

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 | 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. | 1.4 | 6 |
| 2 | Machine Learning Applied to Omics Datasets Predicts Mortality in Patients with Alcoholic Hepatitis. <i>Metabolites</i> , 2022, 12, 41. | 1.3 | 6 |
| 3 | The fecal mycobiome in non-alcoholic fatty liver disease. <i>Journal of Hepatology</i> , 2022, 76, 788-799. | 1.8 | 66 |
| 4 | Clinical challenges treating <i>Stenotrophomonas maltophilia</i> infections: an update. <i>JAC-Antimicrobial Resistance</i> , 2022, 4, dlac040. | 0.9 | 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. | 1.5 | 5 |
| 6 | Imipenem/Relebactam Resistance in Clinical Isolates of Extensively Drug Resistant <i>Pseudomonas aeruginosa</i> : Inhibitor-Resistant β -Lactamases and Their Increasing Importance. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, e0179021. | 1.4 | 8 |
| 7 | A comprehensive and contemporary “snapshot” of β -lactamases in carbapenem resistant <i>Acinetobacter baumannii</i> . <i>Diagnostic Microbiology and Infectious Disease</i> , 2021, 99, 115242. | 0.8 | 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. | 1.3 | 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. | 1.7 | 5 |
| 10 | Dynamic Changes of the Fungal Microbiome in Alcohol Use Disorder. <i>Frontiers in Physiology</i> , 2021, 12, 699253. | 1.3 | 45 |
| 11 | Intestinal virome and therapeutic potential of bacteriophages in liver disease. <i>Journal of Hepatology</i> , 2021, 75, 1465-1475. | 1.8 | 28 |
| 12 | Intestinal Fungal Dysbiosis and Systemic Immune Response to Fungi in Patients With Alcoholic Hepatitis. <i>Hepatology</i> , 2020, 71, 522-538. | 3.6 | 151 |
| 13 | Changes in the fecal bacterial microbiota associated with disease severity in alcoholic hepatitis patients. <i>Gut Microbes</i> , 2020, 12, 1785251. | 4.3 | 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. | 1.3 | 18 |
| 15 | Complete Genome Sequence of Broad-Host-Range <i>Staphylococcus aureus</i> Myophage ESa1. <i>Microbiology Resource Announcements</i> , 2020, 9, . | 0.3 | 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, . | 1.8 | 29 |
| 17 | Intestinal Virome Signature Associated With Severity of Nonalcoholic Fatty Liver Disease. <i>Gastroenterology</i> , 2020, 159, 1839-1852. | 0.6 | 103 |
| 18 | Intestinal Virome in Patients With Alcoholic Hepatitis. <i>Hepatology</i> , 2020, 72, 2182-2196. | 3.6 | 74 |

| # | ARTICLE | IF | CITATIONS |
|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 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, . | 1.4 | 11 |
| 20 | Complete Genome Sequence of <i>Staphylococcus aureus</i> Phage SA75, Isolated from Goat Feces. <i>Microbiology Resource Announcements</i> , 2020, 9, . | 0.3 | 1 |
| 21 | Large-scale comparative analysis of microbial pan-genomes using PanOCT. <i>Bioinformatics</i> , 2019, 35, 1049-1050. | 1.8 | 27 |
| 22 | Population Structure, Molecular Epidemiology, and β -Lactamase Diversity among <i>Stenotrophomonas maltophilia</i> Isolates in the United States. <i>MBio</i> , 2019, 10, . | 1.8 | 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, . | 0.3 | 0 |
| 24 | Emergence of New Delhi Metallo- β -Lactamase (NDM-5) in <i>Klebsiella quasipneumoniae</i> from Neonates in a Nigerian Hospital. <i>MSphere</i> , 2019, 4, . | 1.3 | 37 |
| 25 | Bacteriophage ϕ 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, . | 1.4 | 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, . | 1.8 | 28 |
| 27 | Bacteriophage targeting of gut bacterium attenuates alcoholic liver disease. <i>Nature</i> , 2019, 575, 505-511. | 13.7 | 493 |
| 28 | OMeta: an ontology-based, data-driven metadata tracking system. <i>BMC Bioinformatics</i> , 2019, 20, 8. | 1.2 | 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 β -Lactamases and Carbapenemases. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, . | 1.4 | 81 |
| 30 | GGRaSP: a R-package for selecting representative genomes using Gaussian mixture models. <i>Bioinformatics</i> , 2018, 34, 3032-3034. | 1.8 | 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. | 0.8 | 68 |
| 32 | PanACEA: a bioinformatics tool for the exploration and visualization of bacterial pan-chromosomes. <i>BMC Bioinformatics</i> , 2018, 19, 246. | 1.2 | 9 |
| 33 | Genomic Comparison Among Global Isolates of <i>L. interrogans</i> Serovars Copenhageni and Icterohaemorrhagiae Identified Natural Genetic Variation Caused by an Indel. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 193. | 1.8 | 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. | 1.6 | 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. | 0.8 | 56 |
| 36 | LOCUST: a custom sequence locus typer for classifying microbial isolates. <i>Bioinformatics</i> , 2017, 33, 1725-1726. | 1.8 | 16 |

