

Laurence Van Melderren

List of Publications by Year in descending order

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96
papers

7,679
citations

57758

44
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56724

83
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99
all docs

99
docs citations

99
times ranked

6410
citing authors

#	ARTICLE	IF	CITATIONS
1	Definitions and guidelines for research on antibiotic persistence. <i>Nature Reviews Microbiology</i> , 2019, 17, 441-448.	28.6	748
2	Bacterial Toxin-antitoxin Systems: More Than Selfish Entities?. <i>PLoS Genetics</i> , 2009, 5, e1000437.	3.5	440
3	Diversity of bacterial type II toxin-antitoxin systems: a comprehensive search and functional analysis of novel families. <i>Nucleic Acids Research</i> , 2011, 39, 5513-5525.	14.5	381
4	Toxin-antitoxin systems: why so many, what for?. <i>Current Opinion in Microbiology</i> , 2010, 13, 781-785.	5.1	291
5	A Systematic and Functional Classification of <i>Streptococcus pyogenes</i> That Serves as a New Tool for Molecular Typing and Vaccine Development. <i>Journal of Infectious Diseases</i> , 2014, 210, 1325-1338.	4.0	257
6	Toxins-antitoxins: diversity, evolution and function. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2011, 46, 386-408.	5.2	254
7	Lon-dependent proteolysis of CcdA is the key control for activation of CcdB in plasmid-free segregant bacteria. <i>Molecular Microbiology</i> , 1994, 11, 1151-1157.	2.5	224
8	Overproduction of the Lon protease triggers inhibition of translation in <i>Escherichia coli</i> : involvement of the yefM-yoeB toxin-antitoxin system. <i>Molecular Microbiology</i> , 2004, 51, 1705-1717.	2.5	211
9	Toxin-Antitoxin Systems as Multilevel Interaction Systems. <i>Toxins</i> , 2014, 6, 304-324.	3.4	205
10	ATP-dependent Degradation of CcdA by Lon Protease. <i>Journal of Biological Chemistry</i> , 1996, 271, 27730-27738.	3.4	191
11	What Is the Benefit to <i>Escherichia coli</i> of Having Multiple Toxin-Antitoxin Systems in Its Genome?. <i>Journal of Bacteriology</i> , 2007, 189, 6101-6108.	2.2	191
12	Biological roles of the Lon ATP-dependent protease. <i>Research in Microbiology</i> , 2006, 157, 701-713.	2.1	189
13	Type II Toxin-Antitoxin Systems: Evolution and Revolutions. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	189
14	The F Plasmid CcdB Protein Induces Efficient ATP-dependent DNA Cleavage by Gyrase. <i>Journal of Molecular Biology</i> , 1993, 234, 534-541.	4.2	180
15	Reassessing the Role of Type II Toxin-Antitoxin Systems in Formation of <i>Escherichia coli</i> Type II Persister Cells. <i>MBio</i> , 2018, 9, .	4.1	174
16	Biology and evolution of bacterial toxin-antitoxin systems. <i>Nature Reviews Microbiology</i> , 2022, 20, 335-350.	28.6	174
17	The Staphylococci Phages Family: An Overview. <i>Viruses</i> , 2012, 4, 3316-3335.	3.3	163
18	Crystal structure of CcdB, a topoisomerase poison from <i>E. coli</i> 1 Edited by T. Richmond. <i>Journal of Molecular Biology</i> , 1999, 285, 1667-1677.	4.2	158

