

Stephanie W Lo

List of Publications by Year in descending order

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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	Fast and flexible bacterial genomic epidemiology with PopPUNK. <i>Genome Research</i> , 2019, 29, 304-316.	5.5	258
2	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
3	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. <i>EBioMedicine</i> , 2019, 43, 338-346.	6.1	168
4	Complete Sequencing of pNDM-HK Encoding NDM-1 Carbapenemase from a Multidrug-Resistant <i>Escherichia coli</i> Strain Isolated in Hong Kong. <i>PLoS ONE</i> , 2011, 6, e17989.	2.5	168
5	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
6	Extensive dissemination of CTX-M-producing <i>Escherichia coli</i> 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
7	Prevalence and molecular epidemiology of plasmid-mediated fosfomycin resistance genes among blood and urinary <i>Escherichia coli</i> isolates. <i>Journal of Medical Microbiology</i> , 2013, 62, 1707-1713.	1.8	73
8	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
9	Dissemination of plasmid-mediated fosfomycin resistance <i>fosA3</i> among multidrug-resistant <i>Escherichia coli</i> from livestock and other animals. <i>Journal of Applied Microbiology</i> , 2013, 114, 695-702.	3.1	72
10	Genetic identity of aminoglycoside-resistance genes in <i>Escherichia coli</i> isolates from human and animal sources. <i>Journal of Medical Microbiology</i> , 2010, 59, 702-707.	1.8	58
11	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
12	Dissemination of pHK01-like incompatibility group IncFII plasmids encoding CTX-M-14 in <i>Escherichia coli</i> from human and animal sources. <i>Veterinary Microbiology</i> , 2012, 158, 172-179.	1.9	54
13	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
14	Highly conjugative IncX4 plasmids carrying bla CTX-M in <i>Escherichia coli</i> from humans and food animals. <i>Journal of Medical Microbiology</i> , 2014, 63, 835-840.	1.8	44
15	Molecular Characterization of an Atypical IncX3 Plasmid pKPC-NY79 Carrying bla KPC-2 in a <i>Klebsiella pneumoniae</i> . <i>Current Microbiology</i> , 2013, 67, 493-498.	2.2	43
16	Predominance of pHK01-like incompatibility group FII plasmids encoding CTX-M-14 among extended-spectrum beta-lactamase-producing <i>Escherichia coli</i> in Hong Kong, 1996-2008. <i>Diagnostic Microbiology and Infectious Disease</i> , 2012, 73, 182-186.	1.8	40
17	Clinical outcome of extended-spectrum beta-lactamase-producing <i>Escherichia coli</i> bacteremia in an area with high endemicity. <i>International Journal of Infectious Diseases</i> , 2013, 17, e120-e124.	3.3	31
18	Genomics and epidemiological surveillance. <i>Nature Reviews Microbiology</i> , 2020, 18, 478-478.	28.6	31

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19	Plasmid-mediated fosfomycin resistance in <i>Escherichia coli</i> isolated from pig. <i>Veterinary Microbiology</i> , 2013, 162, 964-967.	1.9	30
20	pIMP-PH114 Carrying bla IMP-4 in a <i>Klebsiella pneumoniae</i> Strain is Closely Related to Other Multidrug-Resistant IncA/C2 Plasmids. <i>Current Microbiology</i> , 2014, 68, 227-232.	2.2	29
21	Complete sequencing of the FII plasmid pHK01, encoding CTX-M-14, and molecular analysis of its variants among <i>Escherichia coli</i> from Hong Kong. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 752-756.	3.0	28
22	Complete Sequence of an IncN Plasmid, pIMP-HZ1, Carrying <i>bla</i> _{IMP-4} in a <i>Klebsiella pneumoniae</i> Strain Associated with Medical Travel to China. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 1561-1562.	3.2	25
23	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
24	Prevalence and characterization of hybrid blaCTX-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
25	The role of interspecies recombination in the evolution of antibiotic-resistant pneumococci. <i>ELife</i> , 2021, 10, .	6.0	21
26	Clonal Diversity of <i>Escherichia coli</i> Isolates Carrying Plasmid-Mediated Fosfomycin Resistance GenefosA3 from Livestock and Other Animals. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 5638-5639.	3.2	20
27	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
28	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
29	Putative novel cps loci in a large global collection of pneumococci. <i>Microbial Genomics</i> , 2019, 5, .	2.0	14
30	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
31	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
32	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
33	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
34	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
35	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
36	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

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37	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
38	<i>Escherichia coli</i> 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
39	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
40	<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
41	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
42	Rare occurrence of vancomycin-resistant <i>Enterococcus faecium</i> among livestock animals in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 2948-2949.	3.0	6
43	Emergence of <i>Staphylococcus lugdunensis</i> Carrying, Multidrug-Resistant Plasmids in <i>Staphylococcus lugdunensis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6411-6414.	3.2	6
44	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
45	Emergence of <i>Klebsiella pneumoniae</i> ST258 with KPC-2 in Hong Kong. <i>International Journal of Antimicrobial Agents</i> , 2011, 37, 386-387.	2.5	5
46	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
47	RCandy: an R package for visualizing homologous recombinations in bacterial genomes. <i>Bioinformatics</i> , 2022, 38, 1450-1451.	4.1	5
48	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
49	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
50	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
51	Effect of applying the new Clinical and Laboratory Standards Institute ceftazidime and ceftriaxone susceptibility breakpoints for <i>Escherichia coli</i> in Hong Kong. <i>International Journal of Antimicrobial Agents</i> , 2011, 37, 270-271.	2.5	3
52	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
53	Comparative Genomics of Disease and Carriage Serotype 1 Pneumococci. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	3
54	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

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55	Genetic background of Cambodian pneumococcal carriage isolates following pneumococcal conjugate vaccine 13. <i>Microbial Genomics</i> , 2022, 8, .	2.0	0