

Stephanie W Lo

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

2,146
citations

279798

23
h-index

254184

43
g-index

59
all docs

59
docs citations

59
times ranked

2682
citing authors

#	ARTICLE	IF	CITATIONS
1	RCandy: an R package for visualizing homologous recombinations in bacterial genomes. <i>Bioinformatics</i> , 2022, 38, 1450-1451.	4.1	5
2	International links between <i>Streptococcus pneumoniae</i> vaccine serotype 4 sequence type (ST) 801 in Northern European shipyard outbreaks of invasive pneumococcal disease. <i>Vaccine</i> , 2022, 40, 1054-1060.	3.8	4
3	Widespread sharing of pneumococcal strains in a rural African setting: proximate villages are more likely to share similar strains that are carried at multiple timepoints. <i>Microbial Genomics</i> , 2022, 8, .	2.0	1
4	Comparative Genomics of Disease and Carriage Serotype 1 Pneumococci. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	3
5	Genetic background of Cambodian pneumococcal carriage isolates following pneumococcal conjugate vaccine 13. <i>Microbial Genomics</i> , 2022, 8, .	2.0	0
6	Variants of <i>Streptococcus pneumoniae</i> Serotype 14 from Papua New Guinea with the Potential to Be Mistyped and Escape Vaccine-Induced Protection. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	5
7	Global genomic pathogen surveillance to inform vaccine strategies: a decade-long expedition in pneumococcal genomics. <i>Genome Medicine</i> , 2021, 13, 84.	8.2	12
8	The role of interspecies recombination in the evolution of antibiotic-resistant pneumococci. <i>ELife</i> , 2021, 10, .	6.0	21
9	Population genetic structure, serotype distribution and antibiotic resistance of <i>Streptococcus pneumoniae</i> causing invasive disease in children in Argentina. <i>Microbial Genomics</i> , 2021, 7, .	2.0	8
10	<i>Streptococcus pneumoniae</i> genomic datasets from an Indian population describing pre-vaccine evolutionary epidemiology using a whole genome sequencing approach. <i>Microbial Genomics</i> , 2021, 7, .	2.0	8
11	Genomic surveillance of invasive <i>Streptococcus pneumoniae</i> isolates in the period pre-PCV10 and post-PCV10 introduction in Brazil. <i>Microbial Genomics</i> , 2021, 7, .	2.0	6
12	A mosaic tetracycline resistance gene tet(S/M) detected in an MDR pneumococcal CC230 lineage that underwent capsular switching in South Africa. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 512-520.	3.0	12
13	Characterization of Pneumococcal Colonization Dynamics and Antimicrobial Resistance Using Shotgun Metagenomic Sequencing in Intensively Sampled South African Infants. <i>Frontiers in Public Health</i> , 2020, 8, 543898.	2.7	4
14	Genomics and epidemiological surveillance. <i>Nature Reviews Microbiology</i> , 2020, 18, 478-478.	28.6	31
15	A Nationwide Outbreak of Invasive Pneumococcal Disease in Israel Caused by <i>Streptococcus Pneumoniae</i> Serotype 2. <i>Clinical Infectious Diseases</i> , 2020, 73, e3768-e3777.	5.8	3
16	Bacterial genome-wide association study of hyper-virulent pneumococcal serotype 1 identifies genetic variation associated with neurotropism. <i>Communications Biology</i> , 2020, 3, 559.	4.4	11
17	A New Pneumococcal Capsule Type, 10D, is the 100th Serotype and Has a Large <i>cps</i> Fragment from an Oral <i>Streptococcus</i> . <i>MBio</i> , 2020, 11, .	4.1	219
18	Carriage Dynamics of Pneumococcal Serotypes in Naturally Colonized Infants in a Rural African Setting During the First Year of Life. <i>Frontiers in Pediatrics</i> , 2020, 8, 587730.	1.9	8

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19	Visualizing variation within Global Pneumococcal Sequence Clusters (GPSCs) and country population snapshots to contextualize pneumococcal isolates. <i>Microbial Genomics</i> , 2020, 6, .	2.0	25
20	Fast and flexible bacterial genomic epidemiology with PopPUNK. <i>Genome Research</i> , 2019, 29, 304-316.	5.5	258
21	Pneumococcal lineages associated with serotype replacement and antibiotic resistance in childhood invasive pneumococcal disease in the post-PCV13 era: an international whole-genome sequencing study. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 759-769.	9.1	165
22	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. <i>EBioMedicine</i> , 2019, 43, 338-346.	6.1	168
23	Putative novel cps loci in a large global collection of pneumococci. <i>Microbial Genomics</i> , 2019, 5, .	2.0	14
24	Identification of Plasmid-Encoded sRNAs in a bla _{NDM-1} -Harboring Multidrug-Resistance Plasmid pNDM-HK in Enterobacteriaceae. <i>Frontiers in Microbiology</i> , 2018, 9, 532.	3.5	5
25	Global Distribution of Invasive Serotype 35D <i>Streptococcus pneumoniae</i> Isolates following Introduction of 13-Valent Pneumococcal Conjugate Vaccine. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	12
26	The CTX-M-14 plasmid pHK01 encodes novel small RNAs and influences host growth and motility. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	12
27	Emergence of <i>ileS2</i> -Carrying, Multidrug-Resistant Plasmids in <i>Staphylococcus lugdunensis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6411-6414.	3.2	6
28	Characterization of carbapenem-resistant <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> from a healthcare region in Hong Kong. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2016, 35, 379-385.	2.9	48
29	Plasmid-Mediated OqxAB Is an Important Mechanism for Nitrofurantoin Resistance in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 537-543.	3.2	55
30	Prevalence of aminoglycoside modifying enzyme and 16S ribosomal RNA methylase genes among aminoglycoside-resistant <i>Escherichia coli</i> isolates. <i>Journal of Microbiology, Immunology and Infection</i> , 2016, 49, 123-126.	3.1	11
31	High prevalence of <i>Escherichia coli</i> sequence type 131 among antimicrobial-resistant <i>E. coli</i> isolates from geriatric patients. <i>Journal of Medical Microbiology</i> , 2015, 64, 243-247.	1.8	19
32	Complete Sequence of the Multidrug-Resistant IncL/M Plasmid pIMP-HB623 Cocarrying <i>bla</i> _{IMP-34} and <i>fosC2</i> in an <i>Enterobacter cloacae</i> Strain Associated with Medical Travel to China. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 5854-5856.	3.2	15
33	Prevalence and characterization of hybrid bla _{CTX-M} among <i>Escherichia coli</i> isolates from livestock and other animals. <i>Diagnostic Microbiology and Infectious Disease</i> , 2015, 82, 148-153.	1.8	24
34	MRSAspat1081, a Highly Transmissible Strain Endemic to Hong Kong, China, in the Netherlands. <i>Emerging Infectious Diseases</i> , 2015, 21, 1074-1076.	4.3	10
35	Clonal diversity of CTX-M-producing, multidrug-resistant <i>Escherichia coli</i> from rodents. <i>Journal of Medical Microbiology</i> , 2015, 64, 185-190.	1.8	13
36	Clonal Diversity of <i>Escherichia coli</i> Isolates Carrying Plasmid-Mediated Fosfomycin Resistance Genes fosA3 from Livestock and Other Animals. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 5638-5639.	3.2	20

