

# Roger C Levesque

## List of Publications by Year in descending order

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195  
papers

8,469  
citations

46918

47  
h-index

62479

80  
g-index

203  
all docs

203  
docs citations

203  
times ranked

8085  
citing authors

#	ARTICLE	IF	CITATIONS
1	Salmonella enterica subsp. enterica virulence potential can be linked to higher survival within a dynamic in vitro human gastrointestinal model. Food Microbiology, 2022, 101, 103877.	2.1	5
2	Genomic and phenotypic analysis of SspH1 identifies a new <i>Salmonella</i> effector, SspH3. Molecular Microbiology, 2022, 117, 770-789.	1.2	3
3	Application of a High-Throughput Targeted Sequence AmpliSeq Procedure to Assess the Presence and Variants of Virulence Genes in Salmonella. Microorganisms, 2022, 10, 369.	1.6	4
4	The Spruce Budworm Genome: Reconstructing the Evolutionary History of Antifreeze Proteins. Genome Biology and Evolution, 2022, 14, .	1.1	3
5	Liverpool Epidemic Strain Isolates of Pseudomonas aeruginosa Display High Levels of Antimicrobial Resistance during Both Planktonic and Biofilm Growth. Microbiology Spectrum, 2022, 10, .	1.2	4
6	Complete Genome Sequence of a Pseudomonas Species Isolated from Tailings Pond Water in Alberta, Canada. Microbiology Resource Announcements, 2021, 10, .	0.3	0
7	Transmission, adaptation and geographical spread of the Pseudomonas aeruginosa Liverpool epidemic strain. Microbial Genomics, 2021, 7, .	1.0	12
8	Sequencing, assembly and annotation of the whole-insect genome of <i>Lymantria dispar dispar</i> , the European gypsy moth. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	5
9	Novel antimicrobial anionic cecropins from the spruce budworm feature a polyaspartic acid C-terminus. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1205-1215.	1.5	6
10	Gene-Gene Interactions Dictate Ciprofloxacin Resistance in Pseudomonas aeruginosa and Facilitate Prediction of Resistance Phenotype from Genome Sequence Data. Antimicrobial Agents and Chemotherapy, 2021, 65, e0269620.	1.4	16
11	Design and Evaluation of New Quinazolin-4(3H)-one Derived PqsR Antagonists as Quorum Sensing Quenchers in Pseudomonas aeruginosa. ACS Infectious Diseases, 2021, 7, 2666-2685.	1.8	22
12	An Organ System-Based Synopsis of Pseudomonas aeruginosa Virulence. Virulence, 2021, 12, 1469-1507.	1.8	35
13	Genome evolution drives transcriptomic and phenotypic adaptation in Pseudomonas aeruginosa during 20 years of infection. Microbial Genomics, 2021, 7, .	1.0	14
14	The Pseudomonas aeruginosa whole genome sequence: A 20th anniversary celebration. Advances in Microbial Physiology, 2021, 79, 25-88.	1.0	7
15	Reuse of voucher specimens provides insights into the genomic associations and taxonomic value of wing colour and genitalic differences in a pest group (Lepidoptera: Tortricidae: Choristoneura ). Systematic Entomology, 2020, 45, 583-593.	1.7	2
16	Inactivation of Salmonella enterica on post-harvest cantaloupe and lettuce by a lytic bacteriophage cocktail. Current Research in Food Science, 2020, 2, 25-32.	2.7	19
17	Reassessment of the status of <i>Lymantria albescens</i> and <i>Lymantria postalba</i> (Lepidoptera: Tortricidae) based on new sequence data. Systematic Entomology, 2020, 45, 493-504.	1.7	6
18	The Salmonella enterica Plasmidome as a Reservoir of Antibiotic Resistance. Microorganisms, 2020, 8, 1016.	1.6	23

