

Swaine L Chen

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

2,932
citations

257357

24
h-index

189801

50
g-index

75
all docs

75
docs citations

75
times ranked

4465
citing authors

#	ARTICLE	IF	CITATIONS
1	Group B Streptococcus in retail food beyond ST283 and raw fish. Food Control, 2022, 133, 108625.	2.8	3
2	Transitional premonocytes emerge in the periphery for host defense against bacterial infections. Science Advances, 2022, 8, eabj4641.	4.7	9
3	Characterisation of Salmonella Enteritidis ST11 and ST1925 Associated with Human Intestinal and Extra-Intestinal Infections in Singapore. International Journal of Environmental Research and Public Health, 2022, 19, 5671.	1.2	5
4	Household transmission of carbapenemase-producing Enterobacteriaceae: a prospective cohort study. Journal of Antimicrobial Chemotherapy, 2021, 76, 1299-1302.	1.3	3
5	Active bacterial modification of the host environment through RNA polymerase II inhibition. Journal of Clinical Investigation, 2021, 131, .	3.9	7
6	Whole-Genome Sequencing Analysis of Salmonella Isolates from Poultry Farms, a Slaughterhouse, and Retail Stalls in Thailand. Microbiology Resource Announcements, 2021, 10, .	0.3	0
7	DNA methylation by three Type I restriction modification systems of Escherichia coli does not influence gene regulation of the host bacterium. Nucleic Acids Research, 2021, 49, 7375-7388.	6.5	2
8	Epidemiology and Transmission of Carbapenemase-Producing Enterobacteriaceae in a Health Care Network of an Acute-Care Hospital and Its Affiliated Intermediate- and Long-Term-Care Facilities in Singapore. Antimicrobial Agents and Chemotherapy, 2021, 65, e0258420.	1.4	7
9	GBS-SBG - GBS Serotyping by Genome Sequencing. Microbial Genomics, 2021, 7, .	1.0	9
10	A Faster and More Accurate Algorithm for Calculating Population Genetics Statistics Requiring Sums of Stirling Numbers of the First Kind. G3: Genes, Genomes, Genetics, 2020, 10, 3959-3967.	0.8	1
11	Sequencing of E. coli strain UTI89 on multiple sequencing platforms. BMC Research Notes, 2020, 13, 487.	0.6	3
12	Adaptation of Arginine Synthesis among Uropathogenic Branches of the Escherichia coli Phylogeny Reveals Adjustment to the Urinary Tract Habitat. MBio, 2020, 11, .	1.8	12
13	Mutations in enterobacterial common antigen biosynthesis restore outer membrane barrier function in <i>Escherichia coli</i> tol mutants. Molecular Microbiology, 2020, 114, 991-1005.	1.2	11
14	Metagenome-wide association analysis identifies microbial determinants of post-antibiotic ecological recovery in the gut. Nature Ecology and Evolution, 2020, 4, 1256-1267.	3.4	98
15	UTIGA: a new society for UTI professionals, researchers and patients. Nature Reviews Urology, 2020, 17, 309-310.	1.9	0
16	Genomic Insights Into the Distribution and Evolution of Group B Streptococcus. Frontiers in Microbiology, 2019, 10, 1447.	1.5	40
17	Comprehensive Identification of Fim-Mediated Inversions in Uropathogenic Escherichia coli with Structural Variation Detection Using Relative Entropy. MSphere, 2019, 4, .	1.3	1
18	One hypervirulent clone, sequence type 283, accounts for a large proportion of invasive Streptococcus agalactiae isolated from humans and diseased tilapia in Southeast Asia. PLoS Neglected Tropical Diseases, 2019, 13, e0007421.	1.3	51

