

Alan McNally

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.

108
papers

4,291
citations

33
h-index

64
g-index

121
ext. papers

6,342
ext. citations

9.3
avg, IF

5.92
L-index

#	Paper	IF	Citations
108	Fine-Scale Reconstruction of the Evolution of FII-33 Multidrug Resistance Plasmids Enables High-Resolution Genomic Surveillance.. <i>MSystems</i> , 2022 , e0083121	7.6	3
107	Characterization of phage resistance and phages capable of intestinal decolonization of carbapenem-resistant <i>Klebsiella pneumoniae</i> in mice.. <i>Communications Biology</i> , 2022 , 5, 48	6.7	4
106	Prokaryote pangenomes are dynamic entities.. <i>Current Opinion in Microbiology</i> , 2022 , 66, 73-78	7.9	2
105	SARS-CoV-2 Testing in the Community: Testing Positive Samples with the TaqMan SARS-CoV-2 Mutation Panel To Find Variants in Real Time.. <i>Journal of Clinical Microbiology</i> , 2022 , e0240821	9.7	1
104	and provide resistance to travel-associated intestinal colonization by multi-drug resistant .. <i>Gut Microbes</i> , 2022 , 14, 2060676	8.8	1
103	Covid-19 testing in the UK was not a "shambles" in 2020.. <i>BMJ, The</i> , 2022 , 377, o916	5.9	
102	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
101	The role of potentiating mutations in the evolution of pandemic <i>Escherichia coli</i> clones. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2021 , 1	5.3	3
100	<i>Klebsiella oxytoca</i> Complex: Update on Taxonomy, Antimicrobial Resistance, and Virulence. <i>Clinical Microbiology Reviews</i> , 2021 , e0000621	34	6
99	Mapping Gene-by-Gene Single-Nucleotide Variation in 8,535 <i>Mycobacterium tuberculosis</i> Genomes: a Resource To Support Potential Vaccine and Drug Development. <i>MSphere</i> , 2021 , 6,	5	2
98	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021 , 593, 266-269	50.4	452
97	Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. <i>Nature</i> , 2021 , 593, 136-141	50.4	376
96	Validation testing to determine the sensitivity of lateral flow testing for asymptomatic SARS-CoV-2 detection in low prevalence settings: Testing frequency and public health messaging is key. <i>PLoS Biology</i> , 2021 , 19, e3001216	9.7	26
95	Limited and Strain-Specific Transcriptional and Growth Responses to Acquisition of a Multidrug Resistance Plasmid in Genetically Diverse <i>Escherichia coli</i> Lineages. <i>MSystems</i> , 2021 , 6,	7.6	6
94	Dynamics of intestinal multidrug-resistant bacteria colonisation contracted by visitors to a high-endemic setting: a prospective, daily, real-time sampling study. <i>Lancet Microbe, The</i> , 2021 , 2, e151-e158	22.2	7
93	Emergence and dissemination of antimicrobial resistance in <i>Escherichia coli</i> causing bloodstream infections in Norway in 2002-17: a nationwide, longitudinal, microbial population genomic study.. <i>Lancet Microbe, The</i> , 2021 , 2, e331-e341	22.2	5
92	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. <i>Lancet Public Health, The</i> , 2021 , 6, e335-e345	22.4	146