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19	Bacteriophage-Induced Lipopolysaccharide Mutations in <i>Escherichia coli</i> Lead to Hypersensitivity to Food Grade Surfactant Sodium Dodecyl Sulfate. <i>Antibiotics</i> , 2020, 9, 552.	1.5	5
20	Structural insights into the putative bacterial acetylcholinesterase ChoE and its substrate inhibition mechanism. <i>Journal of Biological Chemistry</i> , 2020, 295, 8708-8724.	1.6	7
21	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.	1.8	21
22	Similar yet different: phylogenomic analysis to delineate <i>Salmonella</i> and <i>Citrobacter</i> species boundaries. <i>BMC Genomics</i> , 2020, 21, 377.	1.2	15
23	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.	1.8	29
24	Comparative genomic analysis of 142 bacteriophages infecting <i>Salmonella enterica</i> subsp. <i>enterica</i> . <i>BMC Genomics</i> , 2020, 21, 374.	1.2	14
25	Combining Whole-Genome Sequencing and Multimodel Phenotyping To Identify Genetic Predictors of <i>Salmonella</i> Virulence. <i>MSphere</i> , 2020, 5, .	1.3	9
26	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.	1.8	13
27	A megaplasmid family driving dissemination of multidrug resistance in <i>Pseudomonas</i> . <i>Nature Communications</i> , 2020, 11, 1370.	5.8	90
28	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.	0.8	21
29	Model-Informed Drug Development in Pulmonary Delivery: Semimechanistic Pharmacokinetic-Pharmacodynamic Modeling for Evaluation of Treatments against Chronic <i>Pseudomonas aeruginosa</i> Lung Infections. <i>Molecular Pharmaceutics</i> , 2020, 17, 1458-1469.	2.3	8
30	A New Whole Genome Culture-Independent Diagnostic Test (WG-CIDT) for Rapid Detection of <i>Salmonella</i> in Lettuce. <i>Frontiers in Microbiology</i> , 2020, 11, 602.	1.5	8
31	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.	1.5	26
32	Expansion of LINEs and species-specific DNA repeats drives genome expansion in Asian Gypsy Moths. <i>Scientific Reports</i> , 2019, 9, 16413.	1.6	8
33	Reservoirs of resistance: polymyxin resistance in veterinary-associated companion animal isolates of <i>Pseudomonas aeruginosa</i> . <i>Veterinary Record</i> , 2019, 185, 206-206.	0.2	10
34	Culture-Dependent Bioprospecting of Bacterial Isolates From the Canadian High Arctic Displaying Antibacterial Activity. <i>Frontiers in Microbiology</i> , 2019, 10, 1836.	1.5	22
35	Fate of 43 <i>Salmonella</i> Strains on Lettuce and Tomato Seedlings. <i>Journal of Food Protection</i> , 2019, 82, 1045-1051.	0.8	12
36	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.	1.5	32

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37	Species interactions and distinct microbial communities in high Arctic permafrost affected cryosols are associated with the CH <sub>4</sub> and CO <sub>2</sub> gas fluxes. <i>Environmental Microbiology</i> , 2019, 21, 3711-3727.	1.8	23
38	A needle in a haystack: a multigene TaqMan assay for the detection of Asian gypsy moths in bulk pheromone trap samples. <i>Biological Invasions</i> , 2019, 21, 1843-1856.	1.2	7
39	Major Release of 161 Whole-Genome Sequences from the International Pseudomonas Consortium Database. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
40	The <i>Pseudomonas aeruginosa</i> Population among Cystic Fibrosis Patients in Quebec, Canada: a Disease Hot Spot without Known Epidemic Isolates. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	2
41	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.	1.6	14
42	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.	1.1	223
43	Genomics of antibiotic resistance prediction in <i>Pseudomonas aeruginosa</i> . <i>Annals of the New York Academy of Sciences</i> , 2019, 1435, 5-17.	1.8	51
44	Convergent herbivory on conifers by <i>Choristoneura</i> moths after boreal forest formation. <i>Molecular Phylogenetics and Evolution</i> , 2018, 123, 35-43.	1.2	11
45	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.	2.8	15
46	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.	1.5	32
47	A new approach to study attached biofilms and floating communities from <i>Pseudomonas aeruginosa</i> strains of various origins reveals diverse effects of divalent ions. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	11
48	Insights into the Structure of the Spruce Budworm ( <i>Choristoneura fumiferana</i> ) Genome, as Revealed by Molecular Cytogenetic Analyses and a High-Density Linkage Map. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2539-2549.	0.8	12
49	Direct In Vivo Microbial Transcriptomics During Infection. <i>Trends in Microbiology</i> , 2018, 26, 732-735.	3.5	2
50	For the Safety of Fresh Produce: Regulatory Considerations for Canada on the Use of Whole Genome Sequencing to Subtype <i>Salmonella</i> . <i>Frontiers in Sustainable Food Systems</i> , 2018, 2, .	1.8	0
51	<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.	1.5	53
52	A multi-host approach to identify a transposon mutant of <i>Pseudomonas aeruginosa</i> LESB58 lacking full virulence. <i>BMC Research Notes</i> , 2018, 11, 198.	0.6	0
53	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, .	0.7	67
54	Exacerbation induces a microbiota shift in sputa of COPD patients. <i>PLoS ONE</i> , 2018, 13, e0194355.	1.1	34

