

Ewan M Harrison

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

6,766
citations

109321

35
h-index

110387

64
g-index

67
all docs

67
docs citations

67
times ranked

10534
citing authors

#	ARTICLE	IF	CITATIONS
1	Combined epidemiological and genomic analysis of nosocomial SARS-CoV-2 infection early in the pandemic and the role of unidentified cases in transmission. <i>Clinical Microbiology and Infection</i> , 2022, 28, 93-100.	6.0	21
2	Emergence of methicillin resistance predates the clinical use of antibiotics. <i>Nature</i> , 2022, 602, 135-141.	27.8	138
3	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission. <i>Nature Communications</i> , 2022, 13, 751.	12.8	27
4	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	12.8	10
5	Tracking SARS-CoV-2 Mutations & Variants Through the COG-UK-Mutation Explorer. <i>Virus Evolution</i> , 2022, 8, veac023.	4.9	19
6	The NaHCO ₃ -Responsive Phenotype in Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) Is Influenced by <i>mecA</i> Genotype. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, e0025222.	3.2	3
7	Quantifying acquisition and transmission of <i>Enterococcus faecium</i> using genomic surveillance. <i>Nature Microbiology</i> , 2021, 6, 103-111.	13.3	53
8	SARS-CoV-2 variants, spike mutations and immune escape. <i>Nature Reviews Microbiology</i> , 2021, 19, 409-424.	28.6	2,650
9	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. <i>Cell Reports</i> , 2021, 35, 109292.	6.4	375
10	CLIMB-COVID: continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance. <i>Genome Biology</i> , 2021, 22, 196.	8.8	53
11	A Combined Phenotypic-Genotypic Predictive Algorithm for In Vitro Detection of Bicarbonate: β -Lactam Sensitization among Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA). <i>Antibiotics</i> , 2021, 10, 1089.	3.7	7
12	Nasal microbiome research in ANCA-associated vasculitis: Strengths, limitations, and future directions. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 415-423.	4.1	3
13	The impact of viral mutations on recognition by SARS-CoV-2 specific T _H cells. <i>iScience</i> , 2021, 24, 103353.	4.1	57
14	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021, 374, eabl9551.	12.6	111
15	The Evolutionary Genomics of Host Specificity in <i>Staphylococcus aureus</i> . <i>Trends in Microbiology</i> , 2020, 28, 465-477.	7.7	74
16	Definition of a genetic relatedness cutoff to exclude recent transmission of methicillin-resistant <i>Staphylococcus aureus</i> : a genomic epidemiology analysis. <i>Lancet Microbe</i> , The, 2020, 1, e328-e335.	7.3	75
17	The composition and functional protein subsystems of the human nasal microbiome in granulomatosis with polyangiitis: a pilot study. <i>Microbiome</i> , 2019, 7, 137.	11.1	22
18	Genomic identification of cryptic susceptibility to penicillins and β -lactamase inhibitors in methicillin-resistant <i>Staphylococcus aureus</i> . <i>Nature Microbiology</i> , 2019, 4, 1680-1691.	13.3	47

