

# James E Bray

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

3,421  
citations

331670

21  
h-index

395702

33  
g-index

36  
all docs

36  
docs citations

36  
times ranked

4419  
citing authors

#	ARTICLE	IF	CITATIONS
1	Open-access bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications. Wellcome Open Research, 2018, 3, 124.	1.8	1,710
2	MLST revisited: the gene-by-gene approach to bacterial genomics. Nature Reviews Microbiology, 2013, 11, 728-736.	28.6	590
3	Ecological Overlap and Horizontal Gene Transfer in <i>Staphylococcus aureus</i> and <i>Staphylococcus epidermidis</i> . Genome Biology and Evolution, 2015, 7, 1313-1328.	2.5	130
4	Disease-associated genotypes of the commensal skin bacterium <i>Staphylococcus epidermidis</i> . Nature Communications, 2018, 9, 5034.	12.8	115
5	Core Genome Multilocus Sequence Typing Scheme for Stable, Comparative Analyses of <i>Campylobacter jejuni</i> and <i>C. coli</i> Human Disease Isolates. Journal of Clinical Microbiology, 2017, 55, 2086-2097.	3.9	105
6	Defining the Estimated Core Genome of Bacterial Populations Using a Bayesian Decision Model. PLoS Computational Biology, 2014, 10, e1003788.	3.2	72
7	Genomic epidemiology of age-associated meningococcal lineages in national surveillance: an observational cohort study. Lancet Infectious Diseases, The, 2015, 15, 1420-1428.	9.1	63
8	Wild bird-associated <i>Campylobacter jejuni</i> isolates are a consistent source of human disease, in Oxfordshire, United Kingdom. Environmental Microbiology Reports, 2015, 7, 782-788.	2.4	61
9	Diversity and distribution of nuclease bacteriocins in bacterial genomes revealed using Hidden Markov Models. PLoS Computational Biology, 2017, 13, e1005652.	3.2	52
10	Biofilm Morphotypes and Population Structure among <i>Staphylococcus epidermidis</i> from Commensal and Clinical Samples. PLoS ONE, 2016, 11, e0151240.	2.5	49
11	Recombination-Mediated Host Adaptation by Avian <i>Staphylococcus aureus</i> . Genome Biology and Evolution, 2017, 9, 830-842.	2.5	46
12	Genomics Reveals the Worldwide Distribution of Multidrug-Resistant Serotype 6E Pneumococci. Journal of Clinical Microbiology, 2015, 53, 2271-2285.	3.9	44
13	Putatively novel serotypes and the potential for reduced vaccine effectiveness: capsular locus diversity revealed among 5405 pneumococcal genomes. Microbial Genomics, 2016, 2, 000090.	2.0	41
14	A RESTful application programming interface for the PubMLST molecular typing and genome databases. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	33
15	Frequent capsule switching in "ultra-virulent" meningococci " Are we ready for a serogroup B ST-11 complex outbreak?. Journal of Infection, 2017, 75, 95-103.	3.3	30
16	The domestication of the probiotic bacterium <i>Lactobacillus acidophilus</i> . Scientific Reports, 2014, 4, 7202.	3.3	29
17	Heavy Metal Susceptibility of <i>Escherichia coli</i> Isolated from Urine Samples from Sweden, Germany, and Spain. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	27
18	Towards a systematic analysis of human short-chain dehydrogenases/reductases (SDR): Ligand identification and structure-activity relationships. Chemo-Biological Interactions, 2015, 234, 114-125.	4.0	26

#	ARTICLE	IF	CITATIONS
19	A Point Prevalence Survey of Antibiotic Resistance in the Irish Environment, 2018–2019. <i>Environment International</i> , 2021, 152, 106466.	10.0	26
20	Meningococcal carriage in periods of high and low invasive meningococcal disease incidence in the UK: comparison of UKMenCar1–4 cross-sectional survey results. <i>Lancet Infectious Diseases</i> , The, 2021, 21, 677-687.	9.1	24
21	<i>Neisseria</i> genomics: current status and future perspectives. <i>Pathogens and Disease</i> , 2017, 75, .	2.0	23
22	Genomic Analysis of the Evolution and Global Spread of Hyper-invasive Meningococcal Lineage 5. <i>EBioMedicine</i> , 2015, 2, 234-243.	6.1	20
23	Potential Coverage of the 4CMenB Vaccine against Invasive Serogroup B <i>Neisseria meningitidis</i> Isolated from 2009 to 2013 in the Republic of Ireland. <i>MSphere</i> , 2018, 3, .	2.9	18
24	Resolution of a Protracted Serogroup B Meningococcal Outbreak with Whole-Genome Sequencing Shows Interspecies Genetic Transfer. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2891-2899.	3.9	16
25	Hierarchical genomic analysis of carried and invasive serogroup A <i>Neisseria meningitidis</i> during the 2011 epidemic in Chad. <i>BMC Genomics</i> , 2017, 18, 398.	2.8	15
26	<i>Thiomicrothrix heinhorstiae</i> sp. nov. and <i>Thiomicrothrix cannonii</i> sp. nov.: novel sulphur-oxidizing chemolithoautotrophs isolated from the chemocline of Hospital Hole, an anchialine sinkhole in Spring Hill, Florida, USA. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	13
27	Genomic Analyses of >3,100 Nasopharyngeal Pneumococci Revealed Significant Differences Between Pneumococci Recovered in Four Different Geographical Regions. <i>Frontiers in Microbiology</i> , 2019, 10, 317.	3.5	9
28	TypOn: the microbial typing ontology. <i>Journal of Biomedical Semantics</i> , 2014, 5, 43.	1.6	7
29	cgMLST characterisation of invasive <i>Neisseria meningitidis</i> serogroup C and W strains associated with increasing disease incidence in the Republic of Ireland. <i>PLoS ONE</i> , 2019, 14, e0216771.	2.5	7
30	Evolution of Sequence Type 4821 Clonal Complex Hyperinvasive and Quinolone-Resistant Meningococci. <i>Emerging Infectious Diseases</i> , 2021, 27, 1110-1122.	4.3	7
31	Distribution of class 1 integrons in historic and contemporary collections of human pathogenic <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2020, 15, e0233315.	2.5	6
32	Genomic epidemiology of group B streptococci spanning 10 years in an Irish maternity hospital, 2008–2017. <i>Journal of Infection</i> , 2021, 83, 37-45.	3.3	4
33	Complete genome and methylome analysis of <i>Neisseria meningitidis</i> associated with increased serogroup Y disease. <i>Scientific Reports</i> , 2020, 10, 3644.	3.3	2