Stephen Lory

List of Publications by Year
in descending order

54 papers	8,297 citations	126907 33 h-index	175258 52 g-index
55 all docs	55 docs citations	55 times ranked	7116 citing authors

#	Article	IF	Citations
1	A Virulence Locus of Pseudomonas aeruginosa Encodes a Protein Secretion Apparatus. Science, 2006, 312, 1526-1530.	12.6	984
2	A Signaling Network Reciprocally Regulates Genes Associated with Acute Infection and Chronic Persistence in Pseudomonas aeruginosa. Developmental Cell, 2004, 7, 745-754.	7.0	559
3	Analysis of Pseudomonas aeruginosa diguanylate cyclases and phosphodiesterases reveals a role for bis-(3'-5')-cyclic-GMP in virulence. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2839-2844.	7.1	507
4	Dynamics of <i>Pseudomonas aeruginosa</i> genome evolution. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3100-3105.	7.1	492
5	A fourâ€tiered transcriptional regulatory circuit controls flagellar biogenesis in Pseudomonas aeruginosa. Molecular Microbiology, 2003, 50, 809-824.	2.5	404
6	A cyclicâ€diâ€GMP receptor required for bacterial exopolysaccharide production. Molecular Microbiology, 2007, 65, 1474-1484.	2.5	404
7	Multiple sensors control reciprocal expression of Pseudomonas aeruginosa regulatory RNA and virulence genes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 171-176.	7.1	401
8	Coordinate Regulation of Bacterial Virulence Genes by a Novel Adenylate Cyclase-Dependent Signaling Pathway. Developmental Cell, 2003, 4, 253-263.	7.0	362
9	Conservation of genome content and virulence determinants among clinical and environmental isolates ofPseudomonas aeruginosa. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8484-8489.	7.1	356
10	The GacS/GacA signal transduction system of <i>Pseudomonas aeruginosa</i> acts exclusively through its control over the transcription of the RsmY and RsmZ regulatory small RNAs. Molecular Microbiology, 2009, 73, 434-445.	2.5	344
11	The second messenger bisâ€(3â€²â€5â€²)â€cyclicâ€GMP and its PilZ domainâ€containing receptor Alg44 are required for alginate biosynthesis in <i>Pseudomonas aeruginosa</i>. Molecular Microbiology, 2007, 65, 876-895.	2.5	314
12	Determination of the regulon and identification of novel mRNA targets of <i>Pseudomonas aeruginosa</i> RsmA. Molecular Microbiology, 2009, 72, 612-632.	2.5	305
13	A novel two-component system controls the expression of Pseudomonas aeruginosa fimbrial cup genes. Molecular Microbiology, 2004, 55, 368-380.	2.5	278
14	Direct interaction between sensor kinase proteins mediates acute and chronic disease phenotypes in a bacterial pathogen. Genes and Development, 2009, 23, 249-259.	5.9	272
15	The Single-Nucleotide Resolution Transcriptome of Pseudomonas aeruginosa Grown in Body Temperature. PLoS Pathogens, 2012, 8, e1002945.	4.7	240
16	Activities of Pseudomonas aeruginosa Effectors Secreted by the Type III Secretion System In Vitro and during Infection. Infection and Immunity, 2005, 73, 1695-1705.	2.2	220
17	A Comprehensive Analysis of In Vitro and In Vivo Genetic Fitness of Pseudomonas aeruginosa Using High-Throughput Sequencing of Transposon Libraries. PLoS Pathogens, 2013, 9, e1003582.	4.7	178
18	Biofilm Formation in Pseudomonas aeruginosa : Fimbrial cup Gene Clusters Are Controlled by the Transcriptional Regulator MvaT. Journal of Bacteriology, 2004, 186, 2880-2890.	2.2	139

