

Micheál Mac Aogáin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3222191/publications.pdf>

Version: 2024-02-01

65
papers

1,902
citations

304368

22
h-index

276539

41
g-index

70
all docs

70
docs citations

70
times ranked

2668
citing authors

#	ARTICLE	IF	CITATIONS
1	The role of acute and chronic respiratory colonization and infections in the pathogenesis of <scp>COPD</scp>. <i>Respirology</i> , 2017, 22, 634-650.	1.3	143
2	Geographic variation in the aetiology, epidemiology and microbiology of bronchiectasis. <i>BMC Pulmonary Medicine</i> , 2018, 18, 83.	0.8	143
3	Memory Th1 Cells Are Protective in Invasive <i>Staphylococcus aureus</i> Infection. <i>PLoS Pathogens</i> , 2015, 11, e1005226.	2.1	132
4	Immunological corollary of the pulmonary mycobiome in bronchiectasis: the CAMEB study. <i>European Respiratory Journal</i> , 2018, 52, 1800766.	3.1	105
5	Integrative microbiomics in bronchiectasis exacerbations. <i>Nature Medicine</i> , 2021, 27, 688-699.	15.2	105
6	Microbiomes in respiratory health and disease: An Asiaâ€Pacific perspective. <i>Respirology</i> , 2017, 22, 240-250.	1.3	88
7	Transcriptome profiling defines a novel regulon modulated by the LysR-type transcriptional regulator MexT in <i>Pseudomonas aeruginosa</i> . <i>Nucleic Acids Research</i> , 2009, 37, 7546-7559.	6.5	85
8	Inhaled nanomaterials and the respiratory microbiome: clinical, immunological and toxicological perspectives. <i>Particle and Fibre Toxicology</i> , 2018, 15, 46.	2.8	84
9	MexT modulates virulence determinants in <i>Pseudomonas aeruginosa</i> independent of the MexEF-OprN efflux pump. <i>Microbial Pathogenesis</i> , 2009, 47, 237-241.	1.3	58
10	Metagenomics Reveals a Core Macrolide Resistome Related to Microbiota in Chronic Respiratory Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 433-447.	2.5	58
11	Distinct â€œImmunoallertypesâ€ of Disease and High Frequencies of Sensitization in Nonâ€Cystic Fibrosis Bronchiectasis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 199, 842-853.	2.5	57
12	The Mycobiome in Health and Disease: Emerging Concepts, Methodologies and Challenges. <i>Mycopathologia</i> , 2020, 185, 207-231.	1.3	50
13	MexT Functions as a Redox-Responsive Regulator Modulating Disulfide Stress Resistance in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2012, 194, 3502-3511.	1.0	47
14	Understanding COPD-overlap syndromes. <i>Expert Review of Respiratory Medicine</i> , 2017, 11, 285-298.	1.0	47
15	Environmental fungal sensitisation associates with poorer clinical outcomes in COPD. <i>European Respiratory Journal</i> , 2020, 56, 2000418.	3.1	44
16	A high-risk airway mycobiome is associated with frequent exacerbation and mortality in COPD. <i>European Respiratory Journal</i> , 2021, 57, 2002050.	3.1	44
17	Whole-genome sequencing improves discrimination of relapse from reinfection and identifies transmission events among patients with recurrent <i>Clostridium difficile</i> infections. <i>Journal of Hospital Infection</i> , 2015, 90, 108-116.	1.4	40
18	Antimicrobial resistance and molecular epidemiology using whole-genome sequencing of <i>Neisseria gonorrhoeae</i> in Ireland, 2014â€2016: focus on extended-spectrum cephalosporins and azithromycin. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2018, 37, 1661-1672.	1.3	36

