

Ben Pascoe

List of Publications by Year in descending order

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66
papers

2,397
citations

236612

25
h-index

243296

44
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90
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90
docs citations

90
times ranked

2971
citing authors

#	ARTICLE	IF	CITATIONS
1	Combined Analysis of Variation in Core, Accessory and Regulatory Genome Regions Provides a Super-Resolution View into the Evolution of Bacterial Populations. <i>PLoS Genetics</i> , 2016, 12, e1006280.	1.5	177
2	Ecological Overlap and Horizontal Gene Transfer in <i>Staphylococcus aureus</i> and <i>Staphylococcus epidermidis</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 1313-1328.	1.1	130
3	Progressive genome-wide introgression in agricultural <i>Campylobacter coli</i> . <i>Molecular Ecology</i> , 2013, 22, 1051-1064.	2.0	128
4	Rapid host switching in generalist <i>Campylobacter</i> strains erodes the signal for tracing human infections. <i>ISME Journal</i> , 2016, 10, 721-729.	4.4	123
5	A Reference Pan-Genome Approach to Comparative Bacterial Genomics: Identification of Novel Epidemiological Markers in Pathogenic <i>Campylobacter</i> . <i>PLoS ONE</i> , 2014, 9, e92798.	1.1	122
6	Disease-associated genotypes of the commensal skin bacterium <i>Staphylococcus epidermidis</i> . <i>Nature Communications</i> , 2018, 9, 5034.	5.8	115
7	Genome-wide association of functional traits linked with <i>Campylobacter jejuni</i> survival from farm to fork. <i>Environmental Microbiology</i> , 2017, 19, 361-380.	1.8	88
8	Genome-Wide Identification of Host-Segregating Epidemiological Markers for Source Attribution in <i>Campylobacter jejuni</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	82
9	Enhanced biofilm formation and multi-host transmission evolve from divergent genetic backgrounds in <i>Campylobacter jejuni</i> . <i>Environmental Microbiology</i> , 2015, 17, 4779-4789.	1.8	76
10	Genome evolution and the emergence of pathogenicity in avian <i>Escherichia coli</i> . <i>Nature Communications</i> , 2021, 12, 765.	5.8	69
11	Zinc-Responsive Regulation of Alternative Ribosomal Protein Genes in <i>Streptomyces coelicolor</i> Involves Zur and If R. <i>Journal of Bacteriology</i> , 2007, 189, 4078-4086.	1.0	68
12	Gene pool transmission of multidrug resistance among <i>Campylobacter</i> from livestock, sewage and human disease. <i>Environmental Microbiology</i> , 2019, 21, 4597-4613.	1.8	68
13	The Zinc-Responsive Regulator Zur Controls Expression of the Coelibactin Gene Cluster in <i>Streptomyces coelicolor</i> . <i>Journal of Bacteriology</i> , 2010, 192, 608-611.	1.0	65
14	Comparative Genomics Study of <i>Staphylococcus epidermidis</i> Isolates from Orthopedic-Device-Related Infections Correlated with Patient Outcome. <i>Journal of Clinical Microbiology</i> , 2017, 55, 3089-3103.	1.8	55
15	A GWAS on <i>Helicobacter pylori</i> strains points to genetic variants associated with gastric cancer risk. <i>BMC Biology</i> , 2018, 16, 84.	1.7	55
16	Agricultural intensification and the evolution of host specialism in the enteric pathogen <i>Campylobacter jejuni</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11018-11028.	3.3	50
17	Biofilm Morphotypes and Population Structure among <i>Staphylococcus epidermidis</i> from Commensal and Clinical Samples. <i>PLoS ONE</i> , 2016, 11, e0151240.	1.1	49
18	Recombination-Mediated Host Adaptation by Avian <i>Staphylococcus aureus</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 830-842.	1.1	46

