

Louise Cerdeira

List of Publications by Year in descending order

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112
papers

2,074
citations

304368

22
h-index

329751

37
g-index

120
all docs

120
docs citations

120
times ranked

2708
citing authors

#	ARTICLE	IF	CITATIONS
1	Chicken Meat as a Reservoir of Colistin-Resistant <i>Escherichia coli</i> Strains Carrying <i>mcr-1</i> Genes in South America. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	115
2	The Genome of <i>Anopheles darlingi</i> , the main neotropical malaria vector. <i>Nucleic Acids Research</i> , 2013, 41, 7387-7400.	6.5	102
3	Colistin-Resistant <i>mcr-1</i> -Positive <i>Escherichia coli</i> on Public Beaches, an Infectious Threat Emerging in Recreational Waters. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	77
4	Evidence for Reductive Genome Evolution and Lateral Acquisition of Virulence Functions in Two <i>Corynebacterium pseudotuberculosis</i> Strains. <i>PLoS ONE</i> , 2011, 6, e18551.	1.1	75
5	PIPS: Pathogenicity Island Prediction Software. <i>PLoS ONE</i> , 2012, 7, e30848.	1.1	70
6	Characterization of Tn 3000, a Transposon Responsible for <i>bla</i> NDM-1 Dissemination among Enterobacteriaceae in Brazil, Nepal, Morocco, and India. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7387-7395.	1.4	70
7	Global population structure and genotyping framework for genomic surveillance of the major dysentery pathogen, <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2021, 12, 2684.	5.8	65
8	Genomic Features of High-Priority <i>Salmonella enterica</i> Serovars Circulating in the Food Production Chain, Brazil, 2000–2016. <i>Scientific Reports</i> , 2019, 9, 11058.	1.6	61
9	International high-risk clones of <i>Klebsiella pneumoniae</i> KPC-2/CC258 and <i>Escherichia coli</i> CTX-M-15/CC10 in urban lake waters. <i>Science of the Total Environment</i> , 2017, 598, 910-915.	3.9	55
10	Zooanthroponotic Transmission of Drug-Resistant <i>Pseudomonas aeruginosa</i> , Brazil. <i>Emerging Infectious Diseases</i> , 2018, 24, 1160-1162.	2.0	49
11	Wild owls colonized by international clones of extended-spectrum β -lactamase (CTX-M)-producing <i>Escherichia coli</i> and <i>Salmonella</i> <i>Infantis</i> in the Southern Cone of America. <i>Science of the Total Environment</i> , 2019, 674, 554-562.	3.9	49
12	Coexistence of CTX-M-2, CTX-M-55, CMY-2, FosA3, and QnrB19 in Extraintestinal Pathogenic <i>Escherichia coli</i> from Poultry in Brazil. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	48
13	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> I19, a Strain Isolated from a Cow in Israel with Bovine Mastitis. <i>Journal of Bacteriology</i> , 2011, 193, 323-324.	1.0	45
14	Rapid hybrid de novo assembly of a microbial genome using only short reads: <i>Corynebacterium pseudotuberculosis</i> I19 as a case study. <i>Journal of Microbiological Methods</i> , 2011, 86, 218-223.	0.7	40
15	Co-occurrence of clinically relevant β -lactamases and MCR-1 encoding genes in <i>Escherichia coli</i> from companion animals in Argentina. <i>Veterinary Microbiology</i> , 2019, 230, 228-234.	0.8	39
16	WHO Critical Priority <i>Escherichia coli</i> as One Health Challenge for a Post-Pandemic Scenario: Genomic Surveillance and Analysis of Current Trends in Brazil. <i>Microbiology Spectrum</i> , 2022, 10, e0125621.	1.2	31
17	First Characterization of CTX-M-15-Producing <i>Escherichia coli</i> Strains Belonging to Sequence Type (ST) 410, ST224, and ST1284 from Commercial Swine in South America. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 2505-2508.	1.4	30
18	Genome analysis reveals insights of the endophytic <i>Bacillus toyonensis</i> BAC3151 as a potentially novel agent for biocontrol of plant pathogens. <i>World Journal of Microbiology and Biotechnology</i> , 2017, 33, 185.	1.7	30