91	Carbapenem and Colistin Resistance in Enterobacter: Determinants and Clones. <i>Trends in Microbiology</i> , 2021 , 29, 473-476	12.4	5
90	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
89	Transferable Acinetobacter baumannii plasmid pDETAB2 encodes OXA-58 and NDM-1 and represents a new class of antibiotic resistance plasmids. <i>Journal of Antimicrobial Chemotherapy</i> , 2021 , 76, 1130-1134	5.1	6
88	What makes new variants of SARS-CoV-2 concerning is not where they come from, but the mutations they contain. <i>BMJ, The</i> , 2021 , 372, n504	5.9	10
87	S-Variant SARS-CoV-2 Lineage B1.1.7 Is Associated With Significantly Higher Viral Load in Samples Tested by TaqPath Polymerase Chain Reaction. <i>Journal of Infectious Diseases</i> , 2021 , 223, 1666-1670	7	121
86	Spread of Carbapenem-Resistant Klebsiella pneumoniae in an Intensive Care Unit: A Whole-Genome Sequence-Based Prospective Observational Study. <i>Microbiology Spectrum</i> , 2021 , 9, e0005821	8.0	4
85	Gene-gene relationships in an accessory genome are linked to function and mobility. <i>Microbial Genomics</i> , 2021 , 7,	4.4	2
84	Antimicrobial resistance genes and clonal success in Escherichia coli isolates causing bloodstream infection - Authors' reply.. <i>Lancet Microbe, The</i> , 2021 , 2, e493	22.2	1
83	How to establish an academic SARS-CoV-2 testing laboratory. <i>Nature Microbiology</i> , 2020 , 5, 1452-1454	26.6	14
82	Struggle To Survive: the Choir of Target Alteration, Hydrolyzing Enzyme, and Plasmid Expression as a Novel Aztreonam-Avibactam Resistance Mechanism. <i>MSystems</i> , 2020 , 5,	7.6	10
81	Klebsiella pneumoniae type VI secretion system-mediated microbial competition is PhoPQ controlled and reactive oxygen species dependent. <i>PLoS Pathogens</i> , 2020 , 16, e1007969	7.6	29
80	Allelic polymorphism shapes community function in evolving Pseudomonas aeruginosa populations. <i>ISME Journal</i> , 2020 , 14, 1929-1942	11.9	16
79	Pangenomes and Selection: The Public Goods Hypothesis 2020 , 151-167		3
78	Scientific consensus on the COVID-19 pandemic: we need to act now. <i>Lancet, The</i> , 2020 , 396, e71-e72	40	124
77	Pooled testing for SARS-CoV-2 could provide the solution to UK's testing strategy. <i>BMJ, The</i> , 2020 , 371, m4312	5.9	6
76	Handwashing sinks as the source of transmission of ST16 carbapenem-resistant Klebsiella pneumoniae, an international high-risk clone, in an intensive care unit. <i>Journal of Hospital Infection</i> , 2020 , 104, 492-496	6.9	12
75	Key evolutionary events in the emergence of a globally disseminated, carbapenem resistant clone in the ST410 lineage. <i>Communications Biology</i> , 2019 , 2, 322	6.7	17
74	The co-transfer of plasmid-borne colistin-resistant genes mcr-1 and mcr-3.5, the carbapenemase gene bla and the 16S methylase gene rmtB from Escherichia coli. <i>Scientific Reports</i> , 2019 , 9, 696	4.9	27

73	NDM Metallo- β -Lactamases and Their Bacterial Producers in Health Care Settings. <i>Clinical Microbiology Reviews</i> , 2019 , 32,	34	211
72	Bacterial Microcompartment-Mediated Ethanolamine Metabolism in Escherichia coli Urinary Tract Infection. <i>Infection and Immunity</i> , 2019 , 87,	3.7	12
71	Diversification of Colonization Factors in a Multidrug-Resistant Escherichia coli Lineage Evolving under Negative Frequency-Dependent Selection. <i>MBio</i> , 2019 , 10,	7.8	55
70	Antibiotic resistance genes are abundant and diverse in raw sewage used for urban agriculture in Africa and associated with urban population density. <i>Environmental Pollution</i> , 2019 , 251, 146-154	9.3	15
69	Comparative Transcriptomic Profiling of Yersinia enterocolitica O:3 and O:8 Reveals Major Expression Differences of Fitness- and Virulence-Relevant Genes Indicating Ecological Separation. <i>MSystems</i> , 2019 , 4,	7.6	5
68	Genomic and Functional Analysis of Emerging Virulent and Multidrug-Resistant Lineage Sequence Type 648. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 63,	5.9	41
67	Do we really understand how faecal microbiota transplantation works?. <i>EBioMedicine</i> , 2019 , 42, 39	8.8	0
66	Coexistence of three bla genes on an IncF/IncR plasmid in ST11 Klebsiella pneumoniae. <i>Journal of Global Antimicrobial Resistance</i> , 2019 , 17, 90-93	3.4	13
65	The evolution and transmission of multi-drug resistant Escherichia coli and Klebsiella pneumoniae: the complexity of clones and plasmids. <i>Current Opinion in Microbiology</i> , 2019 , 51, 51-56	7.9	59
64	The Ecology and Evolution of Pangenomes. <i>Current Biology</i> , 2019 , 29, R1094-R1103	6.3	81
63	Identification and typing of Yersinia enterocolitica and Yersinia pseudotuberculosis isolated from human clinical specimens in England between 2004 and 2018. <i>Journal of Medical Microbiology</i> , 2019 , 68, 538-548	3.2	14
62	Wastewater used for urban agriculture in West Africa as a reservoir for antibacterial resistance dissemination. <i>Environmental Research</i> , 2019 , 168, 14-24	7.9	38
61	Clinically Relevant Plasmid-Host Interactions Indicate that Transcriptional and Not Genomic Modifications Ameliorate Fitness Costs of Carbapenemase-Carrying Plasmids. <i>MBio</i> , 2018 , 9,	7.8	35
60	Sequence Type 273 Carbapenem-Resistant Klebsiella pneumoniae Carrying and. <i>Antimicrobial Agents and Chemotherapy</i> , 2018 , 62,	5.9	10
59	Convergent Amino Acid Signatures in Polyphyletic Campylobacter jejuni Subpopulations Suggest Human Niche Tropism. <i>Genome Biology and Evolution</i> , 2018 , 10, 763-774	3.9	5
58	Coexistence of Two Genes on an IncF Plasmid as Revealed by Nanopore Sequencing. <i>Antimicrobial Agents and Chemotherapy</i> , 2018 , 62,	5.9	12
57	Cryptic transmission of ST405 Escherichia coli carrying bla in hospital. <i>Scientific Reports</i> , 2018 , 8, 390	4.9	13
56	Occurrence of Enterobacter hormaechei carrying bla and bla in China. <i>Diagnostic Microbiology and Infectious Disease</i> , 2018 , 90, 139-142	2.9	17

