	283
17	Genomewide identification of <i>Pseudomonas syringae</i> pv. tomato 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.	3.3	280
18	Genomic Insights into Methanotrophy: The Complete Genome Sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , 2004, 2, e303.	2.6	275

#	ARTICLE	IF	CITATIONS
19	The genome sequence of <i>Bacillus cereus</i> ATCC 10987 reveals metabolic adaptations and a large plasmid related to <i>Bacillus anthracis</i> pXO1. <i>Nucleic Acids Research</i> , 2004, 32, 977-988.	6.5	273
20	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.	0.6	266
21	Complete Genome Sequence of the N <sub>2</sub> -Fixing Broad Host Range Endophyte <i>Klebsiella pneumoniae</i> 342 and Virulence Predictions Verified in Mice. <i>PLoS Genetics</i> , 2008, 4, e1000141.	1.5	253
22	What Makes a Bacterial Species Pathogenic?:Comparative Genomic Analysis of the Genus <i>Leptospira</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004403.	1.3	253
23	Comparison of the genome of the oral pathogen <i>Treponema denticola</i> with other spirochete genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 5646-5651.	3.3	251
24	Comparative ICE Genomics: Insights into the Evolution of the SXT/R391 Family of ICEs. <i>PLoS Genetics</i> , 2009, 5, e1000786.	1.5	247
25	Next Generation Sequencing to Define Prokaryotic and Fungal Diversity in the Bovine Rumen. <i>PLoS ONE</i> , 2012, 7, e48289.	1.1	234
26	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.	6.5	227
27	Comprehensive Genome Analysis of Carbapenemase-Producing <i>Enterobacter</i> spp.: New Insights into Phylogeny, Population Structure, and Resistance Mechanisms. <i>MBio</i> , 2016, 7, .	1.8	154
28	Intestinal Fungal Dysbiosis and Systemic Immune Response to Fungi in Patients With Alcoholic Hepatitis. <i>Hepatology</i> , 2020, 71, 522-538.	3.6	151
29	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.	13.9	122
30	Intestinal Virome Signature Associated With Severity of Nonalcoholic Fatty Liver Disease. <i>Gastroenterology</i> , 2020, 159, 1839-1852.	0.6	103
31	Comparative genomics of <i>Neisseria meningitidis</i> : core genome, islands of horizontal transfer and pathogen-specific genes. <i>Microbiology (United Kingdom)</i> , 2006, 152, 3733-3749.	0.7	102
32	Leptospiral Pathogenomics. <i>Pathogens</i> , 2014, 3, 280-308.	1.2	94
33	Comparative genomic analysis of <i>Vibrio parahaemolyticus</i> : serotype conversion and virulence. <i>BMC Genomics</i> , 2011, 12, 294.	1.2	82
34	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, .	1.4	81
35	Intestinal Virome in Patients With Alcoholic Hepatitis. <i>Hepatology</i> , 2020, 72, 2182-2196.	3.6	74
36	<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.	0.8	68

#	ARTICLE	IF	CITATIONS
37	The fecal mycobiome in non-alcoholic fatty liver disease. <i>Journal of Hepatology</i> , 2022, 76, 788-799.	1.8	66
38	Whole Genome Analysis of <i>Leptospira licerasiae</i> Provides Insight into Leptospiral Evolution and Pathogenicity. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1853.	1.3	60
39	Changes in the fecal bacterial microbiota associated with disease severity in alcoholic hepatitis patients. <i>Gut Microbes</i> , 2020, 12, 1785251.	4.3	60
40	<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.	0.8	56
41	Population Structure, Molecular Epidemiology, and $\beta$ -Lactamase Diversity among <i>Stenotrophomonas maltophilia</i> Isolates in the United States. <i>MBio</i> , 2019, 10, .	1.8	52
42	Pathogenomic Inference of Virulence-Associated Genes in <i>Leptospira interrogans</i> . <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2468.	1.3	50
43	Sequencing <i>Bacillus anthracis</i> Typing Phages Gamma and Cherry Reveals a Common Ancestry. <i>Journal of Bacteriology</i> , 2006, 188, 3402-3408.	1.0	49
44	Dynamic Changes of the Fungal Microbiome in Alcohol Use Disorder. <i>Frontiers in Physiology</i> , 2021, 12, 699253.	1.3	45
45	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.	1.4	41
46	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.	1.8	39
47	Clinical challenges treating <i>Stenotrophomonas maltophilia</i> infections: an update. <i>JAC-Antimicrobial Resistance</i> , 2022, 4, dlac040.	0.9	39
48	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, .	1.3	37
49	<i>Clostridium perfringens</i> bacteriophages $\phi$ CP390 and $\phi$ CP26F: genomic organization and proteomic analysis of the virions. <i>Archives of Virology</i> , 2011, 156, 25-35.	0.9	32
50	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.	0.7	31
51	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, .	1.8	29
52	Rapid Replacement of <i>Acinetobacter baumannii</i> Strains Accompanied by Changes in Lipooligosaccharide Loci and Resistance Gene Repertoire. <i>MBio</i> , 2019, 10, .	1.8	28
53	Intestinal virome and therapeutic potential of bacteriophages in liver disease. <i>Journal of Hepatology</i> , 2021, 75, 1465-1475.	1.8	28
54	Large-scale comparative analysis of microbial pan-genomes using PanOCT. <i>Bioinformatics</i> , 2019, 35, 1049-1050.	1.8	27

