

# Ewan M Harrison

## List of Publications by Citations

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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 | SARS-CoV-2 variants, spike mutations and immune escape. <i>Nature Reviews Microbiology</i> , <b>2021</b> , 19, 409-424.                                                                                                                                       | 24.2 | 873       |
| 65 | The emergence of mecC methicillin-resistant <i>Staphylococcus aureus</i> . <i>Trends in Microbiology</i> , <b>2014</b> , 22, 42-7                                                                                                                             | 12.4 | 275       |
| 64 | TADB: a web-based resource for Type 2 toxin-antitoxin loci in bacteria and archaea. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D606-11                                                                                                                 | 20.1 | 203       |
| 63 | 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> , <b>2021</b> , 35, 109292                                                                                                            | 10.6 | 172       |
| 62 | Whole genome sequencing identifies zoonotic transmission of MRSA isolates with the novel mecA homologue mecC. <i>EMBO Molecular Medicine</i> , <b>2013</b> , 5, 509-15                                                                                        | 12   | 166       |
| 61 | ICEberg: a web-based resource for integrative and conjugative elements found in Bacteria. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D621-6                                                                                                            | 20.1 | 155       |
| 60 | The effect of genetic structure on molecular dating and tests for temporal signal. <i>Methods in Ecology and Evolution</i> , <b>2016</b> , 7, 80-89                                                                                                           | 7.7  | 90        |
| 59 | Capturing the cloud of diversity reveals complexity and heterogeneity of MRSA carriage, infection and transmission. <i>Nature Communications</i> , <b>2015</b> , 6, 6560                                                                                      | 17.4 | 83        |
| 58 | Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , <b>2018</b> , 2, 1468-1478                                                                                                              | 12.3 | 80        |
| 57 | Longitudinal genomic surveillance of MRSA in the UK reveals transmission patterns in hospitals and the community. <i>Science Translational Medicine</i> , <b>2017</b> , 9,                                                                                    | 17.5 | 70        |
| 56 | A shared population of epidemic methicillin-resistant <i>Staphylococcus aureus</i> 15 circulates in humans and companion animals. <i>MBio</i> , <b>2014</b> , 5, e00985-13                                                                                    | 7.8  | 70        |
| 55 | MobilomeFINDER: web-based tools for in silico and experimental discovery of bacterial genomic islands. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, W97-W104                                                                                             | 20.1 | 66        |
| 54 | 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> , <b>2014</b> , 69, 594-7 | 5.1  | 65        |
| 53 | mGenomeSubtractor: a web-based tool for parallel in silico subtractive hybridization analysis of multiple bacterial genomes. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, W194-200                                                                       | 20.1 | 63        |
| 52 | A novel hybrid SCCmec-mecC region in <i>Staphylococcus sciuri</i> . <i>Journal of Antimicrobial Chemotherapy</i> , <b>2014</b> , 69, 911-8                                                                                                                    | 5.1  | 62        |
| 51 | Genomic insights into the rapid emergence and evolution of MDR in <i>Staphylococcus pseudintermedius</i> . <i>Journal of Antimicrobial Chemotherapy</i> , <b>2015</b> , 70, 997-1007                                                                          | 5.1  | 59        |
| 50 | A <i>Staphylococcus xylosus</i> isolate with a new mecC allotype. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2013</b> , 57, 1524-8                                                                                                                     | 5.9  | 58        |