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55	Complete Genome Sequences of Two Phage-Like Plasmids Carrying the CTX-M-15 Extended-Spectrum $\beta$ -Lactamase Gene. <i>Genome Announcements</i> , 2017, 5, .	0.8	17
56	AnCo3, a New Member of the Emerging Family of Phage-Like Plasmids. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
57	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.	1.2	32
58	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.	1.1	40
59	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.	1.6	36
60	Distinct sources of gene flow produce contrasting population genetic dynamics at different range boundaries of a <i>Choristoneura</i> budworm. <i>Molecular Ecology</i> , 2017, 26, 6666-6684.	2.0	7
61	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, .	0.7	40
62	Whole-Genome Sequencing of <i>Lactobacillus</i> Species from Two Commercial Probiotic Products. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
63	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.	1.7	23
64	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, .	1.3	21
65	A Syst-OMICS Approach to Ensuring Food Safety and Reducing the Economic Burden of Salmonellosis. <i>Frontiers in Microbiology</i> , 2017, 8, 996.	1.5	42
66	Prophage Integrase Typing Is a Useful Indicator of Genomic Diversity in <i>Salmonella enterica</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1283.	1.5	49
67	Characterization of Four Novel Bacteriophages Isolated from British Columbia for Control of Non-typhoidal <i>Salmonella</i> in Vitro and on Sprouting Alfalfa Seeds. <i>Frontiers in Microbiology</i> , 2017, 8, 2193.	1.5	41
68	A Multi-Species TaqMan PCR Assay for the Identification of Asian Gypsy Moths ( <i>Lymantria</i> spp.) and Other Invasive Lymantriines of Biosecurity Concern to North America. <i>PLoS ONE</i> , 2016, 11, e0160878.	1.1	31
69	Temperate phages enhance pathogen fitness in chronic lung infection. <i>ISME Journal</i> , 2016, 10, 2553-2555.	4.4	69
70	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.	1.2	46
71	Cyclic peptides identified by phage display are competitive inhibitors of the tRNA-dependent amidotransferase of <i>Helicobacter pylori</i> . <i>Peptides</i> , 2016, 79, 8-15.	1.2	6
72	Molybdate transporter ModABC is important for <i>Pseudomonas aeruginosa</i> chronic lung infection. <i>BMC Research Notes</i> , 2016, 9, 23.	0.6	22