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19	Post-transcriptional global regulation by CsrA in bacteria. Cellular and Molecular Life Sciences, 2010, 67, 2897-2908.	5.4	157
20	The ratio between CcdA and CcdB modulates the transcriptional repression of the ccd poison-antidote system. Molecular Microbiology, 2001, 41, 73-82.	2.5	137
21	Updated model of group A Streptococcus M proteins based on a comprehensive worldwide study. Clinical Microbiology and Infection, 2013, 19, E222-E229.	6.0	135
22	Molecular Basis of Gyrase Poisoning by the Addiction Toxin CcdB. Journal of Molecular Biology, 2005, 348, 1091-1102.	4.2	130
23	Chromosomal Toxin-Antitoxin Systems May Act as Antiaddiction Modules. Journal of Bacteriology, 2008, 190, 4603-4609.	2.2	128
24	Bacterial death by DNA gyrase poisoning. Trends in Microbiology, 1998, 6, 269-275.	7.7	127
25	Structural Basis for Nucleic Acid and Toxin Recognition of the Bacterial Antitoxin CcdA. Journal of Molecular Biology, 2006, 364, 170-185.	4.2	119
26	Single-cell imaging and characterization of <i>Escherichia coli</i> persister cells to ofloxacin in exponential cultures. Science Advances, 2019, 5, eaav9462.	10.3	119
27	Regulation and quality control by Lon-dependent proteolysis. Research in Microbiology, 2009, 160, 645-651.	2.1	110
28	New toxins homologous to ParE belonging to three-component toxin-antitoxin systems in <i>Escherichia coli</i> O157:H7. Molecular Microbiology, 2010, 76, 719-732.	2.5	110
29	Differences in nasopharyngeal bacterial carriage in preschool children from different socio-economic origins. Clinical Microbiology and Infection, 2011, 17, 907-914.	6.0	76
30	Bacterial toxin-antitoxin systems. Mobile Genetic Elements, 2011, 1, 283-306.	1.8	74
31	AtaT blocks translation initiation by N-acetylation of the initiator tRNA ^{Met} . Nature Chemical Biology, 2017, 13, 640-646.	8.0	71
32	The Highly Conserved TldD and TldE Proteins of <i>Escherichia coli</i> Are Involved in Microcin B17 Processing and in CcdA Degradation. Journal of Bacteriology, 2002, 184, 3224-3231.	2.2	64
33	Conditional Essentiality of the <i>csrA</i> Gene in <i>Escherichia coli</i> . Journal of Bacteriology, 2009, 191, 1722-1724.	2.2	64
34	Small-Angle X-Ray Scattering- and Nuclear Magnetic Resonance-Derived Conformational Ensemble of the Highly Flexible Antitoxin PaaA2. Structure, 2014, 22, 854-865.	3.3	61
35	Differences between Belgian and Brazilian Group A Streptococcus Epidemiologic Landscape. PLoS ONE, 2006, 1, e10.	2.5	60
36	The antidote and autoregulatory functions of the F plasmid CcdA protein: a genetic and biochemical survey. Molecular Genetics and Genomics, 1994, 244, 530-538.	2.4	59

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37	F plasmid CcdB killer protein ccdB gene mutants coding for non-cytotoxic proteins which retain their regulatory functions. <i>Molecular Microbiology</i> , 1995, 15, 1031-1037.	2.5	59
38	Molecular interactions of the CcdB poison with its bacterial target, the DNA gyrase. <i>International Journal of Medical Microbiology</i> , 2001, 291, 537-544.	3.6	57
39	Genetic diversity of Group A Streptococcus M protein: Implications for typing and vaccine development. <i>Vaccine</i> , 2008, 26, 5835-5842.	3.8	57
40	Functional Interactions between Coexisting Toxin-Antitoxin Systems of the ccd Family in <i>Escherichia coli</i> O157:H7. <i>Journal of Bacteriology</i> , 2007, 189, 2712-2719.	2.2	55
41	Regulation of acetate metabolism and coordination with the TCA cycle via a processed small RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1043-1052.	7.1	55
42	The Decay of the Chromosomally Encoded <i>ccdO157</i> Toxin-Antitoxin System in the <i>Escherichia coli</i> Species. <i>Genetics</i> , 2009, 181, 1557-1566.	2.9	53
43	Characterization of Novel Phages Isolated in Coagulase-Negative Staphylococci Reveals Evolutionary Relationships with <i>Staphylococcus aureus</i> Phages. <i>Journal of Bacteriology</i> , 2012, 194, 5829-5839.	2.2	50
44	Substrate sequestration by a proteolytically inactive Lon mutant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 6064-6071.	7.1	49
45	Regulatory crosstalk between type I and type II toxin-antitoxin systems in the human pathogen <i>Enterococcus faecalis</i> . <i>RNA Biology</i> , 2015, 12, 1099-1108.	3.1	49
46	Characterization of the <i>phd-doc</i> and <i>ccd</i> Toxin-Antitoxin Cassettes from <i>Vibrio</i> Superintegrons. <i>Journal of Bacteriology</i> , 2013, 195, 2270-2283.	2.2	46
47	A unique hetero-hexameric architecture displayed by the <i>Escherichia coli</i> O157 PaaA-ParE2 antitoxin-toxin complex. <i>Journal of Molecular Biology</i> , 2016, 428, 1589-1603.	4.2	41
48	Sequential multiplex PCR assay for determining capsular serotypes of colonizing <i>S. pneumoniae</i> . <i>BMC Infectious Diseases</i> , 2011, 11, 100.	2.9	40
49	Reassessing the Role of the Type II MqsRA Toxin-Antitoxin System in Stress Response and Biofilm Formation: <i>mqsA</i> Is Transcriptionally Uncoupled from <i>mqsR</i> . <i>MBio</i> , 2019, 10, .	4.1	40
50	Novel toxins from type II toxin-antitoxin systems with acetyltransferase activity. <i>Plasmid</i> , 2017, 93, 30-35.	1.4	38
51	Pharyngitis in Low-Resources Settings: A Pragmatic Clinical Approach to Reduce Unnecessary Antibiotic Use. <i>Pediatrics</i> , 2006, 118, e1607-e1611.	2.1	37
52	Relaxed Cleavage Specificity within the RelE Toxin Family. <i>Journal of Bacteriology</i> , 2013, 195, 2541-2549.	2.2	34
53	Mechanism of regulation and neutralization of the <i>Ata</i> - <i>AtaT</i> toxin-antitoxin system. <i>Nature Chemical Biology</i> , 2019, 15, 285-294.	8.0	33
54	Commentary: What Is the Link between Stringent Response, Endoribonuclease Encoding Type II Toxin-Antitoxin Systems and Persistence?. <i>Frontiers in Microbiology</i> , 2017, 8, 191.	3.5	31

