Alan McNally

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3879731/publications.pdf

Version: 2024-02-01

106	7,600	87888 38	66911 78
papers	citations	h-index	g-index

121	121	121	12424
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. Nature, 2021, 593, 266-269.	27.8	1,001
2	Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. Nature, 2021, 593, 136-141.	27.8	648
3	NDM Metallo-Î²-Lactamases and Their Bacterial Producers in Health Care Settings. Clinical Microbiology Reviews, 2019, 32, .	13.6	406
4	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. Cell Reports, 2021, 35, 109292.	6.4	375
5	Why prokaryotes have pangenomes. Nature Microbiology, 2017, 2, 17040.	13.3	327
6	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. Lancet Public Health, The, 2021, 6, e335-e345.	10.0	269
7	S-Variant SARS-CoV-2 Lineage B1.1.7 Is Associated With Significantly Higher Viral Load in Samples Tested by TaqPath Polymerase Chain Reaction. Journal of Infectious Diseases, 2021, 223, 1666-1670.	4.0	207
8	The Ecology and Evolution of Pangenomes. Current Biology, 2019, 29, R1094-R1103.	3.9	206
9	Scientific consensus on the COVID-19 pandemic: we need to act now. Lancet, The, 2020, 396, e71-e72.	13.7	189
10	Combined Analysis of Variation in Core, Accessory and Regulatory Genome Regions Provides a Super-Resolution View into the Evolution of Bacterial Populations. PLoS Genetics, 2016, 12, e1006280.	3.5	177
11	Validated H5 Eurasian Real-Time Reverse Transcriptaseâ€“Polymerase Chain Reaction and Its Application in H5N1 Outbreaks in 2005â€“2006. Avian Diseases, 2007, 51, 373-377.	1.0	154
12	Parallel independent evolution of pathogenicity within the genus <i>Yersinia</i>. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6768-6773.	7.1	154
13	Interaction networks, ecological stability, and collective antibiotic tolerance in polymicrobial infections. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10666-10671.	7.1	139
14	Recombination is a key driver of genomic and phenotypic diversity in a Pseudomonas aeruginosa population during cystic fibrosis infection. Scientific Reports, 2015, 5, 7649.	3.3	134
15	'Add, stir and reduce': Yersinia spp. as model bacteria for pathogen evolution. Nature Reviews Microbiology, 2016, 14, 177-190.	28.6	130
16	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. Epidemiology and Infection, 2008, 136, 739-751.	2.1	126
17	The evolution and transmission of multi-drug resistant Escherichia coli and Klebsiella pneumoniae: the complexity of clones and plasmids. Current Opinion in Microbiology, 2019, 51, 51-56.	5.1	113
18	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. Science, 2021, 374, eabl9551.	12.6	111

