

Roger C Levesque

List of Publications by Year in descending order

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197
papers

8,469
citations

47006

47
h-index

62596

80
g-index

203
all docs

203
docs citations

203
times ranked

8085
citing authors

#	ARTICLE	IF	CITATIONS
1	Origin and diversification of endomycorrhizal fungi and coincidence with vascular land plants. <i>Nature</i> , 1993, 363, 67-69.	27.8	756
2	Newly introduced genomic prophage islands are critical determinants of in vivo competitiveness in the Liverpool Epidemic Strain of <i>Pseudomonas aeruginosa</i> . <i>Genome Research</i> , 2009, 19, 12-23.	5.5	317
3	Structure and function of the Mur enzymes: development of novel inhibitors. <i>Molecular Microbiology</i> , 2003, 47, 1-12.	2.5	293
4	Sigma factors in <i>Pseudomonas aeruginosa</i> . <i>FEMS Microbiology Reviews</i> , 2008, 32, 38-55.	8.6	261
5	Antimicrobial Resistance Genes in Enterotoxigenic <i>Escherichia coli</i> O149:K91 Isolates Obtained over a 23-Year Period from Pigs. <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 3214-3221.	3.2	245
6	The <i>Pseudomonas aeruginosa</i> Pan-Genome Provides New Insights on Its Population Structure, Horizontal Gene Transfer, and Pathogenicity. <i>Genome Biology and Evolution</i> , 2019, 11, 109-120.	2.5	223
7	Differential Regulation of Twitching Motility and Elastase Production by Vfr in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2002, 184, 3605-3613.	2.2	175
8	In vivo functional genomics of <i>Pseudomonas aeruginosa</i> for high-throughput screening of new virulence factors and antibacterial targets. <i>Environmental Microbiology</i> , 2003, 5, 1294-1308.	3.8	171
9	Heterogeneity among Virulence and Antimicrobial Resistance Gene Profiles of Extraintestinal <i>Escherichia coli</i> Isolates of Animal and Human Origin. <i>Journal of Clinical Microbiology</i> , 2004, 42, 5444-5452.	3.9	167
10	Clinical utilization of genomics data produced by the international <i>Pseudomonas aeruginosa</i> consortium. <i>Frontiers in Microbiology</i> , 2015, 6, 1036.	3.5	144
11	Phylogeny of LCR-1 and OXA-5 with class A and class D β -lactamases. <i>Molecular Microbiology</i> , 1992, 6, 1693-1705.	2.5	143
12	Identification of endomycorrhizal fungi colonizing roots by fluorescent single-strand conformation polymorphism-polymerase chain reaction. <i>Applied and Environmental Microbiology</i> , 1993, 59, 4211-4215.	3.1	131
13	The sensor kinase PhoQ mediates virulence in <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> 157:103-114. doi:10.1099/mic/0/1570103	1.8	103
14	Decreased outer membrane permeability in imipenem-resistant mutants of <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 1989, 33, 1202-1206.	3.2	101
15	Multiplex polymerase chain reaction for detection and differentiation of the microbial insecticide <i>Bacillus thuringiensis</i> . <i>Applied and Environmental Microbiology</i> , 1993, 59, 523-527.	3.1	97
16	Comparative Genomics of Isolates of a <i>Pseudomonas aeruginosa</i> Epidemic Strain Associated with Chronic Lung Infections of Cystic Fibrosis Patients. <i>PLoS ONE</i> , 2014, 9, e87611.	2.5	95
17	A megaplasmid family driving dissemination of multidrug resistance in <i>Pseudomonas</i> . <i>Nature Communications</i> , 2020, 11, 1370.	12.8	90
18	In Vivo Growth of <i>Pseudomonas aeruginosa</i> Strains PAO1 and PA14 and the Hypervirulent Strain LESB58 in a Rat Model of Chronic Lung Infection. <i>Journal of Bacteriology</i> , 2008, 190, 2804-2813.	2.2	89