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19	Lineage-specific plasmid acquisition and the evolution of specialized pathogens in <i>Bacillus thuringiensis</i> and the <i>Bacillus cereus</i> group. <i>Molecular Ecology</i> , 2018, 27, 1524-1540.	2.0	43
20	Epistasis analysis uncovers hidden antibiotic resistance-associated fitness costs hampering the evolution of MRSA. <i>Genome Biology</i> , 2018, 19, 94.	3.8	43
21	Genome Comparison of Erythromycin Resistant <i>Campylobacter</i> from Turkey's Identifies Hosts and Pathways for Horizontal Spread of <i>erm(B)</i> Genes. <i>Frontiers in Microbiology</i> , 2017, 8, 2240.	1.5	38
22	Local genes for local bacteria: Evidence of allopatry in the genomes of transatlantic <i>Campylobacter</i> populations. <i>Molecular Ecology</i> , 2017, 26, 4497-4508.	2.0	36
23	Molecular epidemiology and comparative genomics of <i>Campylobacter concisus</i> strains from saliva, faeces and gut mucosal biopsies in inflammatory bowel disease. <i>Scientific Reports</i> , 2018, 8, 1902.	1.6	35
24	Genomic structure and insertion sites of <i>Helicobacter pylori</i> prophages from various geographical origins. <i>Scientific Reports</i> , 2017, 7, 42471.	1.6	34
25	Persistent <i>Staphylococcus aureus</i> Isolates from Two Independent Cases of Bacteremia Display Increased Bacterial Fitness and Novel Immune Evasion Phenotypes. <i>Infection and Immunity</i> , 2015, 83, 3311-3324.	1.0	33
26	Dormant Cells of <i>Staphylococcus aureus</i> Are Resuscitated by Spent Culture Supernatant. <i>PLoS ONE</i> , 2014, 9, e85998.	1.1	30
27	<i>Staphylococcus epidermidis</i> in Biomaterial-Associated Infections. , 2013, , 25-56.		29
28	Prevalence of faecal carriage of extended-spectrum β -lactamase (ESBL)-producing <i>Escherichia coli</i> in veterinary hospital staff and students. <i>Veterinary Record Open</i> , 2019, 6, e000307.	0.3	26
29	Domestication of <i>Campylobacter jejuni</i> NCTC 11168. <i>Microbial Genomics</i> , 2019, 5, .	1.0	26
30	Evidence of land-sea transfer of the zoonotic pathogen <i>Campylobacter</i> to a wildlife marine sentinel species. <i>Molecular Ecology</i> , 2015, 24, 208-221.	2.0	25
31	Genetic features of livestock-associated <i>Staphylococcus aureus</i> ST9 isolates from Chinese pigs that carry the <i>Isa(E)</i> gene for quinupristin/dalfopristin resistance. <i>International Journal of Medical Microbiology</i> , 2016, 306, 722-729.	1.5	25
32	<i>Campylobacter jejuni</i> genotypes are associated with post-infection irritable bowel syndrome in humans. <i>Communications Biology</i> , 2021, 4, 1015.	2.0	24
33	A 500-year tale of co-evolution, adaptation, and virulence: <i>Helicobacter pylori</i> in the Americas. <i>ISME Journal</i> , 2021, 15, 78-92.	4.4	23
34	Genetic Diversity of Composite Enterotoxigenic <i>Staphylococcus epidermidis</i> Pathogenicity Islands. <i>Genome Biology and Evolution</i> , 2019, 11, 3498-3509.	1.1	21
35	From Escherich to the <i>Escherichia coli</i> genome. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 634-636.	4.6	20
36	Genomic epidemiology of <i>Campylobacter jejuni</i> associated with asymptomatic pediatric infection in the Peruvian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008533.	1.3	20

