

Ewan M Harrison

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

66

papers

3,520

citations

28

h-index

59

g-index

67

ext. papers

5,563

ext. citations

10.5

avg, IF

5.65

L-index

#	Paper	IF	Citations
66	Emergence of methicillin resistance predates the clinical use of antibiotics.. <i>Nature</i> , 2022 ,	50.4	33
65	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission.. <i>Nature Communications</i> , 2022 , 13, 751	17.4	7
64	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission.. <i>Nature Communications</i> , 2022 , 13, 1012	17.4	2
63	Tracking SARS-CoV-2 mutations and variants through the COG-UK-Mutation Explorer.. <i>Virus Evolution</i> , 2022 , 8, veac023	3.7	1
62	The NaHCO-Responsive Phenotype in Methicillin-Resistant Staphylococcus aureus (MRSA) Is Influenced by Genotype.. <i>Antimicrobial Agents and Chemotherapy</i> , 2022 , e0025222	5.9	0
61	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021 , 374, eabl9551	33.3	31
60	The impact of viral mutations on recognition by SARS-CoV-2 specific T cells. <i>IScience</i> , 2021 , 24, 103353	6.1	12
59	SARS-CoV-2 variants, spike mutations and immune escape. <i>Nature Reviews Microbiology</i> , 2021 , 19, 409-424	24.2	873
58	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	10.6	172
57	Quantifying acquisition and transmission of Enterococcus faecium using genomic surveillance. <i>Nature Microbiology</i> , 2021 , 6, 103-111	26.6	15
56	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> , 2021 ,	9.5	7
55	A Combined Phenotypic-Genotypic Predictive Algorithm for In Vitro Detection of Bicarbonate: β -Lactam Sensitization among Methicillin-Resistant (MRSA). <i>Antibiotics</i> , 2021 , 10,	4.9	3
54	Nasal microbiome research in ANCA-associated vasculitis: Strengths, limitations, and future directions. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 415-423	6.8	1
53	The Evolutionary Genomics of Host Specificity in Staphylococcus aureus. <i>Trends in Microbiology</i> , 2020 , 28, 465-477	12.4	28
52	Definition of a genetic relatedness cutoff to exclude recent transmission of methicillin-resistant : a genomic epidemiology analysis. <i>Lancet Microbe</i> , 2020 , 1, e328-e335	22.2	14
51	Genomic identification of cryptic susceptibility to penicillins and β -lactamase inhibitors in methicillin-resistant Staphylococcus aureus. <i>Nature Microbiology</i> , 2019 , 4, 1680-1691	26.6	24
50	Characterization of mecC gene-carrying coagulase-negative Staphylococcus spp. isolated from various animals. <i>Veterinary Microbiology</i> , 2019 , 230, 138-144	3.3	25

49	The composition and functional protein subsystems of the human nasal microbiome in granulomatosis with polyangiitis: a pilot study. <i>Microbiome</i> , 2019 , 7, 137	16.6	12
48	Prospective genomic surveillance of methicillin-resistant (MRSA) associated with bloodstream infection, England, 1 October 2012 to 30 September 2013. <i>Eurosurveillance</i> , 2019 , 24,	19.8	14
47	Truncation of GdpP mediates β -lactam resistance in clinical isolates of <i>Staphylococcus aureus</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2019 , 74, 1182-1191	5.1	20
46	Nasal carriage of <i>Staphylococcus pseudintermedius</i> in patients with granulomatosis with polyangiitis. <i>Rheumatology</i> , 2019 , 58, 548-550	3.9	8
45	Identification of a staphylococcal complement inhibitor with broad host specificity in equid strains. <i>Journal of Biological Chemistry</i> , 2018 , 293, 4468-4477	5.4	21
44	Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1468-1478	12.3	80
43	Identification of LukPQ, a novel, equid-adapted leukocidin of <i>Staphylococcus aureus</i> . <i>Scientific Reports</i> , 2017 , 7, 40660	4.9	32
42	Longitudinal genomic surveillance of MRSA in the UK reveals transmission patterns in hospitals and the community. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	70
41	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	11.6	8
40	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	4.9	15
39	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	4.5	23
38	The effect of genetic structure on molecular dating and tests for temporal signal. <i>Methods in Ecology and Evolution</i> , 2016 , 7, 80-89	7.7	90
37	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, 447-53	7	25
36	PBP2a substitutions linked to ceftaroline resistance in MRSA isolates from the UK. <i>Journal of Antimicrobial Chemotherapy</i> , 2016 , 71, 268-9	5.1	16
35	Whole-genome sequencing reveals transmission of vancomycin-resistant <i>Enterococcus faecium</i> in a healthcare network. <i>Genome Medicine</i> , 2016 , 8, 4	14.4	46
34	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	3.7	6
33	Genomic Analysis of Companion Rabbit <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2016 , 11, e0151458	3.7	11
32	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	3.2	2