55	Occurrence of colistin-resistant hypervirulent <i>Klebsiella variicola</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018 , 73, 3001-3004	5.1	24
54	Complete genomic characterization of two <i>Escherichia coli</i> lineages responsible for a cluster of carbapenem-resistant infections in a Chinese hospital. <i>Journal of Antimicrobial Chemotherapy</i> , 2018 , 73, 2340-2346	5.1	24
53	blaNDM-21, a new variant of blaNDM in an <i>Escherichia coli</i> clinical isolate carrying blaCTX-M-55 and rmtB. <i>Journal of Antimicrobial Chemotherapy</i> , 2018 , 73, 2336-2339	5.1	34
52	Genomic epidemiology of clinical <i>Campylobacter</i> spp. at a single health trust site. <i>Microbial Genomics</i> , 2018 , 4,	4.4	5
51	Acquisition and Loss of CTX-M-Producing and Non-Producing <i>Escherichia coli</i> in the Fecal Microbiome of Travelers to South Asia. <i>MBio</i> , 2018 , 9,	7.8	13
50	The Occurrence of Colistin-Resistant Hypervirulent in China. <i>Frontiers in Microbiology</i> , 2018 , 9, 2568	5.7	24
49	Identification of <i>Mycobacterium chimaera</i> in heater-cooler units in China. <i>Scientific Reports</i> , 2018 , 8, 7843	4.9	6
48	IncP Plasmid Carrying Colistin Resistance Gene <i>mcr-1</i> in <i>Klebsiella pneumoniae</i> from Hospital Sewage. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	57
47	Why prokaryotes have pangenomes. <i>Nature Microbiology</i> , 2017 , 2, 17040	26.6	182
46	New Variant of in an Extensively Drug-Resistant <i>Escherichia coli</i> Clinical Isolate Carrying and. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	52
45	Interaction networks, ecological stability, and collective antibiotic tolerance in polymicrobial infections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 10666-10671	11.5	72
44	Optimised chronic infection models demonstrate that siderophore 'cheating' in <i>Pseudomonas aeruginosa</i> is context specific. <i>ISME Journal</i> , 2017 , 11, 2492-2509	11.9	20
43	Reply to 'The population genetics of pangenomes'. <i>Nature Microbiology</i> , 2017 , 2, 1575	26.6	7
42	Remarkable Diversity of Carrying from Hospital Sewage with the Identification of Two New Variants. <i>Frontiers in Microbiology</i> , 2017 , 8, 2094	5.7	44
41	Phylogeographic separation and formation of sexually discrete lineages in a global population of. <i>Microbial Genomics</i> , 2017 , 3, e000133	4.4	8
40	'Add, stir and reduce': <i>Yersinia</i> spp. as model bacteria for pathogen evolution. <i>Nature Reviews Microbiology</i> , 2016 , 14, 177-90	22.2	95
39	Increase in bacteraemia cases in the East Midlands region of the UK due to MDR <i>Escherichia coli</i> ST73: high levels of genomic and plasmid diversity in causative isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2016 , 71, 339-43	5.1	16
38	All <i>Yersinia enterocolitica</i> are pathogenic: virulence of phylogroup 1 <i>Y. enterocolitica</i> in a <i>Galleria mellonella</i> infection model. <i>Microbiology (United Kingdom)</i> , 2016 , 162, 1379-1387	2.9	12