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19	Comparative analysis of the 16S to 23S ribosomal intergenic spacer sequences of <i>Bacillus thuringiensis</i> strains and subspecies and of closely related species. <i>Applied and Environmental Microbiology</i> , 1995, 61, 1623-1626.	3.1	89
20	Molecular basis of antibiotic resistance and β -lactamase inhibition by mechanism-based inactivators: perspectives and future directions. <i>FEMS Microbiology Reviews</i> , 2000, 24, 251-262.	8.6	88
21	The biology of <i>Mur</i> ligases as an antibacterial target. <i>Molecular Microbiology</i> , 2014, 94, 242-253.	2.5	88
22	Proteomic, Microarray, and Signature-Tagged Mutagenesis Analyses of Anaerobic <i>Pseudomonas aeruginosa</i> at pH 6.5, Likely Representing Chronic, Late-Stage Cystic Fibrosis Airway Conditions. <i>Journal of Bacteriology</i> , 2008, 190, 2739-2758.	2.2	86
23	The Lon Protease Is Essential for Full Virulence in <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2012, 7, e49123.	2.5	83
24	Animal models of chronic lung infection with <i>Pseudomonas aeruginosa</i> : useful tools for cystic fibrosis studies. <i>Laboratory Animals</i> , 2008, 42, 389-412.	1.0	81
25	An animal source for the ROB-1 beta-lactamase of <i>Haemophilus influenzae</i> type b. <i>Antimicrobial Agents and Chemotherapy</i> , 1986, 29, 212-215.	3.2	80
26	Cloning of SHV-2, OHIO-1, and OXA-6 beta-lactamases and cloning and sequencing of SHV-1 beta-lactamase. <i>Antimicrobial Agents and Chemotherapy</i> , 1990, 34, 1577-1583.	3.2	79
27	Strategies for isolation of in vivo expressed genes from bacteria. <i>FEMS Microbiology Reviews</i> , 1999, 23, 69-91.	8.6	79
28	Characterization of tRNA-dependent Peptide Bond Formation by MurM in the Synthesis of <i>Streptococcus pneumoniae</i> Peptidoglycan. <i>Journal of Biological Chemistry</i> , 2008, 283, 6402-6417.	3.4	70
29	Temperate phages enhance pathogen fitness in chronic lung infection. <i>ISME Journal</i> , 2016, 10, 2553-2555.	9.8	69
30	Genomic characterisation of an international <i>Pseudomonas aeruginosa</i> reference panel indicates that the two major groups draw upon distinct mobile gene pools. <i>FEMS Microbiology Letters</i> , 2018, 365, .	1.8	67
31	Discovery of new MurF inhibitors via pharmacophore modeling and QSAR analysis followed by in-silico screening. <i>Bioorganic and Medicinal Chemistry</i> , 2008, 16, 1218-1235.	3.0	66
32	Genomics of the 35-kbp <i>pvd</i> locus and analysis of novel <i>pvd</i> genes implicated in pyoverdine biosynthesis in <i>Pseudomonas aeruginosa</i> . <i>FEMS Microbiology Letters</i> , 2000, 190, 141-146.	1.8	63
33	Molecular cloning and DNA homology of plasmid-mediated β -lactamase genes. <i>Molecular Genetics and Genomics</i> , 1987, 206, 252-258.	2.4	62
34	Draft genomes of 12 host-adapted and environmental isolates of <i>Pseudomonas aeruginosa</i> and their positions in the core genome phylogeny. <i>Pathogens and Disease</i> , 2014, 71, 20-25.	2.0	62
35	In Vivo-Induced Genes in <i>Pseudomonas aeruginosa</i> . <i>Infection and Immunity</i> , 2000, 68, 2359-2362.	2.2	61
36	A Plasmid-Mediated Cephalosporinase from <i>Achromobacter</i> Species. <i>Journal of Infectious Diseases</i> , 1982, 145, 753-761.	4.0	58