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73	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.	1.9	17
74	Comparative genomics and biological characterization of sequential <i>Pseudomonas aeruginosa</i> isolates from persistent airways infection. <i>BMC Genomics</i> , 2015, 16, 1105.	1.2	50
75	Clinical utilization of genomics data produced by the international <i>Pseudomonas aeruginosa</i> consortium. <i>Frontiers in Microbiology</i> , 2015, 6, 1036.	1.5	144
76	Composition of the Spruce Budworm ( <i>Choristoneura fumiferana</i> ) Midgut Microbiota as Affected by Rearing Conditions. <i>PLoS ONE</i> , 2015, 10, e0144077.	1.1	30
77	Draft Genome Sequences of Two Lipopeptide-Producing Strains of <i>Bacillus methylotrophicus</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	15
78	Glycoside hydrolase family 32 is present in <i>Bacillus subtilis</i> phages. <i>Virology Journal</i> , 2015, 12, 157.	1.4	11
79	Draft Genome Sequence of Triclosan-Resistant Cystic Fibrosis Isolate <i>Achromobacter xylosoxidans</i> CF304. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
80	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.	1.8	47
81	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.	1.1	56
82	Essential Genes in the Infection Model of <i>Pseudomonas aeruginosa</i> -PCR-Based Signature-Tagged Mutagenesis. <i>Methods in Molecular Biology</i> , 2015, 1279, 97-123.	0.4	4
83	Strategy for Genome Sequencing Analysis and Assembly for Comparative Genomics of <i>Pseudomonas</i> Genomes. <i>Methods in Molecular Biology</i> , 2014, 1149, 565-577.	0.4	3
84	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.	1.0	26
85	The biology of <i>Mur</i> ligases as an antibacterial target. <i>Molecular Microbiology</i> , 2014, 94, 242-253.	1.2	88
86	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.	0.8	62
87	Signature-Tagged Mutagenesis. <i>Methods in Molecular Biology</i> , 2014, 1149, 541-554.	0.4	1
88	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.	0.4	33
89	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.	1.1	95
90	Complete Genome Sequence of Persistent Cystic Fibrosis Isolate <i>Pseudomonas aeruginosa</i> Strain RP73. <i>Genome Announcements</i> , 2013, 1, .	0.8	41

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91	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.	0.8	47
92	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.	1.0	15
93	The Lon Protease Is Essential for Full Virulence in <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2012, 7, e49123.	1.1	83
94	Cell Culture Tracking by Multivariate Analysis of Raw LCMS Data. <i>Applied Biochemistry and Biotechnology</i> , 2012, 167, 474-488.	1.4	2
95	Genomics of Banchine Ichnoviruses. , 2012, , 79-87.		8
96	BAC library construction, screening and clone sequencing of lake whitefish (<i>Coregonus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 547 To Ecology Resources, 2011, 11, 541-549.	2.2	11
97	Positive Signature-Tagged Mutagenesis in <i>Pseudomonas aeruginosa</i> : Tracking Patho-Adaptive Mutations Promoting Airways Chronic Infection. <i>PLoS Pathogens</i> , 2011, 7, e1001270.	2.1	55
98	Biophysical studies of the interactions between the phage T-KZ gp144 lytic transglycosylase and model membranes. <i>European Biophysics Journal</i> , 2010, 39, 263-276.	1.2	6
99	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.	2.4	317
100	The sensor kinase PhoQ mediates virulence in <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 38 103	0.7	103
101	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.	1.0	39
102	<i>Pseudomonas aeruginosa</i> MurE amide ligase: enzyme kinetics and peptide inhibitor. <i>Biochemical Journal</i> , 2009, 421, 263-272.	1.7	25
103	Phage display-derived inhibitor of the essential cell wall biosynthesis enzyme MurF. <i>BMC Biochemistry</i> , 2008, 9, 33.	4.4	23
104	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.	1.4	66
105	Sigma factors in<i>Pseudomonas aeruginosa</i>. <i>FEMS Microbiology Reviews</i> , 2008, 32, 38-55.	3.9	261
106	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.	1.0	89
107	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.	0.7	18
108	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.	0.5	81

