Jodi A Lindsay

List of Publications by Year in descending order

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117
papers

9,746
citations

44444
50
h-index

42259
96
g-index

120
all docs

120
docs citations

120
times ranked

9537
citing authors

#	ARTICLE	IF	CITATIONS
1	MRSA surveillance programmes worldwide: moving towards a harmonised international approach. International Journal of Antimicrobial Agents, 2022, 59, 106538.	1.1	8
2	Emergence of methicillin resistance predates the clinical use of antibiotics. Nature, 2022, 602, 135-141.	13.7	138
3	Growth-Dependent Predation and Generalized Transduction of Antimicrobial Resistance by Bacteriophage. MSystems, 2022, 7, e0013522.	1.7	10
4	Understanding MRSA clonal competition within a UK hospital; the possible importance of density dependence. Epidemics, 2021, 37, 100511.	1.5	3
5	Genes on the Move: In Vitro Transduction of Antimicrobial Resistance Genes between Human and Canine Staphylococcal Pathogens. Microorganisms, 2020, 8, 2031.	1.6	19
6	Mathematical modelling to study the horizontal transfer of antimicrobial resistance genes in bacteria: current state of the field and recommendations. Journal of the Royal Society Interface, 2019, 16, 20190260.	1.5	37
7	Genetic resistance determinants to fusidic acid and chlorhexidine in variably susceptible staphylococci from dogs. BMC Microbiology, 2019, 19, 81.	1.3	12
8	Determinants of Phage Host Range in <i>Staphylococcus</i> Species. Applied and Environmental Microbiology, 2019, 85, .	1.4	59
9	<i>Staphylococcus aureus</i> Bacteremia in Children of Rural Areas of The Gambia, 2008â€“2015. Emerging Infectious Diseases, 2019, 25, 701-709.	2.0	9
10	Implications of identifying the recently defined members of the Staphylococcus aureus complex S.Âargenteus and S.Âschweitzeri: a position paper of members of the ESCMID Study Group for Staphylococci and Staphylococcal Diseases (ESGS). Clinical Microbiology and Infection, 2019, 25, 1064-1070.	2.8	58
11	Staphylococci: Evolving Genomes. Microbiology Spectrum, 2019, 7, .	1.2	19
12	Mathematical modelling for antibiotic resistance control policy: do we know enough?. BMC Infectious Diseases, 2019, 19, 1011.	1.3	37
13	The importance of cross-disciplinary research to combat antimicrobial resistance: introducing a new pop-up journal, X-AMR. Microbial Genomics, 2018, 4, .	1.0	2
14	DNA target recognition domains in the Type I restriction and modification systems of Staphylococcus aureus. Nucleic Acids Research, 2017, 45, 3395-3406.	6.5	27
15	Resistance gene transfer: induction of transducing phage by sub-inhibitory concentrations of antimicrobials is not correlated to induction of lytic phage. Journal of Antimicrobial Chemotherapy, 2017, 72, 1624-1631.	1.3	39
16	The Type I Restriction Enzymes as Barriers to Horizontal Gene Transfer: Determination of the DNA Target Sequences Recognised by Livestock-Associated Methicillin-Resistant Staphylococcus aureus Clonal Complexes 133/ST771 and 398. Advances in Experimental Medicine and Biology, 2016, 915, 81-97.	0.8	6
17	Genomic insights into the emergence and spread of international clones of healthcare-, community- and livestock-associated meticillin-resistant Staphylococcus aureus : Blurring of the traditional definitions. Journal of Global Antimicrobial Resistance, 2016, 6, 95-101.	0.9	119
18	Staphylococcal Variation and Evolution. , 2016, , 67-80.		0