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19	Enhanced in vivo fitness of carbapenem-resistant <i>oprD</i> mutants of <i>Pseudomonas aeruginosa</i> revealed through high-throughput sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20747-20752.	7.1	128
20	Fitness cost of antibiotic susceptibility during bacterial infection. Science Translational Medicine, 2015, 7, 297ra114.	12.4	122
21	Identification of a Genomic Island Present in the Majority of Pathogenic Isolates of Pseudomonas aeruginosa. Journal of Bacteriology, 2001, 183, 843-853.	2.2	114
22	The Regulatory Repertoire of Pseudomonas aeruginosa AmpC ÃŸ-Lactamase Regulator AmpR Includes Virulence Genes. PLoS ONE, 2012, 7, e34067.	2.5	108
23	Acquisition and Evolution of the exoU Locus in Pseudomonas aeruginosa. Journal of Bacteriology, 2006, 188, 4037-4050.	2.2	95
24	Probing the sRNA regulatory landscape of <i>P. aeruginosa</i>: postâ€transcriptional control of determinants of pathogenicity and antibiotic susceptibility. Molecular Microbiology, 2017, 106, 919-937.	2.5	91
25	Identification of Small Molecule Inhibitors of Pseudomonas aeruginosa Exoenzyme S Using a Yeast Phenotypic Screen. PLoS Genetics, 2008, 4, e1000005.	3.5	84
26	GRIL-seq provides a method for identifying direct targets of bacterial small regulatory RNA by in vivo proximity ligation. Nature Microbiology, 2017, 2, 16239.	13.3	80
27	<i>Pseudomonas aeruginosa</i> Pore-Forming Exolysin and Type IV Pili Cooperate To Induce Host Cell Lysis. MBio, 2017, 8, .	4.1	69
28	Analysis of regulatory networks in Pseudomonas aeruginosa by genomewide transcriptional profiling. Current Opinion in Microbiology, 2004, 7, 39-44.	5.1	64
29	Deep sequencing analyses expands the Pseudomonas aeruginosa AmpR regulon to include small RNA-mediated regulation of iron acquisition, heat shock and oxidative stress response. Nucleic Acids Research, 2014, 42, 979-998.	14.5	62
30	GPR107, a G-protein-coupled Receptor Essential for Intoxication by Pseudomonas aeruginosa Exotoxin A, Localizes to the Golgi and Is Cleaved by Furin. Journal of Biological Chemistry, 2014, 289, 24005-24018.	3.4	54
31	Phage Morons Play an Important Role in Pseudomonas aeruginosa Phenotypes. Journal of Bacteriology, 2018, 200, .	2.2	53
32	Structural and Functional Characterization of Pseudomonas aeruginosa Global Regulator AmpR. Journal of Bacteriology, 2014, 196, 3890-3902.	2.2	44
33	Complexity of Complement Resistance Factors Expressed by <i>Acinetobacter baumannii</i> Needed for Survival in Human Serum. Journal of Immunology, 2017, 199, 2803-2814.	0.8	43
34	Outer Membrane Targeting of Pseudomonas aeruginosa Proteins Shows Variable Dependence on the Components of Bam and Lol Machineries. MBio, 2011, 2, .	4.1	39
35	Multiple activities of c-di-GMP in Pseudomonas aeruginosa. Nucleic Acids Symposium Series, 2009, 53, 51-52.	0.3	31
36	cAMP and Vfr Control Exolysin Expression and Cytotoxicity of Pseudomonas aeruginosa Taxonomic Outliers. Journal of Bacteriology, 2018, 200, .	2.2	29

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37	Species-specific recruitment of transcription factors dictates toxin expression. Nucleic Acids Research, 2020, 48, 2388-2400.	14.5	28
38	Inhibition of <i>Pseudomonas aeruginosa</i> and <i>Mycobacterium tuberculosis</i> disulfide bond forming enzymes. Molecular Microbiology, 2019, 111, 918-937.	2.5	21
39	Oxygenâ€dependent regulation of câ€diâ€<scp>GMP</scp> synthesis by <scp>SadC</scp> controls alginate production in <scp><i>P</i></scp><i>seudomonas aeruginosa</i>. Environmental Microbiology, 2016, 18, 3390-3402.	3.8	19
40	Insertion sequences drive the emergence of a highly adapted human pathogen. Microbial Genomics, 2020, 6, .	2.0	19
41	The two-component sensor response regulator RoxS/RoxR plays a role in Pseudomonas aeruginosa interactions with airway epithelial cells. Microbes and Infection, 2010, 12, 190-198.	1.9	18
42	The secretome of Acinetobacter baumannii ATCC 17978 type II secretion system reveals a novel plasmid encoded phospholipase that could be implicated in lung colonization. International Journal of Medical Microbiology, 2016, 306, 633-641.	3.6	18
43	Transcriptional Responses of Escherichia coli to a Small-Molecule Inhibitor of LolCDE, an Essential Component of the Lipoprotein Transport Pathway. Journal of Bacteriology, 2016, 198, 3162-3175.	2.2	16
44	The core and accessory Hfq interactomes across Pseudomonas aeruginosa lineages. Nature Communications, 2022, 13, 1258.	12.8	15
45	LTQ-XL mass spectrometry proteome analysis expands the Pseudomonas aeruginosa AmpR regulon to include cyclic di-GMP phosphodiesterases and phosphoproteins, and identifies novel open reading frames. Journal of Proteomics, 2014, 96, 328-342.	2.4	14
46	Pseudomonas-Epithelial Cell Interactions Dissected With DNA Microarrays. Chest, 2002, 121, 36S-39S.	0.8	13
47	Correct Sorting of Lipoproteins into the Inner and Outer Membranes of Pseudomonas aeruginosa by the Escherichia coli LolCDE Transport System. MBio, 2019, 10, .	4.1	13
48	Toward a Comprehensive Analysis of Posttranscriptional Regulatory Networks: a New Tool for the Identification of Small RNA Regulators of Specific mRNAs. MBio, 2021, 12, .	4.1	12
49	The Pseudomonas aeruginosa whole genome sequence: A 20th anniversary celebration. Advances in Microbial Physiology, 2021, 79, 25-88.	2.4	7
50	Conjugative type IVb pilus recognizes lipopolysaccharide of recipient cells to initiate PAPI-1 pathogenicity island transfer in Pseudomonas aeruginosa. BMC Microbiology, 2017, 17, 31.	3.3	6
51	CloG: A pipeline for closing gaps in a draft assembly using short reads. , 2011, , .		4
52	Transcriptional Responses of Pseudomonas aeruginosa to Inhibition of Lipoprotein Transport by a Small Molecule Inhibitor. Journal of Bacteriology, 2020, 202, .	2.2	3
53	In Vitro Activity and the Efficacy of Arbekacin, Cefminox, Fosfomycin, Biapenem Against Gram-Negative Organisms: New Treatment Options?. Proceedings of the National Academy of Sciences India Section B - Biological Sciences, 2016, 86, 749-755.	1.0	2
54	Modulation of Bacterial Lifestyles via Two-Component Regulatory Networks. , 2007, , 311-340.		0