Ian R Monk

List of Publications by Year
in descending order

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62 papers	3,414 citations	147801 31 h-index	155660 55 g-index
72 all docs	72 docs citations	72 times ranked	4449 citing authors

#	Article	IF	Citations
1	RNase III-CLASH of multi-drug resistant Staphylococcus aureus reveals a regulatory mRNA 3â€²UTR required for intermediate vancomycin resistance. Nature Communications, 2022, 13, .	12.8	15
2	Antimicrobial tolerance and its role in the development of resistance: Lessons from enterococci. Advances in Microbial Physiology, 2022, , .	2.4	3
3	Clinical Relevance of Topical Antibiotic Use in Coselecting for Multidrug-Resistant Staphylococcus aureus: Insights from In Vitro and Ex Vivo Models. Antimicrobial Agents and Chemotherapy, 2021, 65, .	3.2	4
4	Accessible Platform for High-Throughput COVID-19 Molecular Diagnostics and Genome Sequencing Using a Repurposed 3D Printer for RNA Extraction. ACS Biomaterials Science and Engineering, 2021, 7, 4669-4676.	5.2	3
5	Low-Cost, Open-Source Device for High-Performance Fluorescence Detection of Isothermal Nucleic Acid Amplification Reactions. ACS Biomaterials Science and Engineering, 2021, 7, 4982-4990.	5.2	6
6	Staphylococcus aureus small colony variants impair host immunity by activating host cell glycolysis and inducing necroptosis. Nature Microbiology, 2020, 5, 141-153.	13.3	65
7	Comprehensive Genomic Investigation of Adaptive Mutations Driving the Low-Level Oxacillin Resistance Phenotype in Staphylococcus aureus. MBio, 2020, 11, .	4.1	27
8	YycH and YycI Regulate Expression of Staphylococcus aureus Autolysins by Activation of WalRK Phosphorylation. Microorganisms, 2020, 8, 870.	3.6	19
9	Comparative Transcriptomic and Functional Assessments of Linezolid-Responsive Small RNA Genes in Staphylococcus aureus. MSystems, 2020, 5, .	3.8	7
10	Neutrophils play an ongoing role in preventing bacterial pneumonia by blocking the dissemination of Staphylococcus aureus from the upper to the lower airways. Immunology and Cell Biology, 2020, 98, 577-594.	2.3	9
11	From cloning to mutant in 5 days: rapid allelic exchange in Staphylococcus aureus. Access Microbiology, 2020, 3, 000193.	0.5	20
12	Validation of a single-step, single-tube reverse transcription loop-mediated isothermal amplification assay for rapid detection of SARS-CoV-2 RNA. Journal of Medical Microbiology, 2020, 69, 1169-1178.	1.8	61
13	Zinc-binding to the cytoplasmic PAS domain regulates the essential WalK histidine kinase of Staphylococcus aureus. Nature Communications, 2019, 10, 3067.	12.8	38
14	Within-host evolution of bovine Staphylococcus aureus selects for a SigB-deficient pathotype characterized by reduced virulence but enhanced proteolytic activity and biofilm formation. Scientific Reports, 2019, 9, 13479.	3.3	20
15	Genomewide Profiling of the Enterococcus faecalis Transcriptional Response to Teixobactin Reveals CroRS as an Essential Regulator of Antimicrobial Tolerance. MSphere, 2019, 4, .	2.9	8
16	Staphylococcus aureus Superantigen-Like Protein SSL1: A Toxic Protease. Pathogens, 2019, 8, 2.	2.8	13
17	Mining the Methylome Reveals Extensive Diversity in Staphylococcus epidermidis Restriction Modification. MBio, 2019, 10, .	4.1	28
18	Unstable chromosome rearrangements in Staphylococcus aureus cause phenotype switching associated with persistent infections. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20135-20140.	7.1	69