| # | ARTICLE | IF | CITATIONS |
|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 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. | 1.0 | 4 |
| 38 | Intestinal fungi contribute to development of alcoholic liver disease. <i>Journal of Clinical Investigation</i> , 2017, 127, 2829-2841. | 3.9 | 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. | 1.3 | 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, . | 1.8 | 154 |
| 41 | Structural proteins of <i>Enterococcus faecalis</i> bacteriophage ϕ 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. | 5.1 | 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. | 13.9 | 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. | 0.6 | 266 |
| 45 | NeatFreq: reference-free data reduction and coverage normalization for De Novo sequence assembly. <i>BMC Bioinformatics</i> , 2014, 15, 357. | 1.2 | 17 |
| 46 | Leptospiral Pathogenomics. <i>Pathogens</i> , 2014, 3, 280-308. | 1.2 | 94 |
| 47 | Sequencing viral genomes from a single isolated plaque. <i>Virology Journal</i> , 2013, 10, 181. | 1.4 | 16 |
| 48 | Pathogenomic Inference of Virulence-Associated Genes in <i>Leptospira interrogans</i> . <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2468. | 1.3 | 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. | 1.3 | 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. | 6.5 | 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. | 1.8 | 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. | 1.8 | 388 |
| 53 | Next Generation Sequencing to Define Prokaryotic and Fungal Diversity in the Bovine Rumen. <i>PLoS ONE</i> , 2012, 7, e48289. | 1.1 | 234 |
| 54 | The annotated complete DNA sequence of <i>Enterococcus faecalis</i> bacteriophage ϕ Ef11 and its comparison with all available phage and predicted prophage genomes. <i>FEMS Microbiology Letters</i> , 2011, 317, 9-26. | 0.7 | 31 |

| # | ARTICLE | IF | CITATIONS |
|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 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. | 0.9 | 32 |
| 56 | Comparative genomic analysis of Vibrio parahaemolyticus: serotype conversion and virulence. BMC Genomics, 2011, 12, 294. | 1.2 | 82 |
| 57 | Enteric dysbiosis associated with a mouse model of alcoholic liver disease. Hepatology, 2011, 53, 96-105. | 3.6 | 636 |
| 58 | Comparative Genome Analysis of Prevotella ruminicola and Prevotella bryantii: Insights into Their Environmental Niche. Microbial Ecology, 2010, 60, 721-729. | 1.4 | 293 |
| 59 | Comparative ICE Genomics: Insights into the Evolution of the SXT/R391 Family of ICEs. PLoS Genetics, 2009, 5, e1000786. | 1.5 | 247 |
| 60 | Complete Genome Sequence of the N ₂ -Fixing Broad Host Range Endophyte Klebsiella pneumoniae 342 and Virulence Predictions Verified in Mice. PLoS Genetics, 2008, 4, e1000141. | 1.5 | 253 |
| 61 | Phage_Finder: Automated identification and classification of prophage regions in complete bacterial genome sequences. Nucleic Acids Research, 2006, 34, 5839-5851. | 6.5 | 283 |
| 62 | Comparative genomics of Neisseria meningitidis: core genome, islands of horizontal transfer and pathogen-specific genes. Microbiology (United Kingdom), 2006, 152, 3733-3749. | 0.7 | 102 |
| 63 | Sequencing Bacillus anthracis Typing Phages Gamma and Cherry Reveals a Common Ancestry. Journal of Bacteriology, 2006, 188, 3402-3408. | 1.0 | 49 |
| 64 | Genome Sequence of the PCE-Dechlorinating Bacterium Dehalococcoides ethenogenes. Science, 2005, 307, 105-108. | 6.0 | 402 |
| 65 | Insights on Evolution of Virulence and Resistance from the Complete Genome Analysis of an Early Methicillin-Resistant Staphylococcus aureus Strain and a Biofilm-Producing Methicillin-Resistant Staphylococcus epidermidis Strain. Journal of Bacteriology, 2005, 187, 2426-2438. | 1.0 | 940 |
| 66 | Major Structural Differences and Novel Potential Virulence Mechanisms from the Genomes of Multiple Campylobacter Species. PLoS Biology, 2005, 3, e15. | 2.6 | 483 |
| 67 | Comparison of the genome of the oral pathogen Treponema denticola with other spirochete genomes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 5646-5651. | 3.3 | 251 |
| 68 | Genomic Insights into Methanotrophy: The Complete Genome Sequence of Methylococcus capsulatus (Bath). PLoS Biology, 2004, 2, e303. | 2.6 | 275 |
| 69 | The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough. Nature Biotechnology, 2004, 22, 554-559. | 9.4 | 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. | 6.5 | 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. | 6.5 | 460 |
| 72 | Environmental Genome Shotgun Sequencing of the Sargasso Sea. Science, 2004, 304, 66-74. | 6.0 | 3,776 |

| # | ARTICLE | IF | CITATIONS |
|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 73 | 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 |
| 74 | 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 |
| 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. | 1.4 | 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. | 3.3 | 280 |