

# Alan McNally

## List of Publications by Year in descending order

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106  
papers

7,600  
citations

87888

38  
h-index

66911

78  
g-index

121  
all docs

121  
docs citations

121  
times ranked

12424  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Klebsiella oxytoca</i> Complex: Update on Taxonomy, Antimicrobial Resistance, and Virulence. <i>Clinical Microbiology Reviews</i> , 2022, 35, e0000621.	13.6	48
2	Fine-Scale Reconstruction of the Evolution of FII-33 Multidrug Resistance Plasmids Enables High-Resolution Genomic Surveillance. <i>MSystems</i> , 2022, 7, e0083121.	3.8	9
3	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.	4.4	32
4	Prokaryote pangenomes are dynamic entities. <i>Current Opinion in Microbiology</i> , 2022, 66, 73-78.	5.1	13
5	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, 60, e0240821.	3.9	7
6	<i>Enterobacteriaceae</i> and <i>Bacteroidaceae</i> provide resistance to travel-associated intestinal colonization by multi-drug resistant <i>Escherichia coli</i> . <i>Gut Microbes</i> , 2022, 14, 2060676.	9.8	11
7	Covid-19 testing in the UK was not a "shambles" in 2020. <i>BMJ</i> , The, 2022, 377, o916.	6.0	0
8	GR13-type plasmids in <i>Acinetobacter</i> potentiate the accumulation and horizontal transfer of diverse accessory genes. <i>Microbial Genomics</i> , 2022, 8, .	2.0	8
9	Genomics and pathotypes of the many faces of <i>Escherichia coli</i> . <i>FEMS Microbiology Reviews</i> , 2022, 46, .	8.6	36
10	Whole-genome sequencing enhances existing pathogen and antimicrobial-resistance surveillance schemes within a neonatal unit. <i>Microbial Genomics</i> , 2022, 8, .	2.0	1
11	Transferable <i>Acinetobacter baumannii</i> 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.	3.0	27
12	What makes new variants of SARS-CoV-2 concerning is not where they come from, but the mutations they contain. <i>BMJ</i> , The, 2021, 372, n504.	6.0	12
13	S-Variant SARS-CoV-2 Lineage B.1.1.7 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.	4.0	207
14	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, .	2.9	4
15	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021, 593, 266-269.	27.8	1,001
16	Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. <i>Nature</i> , 2021, 593, 136-141.	27.8	648
17	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.	5.6	54
18	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, .	3.8	23

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19	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</i> , The, 2021, 2, e151-e158.	7.3	45
20	Emergence and dissemination of antimicrobial resistance in <i>Escherichia coli</i> causing bloodstream infections in Norway in 2002-2017: a nationwide, longitudinal, microbial population genomic study. <i>Lancet Microbe</i> , The, 2021, 2, e331-e341.	7.3	43
21	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. <i>Lancet Public Health</i> , The, 2021, 6, e335-e345.	10.0	269
22	Carbapenem and Colistin Resistance in <i>Enterobacter</i> : Determinants and Clones. <i>Trends in Microbiology</i> , 2021, 29, 473-476.	7.7	29
23	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
24	Spread of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> in an Intensive Care Unit: A Whole-Genome Sequence-Based Prospective Observational Study. <i>Microbiology Spectrum</i> , 2021, 9, e0005821.	3.0	12
25	Gene-gene relationships in an <i>Escherichia coli</i> accessory genome are linked to function and mobility. <i>Microbial Genomics</i> , 2021, 7, .	2.0	11
26	Antimicrobial resistance genes and clonal success in <i>Escherichia coli</i> isolates causing bloodstream infection - Authors' reply. <i>Lancet Microbe</i> , The, 2021, 2, e493.	7.3	1
27	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
28	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.	2.9	30
29	Handwashing sinks as the source of transmission of ST16 carbapenem-resistant <i>Klebsiella pneumoniae</i> , an international high-risk clone, in an intensive care unit. <i>Journal of Hospital Infection</i> , 2020, 104, 492-496.	2.9	21
30	Scientific consensus on the COVID-19 pandemic: we need to act now. <i>Lancet</i> , The, 2020, 396, e71-e72.	13.7	189
31	Pooled testing for SARS-CoV-2 could provide the solution to UK's testing strategy. <i>BMJ</i> , The, 2020, 371, m4312.	6.0	10
32	How to establish an academic SARS-CoV-2 testing laboratory. <i>Nature Microbiology</i> , 2020, 5, 1452-1454.	13.3	23
33	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, .	3.8	22
34	<i>Klebsiella pneumoniae</i> type VI secretion system-mediated microbial competition is PhoPQ controlled and reactive oxygen species dependent. <i>PLoS Pathogens</i> , 2020, 16, e1007969.	4.7	86
35	Allelic polymorphism shapes community function in evolving <i>Pseudomonas aeruginosa</i> populations. <i>ISME Journal</i> , 2020, 14, 1929-1942.	9.8	47
36	Pangenomes and Selection: The Public Goods Hypothesis. , 2020, , 151-167.		10

