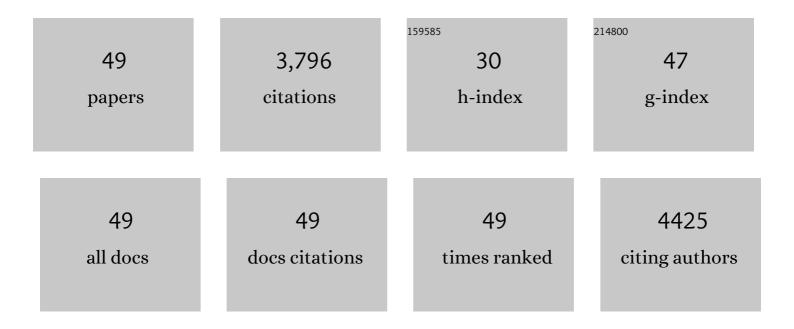
David T Pride

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1514770/publications.pdf Version: 2024-02-01



Πλνίη Τ Ρρίηε

#	Article	IF	CITATIONS
1	Considerations for the Use of Phage Therapy in Clinical Practice. Antimicrobial Agents and Chemotherapy, 2022, 66, AAC0207121.	3.2	151
2	Phage Cocktails Constrain the Growth of <i>Enterococcus</i> . MSystems, 2022, 7, .	3.8	9
3	Animal Models of Phage Therapy. Frontiers in Microbiology, 2021, 12, 631794.	3.5	13
4	Compositional Differences in the Oral Microbiome of E-cigarette Users. Frontiers in Microbiology, 2021, 12, 599664.	3.5	18
5	Comparison of two nucleic acid amplification tests (NAATs) and two antigen tests for detection of SARS-CoV-2 from upper respiratory specimens. Journal of Clinical Virology Plus, 2021, 1, 100011.	1.0	9
6	Molecular Mirror Technology Facilitates High-Throughput, Accurate SARS-CoV-2 Testing. Microbiology Spectrum, 2021, 9, e0039221.	3.0	0
7	Cervicovaginal Microbiome Composition Is Associated with Metabolic Profiles in Healthy Pregnancy. MBio, 2020, 11, .	4.1	30
8	Fecal Viral Community Responses to High-Fat Diet in Mice. MSphere, 2020, 5, .	2.9	33
9	Temporal variations in bacterial community diversity and composition throughout intensive care unit renovations. Microbiome, 2020, 8, 86.	11.1	14
10	Aseptic Barriers Allow a Clean Contact for Contaminated Stethoscope Diaphragms. Mayo Clinic Proceedings Innovations, Quality & Outcomes, 2020, 4, 21-30.	2.4	12
11	The Virome of Cerebrospinal Fluid: Viruses Where We Once Thought There Were None. Frontiers in Microbiology, 2019, 10, 2061.	3.5	48
12	Benchmarking urine storage and collection conditions for evaluating the female urinary microbiome. Scientific Reports, 2019, 9, 13409.	3.3	33
13	Comparison of Three Nucleic Acid Amplification Tests and Culture for Detection of Group B <i>Streptococcus</i> from Enrichment Broth. Journal of Clinical Microbiology, 2019, 57, .	3.9	21
14	Comparison of Multiplex Gastrointestinal Pathogen Panel and Conventional Stool Testing for Evaluation of Diarrhea in Patients with Inflammatory Bowel Diseases. Digestive Diseases and Sciences, 2019, 64, 382-390.	2.3	22
15	A Rapid and Low-Cost Pathogen Detection Platform by Using a Molecular Agglutination Assay. ACS Central Science, 2018, 4, 1485-1494.	11.3	15
16	Shared and Distinct Features of Human Milk and Infant Stool Viromes. Frontiers in Microbiology, 2018, 9, 1162.	3.5	100
17	Draft Genome Sequence of an Enterococcus faecalis ATCC 19433 Siphovirus Isolated from Raw Domestic Sewage. Genome Announcements, 2017, 5, .	0.8	2
18	Transmission of viruses via our microbiomes. Microbiome, 2016, 4, 64.	11.1	70