#	ARTICLE	IF	CITATIONS
19	Diversification of Colonization Factors in a Multidrug-Resistant Escherichia coli Lineage Evolving under Negative Frequency-Dependent Selection. MBio, 2019, 10, .	4.1	106
20	Comparison of the biotypes of Yersinia enterocolitica isolated from pigs, cattle and sheep at slaughter and from humans with yersiniosis in Great Britain during 1999-2000. Letters in Applied Microbiology, 2004, 39, 103-108.	2.2	96
21	Klebsiella pneumoniae type VI secretion system-mediated microbial competition is PhoPQ controlled and reactive oxygen species dependent. PLoS Pathogens, 2020, 16, e1007969.	4.7	86
22	Molecular epidemiology of extraintestinal pathogenic Escherichia coli 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. Journal of Antimicrobial Chemotherapy, 2011, 66, 2501-2508.	3.0	82
23	Increased human pathogenic potential of Escherichia coli from polymicrobial urinary tract infections in comparison to isolates from monomicrobial culture samples. Journal of Medical Microbiology, 2011, 60, 102-109.	1.8	74
24	IncP Plasmid Carrying Colistin Resistance Gene <i>mcr-1</i> in Klebsiella pneumoniae from Hospital Sewage. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	74
25	Differences in Levels of Secreted Locus of Enterocyte Effacement Proteins between Human Disease-Associated and Bovine Escherichia coli O157. Infection and Immunity, 2001, 69, 5107-5114.	2.2	73
26	Genomic and Functional Analysis of Emerging Virulent and Multidrug-Resistant <i>Escherichia coli</i> Lineage Sequence Type 648. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	71
27	New Variant of <i>mcr-3</i> in an Extensively Drug-Resistant Escherichia coli Clinical Isolate Carrying <i>mcr-1</i> and <i>bla</i> _{NDM-5}. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	64
28	Clinically Relevant Plasmid-Host Interactions Indicate that Transcriptional and Not Genomic Modifications Ameliorate Fitness Costs of <i>Klebsiella pneumoniae</i> Carbapenemase-Carrying Plasmids. MBio, 2018, 9, .	4.1	64
29	Remarkable Diversity of Escherichia coli Carrying mcr-1 from Hospital Sewage with the Identification of Two New mcr-1 Variants. Frontiers in Microbiology, 2017, 8, 2094.	3.5	63
30	Infection dynamics of highly pathogenic avian influenza and virulent avian paramyxovirus type 1 viruses in chickens, turkeys and ducks. Avian Pathology, 2010, 39, 265-273.	2.0	58
31	Multidrug-Resistant<i>Escherichia coli</i>Bacteremia. Emerging Infectious Diseases, 2013, 19, 1699-701.	4.3	57
32	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. PLoS Biology, 2021, 19, e3001216.	5.6	54
33	Wastewater used for urban agriculture in West Africa as a reservoir for antibacterial resistance dissemination. Environmental Research, 2019, 168, 14-24.	7.5	52
34	The co-transfer of plasmid-borne colistin-resistant genes mcr-1 and mcr-3.5, the carbapenemase gene blaNDM-5 and the 16S methylase gene rmtB from Escherichia coli. Scientific Reports, 2019, 9, 696.	3.3	48
35	Klebsiella oxytoca Complex: Update on Taxonomy, Antimicrobial Resistance, and Virulence. Clinical Microbiology Reviews, 2022, 35, e0000621.	13.6	48
36	Genomic analysis uncovers a phenotypically diverse but genetically homogeneous Escherichia coli ST131 clone circulating in unrelated urinary tract infections. Journal of Antimicrobial Chemotherapy, 2012, 67, 868-877.	3.0	47