37	Response to 'Refined analyses suggest that recombination is a minor source of genomic diversity in chronic cystic fibrosis infections' by). <i>Microbial Genomics</i> , 2016 , 2, e000054	4.4	1
36	Combined Analysis of Variation in Core, Accessory and Regulatory Genome Regions Provides a Super-Resolution View into the Evolution of Bacterial Populations. <i>PLoS Genetics</i> , 2016 , 12, e1006280	6	117
35	Escherichia coli of sequence type 3835 carrying bla NDM-1, bla CTX-M-15, bla CMY-42 and bla SHV-12. <i>Scientific Reports</i> , 2015 , 5, 12275	4.9	25
34	Gene Loss and Lineage-Specific Restriction-Modification Systems Associated with Niche Differentiation in the Campylobacter jejuni Sequence Type 403 Clonal Complex. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 3641-7	4.8	18
33	Use of whole-genus genome sequence data to develop a multilocus sequence typing tool that accurately identifies Yersinia isolates to the species and subspecies levels. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 35-42	9.7	32
32	Genomic dissection of the 1994 Cronobacter sakazakii outbreak in a French neonatal intensive care unit. <i>BMC Genomics</i> , 2015 , 16, 750	4.5	20
31	Genetic import and phenotype specific alleles associated with hyper-invasion in Campylobacter jejuni. <i>BMC Genomics</i> , 2015 , 16, 852	4.5	11
30	Recombination is a key driver of genomic and phenotypic diversity in a Pseudomonas aeruginosa population during cystic fibrosis infection. <i>Scientific Reports</i> , 2015 , 5, 7649	4.9	81
29	Directional gene flow and ecological separation in. <i>Microbial Genomics</i> , 2015 , 1, e000030	4.4	15
28	Parallel independent evolution of pathogenicity within the genus Yersinia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 6768-73	11.5	114
27	Phenotypic microarrays suggest Escherichia coli ST131 is not a metabolically distinct lineage of extra-intestinal pathogenic E. coli. <i>PLoS ONE</i> , 2014 , 9, e88374	3.7	14
26	Comparative genome analysis identifies few traits unique to the Escherichia coli ST131 H30Rx clade and extensive mosaicism at the capsule locus. <i>BMC Genomics</i> , 2014 , 15, 830	4.5	20
25	Draft Genome Sequence of "Candidatus Cronobacter colletis" NCTC 14934T, a New Species in the Genus Cronobacter. <i>Genome Announcements</i> , 2014 , 2,		6
24	Draft Genome Sequences of Three Newly Identified Species in the Genus Cronobacter, C. helveticus LMG23732T, C. pulveris LMG24059, and C. zurichensis LMG23730T. <i>Genome Announcements</i> , 2013 , 1,		11
23	The evolutionary path to extraintestinal pathogenic, drug-resistant Escherichia coli is marked by drastic reduction in detectable recombination within the core genome. <i>Genome Biology and Evolution</i> , 2013 , 5, 699-710	3.9	38
22	Multidrug-resistant Escherichia coli bacteremia. <i>Emerging Infectious Diseases</i> , 2013 , 19, 1699-701	10.2	45
21	Evolutionary dynamics of the Yersinia enterocolitica complex. <i>Advances in Experimental Medicine and Biology</i> , 2012 , 954, 15-22	3.6	5
20	Genomic analysis uncovers a phenotypically diverse but genetically homogeneous Escherichia coli ST131 clone circulating in unrelated urinary tract infections. <i>Journal of Antimicrobial Chemotherapy</i> , 2012 , 67, 868-77	5.1	40