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55	The Variety in the Common Theme of Translation Inhibition by Type II Toxin-Antitoxin Systems. <i>Frontiers in Genetics</i> , 2020, 11, 262.	2.3	30
56	PinA Inhibits ATP Hydrolysis and Energy-dependent Protein Degradation by Lon Protease. <i>Journal of Biological Chemistry</i> , 1998, 273, 524-527.	3.4	29
57	Characterization of a novel temperate phage originating from a cereulide-producing <i>Bacillus cereus</i> strain. <i>Research in Microbiology</i> , 2011, 162, 446-459.	2.1	25
58	Toxin-Antitoxin Gene Pairs Found in Tn ₃ Family Transposons Appear To Be an Integral Part of the Transposition Module. <i>MBio</i> , 2020, 11, .	4.1	25
59	Emerging fluoroquinolone-non-susceptible group A streptococci in two different paediatric populations. <i>International Journal of Antimicrobial Agents</i> , 2009, 34, 44-49.	2.5	24
60	The emm-type diversity does not always reflect the M protein genetic diversity—Is there a case for designer vaccine against GAS. <i>Vaccine</i> , 2010, 28, 883-885.	3.8	24
61	Evidence for an evolutionary antagonism between Mrr and Type III modification systems. <i>Nucleic Acids Research</i> , 2011, 39, 5991-6001.	14.5	21
62	Crystallization of CcdB in complex with a GyrA fragment. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1132-1134.	2.5	20
63	Nosocomial transmission of necrotising fasciitis. <i>Lancet, The</i> , 2010, 375, 1052.	13.7	19
64	The Ribonucleoprotein Csr Network. <i>International Journal of Molecular Sciences</i> , 2013, 14, 22117-22131.	4.1	19
65	Bacterial behavior in human blood reveals complement evaders with some persister-like features. <i>PLoS Pathogens</i> , 2020, 16, e1008893.	4.7	18
66	Purification, Circular Dichroism Analysis, Crystallization and Preliminary X-ray Diffraction Analysis of the F Plasmid CcdB Killer Protein. <i>Journal of Molecular Biology</i> , 1993, 231, 513-515.	4.2	16
67	Group A Streptococcus virulence and host factors in two toddlers with rheumatic fever following toxic shock syndrome. <i>International Journal of Infectious Diseases</i> , 2010, 14, e403-e409.	3.3	15
68	Expression of the F plasmid ccd toxin-antitoxin system in <i>Escherichia coli</i> cells under nutritional stress. <i>Canadian Journal of Microbiology</i> , 2006, 52, 24-30.	1.7	13
69	Growth-dependent recombinant product formation kinetics can be reproduced through engineering of glucose transport and is prone to phenotypic heterogeneity. <i>Microbial Cell Factories</i> , 2019, 18, 26.	4.0	13
70	Bistable Expression of a Toxin-Antitoxin System Located in a Cryptic Prophage of <i>Escherichia coli</i> O157:H7. <i>MBio</i> , 2021, 12, e0294721.	4.1	13
71	Messing up translation from the start: How AtaT inhibits translation initiation in <i>E. coli</i> . <i>RNA Biology</i> , 2018, 15, 303-307.	3.1	11
72	Identification of a metagenomic gene cluster containing a new class A beta-lactamase and toxin-antitoxin systems. <i>MicrobiologyOpen</i> , 2013, 2, 674-683.	3.0	10