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37	Molecular structure and interrelationships of multiresistance β -lactamase transposons. <i>Plasmid</i> , 1988, 19, 21-29.	1.4	58
38	Nucleotide sequence and phylogeny of SHV-2 beta-lactamase. <i>Antimicrobial Agents and Chemotherapy</i> , 1990, 34, 1725-1732.	3.2	57
39	Physical and genetic mapping of cloned ribosomal DNA from <i>Toxoplasma gondii</i> : primary and secondary structure of the 5S gene. <i>Gene</i> , 1992, 114, 165-171.	2.2	56
40	Primary structure of OXA-3 and phylogeny of oxacillin-hydrolyzing class D beta-lactamases. <i>Antimicrobial Agents and Chemotherapy</i> , 1995, 39, 887-893.	3.2	56
41	Functional Annotation of the <i>Ophiostoma novo-ulmi</i> Genome: Insights into the Phytopathogenicity of the Fungal Agent of Dutch Elm Disease. <i>Genome Biology and Evolution</i> , 2015, 7, 410-430.	2.5	56
42	Defined Oligonucleotide Tag Pools and PCR Screening in Signature-Tagged Mutagenesis of Essential Genes from Bacteria. <i>BioTechniques</i> , 1999, 26, 473-480.	1.8	55
43	Positive Signature-Tagged Mutagenesis in <i>Pseudomonas aeruginosa</i> : Tracking Patho-Adaptive Mutations Promoting Airways Chronic Infection. <i>PLoS Pathogens</i> , 2011, 7, e1001270.	4.7	55
44	<i>Salmonella enterica</i> Prophage Sequence Profiles Reflect Genome Diversity and Can Be Used for High Discrimination Subtyping. <i>Frontiers in Microbiology</i> , 2018, 9, 836.	3.5	53
45	Sequence analysis and evolutionary perspectives of ROB-1 beta-lactamase. <i>Antimicrobial Agents and Chemotherapy</i> , 1990, 34, 1354-1359.	3.2	52
46	Rapid quantitation by PCR of endomycorrhizal fungi colonizing roots.. <i>Genome Research</i> , 1992, 2, 76-80.	5.5	52
47	Transcription of foreign DNA in <i>Escherichia coli</i> . <i>Genome Research</i> , 2008, 18, 1798-1805.	5.5	52
48	Genomics of antibiotic resistance prediction in <i>Pseudomonas aeruginosa</i> . <i>Annals of the New York Academy of Sciences</i> , 2019, 1435, 5-17.	3.8	51
49	Peptidoglycan lytic activity of the <i>Pseudomonas aeruginosa</i> phage ϕ KZ gp144 lytic transglycosylase. <i>FEMS Microbiology Letters</i> , 2007, 266, 201-209.	1.8	50
50	Comparative genomics and biological characterization of sequential <i>Pseudomonas aeruginosa</i> isolates from persistent airways infection. <i>BMC Genomics</i> , 2015, 16, 1105.	2.8	50
51	Site-saturation mutagenesis and three-dimensional modelling of ROB-1 define a substrate binding role of Ser 130 in class A β -lactamases. <i>Protein Engineering, Design and Selection</i> , 1992, 5, 693-701.	2.1	49
52	Prophage Integrase Typing Is a Useful Indicator of Genomic Diversity in <i>Salmonella enterica</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1283.	3.5	49
53	Structural and functional characterization of <i>tnpI</i> , a recombinase locus in Tn21 and related beta-lactamase transposons. <i>Journal of Bacteriology</i> , 1990, 172, 3745-3757.	2.2	47
54	Sequencing of the Dutch Elm Disease Fungus Genome Using the Roche/454 GS-FLX Titanium System in a Comparison of Multiple Genomics Core Facilities. <i>Journal of Biomolecular Techniques</i> , 2013, 24, jbt.12-2401-005.	1.5	47