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| 49 | 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> , <b>2010</b> , 78, 1437-46                                                                   | 3.7  | 56 |
| 48 | 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> , <b>2014</b> , 69, 598-602                                                                | 5.1  | 53 |
| 47 | Prevalence and characterization of human mecC methicillin-resistant <i>Staphylococcus aureus</i> isolates in England. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2014</b> , 69, 907-10                                                                                  | 5.1  | 52 |
| 46 | Whole-genome sequencing reveals transmission of vancomycin-resistant <i>Enterococcus faecium</i> in a healthcare network. <i>Genome Medicine</i> , <b>2016</b> , 8, 4                                                                                                          | 14.4 | 46 |
| 45 | 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> , <b>2006</b> , 74, 4557-65 | 3.7  | 46 |
| 44 | Use of Vitek 2 antimicrobial susceptibility profile to identify mecC in methicillin-resistant <i>Staphylococcus aureus</i> . <i>Journal of Clinical Microbiology</i> , <b>2013</b> , 51, 2732-4                                                                                | 9.7  | 43 |
| 43 | Emergence of methicillin resistance predates the clinical use of antibiotics.. <i>Nature</i> , <b>2022</b> ,                                                                                                                                                                   | 50.4 | 33 |
| 42 | Identification of LukPQ, a novel, equid-adapted leukocidin of <i>Staphylococcus aureus</i> . <i>Scientific Reports</i> , <b>2017</b> , 7, 40660                                                                                                                                | 4.9  | 32 |
| 41 | Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , <b>2021</b> , 374, eabl9551                                                                                                                   | 33.3 | 31 |
| 40 | 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> , <b>2014</b> , 6, 705-8                                                | 3.7  | 29 |
| 39 | The Evolutionary Genomics of Host Specificity in <i>Staphylococcus aureus</i> . <i>Trends in Microbiology</i> , <b>2020</b> , 28, 465-477                                                                                                                                      | 12.4 | 28 |
| 38 | Transmission of methicillin-resistant <i>Staphylococcus aureus</i> in long-term care facilities and their related healthcare networks. <i>Genome Medicine</i> , <b>2016</b> , 8, 102                                                                                           | 14.4 | 28 |
| 37 | 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> , <b>2015</b> , 59, 7396-404                         | 5.9  | 26 |
| 36 | Characterization of mecC gene-carrying coagulase-negative <i>Staphylococcus</i> spp. isolated from various animals. <i>Veterinary Microbiology</i> , <b>2019</b> , 230, 138-144                                                                                                | 3.3  | 25 |
| 35 | 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> , <b>2016</b> , 214, 447-53                                | 7    | 25 |
| 34 | Genomic identification of cryptic susceptibility to penicillins and $\beta$ -lactamase inhibitors in methicillin-resistant <i>Staphylococcus aureus</i> . <i>Nature Microbiology</i> , <b>2019</b> , 4, 1680-1691                                                              | 26.6 | 24 |
| 33 | 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> , <b>2013</b> , 8, e68463                                              | 3.7  | 24 |
| 32 | 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> , <b>2017</b> , 18, 684                                                | 4.5  | 23 |

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| 31 | Identification of a staphylococcal complement inhibitor with broad host specificity in equid strains. <i>Journal of Biological Chemistry</i> , <b>2018</b> , 293, 4468-4477                                               | 5.4  | 21 |
| 30 | Truncation of GdpP mediates $\beta$ -lactam resistance in clinical isolates of <i>Staphylococcus aureus</i> . <i>Journal of Antimicrobial Chemotherapy</i> , <b>2019</b> , 74, 1182-1191                                  | 5.1  | 20 |
| 29 | 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> , <b>2012</b> , 56, 1845-53 | 5.9  | 19 |
| 28 | PBP2a substitutions linked to ceftaroline resistance in MRSA isolates from the UK. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2016</b> , 71, 268-9                                                                 | 5.1  | 16 |
| 27 | Genomic surveillance reveals low prevalence of livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> in the East of England. <i>Scientific Reports</i> , <b>2017</b> , 7, 7406                          | 4.9  | 15 |
| 26 | Quantifying acquisition and transmission of <i>Enterococcus faecium</i> using genomic surveillance. <i>Nature Microbiology</i> , <b>2021</b> , 6, 103-111                                                                 | 26.6 | 15 |
| 25 | Prospective genomic surveillance of methicillin-resistant (MRSA) associated with bloodstream infection, England, 1 October 2012 to 30 September 2013. <i>Eurosurveillance</i> , <b>2019</b> , 24,                         | 19.8 | 14 |
| 24 | Definition of a genetic relatedness cutoff to exclude recent transmission of methicillin-resistant : a genomic epidemiology analysis. <i>Lancet Microbe</i> , <b>2020</b> , 1, e328-e335                                  | 22.2 | 14 |
| 23 | The composition and functional protein subsystems of the human nasal microbiome in granulomatosis with polyangiitis: a pilot study. <i>Microbiome</i> , <b>2019</b> , 7, 137                                              | 16.6 | 12 |
| 22 | The impact of viral mutations on recognition by SARS-CoV-2 specific T $\gamma$ cells. <i>iScience</i> , <b>2021</b> , 24, 103353                                                                                          | 6.1  | 12 |
| 21 | Genomic Analysis of Companion Rabbit <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , <b>2016</b> , 11, e0151458                                                                                                          | 3.7  | 11 |
| 20 | MAJORA: Continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance                                                                                                                    |      | 11 |
| 19 | A Look into the Melting Pot: The mecC-Harboring Region Is a Recombination Hot Spot in <i>Staphylococcus stepanovicii</i> . <i>PLoS ONE</i> , <b>2016</b> , 11, e0147150                                                   | 3.7  | 10 |
| 18 | Investigation of a Cluster of Sequence Type 22 Methicillin-Resistant <i>Staphylococcus aureus</i> Transmission in a Community Setting. <i>Clinical Infectious Diseases</i> , <b>2017</b> , 65, 2069-2077                  | 11.6 | 8  |
| 17 | Draft Genome Sequence of the <i>Streptococcus pneumoniae</i> Avery Strain A66. <i>Genome Announcements</i> , <b>2015</b> , 3,                                                                                             |      | 8  |
| 16 | Nasal carriage of <i>Staphylococcus pseudintermedius</i> in patients with granulomatosis with polyangiitis. <i>Rheumatology</i> , <b>2019</b> , 58, 548-550                                                               | 3.9  | 8  |
| 15 | <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> , <b>2012</b> , 78, 471-80                  | 4.8  | 7  |
| 14 | Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission.. <i>Nature Communications</i> , <b>2022</b> , 13, 751                                                                          | 17.4 | 7  |