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37	The evolution and transmission of multi-drug resistant <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> : the complexity of clones and plasmids. <i>Current Opinion in Microbiology</i> , 2019, 51, 51-56.	5.1	113
38	The Ecology and Evolution of Pangenomes. <i>Current Biology</i> , 2019, 29, R1094-R1103.	3.9	206
39	Key evolutionary events in the emergence of a globally disseminated, carbapenem resistant clone in the <i>Escherichia coli</i> ST410 lineage. <i>Communications Biology</i> , 2019, 2, 322.	4.4	36
40	The co-transfer of plasmid-borne colistin-resistant genes <i>mcr-1</i> and <i>mcr-3.5</i> , the carbapenemase gene <i>bla</i> NDM-5 and the 16S methylase gene <i>rmtB</i> from <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2019, 9, 696.	3.3	48
41	NDM Metallo- $\beta$ -Lactamases and Their Bacterial Producers in Health Care Settings. <i>Clinical Microbiology Reviews</i> , 2019, 32, .	13.6	406
42	Bacterial Microcompartment-Mediated Ethanolamine Metabolism in <i>Escherichia coli</i> Urinary Tract Infection. <i>Infection and Immunity</i> , 2019, 87, .	2.2	21
43	Diversification of Colonization Factors in a Multidrug-Resistant <i>Escherichia coli</i> Lineage Evolving under Negative Frequency-Dependent Selection. <i>MBio</i> , 2019, 10, .	4.1	106
44	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.	7.5	19
45	Comparative Transcriptomic Profiling of <i>Yersinia enterocolitica</i> O:3 and O:8 Reveals Major Expression Differences of Fitness- and Virulence-Relevant Genes Indicating Ecological Separation. <i>MSystems</i> , 2019, 4, .	3.8	8
46	Genomic and Functional Analysis of Emerging Virulent and Multidrug-Resistant <i>Escherichia coli</i> Lineage Sequence Type 648. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	71
47	Do we really understand how faecal microbiota transplantation works?. <i>EBioMedicine</i> , 2019, 42, 39.	6.1	1
48	Coexistence of three <i>bla</i> KPC-2 genes on an <i>IncF/IncR</i> plasmid in ST11 <i>Klebsiella pneumoniae</i> . <i>Journal of Global Antimicrobial Resistance</i> , 2019, 17, 90-93.	2.2	23
49	Wastewater used for urban agriculture in West Africa as a reservoir for antibacterial resistance dissemination. <i>Environmental Research</i> , 2019, 168, 14-24.	7.5	52
50	Identification and typing of <i>Yersinia enterocolitica</i> and <i>Yersinia pseudotuberculosis</i> isolated from human clinical specimens in England between 2004 and 2018. <i>Journal of Medical Microbiology</i> , 2019, 68, 538-548.	1.8	20
51	Clinically Relevant Plasmid-Host Interactions Indicate that Transcriptional and Not Genomic Modifications Ameliorate Fitness Costs of <i>Klebsiella pneumoniae</i> Carbapenemase-Carrying Plasmids. <i>MBio</i> , 2018, 9, .	4.1	64
52	Sequence Type 273 Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Carrying <i>bla</i> <sub>NDM-1</sub> and <i>bla</i> <sub>IMP-4</sub> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	17
53	Convergent Amino Acid Signatures in Polyphyletic <i>Campylobacter jejuni</i> Subpopulations Suggest Human Niche Tropism. <i>Genome Biology and Evolution</i> , 2018, 10, 763-774.	2.5	12
54	Coexistence of Two <i>bla</i> <sub>NDM-5</sub> Genes on an <i>IncF</i> Plasmid as Revealed by Nanopore Sequencing. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	26