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19	Characterization of <i>mecC</i> gene-carrying coagulase-negative <i>Staphylococcus</i> spp. isolated from various animals. <i>Veterinary Microbiology</i> , 2019, 230, 138-144.	1.9	38
20	Truncation of <i>GdpP</i> mediates β -lactam resistance in clinical isolates of <i>Staphylococcus aureus</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1182-1191.	3.0	40
21	Nasal carriage of <i>Staphylococcus pseudintermedius</i> in patients with granulomatosis with polyangiitis. <i>Rheumatology</i> , 2019, 58, 548-550.	1.9	8
22	Prospective genomic surveillance of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) associated with bloodstream infection, England, 1 October 2012 to 30 September 2013. <i>Eurosurveillance</i> , 2019, 24, .	7.0	19
23	Identification of a staphylococcal complement inhibitor with broad host specificity in equid <i>Staphylococcus aureus</i> strains. <i>Journal of Biological Chemistry</i> , 2018, 293, 4468-4477.	3.4	34
24	Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , 2018, 2, 1468-1478.	7.8	156
25	Identification of LukPQ, a novel, equid-adapted leukocidin of <i>Staphylococcus aureus</i> . <i>Scientific Reports</i> , 2017, 7, 40660.	3.3	47
26	Longitudinal genomic surveillance of MRSA in the UK reveals transmission patterns in hospitals and the community. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	103
27	Investigation of a Cluster of Sequence Type 22 Methicillin-Resistant <i>Staphylococcus aureus</i> Transmission in a Community Setting. <i>Clinical Infectious Diseases</i> , 2017, 65, 2069-2077.	5.8	11
28	Genomic surveillance reveals low prevalence of livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> in the East of England. <i>Scientific Reports</i> , 2017, 7, 7406.	3.3	25
29	Evolution of mobile genetic element composition in an epidemic methicillin-resistant <i>Staphylococcus aureus</i> : temporal changes correlated with frequent loss and gain events. <i>BMC Genomics</i> , 2017, 18, 684.	2.8	43
30	Local Persistence of Novel MRSA Lineage after Hospital Ward Outbreak, Cambridge, UK, 2011–2013. <i>Emerging Infectious Diseases</i> , 2016, 22, 1658-1659.	4.3	4
31	A Look into the Melting Pot: The <i>mecC</i> -Harboring Region Is a Recombination Hot Spot in <i>Staphylococcus stepanovicii</i> . <i>PLoS ONE</i> , 2016, 11, e0147150.	2.5	13
32	Transmission of methicillin-resistant <i>Staphylococcus aureus</i> in long-term care facilities and their related healthcare networks. <i>Genome Medicine</i> , 2016, 8, 102.	8.2	30
33	The effect of genetic structure on molecular dating and tests for temporal signal. <i>Methods in Ecology and Evolution</i> , 2016, 7, 80-89.	5.2	143
34	Systematic Surveillance Detects Multiple Silent Introductions and Household Transmission of Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 in the East of England. <i>Journal of Infectious Diseases</i> , 2016, 214, 447-453.	4.0	45
35	PBP2a substitutions linked to ceftaroline resistance in MRSA isolates from the UK: Table 1.. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 268-269.	3.0	16
36	Whole-genome sequencing reveals transmission of vancomycin-resistant <i>Enterococcus faecium</i> in a healthcare network. <i>Genome Medicine</i> , 2016, 8, 4.	8.2	58