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55	The Widespread Multidrug-Resistant Serotype O12 <i>Pseudomonas aeruginosa</i> Clone Emerged through Concomitant Horizontal Transfer of Serotype Antigen and Antibiotic Resistance Gene Clusters. <i>MBio</i> , 2015, 6, e01396-15.	4.1	47
56	Detection of the pathogenic parasite <i>Toxoplasma gondii</i> by specific amplification of ribosomal sequences using comultiplex polymerase chain reaction. <i>Journal of Clinical Microbiology</i> , 1993, 31, 203-207.	3.9	47
57	Increasing genomic diversity and evidence of constrained lifestyle evolution due to insertion sequences in <i>Aeromonas salmonicida</i> . <i>BMC Genomics</i> , 2016, 17, 44.	2.8	46
58	Insights into the Molecular Basis for the Carbenicillinase Activity of PSE-4 β -Lactamase from Crystallographic and Kinetic Studies. <i>Biochemistry</i> , 2001, 40, 395-402.	2.5	44
59	A Syst-OMICS Approach to Ensuring Food Safety and Reducing the Economic Burden of Salmonellosis. <i>Frontiers in Microbiology</i> , 2017, 8, 996.	3.5	42
60	A Study of 33 Bacteriophages of <i>Rhizobium meliloti</i> . <i>Applied and Environmental Microbiology</i> , 1988, 54, 188-196.	3.1	42
61	Complete Genome Sequence of Persistent Cystic Fibrosis Isolate <i>Pseudomonas aeruginosa</i> Strain RP73. <i>Genome Announcements</i> , 2013, 1, .	0.8	41
62	Characterization of Four Novel Bacteriophages Isolated from British Columbia for Control of Non-typhoidal Salmonella in Vitro and on Sprouting Alfalfa Seeds. <i>Frontiers in Microbiology</i> , 2017, 8, 2193.	3.5	41
63	In vitro reconstruction of the biosynthetic pathway of peptidoglycan cytoplasmic precursor in <i>Pseudomonas aeruginosa</i> . <i>FEMS Microbiology Letters</i> , 2001, 201, 229-235.	1.8	40
64	Identification of novel inhibitors of <i>Pseudomonas aeruginosa</i> MurC enzyme derived from phage-displayed peptide libraries. <i>Journal of Antimicrobial Chemotherapy</i> , 2003, 51, 531-543.	3.0	40
65	A Pan-Genomic Approach to Understand the Basis of Host Adaptation in <i>Achromobacter</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1030-1046.	2.5	40
66	Comparative genomics of a drug-resistant <i>Pseudomonas aeruginosa</i> panel and the challenges of antimicrobial resistance prediction from genomes. <i>FEMS Microbiology Letters</i> , 2017, 364, .	1.8	40
67	Characterization of the blaCARB-3 gene encoding the carbenicillinase-3 β -lactamase of <i>Pseudomonas aeruginosa</i> . <i>Gene</i> , 1991, 102, 7-12.	2.2	39
68	Molecular basis of antibiotic resistance and β -lactamase inhibition by mechanism-based inactivators: perspectives and future directions. <i>FEMS Microbiology Reviews</i> , 2000, 24, 251-262.	8.6	39
69	Peptide inhibitors of the essential cell division protein FtsA. <i>Protein Engineering, Design and Selection</i> , 2005, 18, 85-91.	2.1	39
70	Characterization of Alanine Catabolism in <i>Pseudomonas aeruginosa</i> and Its Importance for Proliferation In Vivo. <i>Journal of Bacteriology</i> , 2009, 191, 6329-6334.	2.2	39
71	The Flagellum of <i>Pseudomonas aeruginosa</i> Is Required for Resistance to Clearance by Surfactant Protein A. <i>PLoS ONE</i> , 2007, 2, e564.	2.5	38
72	Secondary structures and features of the 18S, 5.8S and 26S ribosomal RNAs from the Apicomplexan parasite <i>Toxoplasma gondii</i> . <i>Gene</i> , 1996, 173, 129-135.	2.2	36