#	ARTICLE	IF	CITATIONS
55	Bacteriophage $\phi$ Ef11 ORF28 Endolysin, a Multifunctional Lytic Enzyme with Properties Distinct from All Other Identified Enterococcus faecalis Phage Endolysins. Applied and Environmental Microbiology, 2019, 85, .	1.4	24
56	Multidrug resistant pathogens respond differently to the presence of co-pathogen, commensal, probiotic and host cells. Scientific Reports, 2018, 8, 8656.	1.6	19
57	AbGRI4, a novel antibiotic resistance island in multiply antibiotic-resistant Acinetobacter baumannii clinical isolates. Journal of Antimicrobial Chemotherapy, 2020, 75, 2760-2768.	1.3	18
58	Genomic and clinical characterisation of multidrug-resistant carbapenemase-producing ST231 and ST16 Klebsiella pneumoniae isolates colonising patients at Siriraj hospital, Bangkok, Thailand from 2015 to 2017. BMC Infectious Diseases, 2021, 21, 142.	1.3	18
59	NeatFreq: reference-free data reduction and coverage normalization for De Novosequence assembly. BMC Bioinformatics, 2014, 15, 357.	1.2	17
60	OMeta: an ontology-based, data-driven metadata tracking system. BMC Bioinformatics, 2019, 20, 8.	1.2	17
61	Sequencing viral genomes from a single isolated plaque. Virology Journal, 2013, 10, 181.	1.4	16
62	LOCUST: a custom sequence locus typer for classifying microbial isolates. Bioinformatics, 2017, 33, 1725-1726.	1.8	16
63	GGRaSP: a R-package for selecting representative genomes using Gaussian mixture models. Bioinformatics, 2018, 34, 3032-3034.	1.8	16
64	A comprehensive and contemporary "snapshot" of $\beta$ -lactamases in carbapenem resistant Acinetobacter baumannii. Diagnostic Microbiology and Infectious Disease, 2021, 99, 115242.	0.8	16
65	ARGONAUT II Study of the <i>In Vitro</i> Activity of Plazomicin against Carbapenemase-Producing Klebsiella pneumoniae. Antimicrobial Agents and Chemotherapy, 2020, 64, .	1.4	11
66	PanACEA: a bioinformatics tool for the exploration and visualization of bacterial pan-chromosomes. BMC Bioinformatics, 2018, 19, 246.	1.2	9
67	Imipenem/Relebactam Resistance in Clinical Isolates of Extensively Drug Resistant Pseudomonas aeruginosa: Inhibitor-Resistant $\beta$ -Lactamases and Their Increasing Importance. Antimicrobial Agents and Chemotherapy, 2022, 66, e0179021.	1.4	8
68	Structural proteins of Enterococcus faecalis bacteriophage $\phi$ Ef11. Bacteriophage, 2016, 6, e1251381.	1.9	6
69	Cross-Genus "Boot-Up" of Synthetic Bacteriophage in Staphylococcus aureus by Using a New and Efficient DNA Transformation Method. Applied and Environmental Microbiology, 2022, 88, AEM0148621.	1.4	6
70	Machine Learning Applied to Omics Datasets Predicts Mortality in Patients with Alcoholic Hepatitis. Metabolites, 2022, 12, 41.	1.3	6
71	In Vitro Activity of a Novel Siderophore-Cephalosporin LCB10-0200 (GT-1), and LCB10-0200/Avibactam, against Carbapenem-Resistant Escherichia coli, Klebsiella pneumoniae, Acinetobacter baumannii, and Pseudomonas aeruginosa Strains at a Tertiary Hospital in Korea. Pharmaceuticals, 2021, 14, 370.	1.7	5
72	Identification and Characterization of vB_PreP_EPr2, a Lytic Bacteriophage of Pan-Drug Resistant Providencia rettgeri. Viruses, 2022, 14, 708.	1.5	5

#	ARTICLE	IF	CITATIONS
73	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.	1.0	4
74	Complete Genome Sequence of Broad-Host-Range Staphylococcus aureus Myophage ESa1. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
75	Complete Genome Sequence of Staphylococcus aureus Phage SA75, Isolated from Goat Feces. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
76	Closed Genome Sequences of Clinical Neisseria gonorrhoeae Strains Obtained from Combined Oxford Nanopore and Illumina Sequencing. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0