#	ARTICLE	IF	CITATIONS
37	Allelic polymorphism shapes community function in evolving <i>Pseudomonas aeruginosa</i> populations. ISME Journal, 2020, 14, 1929-1942.	9.8	47
38	bla NDM-21, a new variant of blaNDM in an Escherichia coli clinical isolate carrying blaCTX-M-55 and rmtB. Journal of Antimicrobial Chemotherapy, 2018, 73, 2336-2339.	3.0	46
39	The Evolutionary Path to Extraintestinal Pathogenic, Drug-Resistant Escherichia coli Is Marked by Drastic Reduction in Detectable Recombination within the Core Genome. Genome Biology and Evolution, 2013, 5, 699-710.	2.5	45
40	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. Journal of Clinical Microbiology, 2015, 53, 35-42.	3.9	45
41	Dynamics of intestinal multidrug-resistant bacteria colonisation contracted by visitors to a high-endemic setting: a prospective, daily, real-time sampling study. Lancet Microbe, The, 2021, 2, e151-e158.	7.3	45
42	Complete genomic characterization of two Escherichia coli lineages responsible for a cluster of carbapenem-resistant infections in a Chinese hospital. Journal of Antimicrobial Chemotherapy, 2018, 73, 2340-2346.	3.0	44
43	Emergence and dissemination of antimicrobial resistance in Escherichia coli causing bloodstream infections in Norway in 2002â€“17: a nationwide, longitudinal, microbial population genomic study. Lancet Microbe, The, 2021, 2, e331-e341.	7.3	43
44	Development of rapid, automated diagnostics for infectious disease: advances and challenges. Expert Review of Medical Devices, 2009, 6, 641-651.	2.8	38
45	Occurrence of colistin-resistant hypervirulent Klebsiella variicola. Journal of Antimicrobial Chemotherapy, 2018, 73, 3001-3004.	3.0	38
46	Genomic dissection of the 1994 Cronobacter sakazakii outbreak in a French neonatal intensive care unit. BMC Genomics, 2015, 16, 750.	2.8	37
47	Yersinia enterocolitica isolates of differing biotypes from humans and animals are adherent, invasive and persist in macrophages, but differ in cytokine secretion profiles in vitro. Journal of Medical Microbiology, 2006, 55, 1725-1734.	1.8	36
48	The Occurence of Colistin-Resistant Hypervirulent Klebsiellapneumoniae in China. Frontiers in Microbiology, 2018, 9, 2568.	3.5	36
49	Key evolutionary events in the emergence of a globally disseminated, carbapenem resistant clone in the Escherichia coli ST410 lineage. Communications Biology, 2019, 2, 322.	4.4	36
50	Genomics and pathotypes of the many faces of<i>Escherichia coli</i>. FEMS Microbiology Reviews, 2022, 46, .	8.6	36
51	Escherichia coli of sequence type 3835 carrying blaNDM-1, blaCTX-M-15, blaCMY-42 and blaSHV-12. Scientific Reports, 2015, 5, 12275.	3.3	33
52	Characterization of phage resistance and phages capable of intestinal decolonization of carbapenem-resistant Klebsiella pneumoniae in mice. Communications Biology, 2022, 5, 48.	4.4	32
53	Acquisition and Loss of CTX-M-Producing and Non-Producing Escherichia coli in the Fecal Microbiome of Travelers to South Asia. MBio, 2018, 9, .	4.1	30
54	The role of potentiating mutations in the evolution of pandemic Escherichia coli clones. European Journal of Clinical Microbiology and Infectious Diseases, 2021, , 1.	2.9	30

#	Article	IF	Citations
55	Carbapenem and Colistin Resistance in Enterobacter: Determinants and Clones. Trends in Microbiology, 2021, 29, 473-476.	7.7	29
56	An aflagellate mutant Yersinia enterocolitica biotype 1A strain displays altered invasion of epithelial cells, persistence in macrophages, and cytokine secretion profiles in vitro. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	1.8	28
57	Optimised chronic infection models demonstrate that siderophore â€˜cheatingâ€™ in <i>Pseudomonas aeruginosa</i> is context specific. ISME Journal, 2017, 11, 2492-2509.	9.8	28
58	Gene Loss and Lineage-Specific Restriction-Modification Systems Associated with Niche Differentiation in the Campylobacter jejuni Sequence Type 403 Clonal Complex. Applied and Environmental Microbiology, 2015, 81, 3641-3647.	3.1	27
59	Transferable <i>Acinetobacter baumannii</i> plasmid pDETAB2 encodes OXA-58 and NDM-1 and represents a new class of antibiotic resistance plasmids. Journal of Antimicrobial Chemotherapy, 2021, 76, 1130-1134.	3.0	27
60	Coexistence of Two <i>bla</i> _{NDM-5} Genes on an IncF Plasmid as Revealed by Nanopore Sequencing. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	26
61	Cryptic transmission of ST405 Escherichia coli carrying bla NDM-4 in hospital. Scientific Reports, 2018, 8, 390.	3.3	25
62	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. Journal of Antimicrobial Chemotherapy, 2016, 71, 339-343.	3.0	24
63	Occurrence of Enterobacter hormaechei carrying bla NDM-1 and bla KPC-2 in China. Diagnostic Microbiology and Infectious Disease, 2018, 90, 139-142.	1.8	24
64	Cj1136 Is Required for Lipooligosaccharide Biosynthesis, Hyperinvasion, and Chick Colonization by Campylobacter jejuni. Infection and Immunity, 2012, 80, 2361-2370.	2.2	23
65	Comparative genome analysis identifies few traits unique to the Escherichia coli ST131 H30Rx clade and extensive mosaicism at the capsule locus. BMC Genomics, 2014, 15, 830.	2.8	23
66	Coexistence of three blaKPC-2 genes on an IncF/IncR plasmid in ST11 Klebsiella pneumoniae. Journal of Global Antimicrobial Resistance, 2019, 17, 90-93.	2.2	23
67	How to establish an academic SARS-CoV-2 testing laboratory. Nature Microbiology, 2020, 5, 1452-1454.	13.3	23
68	Limited and Strain-Specific Transcriptional and Growth Responses to Acquisition of a Multidrug Resistance Plasmid in Genetically Diverse Escherichia coli Lineages. MSystems, 2021, 6, .	3.8	23
69	Struggle To Survive: the Choir of Target Alteration, Hydrolyzing Enzyme, and Plasmid Expression as a Novel Aztreonam-Avibactam Resistance Mechanism. MSystems, 2020, 5, .	3.8	22
70	All Yersinia enterocolitica are pathogenic: virulence of phylogroup 1 Y. enterocolitica in a Galleria mellonella infection model. Microbiology (United Kingdom), 2016, 162, 1379-1387.	1.8	22
71	Bacterial Microcompartment-Mediated Ethanolamine Metabolism in Escherichia coli Urinary Tract Infection. Infection and Immunity, 2019, 87, .	2.2	21
72	Handwashing sinks as the source of transmission of ST16 carbapenem-resistant Klebsiella pneumoniae, an international high-risk clone, in an intensive care unit. Journal of Hospital Infection, 2020, 104, 492-496.	2.9	21