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19	Evolutionary dynamics of carbapenem-resistant <i>Acinetobacter baumannii</i> circulating in Chilean hospitals. <i>Infection, Genetics and Evolution</i> , 2019, 73, 93-97.	1.0	29
20	Genomic data reveal international lineages of critical priority <i>Escherichia coli</i> harbouring wide resistome in Andean condors (<i>Vultur gryphus</i> Linnaeus, 1758). <i>Molecular Ecology</i> , 2020, 29, 1919-1935.	2.0	29
21	Small IncQ1 and Col-Like Plasmids Harboring <i>bla</i> _{KPC-2} and Non-Tn 4401 Elements (NTE <i>bla</i> _{KPC} -IId) in High-Risk Lineages of <i>Klebsiella pneumoniae</i> CG258. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	27
22	Hypervirulence and biofilm production in KPC-2-producing <i>Klebsiella pneumoniae</i> CG258 isolated in Brazil. <i>Journal of Medical Microbiology</i> , 2018, 67, 523-528.	0.7	27
23	De novo assembly and functional annotation of <i>Myrciaria dubia</i> fruit transcriptome reveals multiple metabolic pathways for L-ascorbic acid biosynthesis. <i>BMC Genomics</i> , 2015, 16, 997.	1.2	25
24	International high-risk clonal lineages of CTX-M-producing <i>Escherichia coli</i> F-ST648 in free-roaming cats, South America. <i>Infection, Genetics and Evolution</i> , 2018, 66, 48-51.	1.0	25
25	IncX3 plasmid harboring a non-Tn 4401 genetic element (NTE KPC) in a hospital-associated clone of KPC-2-producing <i>Klebsiella pneumoniae</i> ST340/CG258. <i>Diagnostic Microbiology and Infectious Disease</i> , 2017, 89, 164-167.	0.8	24
26	Whole genome sequencing of environmental <i>Vibrio cholerae</i> O1 from 10 nanograms of DNA using short reads. <i>Journal of Microbiological Methods</i> , 2011, 87, 208-212.	0.7	23
27	Draft genome sequence of <i>Enterobacter cloacae</i> ST520 harbouring <i>bla</i> _{KPC-2} , <i>bla</i> _{CTX-M-15} and <i>bla</i> _{OXA-17} isolated from coastal waters of the South Atlantic Ocean. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 10, 279-280.	0.9	23
28	Molecular characterization and clonal dynamics of nosocomial <i>bla</i> _{OXA-23} producing XDR <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , 2018, 13, e0198643.	1.1	23
29	Endophytic Lifestyle of Global Clones of Extended-Spectrum β -Lactamase-Producing Priority Pathogens in Fresh Vegetables: a Trojan Horse Strategy Favoring Human Colonization?. <i>MSystems</i> , 2021, 6, .	1.7	23
30	Complete Nucleotide Sequences of Two <i>bla</i> _{KPC-2} -Bearing IncN Plasmids Isolated from Sequence Type 442 <i>Klebsiella pneumoniae</i> Clinical Strains Four Years Apart. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 2958-2960.	1.4	22
31	Multidrug- and colistin-resistant <i>Salmonella enterica</i> 4,[5],12:i:- sequence type 34 carrying the <i>mcr-3.1</i> gene on the IncHI2 plasmid recovered from a human. <i>Journal of Medical Microbiology</i> , 2019, 68, 986-990.	0.7	20
32	Whole-Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> PAT10 Strain Isolated from Sheep in Patagonia, Argentina. <i>Journal of Bacteriology</i> , 2011, 193, 6420-6421.	1.0	19
33	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain CIP 52.97, Isolated from a Horse in Kenya. <i>Journal of Bacteriology</i> , 2011, 193, 7025-7026.	1.0	18
34	Identification of KPC-2-producing <i>Escherichia coli</i> in a companion animal: a new challenge for veterinary clinicians. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 2259-2261.	1.3	18
35	Multidrug-resistant CTX-M-15-positive <i>Klebsiella pneumoniae</i> ST307 causing urinary tract infection in a dog in Brazil. <i>Journal of Global Antimicrobial Resistance</i> , 2019, 19, 96-97.	0.9	18
36	Detection of IncN ϵ pST15 one-health plasmid harbouring <i>bla</i> _{KPC-2} in a hypermucoviscous <i>Klebsiella pneumoniae</i> CG258 isolated from an infected dog, Brazil. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 3083-3088.	1.3	17