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109	Transcription of foreign DNA in <i>Escherichia coli</i> . <i>Genome Research</i> , 2008, 18, 1798-1805.	2.4	52
110	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.	1.6	70
111	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.	1.0	86
112	Essential Genes in the Infection Model of <i>Pseudomonas aeruginosa</i> PCR-Based Signature-Tagged Mutagenesis. <i>Methods in Molecular Biology</i> , 2008, 416, 61-82.	0.4	6
113	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.	1.4	35
114	Peptidoglycan lytic activity of the <i>Pseudomonas aeruginosa</i> phage $\phi$ KZ gp144 lytic transglycosylase. <i>FEMS Microbiology Letters</i> , 2007, 266, 201-209.	0.7	50
115	The Flagellum of <i>Pseudomonas aeruginosa</i> Is Required for Resistance to Clearance by Surfactant Protein A. <i>PLoS ONE</i> , 2007, 2, e564.	1.1	38
116	In Vivo Functional Genomics of <i>Pseudomonas</i> : PCR-Based Signature-Tagged Mutagenesis. , 2006, , 99-120.		4
117	Selection of peptide inhibitors against the <i>Pseudomonas aeruginosa</i> MurD cell wall enzyme. <i>Peptides</i> , 2006, 27, 1693-1700.	1.2	22
118	A peptide inhibitor of MurA UDP-N-acetylglucosamine enolpyruvyl transferase: The first committed step in peptidoglycan biosynthesis. <i>Peptides</i> , 2006, 27, 3115-3121.	1.2	21
119	Letter to the Editor. <i>Journal of Biomolecular NMR</i> , 2006, 36, 11-11.	1.6	6
120	Comparative Signature-Tagged Mutagenesis Identifies <i>Pseudomonas</i> Factors Conferring Resistance to the Pulmonary Collectin SP-A. <i>PLoS Pathogens</i> , 2005, 1, e31.	2.1	33
121	A specific peptide inhibitor of the class B metallo- $\beta$ -lactamase L-1 from <i>Stenotrophomonas maltophilia</i> identified using phage display. <i>Journal of Antimicrobial Chemotherapy</i> , 2005, 55, 252-255.	1.3	24
122	Peptide inhibitors of the essential cell division protein FtsA. <i>Protein Engineering, Design and Selection</i> , 2005, 18, 85-91.	1.0	39
123	Identification of Novel Pathogenicity Genes by PCR Signature-Tagged Mutagenesis and Related Technologies. , 2004, 266, 289-304.		9
124	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.	1.3	18
125	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.	1.8	167
126	Letter to the Editor: $^1\text{H}$ , $^{13}\text{C}$ and $^{15}\text{N}$ backbone resonance assignments for TEM-1, a 28.9 kDa $\beta$ -lactamase from <i>E. coli</i> . <i>Journal of Biomolecular NMR</i> , 2004, 29, 433-434.	1.6	10



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127	Structure and function of the Mur enzymes: development of novel inhibitors. <i>Molecular Microbiology</i> , 2003, 47, 1-12.	1.2	293
128	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.	1.8	171
129	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.	1.4	19
130	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.	1.3	40
131	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.	1.4	245
132	PCR Screening in Signature-Tagged Mutagenesis of Essential Genes. , 2002, 192, 225-234.		4
133	Differential Regulation of Twitching Motility and Elastase Production by Vfr in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2002, 184, 3605-3613.	1.0	175
134	Polymerase Chain Reaction-Based Signature-Tagged Mutagenesis. , 2002, 182, 127-137.		4
135	Broad-Host-Range Mobilizable Suicide Vectors for Promoter Trapping in Gram-Negative Bacteria. <i>BioTechniques</i> , 2002, 33, 1038-1043.	0.8	7
136	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.	0.7	34
137	Discovering essential and infection-related genes. <i>Current Opinion in Microbiology</i> , 2001, 4, 515-519.	2.3	32
138	Insights into the Molecular Basis for the Carbenicillinase Activity of PSE-4 $\beta$ -Lactamase from Crystallographic and Kinetic Studies. <i>Biochemistry</i> , 2001, 40, 395-402.	1.2	44
139	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.	0.7	40
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