2

DAVID T PRIDE

#	Article	IF	CITATIONS
19	Microbial diversity in individuals and their household contacts following typical antibiotic courses. Microbiome, 2016, 4, 39.	11.1	135
20	Immunogenicity and protective efficacy of recombinant <i>Clostridium difficile</i> flagellar protein FliC. Emerging Microbes and Infections, 2016, 5, 1-10.	6.5	44
21	Electronic cigarette inhalation alters innate immunity and airway cytokines while increasing the virulence of colonizing bacteria. Journal of Molecular Medicine, 2016, 94, 667-679.	3.9	204
22	Chemostat culture systems support diverse bacteriophage communities from human feces. Microbiome, 2015, 3, 58.	11.1	50
23	Bacteriophage and their potential roles in the human oral cavity. Journal of Oral Microbiology, 2015, 7, 27423.	2.7	109
24	Identification of staphylococcal phage with reduced transcription in human blood through transcriptome sequencing. Frontiers in Microbiology, 2015, 6, 216.	3.5	4
25	The human urine virome in association with urinary tract infections. Frontiers in Microbiology, 2015, 6, 14.	3.5	173
26	Global transcription of CRISPR loci in the human oral cavity. BMC Genomics, 2015, 16, 401.	2.8	14
27	Library preparation methodology can influence genomic and functional predictions in human microbiome research. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14024-14029.	7.1	179
28	Transcriptome analysis of bacteriophage communities in periodontal health and disease. BMC Genomics, 2015, 16, 549.	2.8	48
29	Effects of Long Term Antibiotic Therapy on Human Oral and Fecal Viromes. PLoS ONE, 2015, 10, e0134941.	2.5	119
30	Characterization of bacteriophage communities and CRISPR profiles from dental plaque. BMC Microbiology, 2014, 14, 175.	3.3	83
31	Altered Oral Viral Ecology in Association with Periodontal Disease. MBio, 2014, 5, e01133-14.	4.1	171
32	Molecular Bases and Role of Viruses in the Human Microbiome. Journal of Molecular Biology, 2014, 426, 3892-3906.	4.2	113
33	Conservation of streptococcal CRISPRs on human skin and saliva. BMC Microbiology, 2014, 14, 146.	3.3	44
34	Human oral viruses are personal, persistent and gender-consistent. ISME Journal, 2014, 8, 1753-1767.	9.8	159
35	Association between living environment and human oral viral ecology. ISME Journal, 2013, 7, 1710-1724.	9.8	108
36	Evidence of a robust resident bacteriophage population revealed through analysis of the human salivary virome. ISME Journal, 2012, 6, 915-926.	9.8	295

DAVID T PRIDE

#	Article	IF	CITATIONS
37	Comparisons of clustered regularly interspaced short palindromic repeats and viromes in human saliva reveal bacterial adaptations to salivary viruses. Environmental Microbiology, 2012, 14, 2564-2576.	3.8	57
38	Analysis of streptococcal CRISPRs from human saliva reveals substantial sequence diversity within and between subjects over time. Genome Research, 2011, 21, 126-136.	5.5	104
39	Metagenomic detection of phage-encoded platelet-binding factors in the human oral cavity. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4547-4553.	7.1	123
40	Genome signature analysis of thermal virus metagenomes reveals Archaea and thermophilic signatures. BMC Genomics, 2008, 9, 420.	2.8	28
41	Superoxide dismutase A antigens derived from molecular analysis of sarcoidosis granulomas elicit systemic Th-1 immune responses. Respiratory Research, 2008, 9, 36.	3.6	40
42	Evidence of host-virus co-evolution in tetranucleotide usage patterns of bacteriophages and eukaryotic viruses. BMC Genomics, 2006, 7, 8.	2.8	112
43	Evolutionary Implications of Microbial Genome Tetranucleotide Frequency Biases. Genome Research, 2003, 13, 145-158.	5.5	232
44	East Asian genotypes of <i>Helicobacter pylori</i> strains in Amerindians provide evidence for its ancient human carriage. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15107-15111.	7.1	115
45	Concerted evolution between duplicated genetic elements in Helicobacter pylori. Journal of Molecular Biology, 2002, 316, 629-642.	4.2	78
46	Molecular Analysis of Sarcoidosis Tissues for <i>Mycobacterium</i> Species DNA. Emerging Infectious Diseases, 2002, 8, 1334-1341.	4.3	128
47	Identification of Horizontally Acquired Genetic Elements in Helicobacter pylori and Other Prokaryotes Using Oligonucleotide Difference Analysis. Journal of Genome Science and Technology, 2002, 1, 2-15.	0.5	19
48	Allelic Variation within Helicobacter pylori babA and babB. Infection and Immunity, 2001, 69, 1160-1171.	2.2	105
49	Increased Innate Immune Susceptibility in Hyperpigmented Bacteriophage-Resistant Mutants of Pseudomonas aeruginosa. Antimicrobial Agents and Chemotherapy, 0, , .	3.2	3