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19	Bystander Activation of Pulmonary Trm Cells Attenuates the Severity of Bacterial Pneumonia by Enhancing Neutrophil Recruitment. Cell Reports, 2019, 29, 4236-4244.e3.	6.4	44
20	Evolution of Daptomycin Resistance in Coagulase-Negative Staphylococci Involves Mutations of the Essential Two-Component Regulator WalKR. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	22
21	Convergent Evolution Driven by Rifampin Exacerbates the Global Burden of Drug-Resistant Staphylococcus aureus. MSphere, 2018, 3, .	2.9	55
22	Topical Antibiotic Use Coselects for the Carriage of Mobile Genetic Elements Conferring Resistance to Unrelated Antimicrobials in Staphylococcus aureus. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	28
23	Daptomycin selects for genetic and phenotypic adaptations leading to antibiotic tolerance in MRSA. Journal of Antimicrobial Chemotherapy, 2018, 73, 2030-2033.	3.0	21
24	Genomic Analysis of Multiresistant Staphylococcus capitis Associated with Neonatal Sepsis. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	34
25	Global spread of three multidrug-resistant lineages of Staphylococcus epidermidis. Nature Microbiology, 2018, 3, 1175-1185.	13.3	206
26	Comprehensive antibiotic-linked mutation assessment by resistance mutation sequencing (RM-seq). Genome Medicine, 2018, 10, 63.	8.2	26
27	Increasing tolerance of hospital Enterococcus faecium to handwash alcohols. Science Translational Medicine, 2018, 10, .	12.4	165
28	Correspondence: Spontaneous secondary mutations confound analysis of the essential two-component system WalKR in Staphylococcus aureus. Nature Communications, 2017, 8, 14403.	12.8	18
29	Vancomycin-intermediate Staphylococcus aureus isolates are attenuated for virulence when compared with susceptible progenitors. Clinical Microbiology and Infection, 2017, 23, 767-773.	6.0	30
30	Evolutionary origins of the emergent ST796 clone of vancomycin resistantEnterococcus faecium. PeerJ, 2017, 5, e2916.	2.0	46
31	Genomic analysis of ST88 community-acquired methicillin resistantStaphylococcus aureusin Ghana. PeerJ, 2017, 5, e3047.	2.0	20
32	A point mutation in AgrC determines cytotoxic or colonizing properties associated with phenotypic variants of ST22 MRSA strains. Scientific Reports, 2016, 6, 31360.	3.3	32
33	De Novo Guanine Biosynthesis but Not the Riboswitch-Regulated Purine Salvage Pathway Is Required for Staphylococcus aureus Infection In Vivo. Journal of Bacteriology, 2016, 198, 2001-2015.	2.2	38
34	Functional analysis of the first complete genome sequence of a multidrug resistant sequence type 2 Staphylococcus epidermidis. Microbial Genomics, 2016, 2, e000077.	2.0	17
35	Competing for Iron: Duplication and Amplification of the isd Locus in Staphylococcus lugdunensis HKU09-01 Provides a Competitive Advantage to Overcome Nutritional Limitation. PLoS Genetics, 2016, 12, e1006246.	3.5	22
36	Complete Bypass of Restriction Systems for Major Staphylococcus aureus Lineages. MBio, 2015, 6, e00308-15.	4.1	168