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55	Cryptic transmission of ST405 <i>Escherichia coli</i> carrying bla NDM-4 in hospital. <i>Scientific Reports</i> , 2018, 8, 390.	3.3	25
56	Occurrence of <i>Enterobacter hormaechei</i> carrying bla NDM-1 and bla KPC-2 in China. <i>Diagnostic Microbiology and Infectious Disease</i> , 2018, 90, 139-142.	1.8	24
57	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, .	4.1	30
58	The Occurrence of Colistin-Resistant Hypervirulent <i>Klebsiella pneumoniae</i> in China. <i>Frontiers in Microbiology</i> , 2018, 9, 2568.	3.5	36
59	Identification of <i>Mycobacterium chimaera</i> in heater-cooler units in China. <i>Scientific Reports</i> , 2018, 8, 7843.	3.3	10
60	Occurrence of colistin-resistant hypervirulent <i>Klebsiella variicola</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 3001-3004.	3.0	38
61	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.	3.0	44
62	bla NDM-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.	3.0	46
63	Genomic epidemiology of clinical <i>Campylobacter</i> spp. at a single health trust site. <i>Microbial Genomics</i> , 2018, 4, .	2.0	15
64	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, .	3.2	74
65	Why prokaryotes have pangenomes. <i>Nature Microbiology</i> , 2017, 2, 17040.	13.3	327
66	New Variant of <i>mcr-3</i> in an Extensively Drug-Resistant <i>Escherichia coli</i> Clinical Isolate Carrying <i>mcr-1</i> and <i>bla</i> <sub>NDM-5</sub> . <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	64
67	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.	7.1	139
68	Optimised chronic infection models demonstrate that siderophore "cheating"™ in <i>Pseudomonas aeruginosa</i> is context specific. <i>ISME Journal</i> , 2017, 11, 2492-2509.	9.8	28
69	Reply to "The population genetics of pangenomes"™. <i>Nature Microbiology</i> , 2017, 2, 1575-1575.	13.3	11
70	Remarkable Diversity of <i>Escherichia coli</i> Carrying <i>mcr-1</i> from Hospital Sewage with the Identification of Two New <i>mcr-1</i> Variants. <i>Frontiers in Microbiology</i> , 2017, 8, 2094.	3.5	63
71	Phylogeographic separation and formation of sexually discrete lineages in a global population of <i>Yersinia pseudotuberculosis</i> . <i>Microbial Genomics</i> , 2017, 3, e000133.	2.0	17
72	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.	3.5	177