19	Cj1136 is required for lipooligosaccharide biosynthesis, hyperinvasion, and chick colonization by <i>Campylobacter jejuni</i> . <i>Infection and Immunity</i> , 2012 , 80, 2361-70	3.7	19
18	Increased human pathogenic potential of <i>Escherichia coli</i> from polymicrobial urinary tract infections in comparison to isolates from monomicrobial culture samples. <i>Journal of Medical Microbiology</i> , 2011 , 60, 102-109	3.2	45
17	Molecular epidemiology of extraintestinal pathogenic <i>Escherichia coli</i> isolates from a regional cohort of elderly patients highlights the prevalence of ST131 strains with increased antimicrobial resistance in both community and hospital care settings. <i>Journal of Antimicrobial Chemotherapy</i> , 2011 , 66, 2501-8	5.1	74
16	Authors' reply to Pathogenic potential of <i>Escherichia coli</i> from polymicrobial urinary tract infections. <i>Journal of Medical Microbiology</i> , 2011 , 60, 1554-1555	3.2	0
15	Infection dynamics of highly pathogenic avian influenza and virulent avian paramyxovirus type 1 viruses in chickens, turkeys and ducks. <i>Avian Pathology</i> , 2010 , 39, 265-73	2.4	46
14	Development of rapid, automated diagnostics for infectious disease: advances and challenges. <i>Expert Review of Medical Devices</i> , 2009 , 6, 641-51	3.5	30
13	Intestinal carriage of verocytotoxigenic <i>Escherichia coli</i> O157, <i>Salmonella</i> , thermophilic <i>Campylobacter</i> and <i>Yersinia enterocolitica</i> , in cattle, sheep and pigs at slaughter in Great Britain during 2003. <i>Epidemiology and Infection</i> , 2008 , 136, 739-51	4.3	108
12	Validated H5 Eurasian real-time reverse transcriptase-polymerase chain reaction and its application in H5N1 outbreaks in 2005-2006. <i>Avian Diseases</i> , 2007 , 51, 373-7	1.6	125
11	An aflagellate mutant <i>Yersinia enterocolitica</i> biotype 1A strain displays altered invasion of epithelial cells, persistence in macrophages, and cytokine secretion profiles in vitro. <i>Microbiology (United Kingdom)</i> , 2007 , 153, 1339-1349	2.9	27
10	<i>Yersinia enterocolitica</i> isolates of differing biotypes from humans and animals are adherent, invasive and persist in macrophages, but differ in cytokine secretion profiles in vitro. <i>Journal of Medical Microbiology</i> , 2006 , 55, 1725-1734	3.2	31
9	Differences in levels of secreted locus of enterocyte effacement proteins between human disease-associated and bovine <i>Escherichia coli</i> O157. <i>Infection and Immunity</i> , 2005 , 73, 2571	3.7	2
8	Comparison of the biotypes of <i>Yersinia enterocolitica</i> isolated from pigs, cattle and sheep at slaughter and from humans with yersiniosis in Great Britain during 1999-2000. <i>Letters in Applied Microbiology</i> , 2004 , 39, 103-8	2.9	79
7	Differences in levels of secreted locus of enterocyte effacement proteins between human disease-associated and bovine <i>Escherichia coli</i> O157. <i>Infection and Immunity</i> , 2001 , 69, 5107-14	3.7	69
6	Complete genomic characterisation of two <i>Escherichia coli</i> lineages responsible for a cluster of carbapenem resistant infections in a Chinese hospital		1
5	Validation testing to determine the effectiveness of lateral flow testing for asymptomatic SARS-CoV-2 detection in low prevalence settings		6
4	S-variant SARS-CoV-2 is associated with significantly higher viral loads in samples tested by ThermoFisher TaqPath RT-QPCR		22
3	Signatures of negative frequency dependent selection in colonisation factors and the evolution of a multi-drug resistant lineage of <i>Escherichia coli</i>		1
2	Allelic polymorphism shapes community function in evolving <i>Pseudomonas aeruginosa</i> populations		1

- 1 Real-time sampling of travelers shows intestinal colonization by multidrug-resistant bacteria to be a dynamic process with multiple transient acquisitions

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