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37	Bayesian identification of bacterial strains from sequencing data. <i>Microbial Genomics</i> , 2016, 2, e000075.	1.0	19
38	The Potential of Isolation Source to Predict Colonization in Avian Hosts: A Case Study in <i>Campylobacter jejuni</i> Strains From Three Bird Species. <i>Frontiers in Microbiology</i> , 2018, 9, 591.	1.5	18
39	Host ecology regulates interspecies recombination in bacteria of the genus <i>Campylobacter</i> . <i>ELife</i> , 2022, 11, .	2.8	17
40	Stress resistance associated with multi-host transmission and enhanced biofilm formation at 42°C among hyper-aerotolerant generalist <i>Campylobacter jejuni</i> . <i>Food Microbiology</i> , 2021, 95, 103706.	2.1	16
41	Core genome sequence analysis to characterize <i>Salmonella enterica</i> serovar Rissen ST469 from a swine production chain. <i>International Journal of Food Microbiology</i> , 2019, 304, 68-74.	2.1	15
42	Genome-Wide Identification of Host-Segregating Single-Nucleotide Polymorphisms for Source Attribution of Clinical <i>Campylobacter coli</i> Isolates. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	15
43	Genomic epidemiology of clinical <i>Campylobacter</i> spp. at a single health trust site. <i>Microbial Genomics</i> , 2018, 4, .	1.0	15
44	High-resolution sweep metagenomics using fast probabilistic inference. <i>Wellcome Open Research</i> , 0, 5, 14.	0.9	14
45	Large Sequence Diversity within the Biosynthesis Locus and Common Biochemical Features of <i>Campylobacter coli</i> Lipooligosaccharides. <i>Journal of Bacteriology</i> , 2016, 198, 2829-2840.	1.0	13
46	High-resolution sweep metagenomics using fast probabilistic inference. <i>Wellcome Open Research</i> , 2020, 5, 14.	0.9	13
47	Whole-genome characterisation of multidrug resistant monophasic variants of <i>Salmonella</i> Typhimurium from pig production in Thailand. <i>PeerJ</i> , 0, 8, e9700.	0.9	13
48	Convergent Amino Acid Signatures in Polyphyletic <i>Campylobacter jejuni</i> Subpopulations Suggest Human Niche Tropism. <i>Genome Biology and Evolution</i> , 2018, 10, 763-774.	1.1	12
49	Genomic epidemiology of the commercially important pathogen <i>Renibacterium salmoninarum</i> within the Chilean salmon industry. <i>Microbial Genomics</i> , 2018, 4, .	1.0	12
50	Quantifying bacterial evolution in the wild: A birthday problem for <i>Campylobacter</i> lineages. <i>PLoS Genetics</i> , 2021, 17, e1009829.	1.5	11
51	Comparative genomic survey of <i>Bacillus cereus</i> sensu stricto isolates from the dairy production chain in Brazil. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	10
52	The emergence of plasmid-borne cfr-mediated linezolid resistant-staphylococci in Vietnam. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 22, 462-465.	0.9	7
53	Genome-wide association study of signature genetic alterations among <i>Pseudomonas aeruginosa</i> cystic fibrosis isolates. <i>PLoS Pathogens</i> , 2021, 17, e1009681.	2.1	7
54	Characterisation of <i>Salmonella enterica</i> clones carrying mcr-1 plasmids in meat products and patients in Northern Thailand using long read sequencing. <i>International Journal of Food Microbiology</i> , 2021, 358, 109314.	2.1	7

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55	Stereoselective Bacterial Metabolism of Antibiotics in Environmental Bacteria – A Novel Biochemical Workflow. <i>Frontiers in Microbiology</i> , 2021, 12, 562157.	1.5	4
56	Signatures of selection in core and accessory genomes indicate different ecological drivers of diversification among <i>Bacillus cereus</i> clades. <i>Molecular Ecology</i> , 2022, 31, 3584-3597.	2.0	4
57	Stereoselective metabolism of chloramphenicol by bacteria isolated from wastewater, and the importance of stereochemistry in environmental risk assessments for antibiotics. <i>Water Research</i> , 2022, 217, 118415.	5.3	3
58	Local accessory gene sharing among Egyptian <i>Campylobacter</i> potentially promotes the spread of antimicrobial resistance. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
59	Draft Genome Sequence of an Enterobacter Species Associated with Illnesses and Powdered Infant Formula. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
60	Molecular evidence for cross boundary spread of <i>Salmonella</i> spp. in meat sold at retail markets in the middle Mekong basin area. <i>PeerJ</i> , 2021, 9, e11255.	0.9	1
61	High Resolution Whole Genome Multilocus Sequence Typing (wgMLST) Schemes for <i>Salmonella enterica</i> Weltevreden Epidemiologic Investigations. <i>Microbiology and Biotechnology Letters</i> , 2018, 46, 162-170.	0.2	1
62	Comparative pangenomics of <i>Campylobacter</i> species. <i>Access Microbiology</i> , 2019, 1, .	0.2	1
63	Genomics for rational autogenous vaccine design to control <i>Campylobacter</i> infection in poultry. <i>Access Microbiology</i> , 2019, 1, .	0.2	0
64	Local genes, for local bacteria: biogeographical variation in <i>Campylobacter</i> accessory genome content. <i>Access Microbiology</i> , 2019, 1, .	0.2	0
65	Genomic epidemiology of <i>Campylobacter jejuni</i> associated with asymptomatic pediatric infection in the Peruvian Amazon. <i>Access Microbiology</i> , 2020, 2, .	0.2	0
66	Identification of <i>Streptococcus suis</i> carriage in healthy pigs in Chiang Mai, Thailand. , 2022, 20, 363-376.		0