

Sima Tokajian

List of Publications by Year in descending order

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49

papers

1,127

citations

430874

18

h-index

454955

30

g-index

54

all docs

54

docs citations

54

times ranked

1878

citing authors

#	ARTICLE	IF	CITATIONS
1	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2 with grinch. Wellcome Open Research, 2021, 6, 121.	1.8	129
2	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2. Wellcome Open Research, 2021, 6, 121.	1.8	115
3	Origin and Evolution of European Community-Acquired Methicillin-Resistant Staphylococcus aureus. MBio, 2014, 5, e01044-14.	4.1	112
4	Molecular characterization of Staphylococcus aureus in Lebanon. Epidemiology and Infection, 2010, 138, 707-712.	2.1	49
5	Phylogenetic assessment of heterotrophic bacteria from a water distribution system using 16S rDNA sequencing. Canadian Journal of Microbiology, 2005, 51, 325-335.	1.7	48
6	Molecular Characterization of Carbapenem Resistant Klebsiella pneumoniae and Klebsiella quasipneumoniae isolated from Lebanon. Scientific Reports, 2019, 9, 531.	3.3	44
7	Molecular characterization of Carbapenem resistant Escherichia coli recovered from a tertiary hospital in Lebanon. PLoS ONE, 2018, 13, e0203323.	2.5	40
8	Extended-spectrum β -lactamase-producing <i>< i>Escherichia coli</i></i> in wastewaters and refugee camp in Lebanon. Future Microbiology, 2018, 13, 81-95.	2.0	36
9	New epidemiology of Staphylococcus aureus infections in the Middle East. Clinical Microbiology and Infection, 2014, 20, 624-628.	6.0	35
10	Molecular characteristics of Staphylococcus aureus isolated from a major hospital in Lebanon. International Journal of Infectious Diseases, 2014, 19, 33-38.	3.3	33
11	COVID-19 Pandemic in Lebanon: One Year Later, What Have We Learnt?. MSystems, 2021, 6, .	3.8	31
12	Antibiotic resistance patterns and sequencing of class I integron from uropathogenic Escherichia coli in Lebanon. Letters in Applied Microbiology, 2010, 51, 456-461.	2.2	28
13	Community-Associated Methicillin-Resistant Staphylococcus aureus Clonal Complex 80 Type IV (CC80-MRSA-IV) Isolated from the Middle East: A Heterogeneous Expanding Clonal Lineage. PLoS ONE, 2014, 9, e103715.	2.5	25
14	emm typing, antibiotic resistance and PFGE analysis of Streptococcus pyogenes in Lebanon. Journal of Medical Microbiology, 2011, 60, 98-101.	1.8	23
15	Genomic mapping of ST85 blaNDM-1 and blaOXA-94 producing Acinetobacter baumannii isolates from Syrian Civil War Victims. International Journal of Infectious Diseases, 2018, 74, 100-108.	3.3	23
16	First report of plasmid-mediated colistin resistance mcr-8.1 gene from a clinical Klebsiella pneumoniae isolate from Lebanon. Antimicrobial Resistance and Infection Control, 2020, 9, 94.	4.1	22
17	Methicillin-resistant Staphylococcus aureus ST80-IV clone in children from Jordan. Diagnostic Microbiology and Infectious Disease, 2012, 73, 228-230.	1.8	21
18	Molecular characterization of Streptococcus pyogenes group A isolates from a tertiary hospital in Lebanon. Journal of Medical Microbiology, 2014, 63, 1197-1204.	1.8	20