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73	Reply to Holden and Errington, "Type II Toxin-Antitoxin Systems and Persister Cells" MBio, 2018, 9, .	4.1	10
74	The ParE2-PaaA2 toxin-antitoxin complex from <i>Escherichia coli</i> O157 forms a heterododecamer in solution and in the crystal. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 724-729.	0.7	9
75	Optimized Method for Measuring Persistence in <i>Escherichia coli</i> with Improved Reproducibility. Methods in Molecular Biology, 2016, 1333, 43-52.	0.9	9
76	Polyclonal dissemination of tetracycline resistance among <i>Streptococcus pyogenes</i> paediatric isolates from Brazil. Journal of Infection in Developing Countries, 2010, 4, 704-711.	1.2	9
77	The role of small proteins in <i>Burkholderia cenocepacia</i> J2315 biofilm formation, persistence and intracellular growth. Biofilm, 2019, 1, 100001.	3.8	7
78	Purification and crystallization of <i>Vibrio fischeri</i> CcdB and its complexes with fragments of gyrase and CcdA. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 356-360.	0.7	5
79	Characterization of culturable <i>Paenibacillus</i> spp. from the snow surface on the high Antarctic Plateau (DOME C) and their dissemination in the Concordia research station. Extremophiles, 2013, 17, 565-573.	2.3	5
80	Carriage-Associated <i>Streptococcus pneumoniae</i> Serotype 1 in Brussels, Belgium. Pediatric Infectious Disease Journal, 2013, 32, 86-87.	2.0	5
81	Crystallization and X-ray analysis of all of the players in the autoregulation of the <i>ataRT</i> toxin-antitoxin system. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 391-401.	0.8	5
82	<i>Escherichia coli</i> Δ EF Toxin-Antitoxin System as a Tool to Target Cell Ablation in Plants. Journal of Molecular Microbiology and Biotechnology, 2016, 26, 277-283.	1.0	4
83	Thermodynamic Stability of the Transcription Regulator PaaR2 from <i>Escherichia coli</i> O157:H7. Biophysical Journal, 2019, 116, 1420-1431.	0.5	4
84	Toxin-Antitoxin Systems and Persistence. , 2019, , 181-202.		4
85	Type II Toxin-Antitoxin Loci: The <i>ccdAB</i> and <i>parDE</i> Families. , 2013, , 45-67.		3
86	Group A <i>Streptococcus</i> Colonies From a Single Throat Swab Can Have Heterogeneous Antimicrobial Susceptibility Patterns. Pediatric Infectious Disease Journal, 2013, 32, 296-298.	2.0	3
87	Crystallization and preliminary X-ray analysis of two variants of the <i>Escherichia coli</i> O157 ParE2-PaaA2 toxin-antitoxin complex. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1284-1291.	0.8	2
88	Sequence-specific ¹ H, ¹⁵ N and ¹³ C resonance assignments of the 23.7-kDa homodimeric toxin CcdB from <i>Vibrio fischeri</i> . Biomolecular NMR Assignments, 2009, 3, 145-147.	0.8	1
89	GhoSTly bacterial persisters. Nature Chemical Biology, 2012, 8, 812-813.	8.0	1
90	¹ H, ¹³ C, and ¹⁵ N backbone and side chain chemical shift assignment of YdaS, a monomeric member of the HigA family. Biomolecular NMR Assignments, 2020, 14, 25-30.	0.8	1

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91	iTDtoest: an Easy-to-Handle and Visual Assay To Detect Tolerant and Persister Cells in an Antibiotic Combination Regimen. MBio, 2022, 13, .	4.1	1
92	Phenotypic Characterization of Antibiotic Persisters at the Single-Cell Level: From Data Acquisition to Data Analysis. Methods in Molecular Biology, 2021, 2357, 95-106.	0.9	0
93	Bacterial behavior in human blood reveals complement evaders with some persister-like features. , 2020, 16, e1008893.		0
94	Bacterial behavior in human blood reveals complement evaders with some persister-like features. , 2020, 16, e1008893.		0
95	Bacterial behavior in human blood reveals complement evaders with some persister-like features. , 2020, 16, e1008893.		0
96	Bacterial behavior in human blood reveals complement evaders with some persister-like features. , 2020, 16, e1008893.		0