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19	Genomic insights into the rapid emergence and evolution of MDR in <i>Staphylococcus pseudintermedius</i>. Journal of Antimicrobial Chemotherapy, 2015, 70, 997-1007.	1.3	77
20	Evolutionary dynamics of methicillin-resistant Staphylococcus aureus within a healthcare system. Genome Biology, 2015, 16, 81.	3.8	129
21	What Is the Origin of Livestock-Associated Methicillin-Resistant Staphylococcus aureus Clonal Complex 398 Isolates from Humans without Livestock Contact? An Epidemiological and Genetic Analysis. Journal of Clinical Microbiology, 2015, 53, 1836-1841.	1.8	46
22	Transmission of antimicrobial resistance in resource-poor healthcare. Trends in Microbiology, 2015, 23, 69-70.	3.5	1
23	Within-host diversity of MRSA antimicrobial resistances. Journal of Antimicrobial Chemotherapy, 2015, 70, 2191-2198.	1.3	49
24	Manipulation of Autophagy in Phagocytes Facilitates Staphylococcus aureus Bloodstream Infection. Infection and Immunity, 2015, 83, 3445-3457.	1.0	81
25	Extensive Horizontal Gene Transfer during Staphylococcus aureus Co-colonization In Vivo. Genome Biology and Evolution, 2014, 6, 2697-2708.	1.1	119
26	Meticillin-resistant Staphylococcus aureus (MRSA) update: New insights into bacterial adaptation and therapeutic targets. Journal of Global Antimicrobial Resistance, 2014, 2, 61-69.	0.9	16
27	Evolution of Staphylococcus aureus and MRSA during outbreaks. Infection, Genetics and Evolution, 2014, 21, 548-553.	1.0	33
28	Staphylococcus aureus genomics and the impact of horizontal gene transfer. International Journal of Medical Microbiology, 2014, 304, 103-109.	1.5	146
29	Fructose transport-deficient Staphylococcus aureus reveals important role of epithelial glucose transporters in limiting sugar-driven bacterial growth in airway surface liquid. Cellular and Molecular Life Sciences, 2014, 71, 4665-4673.	2.4	33
30	Wholeâ€genome comparison of meticillinâ€resistant <i>Staphylococcus aureus</i> CC22 SCC<i>mec</i>IV from people and their inâ€contact pets. Veterinary Dermatology, 2013, 24, 538.	0.4	27
31	Staphylococci. , 2013, , 385-405.		1
32	Hospital-associated MRSA and antibiotic resistanceâ€”What have we learned from genomics?. International Journal of Medical Microbiology, 2013, 303, 318-323.	1.5	81
33	Large mobile genetic elements carrying resistance genes that do not confer a fitness burden in healthcare-associated meticillin-resistant Staphylococcus aureus. Microbiology (United Kingdom), 2013, 159, 1661-1672.	0.7	19
34	Staphylococcus aureus innate immune evasion is lineage-specific: A bioinfomatics study. Infection, Genetics and Evolution, 2013, 19, 7-14.	1.0	95
35	Impact of target site distribution for Type I restriction enzymes on the evolution of methicillin-resistant Staphylococcus aureus (MRSA) populations. Nucleic Acids Research, 2013, 41, 7472-7484.	6.5	58
36	Metformin reduces airway glucose permeability and hyperglycaemia-induced<i>Staphylococcus aureus</i>load independently of effects on blood glucose. Thorax, 2013, 68, 835-845.	2.7	96