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19	Whole genome sequencing of extended-spectrum β -lactamase producing <i>Klebsiella pneumoniae</i> isolated from a patient in Lebanon. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 32.	3.9	20
20	Molecular typing of MRSA isolates by spa and PFGE. <i>Journal of King Saud University - Science</i> , 2019, 31, 999-1004.	3.5	20
21	Genome Analysis of <i>Streptococcus pyogenes</i> Associated with Pharyngitis and Skin Infections. <i>PLoS ONE</i> , 2016, 11, e0168177.	2.5	20
22	Genome sequencing and comparative analysis of an NDM-1-producing <i>Klebsiella pneumoniae</i> ST15 isolated from a refugee patient. <i>Pathogens and Global Health</i> , 2017, 111, 166-175.	2.3	18
23	First report of an <i>Escherichia coli</i> from Lebanon carrying an OXA-181 carbapenemase resistance determinant. <i>Journal of Global Antimicrobial Resistance</i> , 2018, 12, 113-114.	2.2	16
24	Tridecaptin-inspired antimicrobial peptides with activity against multidrug-resistant Gram-negative bacteria. <i>MedChemComm</i> , 2019, 10, 484-487.	3.4	15
25	Expanded genome-wide comparisons give novel insights into population structure and genetic heterogeneity of <i>Leishmania tropica</i> complex. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008684.	3.0	14
26	16S–23S rRNA Gene Intergenic Spacer Region Variability Helps Resolve Closely Related Sphingomonads. <i>Frontiers in Microbiology</i> , 2016, 7, 149.	3.5	13
27	Genome Mining and Comparative Analysis of <i>Streptococcus intermedius</i> Causing Brain Abscess in a Child. <i>Pathogens</i> , 2019, 8, 22.	2.8	13
28	Genotypic and phenotypic characterization of <i>Candida albicans</i> Lebanese hospital isolates resistant and sensitive to caspofungin. <i>Fungal Genetics and Biology</i> , 2019, 127, 12-22.	2.1	12
29	Typing and comparative genome analysis of <i>Brucella melitensis</i> isolated from Lebanon. <i>FEMS Microbiology Letters</i> , 2017, 364, .	1.8	11
30	Genomic attributes of extended-spectrum β -lactamase-producing <i>Escherichia coli</i> isolated from patients in Lebanon. <i>Future Microbiology</i> , 2017, 12, 213-226.	2.0	10
31	Genomic Characterization of MDR <i>Escherichia coli</i> Harboring <i>blaOXA-48</i> on the IncL/M-type Plasmid Isolated from Blood Stream Infection. <i>BioMed Research International</i> , 2018, 2018, 1-8.	1.9	9
32	Detection and genomic characterization of mcr-9 in <i>Enterobacter hormaechei</i> recovered from a pediatric patient in Lebanon. <i>Infection, Genetics and Evolution</i> , 2021, 94, 105014.	2.3	9
33	Draft Genome Sequences of <i>Acinetobacter baumannii</i> Strains Harboring the <i>blaNDM-1</i> Gene Isolated in Lebanon from Civilians Wounded during the Syrian Civil War. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
34	First insights on the genetic diversity of MDR <i>Mycobacterium tuberculosis</i> in Lebanon. <i>BMC Infectious Diseases</i> , 2018, 18, 710.	2.9	7
35	Genomic Features of <i>Vibrio parahaemolyticus</i> from Lebanon and Comparison to Globally Diverse Strains by Whole-Genome Sequencing. <i>Foodborne Pathogens and Disease</i> , 2019, 16, 778-787.	1.8	7
36	Detailed characterization of an IncFII plasmid carrying <i>blaOXA-48</i> from Lebanon. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2462-2465.	3.0	7

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37	Molecular mechanism of fluconazole resistance and pathogenicity attributes of Lebanese <i>Candida albicans</i> hospital isolates. <i>Fungal Genetics and Biology</i> , 2021, 153, 103575.	2.1	7
38	Use of the 16Sâ€“23S ribosomal genes spacer region for the molecular typing of sphingomonads. <i>Canadian Journal of Microbiology</i> , 2008, 54, 668-676.	1.7	5
39	Draft Genome Sequences of <i>Streptococcus pyogenes</i> Strains Associated with Throat and Skin Infections in Lebanon. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
40	The dissemination of antimicrobial resistance determinants in surface water sources in Lebanon. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	5
41	Molecular characterization of a carbapenem-resistant <i>Enterobacter hormaechei</i> ssp. <i>xiangfangensis</i> co-harbouring blaNDM-1 and a chromosomally encoded phage-linked blaCTX-M-15 genes. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104924.	2.3	5
42	Incidence of Antibiotic Resistance in Coliforms from Drinking Water and Their Identification Using the Biolog and the API Identification Systems. <i>Journal of Chemotherapy</i> , 2004, 16, 45-50.	1.5	4
43	Antimicrobial Resistance in Relation to Virulence Determinants and Phylogenetic Background Among Uropathogenic <i>Escherichia coli</i> in Lebanon. <i>Journal of Chemotherapy</i> , 2009, 21, 153-158.	1.5	4
44	Draft Genome Sequence of <i>Klebsiella pneumoniae</i> KGM-IMP216 Harboring <i>bla</i> CTX-M-15, <i>bla</i> DHA-1, <i>bla</i> TEM-1B, <i>bla</i> NDM-1, <i>bla</i> SHV-28, and <i>bla</i> OXA-1, isolated from a Patient in Lebanon. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
45	Insights into the genome diversity and virulence of two clinical isolates of <i>Burkholderia cenocepacia</i> . <i>Journal of Medical Microbiology</i> , 2018, 67, 1157-1167.	1.8	4
46	Integration of two pKPx-2-derived antibiotic resistance islands in the genome of an ESBL-producing <i>Klebsiella pneumoniae</i> ST3483 from Lebanon. <i>Journal of Global Antimicrobial Resistance</i> , 2019, 18, 257-259.	2.2	3
47	Genome analysis of a MDR <i>Streptococcus pneumoniae</i> 23F serotype causing meningoencephalitis in a 10-months refugee infant. <i>Journal of Infection in Developing Countries</i> , 2018, 12, 196-203.	1.2	3
48	Molecular epidemiology of nonpharyngeal group A streptococci isolates in northern Lebanon. <i>Future Microbiology</i> , 2020, 15, 1555-1569.	2.0	2
49	Reconstruction of Metagenome-Assembled Genomes from Aquaria. <i>Microbiology Resource Announcements</i> , 2021, 10, e0055721.	0.6	1