

# 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	COVID-19 Pandemic in Lebanon: One Year Later, What Have We Learnt?. <i>MSystems</i> , 2021, 6, .	3.8	31
2	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2. <i>Wellcome Open Research</i> , 2021, 6, 121.	1.8	115
3	The dissemination of antimicrobial resistance determinants in surface water sources in Lebanon. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	5
4	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
5	Reconstruction of Metagenome-Assembled Genomes from Aquaria. <i>Microbiology Resource Announcements</i> , 2021, 10, e0055721.	0.6	1
6	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
7	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2 with grinch. <i>Wellcome Open Research</i> , 2021, 6, 121.	1.8	129
8	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
9	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
10	Detailed characterization of an IncFII plasmid carrying blaOXA-48 from Lebanon. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2462-2465.	3.0	7
11	First report of plasmid-mediated colistin resistance mcr-8.1 gene from a clinical <i>Klebsiella pneumoniae</i> isolate from Lebanon. <i>Antimicrobial Resistance and Infection Control</i> , 2020, 9, 94.	4.1	22
12	Molecular epidemiology of nonpharyngeal group A streptococci isolates in northern Lebanon. <i>Future Microbiology</i> , 2020, 15, 1555-1569.	2.0	2
13	Molecular typing of MRSA isolates by spa and PFGE. <i>Journal of King Saud University - Science</i> , 2019, 31, 999-1004.	3.5	20
14	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
15	Molecular Characterization of Carbapenem Resistant <i>Klebsiella pneumoniae</i> and <i>Klebsiella quasipneumoniae</i> Isolated from Lebanon. <i>Scientific Reports</i> , 2019, 9, 531.	3.3	44
16	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
17	Tridecaptin-inspired antimicrobial peptides with activity against multidrug-resistant Gram-negative bacteria. <i>MedChemComm</i> , 2019, 10, 484-487.	3.4	15
18	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

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19	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
20	Extended-spectrum $\beta$ -lactamase-producing <i>&lt; i&gt;Escherichia coli&lt;/i&gt;</i> in wastewaters and refugee camp in Lebanon. <i>Future Microbiology</i> , 2018, 13, 81-95.	2.0	36
21	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
22	Molecular characterization of Carbapenem resistant <i>Escherichia coli</i> recovered from a tertiary hospital in Lebanon. <i>PLoS ONE</i> , 2018, 13, e0203323.	2.5	40
23	Genomic Characterization of MDR <i>&lt; i&gt;Escherichia coli&lt;/i&gt;</i> Harboring <i>&lt; i&gt;bla&lt;/i&gt;&lt;sub&gt;OXA-48&lt;/sub&gt;</i> on the Incl/M-type Plasmid Isolated from Blood Stream Infection. <i>BioMed Research International</i> , 2018, 2018, 1-8.	1.9	9
24	Genomic mapping of ST85 <i>blaNDM-1</i> and <i>blaOXA-94</i> producing <i>Acinetobacter baumannii</i> isolates from Syrian Civil War Victims. <i>International Journal of Infectious Diseases</i> , 2018, 74, 100-108.	3.3	23
25	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
26	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
27	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
28	Genomic attributes of extended-spectrum $\beta$ -lactamase-producing <i>Escherichia coli</i> isolated from patients in Lebanon. <i>Future Microbiology</i> , 2017, 12, 213-226.	2.0	10
29	Genome sequencing and comparative analysis of an NDM-1-producing <i>&lt; i&gt;Klebsiella pneumoniae&lt;/i&gt;</i> ST15 isolated from a refugee patient. <i>Pathogens and Global Health</i> , 2017, 111, 166-175.	2.3	18
30	Typing and comparative genome analysis of <i>Brucella melitensis</i> isolated from Lebanon. <i>FEMS Microbiology Letters</i> , 2017, 364, .	1.8	11
31	16S–23S rRNA Gene Intergenic Spacer Region Variability Helps Resolve Closely Related Sphingomonads. <i>Frontiers in Microbiology</i> , 2016, 7, 149.	3.5	13
32	Draft Genome Sequences of <i>Acinetobacter baumannii</i> Strains Harboring the <i>&lt; i&gt;bla&lt;/i&gt;&lt;sub&gt;NDM-1&lt;/sub&gt;</i> Gene Isolated in Lebanon from Civilians Wounded during the Syrian Civil War. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
33	Draft Genome Sequence of <i>Klebsiella pneumoniae</i> KGM-IMP216 Harboring <i>&lt; i&gt;bla&lt;/i&gt;&lt;sub&gt;CTX-M-15&lt;/sub&gt;</i> , <i>&lt; i&gt;bla&lt;/i&gt;&lt;sub&gt;DHA-1&lt;/sub&gt;</i> , <i>&lt; i&gt;bla&lt;/i&gt;&lt;sub&gt;TEM-1B&lt;/sub&gt;</i> , <i>&lt; i&gt;bla&lt;/i&gt;&lt;sub&gt;NDM-1&lt;/sub&gt;</i> , <i>&lt; i&gt;bla&lt;/i&gt;&lt;sub&gt;SHV-28&lt;/sub&gt;</i> , and <i>&lt; i&gt;bla&lt;/i&gt;&lt;sub&gt;OXA-1&lt;/sub&gt;</i> , Isolated from a Patient in Lebanon. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
34	Genome Analysis of <i>Streptococcus pyogenes</i> Associated with Pharyngitis and Skin Infections. <i>PLoS ONE</i> , 2016, 11, e0168177.	2.5	20
35	Whole genome sequencing of extended-spectrum $\beta$ -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
36	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

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37	New epidemiology of <i>Staphylococcus aureus</i> infections in the Middle East. <i>Clinical Microbiology and Infection</i> , 2014, 20, 624-628.	6.0	35
38	Origin and Evolution of European Community-Acquired Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2014, 5, e01044-14.	4.1	112
39	Molecular characterization of <i>Streptococcus pyogenes</i> group A isolates from a tertiary hospital in Lebanon. <i>Journal of Medical Microbiology</i> , 2014, 63, 1197-1204.	1.8	20
40	Molecular characteristics of <i>Staphylococcus aureus</i> isolated from a major hospital in Lebanon. <i>International Journal of Infectious Diseases</i> , 2014, 19, 33-38.	3.3	33
41	Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Clonal Complex 80 Type IV (CC80-MRSA-IV) Isolated from the Middle East: A Heterogeneous Expanding Clonal Lineage. <i>PLoS ONE</i> , 2014, 9, e103715.	2.5	25
42	Methicillin-resistant <i>Staphylococcus aureus</i> ST80-IV clone in children from Jordan. <i>Diagnostic Microbiology and Infectious Disease</i> , 2012, 73, 228-230.	1.8	21
43	emm typing, antibiotic resistance and PFGE analysis of <i>Streptococcus pyogenes</i> in Lebanon. <i>Journal of Medical Microbiology</i> , 2011, 60, 98-101.	1.8	23
44	Molecular characterization of <i>Staphylococcus aureus</i> in Lebanon. <i>Epidemiology and Infection</i> , 2010, 138, 707-712.	2.1	49
45	Antibiotic resistance patterns and sequencing of class I integron from uropathogenic <i>Escherichia coli</i> in Lebanon. <i>Letters in Applied Microbiology</i> , 2010, 51, 456-461.	2.2	28
46	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
47	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
48	Phylogenetic assessment of heterotrophic bacteria from a water distribution system using 16S rDNA sequencing. <i>Canadian Journal of Microbiology</i> , 2005, 51, 325-335.	1.7	48
49	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