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37	Complete Genome Sequence of Type Strain <i>Campylobacter fetus</i> subsp. <i>venerealis</i> NCTC 10354T. <i>Journal of Bacteriology</i> , 2011, 193, 5871-5872.	1.0	16
38	High-virulence CMY-2- and CTX-M-2-producing avian pathogenic <i>Escherichia coli</i> strains isolated from commercial turkeys. <i>Diagnostic Microbiology and Infectious Disease</i> , 2017, 87, 64-67.	0.8	16
39	Genome sequence analysis of a hypermucoviscous/hypervirulent and MDR CTX-M-15/K19/ST29 <i>Klebsiella pneumoniae</i> isolated from human infection. <i>Pathogens and Disease</i> , 2017, 75, .	0.8	16
40	Multidrug-resistant CTX-M-15-producing <i>Klebsiella pneumoniae</i> ST231 associated with infection and persistent colonization of dog. <i>Diagnostic Microbiology and Infectious Disease</i> , 2018, 92, 259-261.	0.8	16
41	Emergence of CTX-M-27-producing <i>Escherichia coli</i> of ST131 and clade C1-M27 in an impacted ecosystem with international maritime traffic in South America. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1647-1649.	1.3	16
42	Draft genome sequences of two fluoroquinolone-resistant CTX-M-15-producing <i>Escherichia coli</i> ST90 (ST23 complex) isolated from a calf and a dairy cow in South America. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 11, 145-147.	0.9	15
43	Novel mcr-5.3 variant in a CTX-M-8-producing <i>Escherichia coli</i> ST711 isolated from an infected horse. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 3520-3522.	1.3	15
44	Multidrug-resistant <i>Klebsiella pneumoniae</i> : a retrospective study in Manaus, Brazil. <i>Archives of Microbiology</i> , 2022, 204, 202.	1.0	15
45	Complete Genome Sequences of <i>Corynebacterium pseudotuberculosis</i> Strains 3/99-5 and 42/02-A, Isolated from Sheep in Scotland and Australia, Respectively. <i>Journal of Bacteriology</i> , 2012, 194, 4736-4737.	1.0	14
46	Changed epidemiology during intra and interhospital spread of high-risk clones of <i>vanA</i> -containing <i>Enterococcus</i> in Brazilian hospitals. <i>Diagnostic Microbiology and Infectious Disease</i> , 2017, 88, 348-351.	0.8	14
47	Draft genome sequence of a <i>bla</i> CMY-2/ <i>Inc11</i> -harbouring <i>Escherichia coli</i> D:ST457 isolated from coastal benthic organisms. <i>Journal of Global Antimicrobial Resistance</i> , 2018, 14, 83-84.	0.9	14
48	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain 1/06-A, Isolated from a Horse in North America. <i>Journal of Bacteriology</i> , 2012, 194, 4476-4476.	1.0	13
49	Complete Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Cp31, Isolated from an Egyptian Buffalo. <i>Journal of Bacteriology</i> , 2012, 194, 6663-6664.	1.0	13
50	Draft genome sequence of a CTX-M-15-producing <i>Escherichia coli</i> ST345 from commercial chicken meat in Brazil. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 9, 124-125.	0.9	13
51	Draft genome sequence of a multidrug-resistant <i>Aeromonas hydrophila</i> ST508 strain carrying <i>rmtD</i> and <i>bla</i> CTX-M-131 isolated from a bloodstream infection. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 10, 289-290.	0.9	13
52	A Novel Multifunctional Î ² -N-Acetylhexosaminidase Revealed through Metagenomics of an Oil-Spilled Mangrove. <i>Bioengineering</i> , 2017, 4, 62.	1.6	13
53	Complete DNA Sequence of an <i>IncM1</i> Plasmid Bearing the Novel <i>qnrE1</i> Plasmid-Mediated Quinolone Resistance Variant and <i>bla</i> CTX-M-8 from <i>Klebsiella pneumoniae</i> Sequence Type 147. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	12
54	Genomic insights of high-risk clones of ESBL-producing <i>Escherichia coli</i> isolated from community infections and commercial meat in southern Brazil. <i>Scientific Reports</i> , 2022, 12, .	1.6	12