#	ARTICLE	IF	CITATIONS
19	Optimisation and Benchmarking of Targeted Amplicon Sequencing for Mycobiome Analysis of Respiratory Specimens. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4991.	1.8	28
20	A step-by-step beginner. <i>Journal of Biological Methods</i> , 2019, 6, e110.	1.0	27
21	Airway microbiome composition correlates with lung function and arterial stiffness in an age-dependent manner. <i>PLoS ONE</i> , 2019, 14, e0225636.	1.1	26
22	Detailed characterization of the first high-level azithromycin-resistant <i>Neisseria gonorrhoeae</i> cases in Ireland. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2411-2413.	1.3	25
23	Mycopathologia GENOMES: The New "Home"™ for the Publication of Fungal Genomes. <i>Mycopathologia</i> , 2019, 184, 551-554.	1.3	25
24	Characterization of <i>Escherichia coli</i> bloodstream isolates associated with mortality. <i>Journal of Medical Microbiology</i> , 2016, 65, 71-79.	0.7	22
25	The non-classical ArsR-family repressor PyeR (PA4354) modulates biofilm formation in <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> , 2012, 158, 2598-2609.	0.7	20
26	Identification of emergent bla _{CMY-2} -carrying <i>Proteus mirabilis</i> lineages by whole-genome sequencing. <i>New Microbes and New Infections</i> , 2016, 9, 58-62.	0.8	20
27	Enhanced Tracking of Nosocomial Transmission of Endemic Sequence Type 22 Methicillin-Resistant <i>Staphylococcus aureus</i> Type IV Isolates among Patients and Environmental Sites by Use of Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2016, 54, 445-448.	1.8	19
28	Surface layer proteins from virulent <i>Clostridium difficile</i> ribotypes exhibit signatures of positive selection with consequences for innate immune response. <i>BMC Evolutionary Biology</i> , 2017, 17, 90.	3.2	19
29	Similarity network fusion for the integration of multi-omics and microbiomes in respiratory disease. <i>European Respiratory Journal</i> , 2021, 58, 2101016.	3.1	19
30	The Airway Microbiome: Present and Future Applications. <i>Archivos De Bronconeumologia</i> , 2022, 58, 8-10.	0.4	19
31	Increased Chitotriosidase Is Associated With <i>Aspergillus</i> and Frequent Exacerbations in South-East Asian Patients With Bronchiectasis. <i>Chest</i> , 2020, 158, 512-522.	0.4	15
32	Respiratory Mycoses in COPD and Bronchiectasis. <i>Mycopathologia</i> , 2021, 186, 623-638.	1.3	15
33	"High-Risk" Clinical and Inflammatory Clusters in COPD of Chinese Descent. <i>Chest</i> , 2020, 158, 145-156.	0.4	14
34	Draft Genome Sequences of Three <i>Mycobacterium chimaera</i> Respiratory Isolates. <i>Genome Announcements</i> , 2015, 3, .	0.8	13
35	Differential carriage of virulence-associated loci in the New Zealand Rangipo outbreak strain of <i>Mycobacterium tuberculosis</i> . <i>Infectious Diseases</i> , 2017, 49, 680-688.	1.4	13
36	Mathematical-based microbiome analytics for clinical translation. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6272-6281.	1.9	13