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73	Comparative analysis of mitochondrial genomes of geographic variants of the gypsy moth, <i>Lymantria dispar</i> , reveals a previously undescribed genotypic entity. <i>Scientific Reports</i> , 2017, 7, 14245.	3.3	36
74	Parallel solid synthesis of inhibitors of the essential cell division FtsZ enzyme as a new potential class of antibacterials. <i>Bioorganic and Medicinal Chemistry</i> , 2007, 15, 1330-1340.	3.0	35
75	An Organ System-Based Synopsis of <i>Pseudomonas aeruginosa</i> Virulence. <i>Virulence</i> , 2021, 12, 1469-1507.	4.4	35
76	Cloning and expression of the imipenem-hydrolyzing beta-lactamase operon from <i>Pseudomonas maltophilia</i> in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 1988, 32, 819-826.	3.2	34
77	Molecular Heterogeneity of the L-1 Metallo- β -Lactamase Family from <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 1998, 42, 1245-1248.	3.2	34
78	Identification of in vivo essential genes from <i>Pseudomonas aeruginosa</i> by PCR-based signature-tagged mutagenesis. <i>FEMS Microbiology Letters</i> , 2002, 210, 73-80.	1.8	34
79	Exacerbation induces a microbiota shift in sputa of COPD patients. <i>PLoS ONE</i> , 2018, 13, e0194355.	2.5	34
80	Comparative Signature-Tagged Mutagenesis Identifies <i>Pseudomonas</i> Factors Conferring Resistance to the Pulmonary Collectin SP-A. <i>PLoS Pathogens</i> , 2005, 1, e31.	4.7	33
81	Assessing <i>Pseudomonas aeruginosa</i> Virulence and the Host Response Using Murine Models of Acute and Chronic Lung Infection. <i>Methods in Molecular Biology</i> , 2014, 1149, 757-771.	0.9	33
82	Construction of a DNA probe and detection of <i>Actinobacillus pleuropneumoniae</i> by using polymerase chain reaction. <i>Journal of Clinical Microbiology</i> , 1991, 29, 1183-1187.	3.9	33
83	Discovering essential and infection-related genes. <i>Current Opinion in Microbiology</i> , 2001, 4, 515-519.	5.1	32
84	Genome-wide SNPs resolve phylogenetic relationships in the North American spruce budworm (<i>Choristoneura fumiferana</i>) species complex. <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 158-168.	2.7	32
85	Assessing the potential of genotyping-by-sequencing-derived single nucleotide polymorphisms to identify the geographic origins of intercepted gypsy moth (<i>Lymantria dispar</i>) specimens: A proof-of-concept study. <i>Evolutionary Applications</i> , 2018, 11, 325-339.	3.1	32
86	Diversity and Host Specificity Revealed by Biological Characterization and Whole Genome Sequencing of Bacteriophages Infecting <i>Salmonella enterica</i> . <i>Viruses</i> , 2019, 11, 854.	3.3	32
87	A Multi-Species TaqMan PCR Assay for the Identification of Asian Gypsy Moths (<i>Lymantria</i> spp.) and Other Invasive <i>Lymantria</i> Species of Biosecurity Concern to North America. <i>PLoS ONE</i> , 2016, 11, e0160878.	2.5	31
88	Detection of genes essential in specific niches by signature-tagged mutagenesis. <i>Current Opinion in Biotechnology</i> , 2000, 11, 434-439.	6.6	30
89	Composition of the Spruce Budworm (<i>Choristoneura fumiferana</i>) Midgut Microbiota as Affected by Rearing Conditions. <i>PLoS ONE</i> , 2015, 10, e0144077.	2.5	30
90	Hit Identification of New Potent PqsR Antagonists as Inhibitors of Quorum Sensing in Planktonic and Biofilm Grown <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Chemistry</i> , 2020, 8, 204.	3.6	29