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19	The higher prevalence of extended spectrum beta-lactamases among <i>Escherichia coli</i> ST131 in Southeast Asia is driven by expansion of a single, locally prevalent subclone. <i>Scientific Reports</i> , 2019, 9, 13245.	1.6	18
20	Isolation of Single Intracellular Bacterial Communities Generated from a Murine Model of Urinary Tract Infection for Downstream Single-cell Analysis. <i>Journal of Visualized Experiments</i> , 2019, , .	0.2	3
21	Implementation of a Stirling number estimator enables direct calculation of population genetics tests for large sequence datasets. <i>Bioinformatics</i> , 2019, 35, 2668-2670.	1.8	4
22	MRGPR-mediated activation of local mast cells clears cutaneous bacterial infection and protects against reinfection. <i>Science Advances</i> , 2019, 5, eaav0216.	4.7	78
23	Purification of Intracellular Bacterial Communities during Experimental Urinary Tract Infection Reveals an Abundant and Viable Bacterial Reservoir. <i>Infection and Immunity</i> , 2018, 86, .	1.0	12
24	Draft Genome Sequence of Singapore <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> Isolate DS32358_14, Which Contains the Carbapenemase Gene <i>bla</i> _{VIM-1} . <i>Genome Announcements</i> , 2018, 6, .	0.8	0
25	A Sub-population of Group A <i>Streptococcus</i> Elicits a Population-wide Production of Bacteriocins to Establish Dominance in the Host. <i>Cell Host and Microbe</i> , 2018, 23, 312-323.e6.	5.1	11
26	Putative Integrative Mobile Elements That Exploit the Xer Recombination Machinery Carrying <i>bla</i> _{IMI} -Type Carbapenemase Genes in <i>Enterobacter cloacae</i> Complex Isolates in Singapore. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	8
27	Complete Genome Sequence of <i>Photobacterium leiognathi</i> Strain JS01. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
28	Premenopausal women with recurrent urinary tract infections have lower quality of life. <i>International Journal of Urology</i> , 2018, 25, 684-689.	0.5	20
29	Long-read whole genome sequencing and comparative analysis of six strains of the human pathogen <i>Orientia tsutsugamushi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006566.	1.3	50
30	No association between resistance mutations, empiric antibiotic, and mortality in ceftriaxone-resistant <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> bacteremia. <i>Scientific Reports</i> , 2018, 8, 12785.	1.6	7
31	Complete Genome Sequence of the Uropathogenic <i>Escherichia coli</i> Strain NU14. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
32	2015 Epidemic of Severe <i>Streptococcus agalactiae</i> Sequence Type 283 Infections in Singapore Associated With the Consumption of Raw Freshwater Fish: A Detailed Analysis of Clinical, Epidemiological, and Bacterial Sequencing Data. <i>Clinical Infectious Diseases</i> , 2017, 64, S145-S152.	2.9	80
33	Complete Genome Sequence of <i>Streptococcus pyogenes</i> emm14 JS95, a Necrotizing Fasciitis Strain Isolated in Israel. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
34	Flow-aligned, single-shot fiber diffraction using a femtosecond X-ray free-electron laser. <i>Cytoskeleton</i> , 2017, 74, 472-481.	1.0	12
35	Virulence profile: Swaine L. Chen. <i>Virulence</i> , 2017, 8, 494-496.	1.8	0
36	Direct and convenient measurement of plasmid stability in lab and clinical isolates of <i>E. coli</i> . <i>Scientific Reports</i> , 2017, 7, 4788.	1.6	25