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37	Modeling staphylococcal pneumonia in a human 3D lung tissue model system delineates toxin-mediated pathology. DMM Disease Models and Mechanisms, 2015, 8, 1413-25.	2.4	47
38	Manipulation of Autophagy in Phagocytes Facilitates Staphylococcus aureus Bloodstream Infection. Infection and Immunity, 2015, 83, 3445-3457.	2.2	81
39	Fibronectin Binding Proteins SpsD and SpsL Both Support Invasion of Canine Epithelial Cells by Staphylococcus pseudintermedius. Infection and Immunity, 2015, 83, 4093-4102.	2.2	35
40	Large tandem chromosome expansions facilitate niche adaptation during persistent infection with drug-resistant Staphylococcus aureus. Microbial Genomics, 2015, 1, e000026.	2.0	16
41	LSC Abstract â€“ Severity of lung tissue pathology is dictated by S. aureus toxins eliciting series of cytolytic and chemotactic responses. , 2015, , .		0
42	Two TIR-like domain containing proteins in a newly emerging zoonotic Staphylococcus aureus strain sequence type 398 are potential virulence factors by impacting on the host innate immune response. Frontiers in Microbiology, 2014, 5, 662.	3.5	11
43	Hyperexpression of Î±-hemolysin explains enhanced virulence of sequence type 93 community-associated methicillin-resistant Staphylococcus aureus. BMC Microbiology, 2014, 14, 31.	3.3	68
44	Sortase A promotes virulence in experimental Staphylococcus lugdunensis endocarditis. Microbiology (United Kingdom), 2013, 159, 2141-2152.	1.8	40
45	The phage integrase vector pIPI03 allows RecA -independent, site-specific labelling of Staphylococcus lugdunensis strains. Plasmid, 2013, 70, 377-384.	1.4	5
46	Subdomains N2N3 of Fibronectin Binding Protein A Mediate Staphylococcus aureus Biofilm Formation and Adherence to Fibrinogen Using Distinct Mechanisms. Journal of Bacteriology, 2013, 195, 2675-2683.	2.2	90
47	Nasal Colonisation by Staphylococcus aureus Depends upon Clumping Factor B Binding to the Squamous Epithelial Cell Envelope Protein Loricrin. PLoS Pathogens, 2012, 8, e1003092.	4.7	133
48	Transforming the Untransformable: Application of Direct Transformation To Manipulate Genetically Staphylococcus aureus and Staphylococcus epidermidis. MBio, 2012, 3, .	4.1	458
49	Genetic manipulation of Staphylococciâ€"breaking through the barrier. Frontiers in Cellular and Infection Microbiology, 2012, 2, 49.	3.9	76
50	Directed evolution and targeted mutagenesis to murinize listeria monocytogenes internalin A for enhanced infectivity in the murine oral infection model. BMC Microbiology, 2010, 10, 318.	3.3	36
51	A NovelListeria monocytogenes-Based DNA Delivery System for Cancer Gene Therapy. Human Gene Therapy, 2010, 21, 405-416.	2.7	69
52	AgrDâ€dependent quorum sensing affects biofilm formation, invasion, virulence and global gene expression profiles in Listeria monocytogenes. Molecular Microbiology, 2009, 71, 1177-1189.	2.5	158
53	Screening of rationally designed oligopeptides for Listeria monocytogenes detection by means of a high density colorimetric microarray. Mikrochimica Acta, 2008, 163, 227-235.	5.0	9
54	Development of multiple strain competitive index assays for Listeria monocytogenes using pIMC; a new site-specific integrative vector. BMC Microbiology, 2008, 8, 96.	3.3	37

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55	Tools for Functional Postgenomic Analysis ofListeria monocytogenes. Applied and Environmental Microbiology, 2008, 74, 3921-3934.	3.1	205
56	Improved Luciferase Tagging System for Listeria monocytogenes Allows Real-Time Monitoring In Vivo and In Vitro. Applied and Environmental Microbiology, 2007, 73, 3091-3094.	3.1	101
57	Novel Luciferase Reporter System for In Vitro and Organ-Specific Monitoring of Differential Gene Expression in Listeria monocytogenes. Applied and Environmental Microbiology, 2006, 72, 2876-2884.	3.1	69
58	Morphotypic Conversion in Listeria monocytogenes Biofilm Formation: Biological Significance of Rough Colony Isolates. Applied and Environmental Microbiology, 2004, 70, 6686-6694.	3.1	50
59	Inactivation of Listeria monocytogenes/Flavobacterium spp. biofilms using chlorine: impact of substrate, pH, time and concentration. Letters in Applied Microbiology, 2002, 35, 321-325.	2.2	74
60	Development of a Steam Treatment to Eliminate Listeria monocytogenes From King Salmon (Oncorhynchus tshawytscha). Journal of Food Science, 2002, 67, 2282-2287.	3.1	14
61	Survival of Listeria monocytogenes Attached to Stainless Steel Surfaces in the Presence or Absence of Flavobacterium spp.. Journal of Food Protection, 2001, 64, 1369-1376.	1.7	106
62	Staphylococcus aureus specific lung resident memory CD4+ Th1 cells attenuate the severity of influenza virus induced secondary bacterial pneumonia. Mucosal Immunology, 0, , .	6.0	6