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91	Evolutionary perspectives on multiresistance beta-lactamase transposons. <i>Journal of Bacteriology</i> , 1989, 171, 6423-6429.	2.2	28
92	Development of natural and synthetic DNA probes for OXA-2 and TEM-1 beta-lactamases. <i>Antimicrobial Agents and Chemotherapy</i> , 1987, 31, 728-734.	3.2	27
93	Cloning, sequencing and expression in <i>Escherichia coli</i> of the <i>ptsI</i> gene encoding enzyme I of the phosphoenolpyruvate:sugar phosphotransferase transport system from <i>Streptococcus salivarius</i> . <i>Gene</i> , 1992, 121, 71-78.	2.2	26
94	Requirement of the <i>Pseudomonas aeruginosa</i> CbrA Sensor Kinase for Full Virulence in a Murine Acute Lung Infection Model. <i>Infection and Immunity</i> , 2014, 82, 1256-1267.	2.2	26
95	Temporal variation in spatial genetic structure during population outbreaks: Distinguishing among different potential drivers of spatial synchrony. <i>Evolutionary Applications</i> , 2019, 12, 1931-1945.	3.1	26
96	<i>Pseudomonas aeruginosa</i> MurE amide ligase: enzyme kinetics and peptide inhibitor. <i>Biochemical Journal</i> , 2009, 421, 263-272.	3.7	25
97	A specific peptide inhibitor of the class B metallo- β -lactamase L-1 from <i>Stenotrophomonas maltophilia</i> identified using phage display. <i>Journal of Antimicrobial Chemotherapy</i> , 2005, 55, 252-255.	3.0	24
98	Molecular distribution of ROB-1 beta-lactamase in <i>Actinobacillus pleuropneumoniae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 1991, 35, 1397-1402.	3.2	23
99	Molecular cloning, complete sequence of the small subunit ribosomal RNA coding region and phylogeny of <i>Toxoplasma gondii</i> . <i>Molecular and Biochemical Parasitology</i> , 1993, 60, 145-148.	1.1	23
100	Phage display-derived inhibitor of the essential cell wall biosynthesis enzyme MurF. <i>BMC Biochemistry</i> , 2008, 9, 33.	4.4	23
101	Two's company, three's a crowd: new insights on spruce budworm species boundaries using genotyping-by-sequencing in an integrative species assessment (Lepidoptera: Tortricidae). <i>Systematic Entomology</i> , 2017, 42, 317-328.	3.9	23
102	Species interactions and distinct microbial communities in high Arctic permafrost affected cryosols are associated with the CH ₄ and CO ₂ gas fluxes. <i>Environmental Microbiology</i> , 2019, 21, 3711-3727.	3.8	23
103	The <i>Salmonella enterica</i> Plasmidome as a Reservoir of Antibiotic Resistance. <i>Microorganisms</i> , 2020, 8, 1016.	3.6	23
104	Physical mapping of 32 genetic markers on the <i>Pseudomonas aeruginosa</i> PAO1 chromosome. <i>Microbiology (United Kingdom)</i> , 1996, 142, 79-86.	1.8	22
105	ASD-GFP Vectors for In Vivo Expression Technology in <i>Pseudomonas aeruginosa</i> and Other Gram-Negative Bacteria. <i>BioTechniques</i> , 1998, 24, 261-264.	1.8	22
106	Structure of CARB-4 and AER-1 CarbenicillinHydrolyzing β -Lactamases. <i>Antimicrobial Agents and Chemotherapy</i> , 1998, 42, 1966-1972.	3.2	22
107	Selection of peptide inhibitors against the <i>Pseudomonas aeruginosa</i> MurD cell wall enzyme. <i>Peptides</i> , 2006, 27, 1693-1700.	2.4	22
108	Molybdate transporter ModABC is important for <i>Pseudomonas aeruginosa</i> chronic lung infection. <i>BMC Research Notes</i> , 2016, 9, 23.	1.4	22