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73	'Add, stir and reduce': <i>Yersinia</i> spp. as model bacteria for pathogen evolution. <i>Nature Reviews Microbiology</i> , 2016, 14, 177-190.	28.6	130
74	Increase in bacteraemia cases in the East Midlands region of the UK due to MDREscherichia coliST73: high levels of genomic and plasmid diversity in causative isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 339-343.	3.0	24
75	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.	1.8	22
76	Response to "Refined analyses suggest that recombination is a minor source of genomic diversity in <i>Pseudomonas aeruginosa</i> chronic cystic fibrosis infections" by Williams et al. (2016). <i>Microbial Genomics</i> , 2016, 2, e000054.	2.0	1
77	Genomic dissection of the 1994 <i>Cronobacter sakazakii</i> outbreak in a French neonatal intensive care unit. <i>BMC Genomics</i> , 2015, 16, 750.	2.8	37
78	Genetic import and phenotype specific alleles associated with hyper-invasion in <i>Campylobacter jejuni</i> . <i>BMC Genomics</i> , 2015, 16, 852.	2.8	14
79	Recombination is a key driver of genomic and phenotypic diversity in a <i>Pseudomonas aeruginosa</i> population during cystic fibrosis infection. <i>Scientific Reports</i> , 2015, 5, 7649.	3.3	134
80	<i>Escherichia coli</i> of sequence type 3835 carrying blaNDM-1, blaCTX-M-15, blaCMY-42 and blaSHV-12. <i>Scientific Reports</i> , 2015, 5, 12275.	3.3	33
81	Gene Loss and Lineage-Specific Restriction-Modification Systems Associated with Niche Differentiation in the <i>Campylobacter jejuni</i> Sequence Type 403 Clonal Complex. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3641-3647.	3.1	27
82	Use of Whole-Genus Genome Sequence Data To Develop a Multilocus Sequence Typing Tool That Accurately Identifies <i>Yersinia</i> Isolates to the Species and Subspecies Levels. <i>Journal of Clinical Microbiology</i> , 2015, 53, 35-42.	3.9	45
83	Directional gene flow and ecological separation in <i>Yersinia enterocolitica</i> . <i>Microbial Genomics</i> , 2015, 1, e000030.	2.0	16
84	Phenotypic Microarrays Suggest <i>Escherichia coli</i> ST131 Is Not a Metabolically Distinct Lineage of Extra-Intestinal Pathogenic <i>E. coli</i> . <i>PLoS ONE</i> , 2014, 9, e88374.	2.5	18
85	Comparative genome analysis identifies few traits unique to the <i>Escherichia coli</i> ST131 H30Rx clade and extensive mosaicism at the capsule locus. <i>BMC Genomics</i> , 2014, 15, 830.	2.8	23
86	Draft Genome Sequence of "Candidate <i>Cronobacter collettis</i> " NCTC 14934 T, a New Species in the Genus <i>Cronobacter</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	11
87	Parallel independent evolution of pathogenicity within the genus <i>Yersinia</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6768-6773.	7.1	154
88	Nanoparticles detect infection. <i>Nature Nanotechnology</i> , 2013, 8, 315-316.	31.5	5
89	Draft Genome Sequences of Three Newly Identified Species in the Genus <i>Cronobacter</i> , <i>C. helveticus</i> LMG23732 T, <i>C. pulveris</i> LMG24059, and <i>C. zurichensis</i> LMG23730 T. <i>Genome Announcements</i> , 2013, 1, .	0.8	11
90	The Evolutionary Path to Extraintestinal Pathogenic, Drug-Resistant <i>Escherichia coli</i> Is Marked by Drastic Reduction in Detectable Recombination within the Core Genome. <i>Genome Biology and Evolution</i> , 2013, 5, 699-710.	2.5	45

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91	Multidrug-Resistant <i>Escherichia coli</i> Bacteremia. <i>Emerging Infectious Diseases</i> , 2013, 19, 1699-701.	4.3	57
92	Genomic analysis uncovers a phenotypically diverse but genetically homogeneous <i>Escherichia coli</i> ST131 clone circulating in unrelated urinary tract infections. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 868-877.	3.0	47
93	Cj1136 Is Required for Lipooligosaccharide Biosynthesis, Hyperinvasion, and Chick Colonization by <i>Campylobacter jejuni</i> . <i>Infection and Immunity</i> , 2012, 80, 2361-2370.	2.2	23
94	Evolutionary Dynamics of the <i>Yersinia enterocolitica</i> Complex. <i>Advances in Experimental Medicine and Biology</i> , 2012, 954, 15-22.	1.6	5
95	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.	1.8	74
96	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, 2501-2508.	3.0	82
97	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.	1.8	1
98	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, 265-273.	2.0	58
99	Development of rapid, automated diagnostics for infectious disease: advances and challenges. <i>Expert Review of Medical Devices</i> , 2009, 6, 641-651.	2.8	38
100	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, 739-751.	2.1	126
101	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> 154, 1474-1484. doi:10.1099/mic/0/01541474-1484	1.0	14
102	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, 373-377.	1.0	154
103	<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.	1.8	36
104	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, 2571-2571.	2.2	2
105	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, 103-108.	2.2	96
106	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, 5107-5114.	2.2	73