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55	Genome Sequence of the <i>Corynebacterium pseudotuberculosis</i> Cp316 Strain, Isolated from the Abscess of a Californian Horse. <i>Journal of Bacteriology</i> , 2012, 194, 6620-6621.	1.0	11
56	Novel class 1 integron (In 1390) harboring bla GES-5 in a <i>Morganella morganii</i> strain recovered from a remote community. <i>Diagnostic Microbiology and Infectious Disease</i> , 2018, 91, 345-347.	0.8	11
57	Genomic insights of <i>Klebsiella pneumoniae</i> isolated from a native Amazonian fish reveal wide resistome against heavy metals, disinfectants, and clinically relevant antibiotics. <i>Genomics</i> , 2020, 112, 5143-5146.	1.3	11
58	Genome and plasmid context of two rmtG-carrying <i>Enterobacter hormaechei</i> isolated from urinary tract infections in Brazil. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 20, 36-40.	0.9	10
59	First report of hypermucoviscous <i>Klebsiella variicola</i> subsp. <i>variicola</i> causing primary endodontic infection. <i>Clinical Microbiology and Infection</i> , 2021, 27, 303-304.	2.8	10
60	Draft genome sequence of a CTX-M-15-producing <i>Klebsiella pneumoniae</i> sequence type 340 (clonal) Tj ETQq0 0 0 rgBT /Overlock 10 TF 5 7, 67-68.	0.9	9
61	Draft genome sequence of an environmental multidrug-resistant <i>Klebsiella pneumoniae</i> ST340/CC258 harbouring bla CTX-M-15 and bla KPC-2 genes. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 8, 108-109.	0.9	9
62	Tn <i>6350</i> , a Novel Transposon Carrying Pyocin S8 Genes Encoding a Bacteriocin with Activity against Carbapenemase-Producing <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	9
63	Draft Genome Sequences of Colistin-Resistant MCR-1-Producing <i>Escherichia coli</i> ST1850 and ST74 Strains Isolated from Commercial Chicken Meat. <i>Genome Announcements</i> , 2017, 5, .	0.8	9
64	Draft Genome Sequence of the First New Delhi Metallo-β-Lactamase (NDM-1)-Producing <i>Escherichia coli</i> Strain Isolated in Peru. <i>Genome Announcements</i> , 2018, 6, .	0.8	9
65	Insights into a novel Tn4401 deletion (Tn4401i) in a multidrug-resistant <i>Klebsiella pneumoniae</i> clinical strain belonging to the high-risk clonal group 258 producing KPC-2. <i>International Journal of Antimicrobial Agents</i> , 2018, 52, 525-527.	1.1	9
66	Early Dissemination of qnrE1 in <i>Salmonella enterica</i> Serovar Typhimurium from Livestock in South America. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	9
67	Detection and Whole-Genome Analysis of a High-Risk Clone of <i>Klebsiella pneumoniae</i> ST340/CG258 Producing CTX-M-15 in a Companion Animal. <i>Microbial Drug Resistance</i> , 2020, 26, 611-615.	0.9	9
68	Multidrug-Resistant (MDR) <i>Klebsiella variicola</i> Strains Isolated in a Brazilian Hospital Belong to New Clones. <i>Frontiers in Microbiology</i> , 2021, 12, 604031.	1.5	9
69	Whole-Genome Analysis of a High-Risk Clone of <i>Klebsiella pneumoniae</i> ST147 Carrying Both <i>mcr-1</i> and <i>bla</i> _{NDM-1} Genes in Peru. <i>Microbial Drug Resistance</i> , 2022, 28, 171-179.	0.9	9
70	Complete genome sequence of <i>Corynebacterium pseudotuberculosis</i> biovar <i>ovis</i> strain P54B96 isolated from antelope in South Africa obtained by rapid next generation sequencing technology. <i>Standards in Genomic Sciences</i> , 2012, 7, 189-199.	1.5	8
71	Draft Genome Sequence of the Fungus <i>Penicillium brasilianum</i> (Strain LaBioMMi 136), a Plant Endophyte from <i>Melia azedarach</i> . <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	8
72	Molecular Detection of Class 1 Integron-Associated Gene Cassettes in KPC-2-Producing <i>Klebsiella pneumoniae</i> Clones by Whole-Genome Sequencing. <i>Microbial Drug Resistance</i> , 2019, 25, 1127-1131.	0.9	8

