

Nouri L Ben Zakour

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

6,146
citations

172207

29
h-index

205818

48
g-index

61
all docs

61
docs citations

61
times ranked

8252
citing authors

#	ARTICLE	IF	CITATIONS
1	BLAST Ring Image Generator (BRIG): simple prokaryote genome comparisons. BMC Genomics, 2011, 12, 402.	1.2	2,691
2	Global dissemination of a multidrug resistant <i>Escherichia coli</i> clone. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5694-5699.	3.3	498
3	Recent human-to-poultry host jump, adaptation, and pandemic spread of <i>Staphylococcus aureus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19545-19550.	3.3	363
4	Safety of bacteriophage therapy in severe <i>Staphylococcus aureus</i> infection. Nature Microbiology, 2020, 5, 465-472.	5.9	258
5	Population Genetic Structure of the <i>Staphylococcus intermedius</i> Group: Insights into <i>agr</i> Diversification and the Emergence of Methicillin-Resistant Strains. Journal of Bacteriology, 2007, 189, 8685-8692.	1.0	241
6	Evolutionary Genomics of <i>Staphylococcus aureus</i> Reveals Insights into the Origin and Molecular Basis of Ruminant Host Adaptation. Genome Biology and Evolution, 2010, 2, 454-466.	1.1	174
7	Sequential Acquisition of Virulence and Fluoroquinolone Resistance Has Shaped the Evolution of <i>Escherichia coli</i> ST131. MBio, 2016, 7, e00347-16.	1.8	164
8	Emergence of scarlet fever <i>Streptococcus pyogenes</i> emm12 clones in Hong Kong is associated with toxin acquisition and multidrug resistance. Nature Genetics, 2015, 47, 84-87.	9.4	135
9	The Complete Genome Sequence of <i>Escherichia coli</i> EC958: A High Quality Reference Sequence for the Globally Disseminated Multidrug Resistant <i>E. coli</i> O25b:H4-ST131 Clone. PLoS ONE, 2014, 9, e104400.	1.1	116
10	Bacteriophage Therapy of Ventilator-associated Pneumonia and Empyema Caused by <i>Pseudomonas aeruginosa</i> . American Journal of Respiratory and Critical Care Medicine, 2019, 200, 1179-1181.	2.5	86
11	Low occurrence of safety hazards in coagulase negative staphylococci isolated from fermented foodstuffs. International Journal of Food Microbiology, 2010, 139, 87-95.	2.1	79
12	Tandem repeat sequence analysis of staphylococcal protein A (<i>spa</i>) gene in methicillin-resistant <i>Staphylococcus pseudintermedius</i> . Veterinary Microbiology, 2009, 135, 320-326.	0.8	77
13	Development of a PCR Test To Differentiate between <i>Staphylococcus aureus</i> and <i>Staphylococcus intermedius</i> . Journal of Food Protection, 2004, 67, 2302-2305.	0.8	76
14	Complete Genome Sequence of the Canine Pathogen <i>Staphylococcus pseudintermedius</i> . Journal of Bacteriology, 2011, 193, 2363-2364.	1.0	72
15	Genomic and Surface Proteomic Analysis of the Canine Pathogen <i>Staphylococcus pseudintermedius</i> Reveals Proteins That Mediate Adherence to the Extracellular Matrix. Infection and Immunity, 2011, 79, 3074-3086.	1.0	63
16	<i>Staphylococcus aureus</i> Virulence Expression Is Impaired by <i>Lactococcus lactis</i> in Mixed Cultures. Applied and Environmental Microbiology, 2009, 75, 4459-4472.	1.4	59
17	Genome-Wide Analysis of Ruminant <i>Staphylococcus aureus</i> Reveals Diversification of the Core Genome. Journal of Bacteriology, 2008, 190, 6302-6317.	1.0	57
18	Transfer of scarlet fever-associated elements into the group A <i>Streptococcus</i> M1T1 clone. Scientific Reports, 2015, 5, 15877.	1.6	57