#	ARTICLE	IF	CITATIONS
37	Molecular epidemiology of tuberculosis in Tasmania and genomic characterisation of its first known multi-drug resistant case. PLoS ONE, 2018, 13, e0192351.	1.1	12
38	Human and Porcine Transmission of <i>Clostridioides difficile</i> Ribotype 078, Europe. Emerging Infectious Diseases, 2021, 27, 2294-2300.	2.0	12
39	Identification of a novel mutation at the primary dimer interface of GyrA conferring fluoroquinolone resistance in <i>Clostridium difficile</i> . Journal of Global Antimicrobial Resistance, 2015, 3, 295-299.	0.9	11
40	Field of genes: using Apache Kafka as a bioinformatic data repository. GigaScience, 2018, 7, .	3.3	11
41	The Healthy Airway Mycobiome in Individuals of Asian Descent. Chest, 2021, 159, 544-548.	0.4	11
42	The current understanding and future directions for sputum microbiome profiling in chronic obstructive pulmonary disease. Current Opinion in Pulmonary Medicine, 2022, 28, 121-133.	1.2	11
43	Sex Steroids Induce Membrane Stress Responses and Virulence Properties in <i>Pseudomonas aeruginosa</i> . MBio, 2020, 11, .	1.8	10
44	Microbiology and the Microbiome in Bronchiectasis. Clinics in Chest Medicine, 2022, 43, 23-34.	0.8	10
45	The Microbial Endocrinology of <i>Pseudomonas aeruginosa</i> : Inflammatory and Immune Perspectives. Archivum Immunologiae Et Therapiae Experimentalis, 2018, 66, 329-339.	1.0	9
46	Emergence of extended-spectrum β -lactamase and fluoroquinolone resistance genes among Irish multidrug-resistant isolates. Diagnostic Microbiology and Infectious Disease, 2010, 67, 106-109.	0.8	8
47	Typhlocolitis associated with <i>Clostridium difficile</i> ribotypes 078 and 110 in neonatal piglets from a commercial Irish pig herd. Irish Veterinary Journal, 2015, 69, 10.	0.8	8
48	High Frequency of Allergic Bronchopulmonary Aspergillosis in Bronchiectasis-COPD Overlap. Chest, 2022, 161, 40-53.	0.4	8
49	Whole-Genome Sequencing of <i>Aspergillus terreus</i> Species Complex. Mycopathologia, 2020, 185, 405-408.	1.3	7
50	Draft Genome Sequence of the First Isolate of Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> in New Zealand. Genome Announcements, 2014, 2, .	0.8	6
51	Draft Genome Sequence of a New Zealand Rangipo Strain of <i>Mycobacterium tuberculosis</i> . Genome Announcements, 2016, 4, .	0.8	6
52	On Bugs and Blowholes: Why Is Aspiration the Rule, Not the Exception?. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 1049-1051.	2.5	6
53	<i>Aspergillus</i> -Associated Endophenotypes in Bronchiectasis. Seminars in Respiratory and Critical Care Medicine, 2021, 42, 556-566.	0.8	6
54	Characterization of imipenem resistance mechanisms in <i>Pseudomonas aeruginosa</i> isolates from Turkey. Clinical Microbiology and Infection, 2012, 18, E262-E265.	2.8	5

#	ARTICLE	IF	CITATIONS
55	Bronchiectasis and cough: An old relationship in need of renewed attention. <i>Pulmonary Pharmacology and Therapeutics</i> , 2019, 57, 101812.	1.1	5
56	Reply to de Steenhuijsen Piters and Bogaert: Bacterial DNA in Fetal Lung Samples May Be Explained by Sample Contamination. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 201, 1311-1312.	2.5	5
57	Draft Genome Sequence of the First Isolate of Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> in Ireland. <i>Genome Announcements</i> , 2014, 2, .	0.8	3
58	Possible Interplay Between Hospital and Community Transmission of a Novel <i>Clostridium Difficile</i> Sequence Type 295 Recognized by Next-Generation Sequencing. <i>Infection Control and Hospital Epidemiology</i> , 2016, 37, 680-684.	1.0	3
59	Fourteen Draft Genome Sequences for the First Reported Cases of Azithromycin-Resistant <i>Neisseria gonorrhoeae</i> in Ireland. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
60	Draft Genome Sequence of a Multidrug-Resistant New Zealand Isolate of <i>Mycobacterium tuberculosis</i> Lineage 3. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
61	Fungal Infections and ABPA. <i>Respiratory Medicine</i> , 2020, , 93-126.	0.1	2
62	Intercontinental translocation of latent multidrug-resistant tuberculosis to Australia demonstrated by whole genome sequencing. <i>Medical Journal of Australia</i> , 2019, 210, 236.	0.8	1
63	Draft Genome Sequence of a Drug-Susceptible New Zealand Isolate of <i>Mycobacterium tuberculosis</i> Lineage 3. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
64	Draft Genome Sequence of the First Confirmed Isolate of Multidrug-Resistant <i>Mycobacterium tuberculosis</i> in Tasmania. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
65	Identification of a novel sequence type of <i>Escherichia coli</i> as the causative agent of pyelonephritis and bloodstream infection. <i>JMM Case Reports</i> , 2016, 3, e005061.	1.3	0