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73	Genomic background of a colistin-resistant and highly virulent MCR-1-positive <i>Escherichia coli</i> ST6395 from a broiler chicken in Pakistan. <i>Pathogens and Disease</i> , 2019, 77, .	0.8	8
74	Novel small IncX3 plasmid carrying the blaKPC-2 gene in high-risk <i>Klebsiella pneumoniae</i> ST11/CG258. <i>Diagnostic Microbiology and Infectious Disease</i> , 2020, 96, 114900.	0.8	8
75	Draft genome sequence of a CTX-M-15-producing endophytic <i>Klebsiella pneumoniae</i> ST198 isolate from commercial lettuce. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 10, 19-20.	0.9	7
76	Genomic features of a carbapenem-resistant OXA-219-positive <i>Acinetobacter baumannii</i> of international ST15 (CC15) from a patient with community-onset urinary tract infection in Chilean Patagonia. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 22, 756-758.	0.9	7
77	Genomic data reveals the emergence of an IncQ1 small plasmid carrying blaKPC-2 in <i>Escherichia coli</i> of the pandemic sequence type 648. <i>Journal of Global Antimicrobial Resistance</i> , 2021, 25, 8-13.	0.9	7
78	Draft Genome Sequence of a Hospital-Associated Clone of <i>Klebsiella pneumoniae</i> ST340/CC258 Coproducing RmtG and KPC-2 Isolated from a Pediatric Patient. <i>Genome Announcements</i> , 2016, 4, .	0.8	6
79	Genomic characterisation of a multidrug-resistant TEM-52b extended-spectrum β -lactamase-positive <i>Escherichia coli</i> ST219 isolated from a cat in France. <i>Journal of Global Antimicrobial Resistance</i> , 2019, 18, 223-224.	0.9	6
80	VanA-type vancomycin-resistant <i>Enterococcus faecium</i> ST1336 isolated from mussels in an anthropogenically impacted ecosystem. <i>Marine Pollution Bulletin</i> , 2019, 142, 533-536.	2.3	6
81	Genomic Analysis of SXT/R391 Integrative Conjugative Elements From <i>Proteus mirabilis</i> Isolated in Brazil. <i>Frontiers in Microbiology</i> , 2020, 11, 571472.	1.5	6
82	IncX4 Plasmid-Mediated mcr-1.1 in Polymyxin-Resistant <i>Escherichia coli</i> from Outpatients in Santa Catarina, Southern Brazil. <i>Microbial Drug Resistance</i> , 2020, 26, 1326-1333.	0.9	6
83	Genome Sequences of Clinical Isolates of NDM-1-Producing <i>Klebsiella quasipneumoniae</i> subsp. <i>similipneumoniae</i> and KPC-2-Producing <i>Klebsiella quasipneumoniae</i> subsp. <i>quasipneumoniae</i> from Brazil. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
84	Novel ST1465/CC216 Nosocomial Lineage of Carbapenem-Resistant <i>Acinetobacter baumannii</i> Harboring an Unusual Plasmid Carrying bla _{NDM-1} Gene. <i>Microbial Drug Resistance</i> , 2021, 27, 471-475.	0.9	6
85	Genomic insights of <i>Acinetobacter baumannii</i> ST374 reveal wide and increasing resistome and virulome. <i>Infection, Genetics and Evolution</i> , 2022, 97, 105148.	1.0	6
86	Environmental dissemination of vanA-containing <i>Enterococcus faecium</i> strains belonging to hospital-associated clonal lineages: Table 1.. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 264-266.	1.3	5
87	Identification of the cfr methyltransferase gene in <i>Enterococcus faecalis</i> isolated from swine: First report in Brazil. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 8, 192-193.	0.9	5
88	Draft genome sequence of a multidrug-resistant CMY-2-producing <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Minnesota ST3088 isolated from chicken meat. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 8, 67-69.	0.9	5
89	Draft genome sequence of an aminoglycoside-resistant RmtD2-producing <i>Enterobacter cloacae</i> subsp. <i>cloacae</i> ST395 in Brazil. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 10, 308-309.	0.9	5
90	MCR-1-positive colistin-resistant <i>Escherichia coli</i> in immunocompromised hospitalised patients. <i>International Journal of Antimicrobial Agents</i> , 2018, 52, 438-440.	1.1	5