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37	pIMP-PH114 Carrying bla IMP-4 in a Klebsiella pneumoniae Strain is Closely Related to Other Multidrug-Resistant IncA/C2 Plasmids. <i>Current Microbiology</i> , 2014, 68, 227-232.	2.2	29
38	Highly conjugative IncX4 plasmids carrying bla CTX-M in Escherichia coli from humans and food animals. <i>Journal of Medical Microbiology</i> , 2014, 63, 835-840.	1.8	44
39	Molecular Characterization of an Atypical IncX3 Plasmid pKPC-NY79 Carrying bla KPC-2 in a Klebsiella pneumoniae. <i>Current Microbiology</i> , 2013, 67, 493-498.	2.2	43
40	Plasmid-mediated fosfomycin resistance in Escherichia coli isolated from pig. <i>Veterinary Microbiology</i> , 2013, 162, 964-967.	1.9	30
41	Prevalence and molecular epidemiology of plasmid-mediated fosfomycin resistance genes among blood and urinary Escherichia coli isolates. <i>Journal of Medical Microbiology</i> , 2013, 62, 1707-1713.	1.8	73
42	Clinical outcome of extended-spectrum beta-lactamase-producing Escherichia coli bacteremia in an area with high endemicity. <i>International Journal of Infectious Diseases</i> , 2013, 17, e120-e124.	3.3	31
43	Rare occurrence of vancomycin-resistant Enterococcus faecium among livestock animals in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 2948-2949.	3.0	6
44	Complete Sequence of an IncN Plasmid, pIMP-HZ1, Carrying bla IMP-4 in a Klebsiella pneumoniae Strain Associated with Medical Travel to China. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 1561-1562.	3.2	25
45	Dissemination of plasmid-mediated fosfomycin resistance fosA3 among multidrug-resistant Escherichia coli from livestock and other animals. <i>Journal of Applied Microbiology</i> , 2013, 114, 695-702.	3.1	72
46	Escherichia coli O25b-ST131 is an important cause of antimicrobial-resistant infections in women with uncomplicated cystitis. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 2534-2535.	3.0	9
47	Predominance of pHK01-like incompatibility group FII plasmids encoding CTX-M-14 among extended-spectrum beta-lactamase-producing Escherichia coli in Hong Kong, 1996-2008. <i>Diagnostic Microbiology and Infectious Disease</i> , 2012, 73, 182-186.	1.8	40
48	Dissemination of pHK01-like incompatibility group IncFII plasmids encoding CTX-M-14 in Escherichia coli from human and animal sources. <i>Veterinary Microbiology</i> , 2012, 158, 172-179.	1.9	54
49	Extensive dissemination of CTX-M-producing Escherichia coli with multidrug resistance to 'critically important' antibiotics among food animals in Hong Kong, 2008-10. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 765-768.	3.0	102
50	Effect of applying the new Clinical and Laboratory Standards Institute ceftazidime and ceftriaxone susceptibility breakpoints for Escherichia coli in Hong Kong. <i>International Journal of Antimicrobial Agents</i> , 2011, 37, 270-271.	2.5	3
51	Emergence of Klebsiella pneumoniae ST258 with KPC-2 in Hong Kong. <i>International Journal of Antimicrobial Agents</i> , 2011, 37, 386-387.	2.5	5
52	Complete sequencing of the FII plasmid pHK01, encoding CTX-M-14, and molecular analysis of its variants among Escherichia coli from Hong Kong. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 752-756.	3.0	28
53	Complete Sequencing of pNDM-HK Encoding NDM-1 Carbapenemase from a Multidrug-Resistant Escherichia coli Strain Isolated in Hong Kong. <i>PLoS ONE</i> , 2011, 6, e17989.	2.5	168
54	Fecal carriage of CTXM type extended-spectrum beta-lactamase-producing organisms by children and their household contacts. <i>Journal of Infection</i> , 2010, 60, 286-292.	3.3	72

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55	Genetic identity of aminoglycoside-resistance genes in Escherichia coli isolates from human and animal sources. Journal of Medical Microbiology, 2010, 59, 702-707.	1.8	58