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37	Characterization and Comparison of 2 Distinct Epidemic Community-Associated Methicillin-Resistant Staphylococcus aureus Clones of ST59 Lineage. PLoS ONE, 2013, 8, e63210.	1.1	57
38	Shuffling of mobile genetic elements (MGEs) in successful healthcare-associated MRSA (HA-MRSA). Mobile Genetic Elements, 2012, 2, 239-243.	1.8	22
39	Detection of Mobile-Genetic-Element Variation between Colonizing and Infecting Hospital-Associated Methicillin-Resistant Staphylococcus aureus Isolates. Journal of Clinical Microbiology, 2012, 50, 1073-1075.	1.8	43
40	Identification of a Highly Transmissible Animal-Independent Staphylococcus aureus ST398 Clone with Distinct Genomic and Cell Adhesion Properties. MBio, 2012, 3, .	1.8	180
41	Staphylococcus aureus CC398 Clade Associated with Human-to-Human Transmission. Applied and Environmental Microbiology, 2012, 78, 8845-8848.	1.4	75
42	Shift in dominant hospital-associated methicillin-resistant Staphylococcus aureus (HA-MRSA) clones over time. Journal of Antimicrobial Chemotherapy, 2012, 67, 2514-2522.	1.3	121
43	The distribution of plasmids that carry virulence and resistance genes in Staphylococcus aureus is lineage associated. BMC Microbiology, 2012, 12, 104.	1.3	138
44	Meticillin-resistant Staphylococcus aureus (MRSA): global epidemiology and harmonisation of typing methods. International Journal of Antimicrobial Agents, 2012, 39, 273-282.	1.1	473
45	Comparative Host Specificity of Human- and Pig- Associated Staphylococcus aureus Clonal Lineages. PLoS ONE, 2012, 7, e49344.	1.1	17
46	Staphylococcus aureus Temperate Bacteriophage: Carriage and Horizontal Gene Transfer is Lineage Associated. Frontiers in Cellular and Infection Microbiology, 2012, 2, 6.	1.8	85
47	Are all meticillinâ€resistant <i>Staphylococcus aureus</i> (MRSA) equal in all hosts? Epidemiological and genetic comparison between animal and human MRSA. Veterinary Dermatology, 2012, 23, 267.	0.4	58
48	Survival of Staphylococcus aureus ST398 in the Human Nose after Artificial Inoculation. PLoS ONE, 2012, 7, e48896.	1.1	23
49	Developing An In Vitro Model To Determine The Effect Of Glucose On Epithelial-Bacterial Interactions In Airway Infection. , 2011, , .		0
50	Genetic Variation in Spatio-Temporal Confined USA300 Community-Associated MRSA Isolates: A Shift from Clonal Dispersion to Genetic Evolution?. PLoS ONE, 2011, 6, e16419.	1.1	15
51	The Distribution of Mobile Genetic Elements (MGEs) in MRSA CC398 Is Associated with Both Host and Country. Genome Biology and Evolution, 2011, 3, 1164-1174.	1.1	82
52	Reduced Sensitivity of Oxacillin-Screening Agar for Detection of MRSA ST398 from Colonized Pigs. Journal of Clinical Microbiology, 2011, 49, 3103-3104.	1.8	1
53	Are Nasal Carriers of <i>Staphylococcus aureus</i> More Likely To Become Colonized or Infected with Methicillin-Resistant <i>Staphylococcus aureus</i> on Admission to a Hospital?. Journal of Clinical Microbiology, 2011, 49, 430-432.	1.8	18
54	Major Families of Multiresistant Plasmids from Geographically and Epidemiologically Diverse Staphylococci. G3: Genes, Genomes, Genetics, 2011, 1, 581-591.	0.8	92

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55	Rapid PCR Detection of Staphylococcus aureus Clonal Complex 398 by Targeting the Restriction-Modification System Carrying <i>sau1-hsdS1</i>. Journal of Clinical Microbiology, 2011, 49, 732-734.	1.8	104
56	Prevalence of and risk factors for MRSA carriage in companion animals: a survey of dogs, cats and horses. Epidemiology and Infection, 2011, 139, 1019-1028.	1.0	61
57	Genomics of Staphylococcus. , 2011, , 237-265.		5
58	Evolution of MRSA During Hospital Transmission and Intercontinental Spread. Science, 2010, 327, 469-474.	6.0	1,054
59	Meticillin-resistant Staphylococcus aureus carriage in UK veterinary staff and owners of infected pets: new risk groups. Journal of Hospital Infection, 2010, 74, 282-288.	1.4	73
60	Genetic variation in Staphylococcus aureus surface and immune evasion genes is lineage associated: implications for vaccine design and host-pathogen interactions. BMC Microbiology, 2010, 10, 173.	1.3	194
61	Lack of transmission of methicillin-resistant Staphylococcus aureus (MRSA) between apparently healthy dogs in a rescue kennel. Veterinary Microbiology, 2010, 141, 178-181.	0.8	33
62	Genetic diversity in CC398 methicillin-resistant Staphylococcus aureus isolates of different geographical origin. Clinical Microbiology and Infection, 2010, 16, 1017-1019.	2.8	52
63	Risk factors for methicillin-resistant<i>Staphylococcus aureus</i>(MRSA) infection in dogs and cats: a case-control study. Veterinary Research, 2010, 41, 55.	1.1	84
64	Clinical and Microbiological Determinants of Outcome inStaphylococcus aureusBacteraemia. International Journal of Microbiology, 2010, 2010, 1-7.	0.9	18
65	Genome Sequence of a Recently Emerged, Highly Transmissible, Multi-Antibiotic- and Antiseptic-Resistant Variant of Methicillin-Resistant <i>Staphylococcus aureus</i> , Sequence Type 239 (TW). Journal of Bacteriology, 2010, 192, 888-892.	1.0	211
66	Evolutionary Genomics of Staphylococcus aureus Reveals Insights into the Origin and Molecular Basis of Ruminant Host Adaptation. Genome Biology and Evolution, 2010, 2, 454-466.	1.1	174
67	Genomic variation and evolution of Staphylococcus aureus. International Journal of Medical Microbiology, 2010, 300, 98-103.	1.5	222
68	The RM Test for Determining Methicillin-Resistant Staphylococcus aureus Lineages. Methods in Molecular Biology, 2010, 642, 3-11.	0.4	4
69	Transcriptional Signature following Inhibition of Early-Stage Cell Wall Biosynthesis in Staphylococcus aureus. Antimicrobial Agents and Chemotherapy, 2009, 53, 1701-1704.	1.4	11
70	Two Distinct Clones of Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) with the Same USA300 Pulsed-Field Gel Electrophoresis Profile: a Potential Pitfall for Identification of USA300 Community-Associated MRSA. Journal of Clinical Microbiology, 2009, 47, 3765-3768.	1.8	46
71	Association of Mannoseâ€Binding Lectin Deficiency with Acute Invasive Aspergillosis in Immunocompromised Patients. Clinical Infectious Diseases, 2009, 49, 1486-1491.	2.9	75
72	First isolation of MRSA ST398 from UK animals: a new challenge for infection control teams?. Journal of Hospital Infection, 2009, 72, 269-271.	1.4	42