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37	Validation of self-administered nasal swabs and postage for the isolation of <i>Staphylococcus aureus</i> . <i>Journal of Medical Microbiology</i> , 2016, 65, 1434-1437.	1.8	3
38	A Site-Specific Integrative Plasmid Found in <i>Pseudomonas aeruginosa</i> Clinical Isolate HS87 along with A Plasmid Carrying an Aminoglycoside-Resistant Gene. <i>PLoS ONE</i> , 2016, 11, e0148367.	2.5	7
39	Genomic Analysis of Companion Rabbit <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2016, 11, e0151458.	2.5	12
40	Genomic insights into the rapid emergence and evolution of MDR in <i>Staphylococcus pseudintermedius</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 997-1007.	3.0	77
41	Old Drugs To Treat Resistant Bugs: Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates with <i>mecC</i> Are Susceptible to a Combination of Penicillin and Clavulanic Acid. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7396-7404.	3.2	32
42	Capturing the cloud of diversity reveals complexity and heterogeneity of MRSA carriage, infection and transmission. <i>Nature Communications</i> , 2015, 6, 6560.	12.8	105
43	Draft Genome Sequence of the <i>Streptococcus pneumoniae</i> Avery Strain A66. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
44	A Shared Population of Epidemic Methicillin-Resistant <i>Staphylococcus aureus</i> 15 Circulates in Humans and Companion Animals. <i>MBio</i> , 2014, 5, e00985-13.	4.1	95
45	Detection of <i>mecC</i> - <i>M</i> -methicillin-resistant <i>Staphylococcus aureus</i> isolates in river water: a potential role for water in the environmental dissemination. <i>Environmental Microbiology Reports</i> , 2014, 6, 705-708.	2.4	35
46	Conjugative transfer frequencies of <i>mef</i> (A)-containing Tn 1207.3 to macrolide-susceptible <i>S. treptococcus pyogenes</i> belonging to different emm types. <i>Letters in Applied Microbiology</i> , 2014, 58, 299-302.	2.2	6
47	The emergence of <i>mecC</i> methicillin-resistant <i>Staphylococcus aureus</i> . <i>Trends in Microbiology</i> , 2014, 22, 42-47.	7.7	351
48	Novel mutations in penicillin-binding protein genes in clinical <i>Staphylococcus aureus</i> isolates that are methicillin resistant on susceptibility testing, but lack the <i>mec</i> gene. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 594-597.	3.0	80
49	Prevalence and properties of <i>mecC</i> methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) in bovine bulk tank milk in Great Britain. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 598-602.	3.0	66
50	A novel hybrid SCCmec-mecC region in <i>Staphylococcus sciuri</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 911-918.	3.0	73
51	Prevalence and characterization of human <i>mecC</i> methicillin-resistant <i>Staphylococcus aureus</i> isolates in England. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 907-910.	3.0	62
52	Whole genome sequencing identifies zoonotic transmission of MRSA isolates with the novel <i>mecA</i> homologue <i>mecC</i> . <i>EMBO Molecular Medicine</i> , 2013, 5, 509-515.	6.9	192
53	Use of Vitek 2 Antimicrobial Susceptibility Profile To Identify <i>mecC</i> in Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Journal of Clinical Microbiology</i> , 2013, 51, 2732-2734.	3.9	53
54	A <i>Staphylococcus xylosus</i> Isolate with a New <i>mecC</i> Allotype. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 1524-1528.	3.2	67

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55	Incidence and Characterisation of Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) from Nasal Colonisation in Participants Attending a Cattle Veterinary Conference in the UK. <i>PLoS ONE</i> , 2013, 8, e68463.	2.5	28
56	Deletion of TnAbaR23 Results in both Expected and Unexpected Antibigram Changes in a Multidrug-Resistant <i>Acinetobacter baumannii</i> Strain. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 1845-1853.	3.2	37
57	ICEberg: a web-based resource for integrative and conjugative elements found in Bacteria. <i>Nucleic Acids Research</i> , 2012, 40, D621-D626.	14.5	206
58	<i>Acinetobacter</i> Insertion Sequence IS <i>Aba11</i> Belongs to a Novel Family That Encodes Transposases with a Signature HHEK Motif. <i>Applied and Environmental Microbiology</i> , 2012, 78, 471-480.	3.1	7
59	Characterization of a novel chaperone/usher fimbrial operon present on KpGI-5, a methionine tRNA gene-associated genomic island in <i>Klebsiella pneumoniae</i> . <i>BMC Microbiology</i> , 2012, 12, 59.	3.3	8
60	TADB: a web-based resource for Type 2 toxin antitoxin loci in bacteria and archaea. <i>Nucleic Acids Research</i> , 2011, 39, D606-D611.	14.5	271
61	mGenomeSubtractor: a web-based tool for parallel in silico subtractive hybridization analysis of multiple bacterial genomes. <i>Nucleic Acids Research</i> , 2010, 38, W194-W200.	14.5	74
62	Pathogenicity Islands PAPI-1 and PAPI-2 Contribute Individually and Synergistically to the Virulence of <i>Pseudomonas aeruginosa</i> Strain PA14. <i>Infection and Immunity</i> , 2010, 78, 1437-1446.	2.2	69
63	MobilomeFINDER: web-based tools for in silico and experimental discovery of bacterial genomic islands. <i>Nucleic Acids Research</i> , 2007, 35, W97-W104.	14.5	74
64	Comparison and Correlation of <i>Neisseria meningitidis</i> Serogroup B Immunologic Assay Results and Human Antibody Responses following Three Doses of the Norwegian Meningococcal Outer Membrane Vesicle Vaccine MenBvac. <i>Infection and Immunity</i> , 2006, 74, 4557-4565.	2.2	47