#	ARTICLE	IF	CITATIONS
73	Identification and typing of Yersinia enterocolitica and Yersinia pseudotuberculosis isolated from human clinical specimens in England between 2004 and 2018. Journal of Medical Microbiology, 2019, 68, 538-548.	1.8	20
74	Antibiotic resistance genes are abundant and diverse in raw sewage used for urban agriculture in Africa and associated with urban population density. Environmental Pollution, 2019, 251, 146-154.	7.5	19
75	Phenotypic Microarrays Suggest Escherichia coli ST131 Is Not a Metabolically Distinct Lineage of Extra-Intestinal Pathogenic E. coli. PLoS ONE, 2014, 9, e88374.	2.5	18
76	Sequence Type 273 Carbapenem-Resistant Klebsiella pneumoniae Carrying <i>bla</i> _{NDM-1} and <i>bla</i> _{IMP-4}. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	17
77	Phylogeographic separation and formation of sexually discrete lineages in a global population of Yersinia pseudotuberculosis. Microbial Genomics, 2017, 3, e000133.	2.0	17
78	Directional gene flow and ecological separation in Yersinia enterocolitica. Microbial Genomics, 2015, 1, e000030.	2.0	16
79	Genomic epidemiology of clinical Campylobacter spp. at a single health trust site. Microbial Genomics, 2018, 4, .	2.0	15
80	Genetic import and phenotype specific alleles associated with hyper-invasion in Campylobacter jejuni. BMC Genomics, 2015, 16, 852.	2.8	14
81	Prokaryote pangenomes are dynamic entities. Current Opinion in Microbiology, 2022, 66, 73-78.	5.1	13
82	Convergent Amino Acid Signatures in Polyphyletic Campylobacter jejuni Subpopulations Suggest Human Niche Tropism. Genome Biology and Evolution, 2018, 10, 763-774.	2.5	12
83	What makes new variants of SARS-CoV-2 concerning is not where they come from, but the mutations they contain. BMJ, The, 2021, 372, n504.	6.0	12
84	Spread of Carbapenem-Resistant Klebsiella pneumoniae in an Intensive Care Unit: A Whole-Genome Sequence-Based Prospective Observational Study. Microbiology Spectrum, 2021, 9, e0005821.	3.0	12
85	Draft Genome Sequences of Three Newly Identified Species in the Genus Cronobacter , C. helveticus LMG23732 T , C. pulveris LMG24059, and C . zurichensis LMG23730 T. Genome Announcements, 2013, 1, .	0.8	11
86	Draft Genome Sequence of â€œ Candidatus Cronobacter colletisâ€•NCTC 14934 T , a New Species in the Genus Cronobacter. Genome Announcements, 2014, 2, .	0.8	11
87	Reply to â€˜The population genetics of pangenomesâ€™. Nature Microbiology, 2017, 2, 1575-1575.	13.3	11
88	Gene-gene relationships in an Escherichia coli accessory genome are linked to function and mobility. Microbial Genomics, 2021, 7, .	2.0	11
89	<i>Enterobacteriaceae</i> and <i>Bacteroidaceae</i> provide resistance to travel-associated intestinal colonization by multi-drug resistant <i>Escherichia coli</i>. Gut Microbes, 2022, 14, 2060676.	9.8	11
90	Identification of Mycobacterium chimaera in heater-cooler units in China. Scientific Reports, 2018, 8, 7843.	3.3	10