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73	New methods to analyse microarray data that partially lack a reference signal. BMC Genomics, 2009, 10, 522.	1.2	3
74	Difference in virulence between<i>Staphylococcus aureus</i>isolates causing gangrenous mastitis versus subclinical mastitis in a dairy sheep flock. Veterinary Research, 2009, 40, 56.	1.1	26
75	The Staphylococcus aureus Response to Unsaturated Long Chain Free Fatty Acids: Survival Mechanisms and Virulence Implications. PLoS ONE, 2009, 4, e4344.	1.1	152
76	For CA-MRSA, how much PVL is too much?. Microbiology (United Kingdom), 2009, 155, 3473-3474.	0.7	4
77	The rise of invasive s. aureus infection in brighton; poor practice or bad bugs?. Journal of Infection, 2008, 56, 302-303.	1.7	0
78	Antiâ€MRSA Agent Discovery Using Diversityâ€Oriented Synthesis. Angewandte Chemie - International Edition, 2008, 47, 2808-2812.	7.2	122
79	Staphylococcus aureus host specificity: comparative genomics of human versus animal isolates by multi-strain microarray. Microbiology (United Kingdom), 2008, 154, 1949-1959.	0.7	274
80	Clones and Drones: Do Variants of Pantonâ€Valentine Leukocidin Extend the Reach of Communityâ€Associated Methicillinâ€Resistant<i>Staphylococcus aureus</i>?. Journal of Infectious Diseases, 2008, 197, 175-178.	1.9	10
81	Staphylococcus aureus Strains That are Hypersusceptible to Resistance Gene Transfer from Enterococci. Antimicrobial Agents and Chemotherapy, 2007, 51, 2189-2191.	1.4	55
82	Prospects for a MRSA vaccine. Future Microbiology, 2007, 2, 1-3.	1.0	12
83	An Outbreak in an Intensive Care Unit of a Strain of Methicillin-Resistant Staphylococcus aureus Sequence Type 239 Associated with an Increased Rate of Vascular Access Device--Related Bacteremia. Clinical Infectious Diseases, 2007, 44, 493-501.	2.9	95
84	Rapid determination of hospital-acquired meticillin-resistant Staphylococcus aureus lineages. Journal of Medical Microbiology, 2007, 56, 614-619.	0.7	72
85	An Outbreak of Severe Infections with Community-Acquired MRSA Carrying the Panton-Valentine Leukocidin Following Vaccination. PLoS ONE, 2007, 2, e822.	1.1	40
86	The grapes of wrath. Nature Reviews Microbiology, 2006, 4, 806-807.	13.6	3
87	Understanding the rise of the superbug: investigation of the evolution and genomic variation of Staphylococcus aureus. Functional and Integrative Genomics, 2006, 6, 186-201.	1.4	181
88	Microarrays Reveal that Each of the Ten Dominant Lineages of Staphylococcus aureus Has a Unique Combination of Surface-Associated and Regulatory Genes. Journal of Bacteriology, 2006, 188, 669-676.	1.0	303
89	Sau1: a Novel Lineage-Specific Type I Restriction-Modification System That Blocks Horizontal Gene Transfer into Staphylococcus aureus and between S. aureus Isolates of Different Lineages. Journal of Bacteriology, 2006, 188, 5578-5585.	1.0	279
90	Investigation of MRSA in small animal practice. Veterinary Record, 2005, 157, 179-180.	0.2	2

