

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	Thiomicrothabodus heinhorstiae sp. nov. and Thiomicrothabodus cannonii 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
2	Evolution of Sequence Type 4821 Clonal Complex Hyperinvasive and Quinolone-Resistant Meningococci. <i>Emerging Infectious Diseases</i> , 2021, 27, 1110-1122.	4.3	7
3	Meningococcal carriage in periods of high and low invasive meningococcal disease incidence in the UK: comparison of UKMenCar1â€™4 cross-sectional survey results. <i>Lancet Infectious Diseases</i> , The, 2021, 21, 677-687.	9.1	24
4	Genomic epidemiology of group B streptococci spanning 10 years in an Irish maternity hospital, 2008â€™2017. <i>Journal of Infection</i> , 2021, 83, 37-45.	3.3	4
5	A Point Prevalence Survey of Antibiotic Resistance in the Irish Environment, 2018â€™2019. <i>Environment International</i> , 2021, 152, 106466.	10.0	26
6	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
7	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
8	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
9	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
10	Heavy Metal Susceptibility of <i>Escherichia coli</i> Isolated from Urine Samples from Sweden, Germany, and Spain. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	27
11	Disease-associated genotypes of the commensal skin bacterium <i>Staphylococcus epidermidis</i> . <i>Nature Communications</i> , 2018, 9, 5034.	12.8	115
12	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
13	Open-access bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications. <i>Wellcome Open Research</i> , 2018, 3, 124.	1.8	1,710
14	Recombination-Mediated Host Adaptation by Avian <i>Staphylococcus aureus</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 830-842.	2.5	46
15	Core Genome Multilocus Sequence Typing Scheme for Stable, Comparative Analyses of <i>Campylobacter jejuni</i> and <i>C. coli</i> Human Disease Isolates. <i>Journal of Clinical Microbiology</i> , 2017, 55, 2086-2097.	3.9	105
16	Frequent capsule switching in â€™ultra-virulentâ€™ meningococci â€™ Are we ready for a serogroup B ST-11 complex outbreak?. <i>Journal of Infection</i> , 2017, 75, 95-103.	3.3	30
17	<i>Neisseria</i> genomics: current status and future perspectives. <i>Pathogens and Disease</i> , 2017, 75, .	2.0	23
18	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

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19	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
20	Diversity and distribution of nuclease bacteriocins in bacterial genomes revealed using Hidden Markov Models. PLoS Computational Biology, 2017, 13, e1005652.	3.2	52
21	Resolution of a Protracted Serogroup B Meningococcal Outbreak with Whole-Genome Sequencing Shows Interspecies Genetic Transfer. Journal of Clinical Microbiology, 2016, 54, 2891-2899.	3.9	16
22	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
23	Biofilm Morphotypes and Population Structure among Staphylococcus epidermidis from Commensal and Clinical Samples. PLoS ONE, 2016, 11, e0151240.	2.5	49
24	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
25	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
26	Towards a systematic analysis of human short-chain dehydrogenases/reductases (SDR): Ligand identification and structure-activity relationships. Chemico-Biological Interactions, 2015, 234, 114-125.	4.0	26
27	Genomic Analysis of the Evolution and Global Spread of Hyper-invasive Meningococcal Lineage 5. EBioMedicine, 2015, 2, 234-243.	6.1	20
28	Ecological Overlap and Horizontal Gene Transfer in Staphylococcus aureus and Staphylococcus epidermidis. Genome Biology and Evolution, 2015, 7, 1313-1328.	2.5	130
29	Genomics Reveals the Worldwide Distribution of Multidrug-Resistant Serotype 6E Pneumococci. Journal of Clinical Microbiology, 2015, 53, 2271-2285.	3.9	44
30	Defining the Estimated Core Genome of Bacterial Populations Using a Bayesian Decision Model. PLoS Computational Biology, 2014, 10, e1003788.	3.2	72
31	TypOn: the microbial typing ontology. Journal of Biomedical Semantics, 2014, 5, 43.	1.6	7
32	The domestication of the probiotic bacterium Lactobacillus acidophilus. Scientific Reports, 2014, 4, 7202.	3.3	29
33	MLST revisited: the gene-by-gene approach to bacterial genomics. Nature Reviews Microbiology, 2013, 11, 728-736.	28.6	590