#	ARTICLE	IF	CITATIONS
91	Pooled testing for SARS-CoV-2 could provide the solution to UKâ€™s testing strategy. BMJ, The, 2020, 371, m4312.	6.0	10
92	Pangenomes and Selection: The Public Goods Hypothesis. , 2020, , 151-167.		10
93	Fine-Scale Reconstruction of the Evolution of FII-33 Multidrug Resistance Plasmids Enables High-Resolution Genomic Surveillance. MSystems, 2022, 7, e0083121.	3.8	9
94	Comparative Transcriptomic Profiling of Yersinia enterocolitica O:3 and O:8 Reveals Major Expression Differences of Fitness- and Virulence-Relevant Genes Indicating Ecological Separation. MSystems, 2019, 4, .	3.8	8
95	GR13-type plasmids in Acinetobacter potentiate the accumulation and horizontal transfer of diverse accessory genes. Microbial Genomics, 2022, 8, .	2.0	8
96	SARS-CoV-2 Testing in the Community: Testing Positive Samples with the TaqMan SARS-CoV-2 Mutation Panel To Find Variants in Real Time. Journal of Clinical Microbiology, 2022, 60, e0240821.	3.9	7
97	Evolutionary Dynamics of the Yersinia enterocolitica Complex. Advances in Experimental Medicine and Biology, 2012, 954, 15-22.	1.6	5
98	Nanoparticles detect infection. Nature Nanotechnology, 2013, 8, 315-316.	31.5	5
99	Mapping Gene-by-Gene Single-Nucleotide Variation in 8,535 Mycobacterium tuberculosis Genomes: a Resource To Support Potential Vaccine and Drug Development. MSphere, 2021, 6, .	2.9	4
100	Differences in Levels of Secreted Locus of Enterocyte Effacement Proteins between Human Disease-Associated and Bovine Escherichia coli O157. Infection and Immunity, 2005, 73, 2571-2571.	2.2	2
101	Authorsâ€™ reply to â€˜Pathogenic potential of Escherichia coli from polymicrobial urinary tract infectionsâ€™. Journal of Medical Microbiology, 2011, 60, 1554-1555.	1.8	1
102	Do we really understand how faecal microbiota transplantation works?. EBioMedicine, 2019, 42, 39.	6.1	1
103	Antimicrobial resistance genes and clonal success in Escherichia coli isolates causing bloodstream infection â€“ Authorsâ€™ reply. Lancet Microbe, The, 2021, 2, e493.	7.3	1
104	Response to â€˜Refined analyses suggest that recombination is a minor source of genomic diversity in Pseudomonas aeruginosa chronic cystic fibrosis infectionsâ€™ by Williams et al. (2016). Microbial Genomics, 2016, 2, e000054.	2.0	1
105	Whole-genome sequencing enhances existing pathogen and antimicrobial-resistance surveillance schemes within a neonatal unit. Microbial Genomics, 2022, 8, .	2.0	1
106	Covid-19 testing in the UK was not a â€œshamblesâ€•in 2020. BMJ, The, 2022, 377, o916.	6.0	0