31	Local Persistence of Novel MRSA Lineage after Hospital Ward Outbreak, Cambridge, UK, 2011-2013. <i>Emerging Infectious Diseases</i> , 2016 , 22, 1658-9	10.2	4
30	A Look into the Melting Pot: The mecC-Harboring Region Is a Recombination Hot Spot in <i>Staphylococcus stepanovicii</i> . <i>PLoS ONE</i> , 2016 , 11, e0147150	3.7	10
29	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	14.4	28
28	Old Drugs To Treat Resistant Bugs: Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates with mecC Are Susceptible to a Combination of Penicillin and Clavulanic Acid. <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 7396-404	5.9	26
27	Capturing the cloud of diversity reveals complexity and heterogeneity of MRSA carriage, infection and transmission. <i>Nature Communications</i> , 2015 , 6, 6560	17.4	83
26	Draft Genome Sequence of the <i>Streptococcus pneumoniae</i> Avery Strain A66. <i>Genome Announcements</i> , 2015 , 3,		8
25	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	5.1	59
24	The emergence of mecC methicillin-resistant <i>Staphylococcus aureus</i> . <i>Trends in Microbiology</i> , 2014 , 22, 42-7	12.4	275
23	Novel mutations in penicillin-binding protein genes in clinical <i>Staphylococcus aureus</i> isolates that are methicillin resistant on susceptibility testing, but lack the mec gene. <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 594-7	5.1	65
22	Prevalence and properties of mecC 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	5.1	53
21	A novel hybrid SCCmec-mecC region in <i>Staphylococcus sciuri</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 911-8	5.1	62
20	Prevalence and characterization of human mecC methicillin-resistant <i>Staphylococcus aureus</i> isolates in England. <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 907-10	5.1	52
19	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	7.8	70
18	Detection of mecC-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, 705-8	3.7	29
17	Conjugative transfer frequencies of mef(A)-containing Tn1207.3 to macrolide-susceptible <i>Streptococcus pyogenes</i> belonging to different emm types. <i>Letters in Applied Microbiology</i> , 2014 , 58, 299-302	2.9	6
16	Whole genome sequencing identifies zoonotic transmission of MRSA isolates with the novel mecA homologue mecC. <i>EMBO Molecular Medicine</i> , 2013 , 5, 509-15	12	166
15	Use of Vitek 2 antimicrobial susceptibility profile to identify mecC in methicillin-resistant <i>Staphylococcus aureus</i> . <i>Journal of Clinical Microbiology</i> , 2013 , 51, 2732-4	9.7	43
14	A <i>Staphylococcus xylosus</i> isolate with a new mecC allotype. <i>Antimicrobial Agents and Chemotherapy</i> , 2013 , 57, 1524-8	5.9	58

13	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	3.7	24
12	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	4.5	6
11	Deletion of TnAbaR23 results in both expected and unexpected antibiogram changes in a multidrug-resistant <i>Acinetobacter baumannii</i> strain. <i>Antimicrobial Agents and Chemotherapy</i> , 2012 , 56, 1845-53	5.9	19
10	ICEberg: a web-based resource for integrative and conjugative elements found in Bacteria. <i>Nucleic Acids Research</i> , 2012 , 40, D621-6	20.1	155
9	<i>Acinetobacter</i> insertion sequence ISAb11 belongs to a novel family that encodes transposases with a signature HHEK motif. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 471-80	4.8	7
8	TADB: a web-based resource for Type 2 toxin-antitoxin loci in bacteria and archaea. <i>Nucleic Acids Research</i> , 2011 , 39, D606-11	20.1	203
7	mGenomeSubtractor: a web-based tool for parallel in silico subtractive hybridization analysis of multiple bacterial genomes. <i>Nucleic Acids Research</i> , 2010 , 38, W194-200	20.1	63
6	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, 1437-46	3.7	56
5	MobilomeFINDER: web-based tools for in silico and experimental discovery of bacterial genomic islands. <i>Nucleic Acids Research</i> , 2007 , 35, W97-W104	20.1	66
4	Comparison and correlation of neisseria meningitidis 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, 4557-65	3.7	46
3	MAJORA: Continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance		11
2	An integrated analysis of contact tracing and genomics to assess the efficacy of travel restrictions on SARS-CoV-2 introduction and transmission in England from June to September, 2020		3
1	The origins and molecular evolution of SARS-CoV-2 lineage B.1.1.7 in the UK		2