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37	Complete Genome Sequence of the Original Escherichia coli Isolate, Strain NCTC86. Genome Announcements, 2017, 5, .	0.8	7
38	Group B <i>Streptococcus</i> Infections Caused by Improper Sourcing and Handling of Fish for Raw Consumption, Singapore, 2015–2016. Emerging Infectious Diseases, 2017, 23, .	2.0	29
39	Brighter Fluorescent Derivatives of UTI89 Utilizing a Monomeric vGFP. Pathogens, 2016, 5, 3.	1.2	6
40	Application and Optimization of relE as a Negative Selection Marker for Making Definitive Genetic Constructs in Uropathogenic Escherichia coli. Pathogens, 2016, 5, 9.	1.2	2
41	Developmental transcriptome of resting cell formation in Mycobacterium smegmatis. BMC Genomics, 2016, 17, 837.	1.2	30
42	Fast and sensitive mapping of nanopore sequencing reads with GraphMap. Nature Communications, 2016, 7, 11307.	5.8	331
43	Comprehensive mutagenesis of the fimSPromoter regulatory switch reveals novel regulation of type 1 pili in uropathogenic Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4182-4187.	3.3	8
44	Point mutations in the major outer membrane protein drive hypervirulence of a rapidly expanding clone of <i>Campylobacter jejuni</i> . Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10690-10695.	3.3	56
45	Enterococcal Metabolite Cues Facilitate Interspecies Niche Modulation and Polymicrobial Infection. Cell Host and Microbe, 2016, 20, 493-503.	5.1	131
46	Rational Structure-Based Design of Bright GFP-Based Complexes with Tunable Dimerization. Angewandte Chemie - International Edition, 2015, 54, 13952-13956.	7.2	18
47	Complete Genome Sequence of Uropathogenic Escherichia coli Strain CI5. Genome Announcements, 2015, 3, .	0.8	5
48	A set of powerful negative selection systems for unmodified Enterobacteriaceae. Nucleic Acids Research, 2015, 43, e83-e83.	6.5	66
49	Complete Genome Sequence of Streptococcus agalactiae Serotype III, Multilocus Sequence Type 283 Strain SG-M1. Genome Announcements, 2015, 3, .	0.8	10
50	Human Urine Decreases Function and Expression of Type 1 Pili in Uropathogenic Escherichia coli. MBio, 2015, 6, e00820.	1.8	58
51	<i>Burkholderia pseudomallei</i> sequencing identifies genomic clades with distinct recombination, accessory, and epigenetic profiles. Genome Research, 2015, 25, 129-141.	2.4	61
52	Intracellular Uropathogenic E. coli Exploits Host Rab35 for Iron Acquisition and Survival within Urinary Bladder Cells. PLoS Pathogens, 2015, 11, e1005083.	2.1	44
53	Positively selected FimH residues enhance virulence during urinary tract infection by altering FimH conformation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15530-15537.	3.3	105
54	Genomic Diversity and Fitness of <i>E. coli</i> Strains Recovered from the Intestinal and Urinary Tracts of Women with Recurrent Urinary Tract Infection. Science Translational Medicine, 2013, 5, 184ra60.	5.8	148

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55	Population Dynamics and Niche Distribution of Uropathogenic <i>Escherichia coli</i> during Acute and Chronic Urinary Tract Infection. <i>Infection and Immunity</i> , 2011, 79, 4250-4259.	1.0	146
56	A central metabolic circuit controlled by QseC in pathogenic <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2011, 80, 1516-1529.	1.2	107
57	Positive selection identifies an in vivo role for FimH during urinary tract infection in addition to mannose binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 22439-22444.	3.3	165
58	Diabetes Mellitus and Urinary Tract Infection: Epidemiology, Pathogenesis and Proposed Studies in Animal Models. <i>Journal of Urology</i> , 2009, 182, S51-6.	0.2	80
59	<i>LeuX</i> tRNA-dependent and -independent mechanisms of <i>Escherichia coli</i> pathogenesis in acute cystitis. <i>Molecular Microbiology</i> , 2008, 67, 116-128.	1.2	67
60	Identification of genes subject to positive selection in uropathogenic strains of <i>Escherichia coli</i> : A comparative genomics approach. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 5977-5982.	3.3	509
61	A Chemical Method for Site-Specific Modification of RNA: The Convertible Nucleoside Approach. <i>Journal of the American Chemical Society</i> , 1997, 119, 7423-7433.	6.6	118
62	Invasive <i>Streptococcus agalactiae</i> ST283 infection after fish consumption in two sisters, Lao PDR. <i>Wellcome Open Research</i> , 0, 7, 148.	0.9	4