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109	Culture-Dependent Bioprospecting of Bacterial Isolates From the Canadian High Arctic Displaying Antibacterial Activity. <i>Frontiers in Microbiology</i> , 2019, 10, 1836.	3.5	22
110	Design and Evaluation of New Quinazolin-4(3 <i>H</i>)-one Derived PqsR Antagonists as Quorum Sensing Quenchers in <i>Pseudomonas aeruginosa</i> . <i>ACS Infectious Diseases</i> , 2021, 7, 2666-2685.	3.8	22
111	Comparative study of the beta-lactamase activity found in <i>Achromobacter</i> . <i>Canadian Journal of Microbiology</i> , 1983, 29, 819-826.	1.7	21
112	<i>Pseudomonas aeruginosa</i> PA01 Bacterial Artificial Chromosomes: Strategies for Mapping, Screening, and Sequencing 100 kb Loci of the 5.9 Mb Genome. <i>Microbial & Comparative Genomics</i> , 1998, 3, 105-117.	0.4	21
113	A peptide inhibitor of MurA UDP-N-acetylglucosamine enolpyruvyl transferase: The first committed step in peptidoglycan biosynthesis. <i>Peptides</i> , 2006, 27, 3115-3121.	2.4	21
114	Genomic characterization of environmental <i>Pseudomonas aeruginosa</i> isolated from dental unit waterlines revealed the insertion sequence ISPa11 as a chaotropic element. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	21
115	Phenomic and genomic approaches to studying the inhibition of multiresistant <i>Salmonella enterica</i> by microcin J25. <i>Environmental Microbiology</i> , 2020, 22, 2907-2920.	3.8	21
116	Continent-wide population genomic structure and phylogeography of North America's most destructive conifer defoliator, the spruce budworm (<i>Choristoneura fumiferana</i>). <i>Ecology and Evolution</i> , 2020, 10, 914-927.	1.9	21
117	Mapping of a plasmid (pLQ3) from <i>Achromobacter</i> and cloning of its cephalosporinase gene in <i>Escherichia coli</i> . <i>Gene</i> , 1982, 18, 69-75.	2.2	20
118	Structure-Function Studies of Ser-289 in the Class C β -Lactamase from <i>Enterobacter cloacae</i> P99. <i>Antimicrobial Agents and Chemotherapy</i> , 1999, 43, 543-548.	3.2	20
119	Combinatorial enzymatic assay for the screening of a new class of bacterial cell wall inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 2003, 11, 1583-1592.	3.0	19
120	Inactivation of <i>Salmonella enterica</i> on post-harvest cantaloupe and lettuce by a lytic bacteriophage cocktail. <i>Current Research in Food Science</i> , 2020, 2, 25-32.	5.8	19
121	Identification of <i>Pseudomonas aeruginosa</i> FtsZ peptide inhibitors as a tool for development of novel antimicrobials. <i>Journal of Antimicrobial Chemotherapy</i> , 2004, 54, 278-280.	3.0	18
122	Functional genomics of PycR, a LysR family transcriptional regulator essential for maintenance of <i>Pseudomonas aeruginosa</i> in the rat lung. <i>Microbiology (United Kingdom)</i> , 2008, 154, 2106-2118.	1.8	18
123	Genes Required for Free Phage Production are Essential for <i>Pseudomonas aeruginosa</i> Chronic Lung Infections. <i>Journal of Infectious Diseases</i> , 2016, 213, 395-402.	4.0	17
124	Complete Genome Sequences of Two Phage-Like Plasmids Carrying the CTX-M-15 Extended-Spectrum β -Lactamase Gene. <i>Genome Announcements</i> , 2017, 5, .	0.8	17
125	Gene-Gene Interactions Dictate Ciprofloxacin Resistance in <i>Pseudomonas aeruginosa</i> and Facilitate Prediction of Resistance Phenotype from Genome Sequence Data. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0269620.	3.2	16
126	Complete Genome Sequences of Three <i>Pseudomonas aeruginosa</i> Isolates with Phenotypes of Polymyxin B Adaptation and Inducible Resistance. <i>Journal of Bacteriology</i> , 2012, 194, 529-530.	2.2	15

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127	Draft Genome Sequences of Two Lipopeptide-Producing Strains of <i>Bacillus methylotrophicus</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	15
128	Prophage induction reduces Shiga toxin producing <i>Escherichia coli</i> (STEC) and <i>Salmonella enterica</i> on tomatoes and spinach: A model study. <i>Food Control</i> , 2018, 89, 250-259.	5.5	15
129	Similar yet different: phylogenomic analysis to delineate <i>Salmonella</i> and <i>Citrobacter</i> species boundaries. <i>BMC Genomics</i> , 2020, 21, 377.	2.8	15
130	Model-Based Drug Development in Pulmonary Delivery: Pharmacokinetic Analysis of Novel Drug Candidates for Treatment of <i>Pseudomonas aeruginosa</i> Lung Infection. <i>Journal of Pharmaceutical Sciences</i> , 2019, 108, 630-640.	3.3	14
131	Comparative genomic analysis of 142 bacteriophages infecting <i>Salmonella enterica</i> subsp. <i>enterica</i> . <i>BMC Genomics</i> , 2020, 21, 374.	2.8	14
132	Genome evolution drives transcriptomic and phenotypic adaptation in <i>Pseudomonas aeruginosa</i> during 20 years of infection. <i>Microbial Genomics</i> , 2021, 7, .	2.0	14
133	Bacteriophage-Insensitive Mutants of Antimicrobial-Resistant <i>Salmonella Enterica</i> are Altered in their Tetracycline Resistance and Virulence in Caco-2 Intestinal Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1883.	4.1	13
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