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|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|---|
| 13 | 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> , <b>2021</b> ,                     | 9.5  | 7 |
| 12 | Conjugative transfer frequencies of <i>mef(A)</i> -containing Tn1207.3 to macrolide-susceptible <i>Streptococcus pyogenes</i> belonging to different <i>emm</i> types. <i>Letters in Applied Microbiology</i> , <b>2014</b> , 58, 299-302 | 2.9  | 6 |
| 11 | 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> , <b>2012</b> , 12, 59                          | 4.5  | 6 |
| 10 | 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> , <b>2016</b> , 11, e0148367                             | 3.7  | 6 |
| 9  | Local Persistence of Novel MRSA Lineage after Hospital Ward Outbreak, Cambridge, UK, 2011-2013. <i>Emerging Infectious Diseases</i> , <b>2016</b> , 22, 1658-9                                                                            | 10.2 | 4 |
| 8  | 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 |
| 7  | A Combined Phenotypic-Genotypic Predictive Algorithm for In Vitro Detection of Bicarbonate: $\beta$ -Lactam Sensitization among Methicillin-Resistant (MRSA). <i>Antibiotics</i> , <b>2021</b> , 10,                                      | 4.9  | 3 |
| 6  | Validation of self-administered nasal swabs and postage for the isolation of <i>Staphylococcus aureus</i> . <i>Journal of Medical Microbiology</i> , <b>2016</b> , 65, 1434-1437                                                          | 3.2  | 2 |
| 5  | Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission.. <i>Nature Communications</i> , <b>2022</b> , 13, 1012                                                                                      | 17.4 | 2 |
| 4  | The origins and molecular evolution of SARS-CoV-2 lineage B.1.1.7 in the UK                                                                                                                                                               |      | 2 |
| 3  | Nasal microbiome research in ANCA-associated vasculitis: Strengths, limitations, and future directions. <i>Computational and Structural Biotechnology Journal</i> , <b>2021</b> , 19, 415-423                                             | 6.8  | 1 |
| 2  | Tracking SARS-CoV-2 mutations and variants through the COG-UK-Mutation Explorer.. <i>Virus Evolution</i> , <b>2022</b> , 8, veac023                                                                                                       | 3.7  | 1 |
| 1  | The NaHCO <sub>3</sub> -Responsive Phenotype in Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) Is Influenced by Genotype.. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2022</b> , e0025222                               | 5.9  | 0 |