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91	Early Dissemination of IncQ1 Plasmids in KPC-2-Producing <i>Klebsiella pneumoniae</i> CG258. <i>Microbial Drug Resistance</i> , 2019, 25, 1257-1259.	0.9	5
92	Draft genome sequences of KPC-2- and CTX-M-15-producing <i>Klebsiella pneumoniae</i> ST437 isolated from a clinical sample and urban rivers in Sao Paulo, Brazil. <i>Journal of Global Antimicrobial Resistance</i> , 2019, 16, 74-75.	0.9	5
93	Draft genome sequence of a multidrug-resistant KPC-2 and SRT-2 co-producing <i>Serratia marcescens</i> strain isolated from a hospitalised patient in Chile. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 21, 1-2.	0.9	5
94	Draft genome sequences of PDR and XDR <i>Klebsiella pneumoniae</i> belonging to high-risk CG258 isolated from a Brazilian tertiary hospital. <i>Infection, Genetics and Evolution</i> , 2021, 87, 104643.	1.0	5
95	A Variant Detection Pipeline for Inherited Cardiomyopathy-Associated Genes Using Next-Generation Sequencing. <i>Journal of Molecular Diagnostics</i> , 2015, 17, 420-430.	1.2	4
96	Detection of ISE cp1- associated bla CTX-M-15 mediated resistance to colistin in KPC-producing <i>Klebsiella pneumoniae</i> isolates. <i>International Journal of Antimicrobial Agents</i> , 2018, 51, 810-811.	1.1	4
97	Genomic features of a clinical ESBL-producing and colistin-resistant hypermucoviscous <i>K. quasipneumoniae</i> subsp. <i>similipneumoniae</i> from Brazil. <i>Brazilian Journal of Infectious Diseases</i> , 2019, 23, 207-209.	0.3	4
98	Genomic features of a polymyxin-resistant <i>Klebsiella pneumoniae</i> ST491 isolate co-harboring blaCTX-M-8 and qnrE1 genes from a hospitalised cat in São Paulo, Brazil. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 21, 186-187.	0.9	4
99	Genomic insights of international clones of <i>Haemophilus influenzae</i> causing invasive infections in vaccinated and unvaccinated infants. <i>Microbial Pathogenesis</i> , 2021, 150, 104644.	1.3	4
100	Carbapenem-resistant IMP-1-producing <i>Pseudocitrobacter vendiensis</i> emerging in a hemodialysis unit. <i>Brazilian Journal of Microbiology</i> , 2022, 53, 251-254.	0.8	4
101	Identification of new sequence types among <i>Enterococcus faecium</i> and <i>Enterococcus faecalis</i> carrying the vanA gene in retail chicken meat. <i>Journal of Global Antimicrobial Resistance</i> , 2016, 4, 72-73.	0.9	3
102	Draft genome sequence of an aminoglycoside-resistant RmtG-producing <i>Pseudomonas aeruginosa</i> ST235 isolated from a cystic fibrosis patient. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 8, 106-107.	0.9	3
103	Transfer of KPC-2 carbapenemase from <i>Klebsiella pneumoniae</i> to <i>Enterobacter cloacae</i> in a patient receiving meropenem therapy. <i>Diagnostic Microbiology and Infectious Disease</i> , 2017, 88, 287-289.	0.8	3
104	Draft genome sequence of an extensively drug-resistant <i>Pseudomonas aeruginosa</i> isolate belonging to ST644 isolated from a footpad infection in a Magellanic penguin (<i>Spheniscus magellanicus</i>). <i>Journal of Global Antimicrobial Resistance</i> , 2018, 12, 88-89.	0.9	3
105	Linear plasmids in <i>Klebsiella</i> and other <i>Enterobacteriaceae</i> . <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
106	<i>Wolbachia</i> endosymbionts in two <i>Anopheles</i> species indicates independent acquisitions and lack of prophage elements. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
107	Draft genome sequence of a KPC-2-producing <i>Klebsiella pneumoniae</i> ST340 carrying bla CTX-M-15 and bla CTX-M-59 genes: a rich genome of mobile genetic elements and genes encoding antibiotic resistance. <i>Journal of Global Antimicrobial Resistance</i> , 2018, 13, 35-36.	0.9	2
108	Draft Genome Sequence of a <i>Pseudomonas aeruginosa</i> Sequence Type 3351 Strain Exhibiting High-Level Resistance to Polymyxins in a Pediatric Patient with Cystic Fibrosis in Mexico. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2

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109	A novel hypermucoviscous <i>Klebsiella pneumoniae</i> ST3994-K2 clone belonging to Clonal Group 86. <i>Pathogens and Disease</i> , 2021, 79, .	0.8	2
110	FONA-7, a Novel Extended-Spectrum β -Lactamase Variant of the FONA Family Identified in <i>Serratia fonticola</i> . <i>Microbial Drug Resistance</i> , 2021, 27, 585-589.	0.9	2
111	A Scheduling Algorithm for Computational Grids that Minimizes Centralized Processing in Genome Assembly of Next-Generation Sequencing Data. <i>Frontiers in Genetics</i> , 2012, 3, 38.	1.1	1
112	Draft genome sequence of a multidrug-resistant KPC-2-producing <i>Enterobacter aerogenes</i> isolated from a hospitalised patient in Brazil. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 10, 277-278.	0.9	1