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91	Clonal Distribution and Phase-Variable Expression of a Major Histocompatibility Complex Analogue Protein in Staphylococcus aureus. Journal of Bacteriology, 2005, 187, 2917-2919.	1.0	15
92	Design, Validation, and Application of a Seven-Strain Staphylococcus aureus PCR Product Microarray for Comparative Genomics. Applied and Environmental Microbiology, 2005, 71, 7504-7514.	1.4	77
93	Prevalence of methicillin-resistant Staphylococcus aureus among staff and pets in a small animal referral hospital in the UK. Journal of Antimicrobial Chemotherapy, 2005, 56, 692-697.	1.3	236
94	Complete genomes of two clinical Staphylococcus aureus strains: Evidence for the rapid evolution of virulence and drug resistance. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9786-9791.	3.3	830
95	Staphylococcus aureus : superbug, super genome?. Trends in Microbiology, 2004, 12, 378-385.	3.5	353
96	Three steps to targeting anthrax toxin. Trends in Molecular Medicine, 2002, 8, 6.	3.5	0
97	PIs â€“ do they really have all the answers?. Trends in Molecular Medicine, 2001, 7, 10.	3.5	0
98	Capsule essential for fatal tropical disease pathogen. Trends in Molecular Medicine, 2001, 7, 99.	3.5	0
99	Attracting the right cells to control tuberculosis. Trends in Molecular Medicine, 2001, 7, 432.	3.5	0
100	Molecular genetics of SaPI1 - a mobile pathogenicity island in Staphylococcus aureus. Molecular Microbiology, 2001, 41, 365-377.	1.2	197
101	Genetic Variation among Hospital Isolates of Methicillin-Sensitive Staphylococcus aureus : Evidence for Horizontal Transfer of Virulence Genes. Journal of Clinical Microbiology, 2001, 39, 2760-2767.	1.8	151
102	zur: a Zn2+-responsive regulatory element of Staphylococcus aureus The GenBank accession number for the sequence reported in this paper is AF101263.. Microbiology (United Kingdom), 2001, 147, 1259-1266.	0.7	79
103	Sic in epidemic waves of GAS. Trends in Molecular Medicine, 2000, 6, 187.	2.6	0
104	Conserved virulence-control in Gram-positive bacteria?. Trends in Molecular Medicine, 2000, 6, 262.	2.6	0
105	Peptic ulcer irony. Trends in Molecular Medicine, 2000, 6, 382.	2.6	0
106	Typing pathogenic bugs on the net. Trends in Molecular Medicine, 2000, 6, 100.	2.6	1
107	Interactive regulatory pathways control virulence determinant production and stability in response to environmental conditions in Staphylococcus aureus. Molecular Genetics and Genomics, 1999, 262, 323-331.	2.4	68
108	The importance of location. Trends in Molecular Medicine, 1999, 5, 54.	2.6	1

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109	Streptococcal invasive mechanisms and flesh-eating disease. Trends in Molecular Medicine, 1999, 5, 193.	2.6	0
110	Viruses that turn bacteria pathogenic. Trends in Molecular Medicine, 1999, 5, 329.	2.6	0
111	UTI inflammation â€" is LPS not the key?. Trends in Molecular Medicine, 1999, 5, 507.	2.6	0
112	Vaccine evasion by pneumococci: as easy as changing a cassette. Trends in Molecular Medicine, 1998, 4, 99.	2.6	0
113	Keeping antibacterials inside bacteria. Trends in Molecular Medicine, 1998, 4, 465.	2.6	0
114	The gene for toxic shock toxin is carried by a family of mobile pathogenicity islands inStaphylococcus aureus. Molecular Microbiology, 1998, 29, 527-543.	1.2	400
115	Production of siderophore by coagulase-negative staphylococci and its relation to virulence. European Journal of Clinical Microbiology and Infectious Diseases, 1994, 13, 1063-1066.	1.3	15
116	Identification ofStaphylococcus epidermidis andStaphylococcus hominis from blood cultures by testing susceptibility to desferrioxamine. European Journal of Clinical Microbiology and Infectious Diseases, 1993, 12, 127-131.	1.3	11
117	The Staphylococci: A Postgenomic View. , 0, , 120-140.		1