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19	Whole genome analysis of cephalosporin-resistant <i>Escherichia coli</i> from bloodstream infections in Australia, New Zealand and Singapore: high prevalence of CMY-2 producers and ST131 carrying blaCTX-M-15 and blaCTX-M-27. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 634-642.	1.3	56
20	Host adaptation and convergent evolution increases antibiotic resistance without loss of virulence in a major human pathogen. <i>PLoS Pathogens</i> , 2019, 15, e1007218.	2.1	56
21	Analysis of a <i>Streptococcus pyogenes</i> Puerperal Sepsis Cluster by Use of Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2012, 50, 2224-2228.	1.8	55
22	Hospital-wide Eradication of a Nosocomial <i>Legionella pneumophila</i> Serogroup 1 Outbreak. <i>Clinical Infectious Diseases</i> , 2016, 62, 273-279.	2.9	49
23	Tracing the evolutionary history of the pandemic group A streptococcal M1T1 clone. <i>FASEB Journal</i> , 2012, 26, 4675-4684.	0.2	48
24	Molecular Characterization of a Multidrug Resistance IncF Plasmid from the Globally Disseminated <i>Escherichia coli</i> ST131 Clone. <i>PLoS ONE</i> , 2015, 10, e0122369.	1.1	48
25	Pathogenomics of the staphylococci: insights into niche adaptation and the emergence of new virulent strains. <i>FEMS Microbiology Letters</i> , 2008, 289, 1-12.	0.7	45
26	Comparative Genomics of the <i>Staphylococcus intermedius</i> Group of Animal Pathogens. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 44.	1.8	45
27	Molecular Characterization of the Multidrug Resistant <i>Escherichia coli</i> ST131 Clone. <i>Pathogens</i> , 2015, 4, 422-430.	1.2	39
28	Phage therapy for severe bacterial infections: a narrative review. <i>Medical Journal of Australia</i> , 2020, 212, 279-285.	0.8	37
29	Integrating multiple genomic technologies to investigate an outbreak of carbapenemase-producing <i>Enterobacter hormaechei</i> . <i>Nature Communications</i> , 2020, 11, 466.	5.8	34
30	Microevolution of <i>Streptococcus agalactiae</i> ST-261 from Australia Indicates Dissemination via Imported Tilapia and Ongoing Adaptation to Marine Hosts or Environment. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	33
31	Within-host whole genome analysis of an antibiotic resistant <i>Pseudomonas aeruginosa</i> strain sub-type in cystic fibrosis. <i>PLoS ONE</i> , 2017, 12, e0172179.	1.1	31
32	Mutual Exclusivity of Hyaluronan and Hyaluronidase in Invasive Group A <i>Streptococcus</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 32303-32315.	1.6	30
33	Genome analysis and CRISPR typing of <i>Salmonella enterica</i> serovar Virchow. <i>BMC Genomics</i> , 2014, 15, 389.	1.2	25
34	GenoFrag: software to design primers optimized for whole genome scanning by long-range PCR amplification. <i>Nucleic Acids Research</i> , 2004, 32, 17-24.	6.5	24
35	Molecular Analysis of Asymptomatic Bacteriuria <i>Escherichia coli</i> Strain VR50 Reveals Adaptation to the Urinary Tract by Gene Acquisition. <i>Infection and Immunity</i> , 2015, 83, 1749-1764.	1.0	24
36	Discovery and Characterization of Human-Urine Utilization by Asymptomatic-Bacteriuria-Causing <i>Streptococcus agalactiae</i> . <i>Infection and Immunity</i> , 2016, 84, 307-319.	1.0	24

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37	Characterisation of a cell wall-anchored protein of <i>Staphylococcus saprophyticus</i> associated with linoleic acid resistance. <i>BMC Microbiology</i> , 2012, 12, 8.	1.3	19
38	Acquisition of the Sda1-Encoding Bacteriophage Does Not Enhance Virulence of the Serotype M1 <i>Streptococcus pyogenes</i> Strain SF370. <i>Infection and Immunity</i> , 2013, 81, 2062-2069.	1.0	19
39	Streptococcal collagen-like protein A and general stress protein 24 are immunomodulating virulence factors of group A <i>Streptococcus</i> . <i>FASEB Journal</i> , 2013, 27, 2633-2643.	0.2	18
40	Fine capsule variation affects bacteriophage susceptibility in <i>Klebsiella pneumoniae</i> ST258. <i>FASEB Journal</i> , 2020, 34, 10801-10817.	0.2	17
41	Whole genome sequencing reveals the emergence of a <i>Pseudomonas aeruginosa</i> shared strain sub-lineage among patients treated within a single cystic fibrosis centre. <i>BMC Genomics</i> , 2018, 19, 644.	1.2	16
42	Complete Genome Sequence of Serotype III <i>Streptococcus agalactiae</i> Sequence Type 17 Strain 874391. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
43	Polyclonal <i>Staphylococcus aureus</i> Bacteremia. <i>Annals of Internal Medicine</i> , 2019, 171, 940.	2.0	8
44	Testing of a whole genome PCR scanning approach to identify genomic variability in four different species of lactic acid bacteria. <i>Research in Microbiology</i> , 2006, 157, 386-394.	1.0	3
45	Co-Occurrence of Multidrug Resistant <i>Klebsiella pneumoniae</i> Pathogenic Clones of Human Relevance in an Equine Pneumonia Case. <i>Microbiology Spectrum</i> , 2022, , e0215821.	1.2	3
46	Designing Primers for Whole Genome PCR Scanning Using the Software Package GenoFrag. <i>Methods in Molecular Biology</i> , 2007, 402, 348-368.	0.4	1
47	A high-quality reference genome for the fish pathogen <i>Streptococcus iniae</i> . <i>Microbial Genomics</i> , 2022, 8, .	1.0	0