

# Laurence Van Melderren

## List of Publications by Year in descending order

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96  
papers

7,679  
citations

57758

44  
h-index

56724

83  
g-index

99  
all docs

99  
docs citations

99  
times ranked

6410  
citing authors

#	ARTICLE	IF	CITATIONS
1	Biology and evolution of bacterial toxin-antitoxin systems. <i>Nature Reviews Microbiology</i> , 2022, 20, 335-350.	28.6	174
2	iTDtest: an Easy-to-Handle and Visual Assay To Detect Tolerant and Persister Cells in an Antibiotic Combination Regimen. <i>MBio</i> , 2022, 13, .	4.1	1
3	Phenotypic Characterization of Antibiotic Persisters at the Single-Cell Level: From Data Acquisition to Data Analysis. <i>Methods in Molecular Biology</i> , 2021, 2357, 95-106.	0.9	0
4	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
5	<sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N backbone and side chain chemical shift assignment of YdaS, a monomeric member of the HigA family. <i>Biomolecular NMR Assignments</i> , 2020, 14, 25-30.	0.8	1
6	Type II Toxin-Antitoxin Systems: Evolution and Revolutions. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	189
7	Toxin-Antitoxin Gene Pairs Found in Tn <i>3</i> Family Transposons Appear To Be an Integral Part of the Transposition Module. <i>MBio</i> , 2020, 11, .	4.1	25
8	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
9	Bacterial behavior in human blood reveals complement evaders with some persister-like features. <i>PLoS Pathogens</i> , 2020, 16, e1008893.	4.7	18
10	Bacterial behavior in human blood reveals complement evaders with some persister-like features. , 2020, 16, e1008893.		0
11	Bacterial behavior in human blood reveals complement evaders with some persister-like features. , 2020, 16, e1008893.		0
12	Bacterial behavior in human blood reveals complement evaders with some persister-like features. , 2020, 16, e1008893.		0
13	Bacterial behavior in human blood reveals complement evaders with some persister-like features. , 2020, 16, e1008893.		0
14	The role of small proteins in <i>Burkholderia cenocepacia</i> J2315 biofilm formation, persistence and intracellular growth. <i>Biofilm</i> , 2019, 1, 100001.	3.8	7
15	Single-cell imaging and characterization of <i>Escherichia coli</i> persister cells to ofloxacin in exponential cultures. <i>Science Advances</i> , 2019, 5, eaav9462.	10.3	119
16	Thermodynamic Stability of the Transcription Regulator PaaR2 from <i>Escherichia coli</i> O157:H7. <i>Biophysical Journal</i> , 2019, 116, 1420-1431.	0.5	4
17	Definitions and guidelines for research on antibiotic persistence. <i>Nature Reviews Microbiology</i> , 2019, 17, 441-448.	28.6	748
18	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

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19	Regulation of acetate metabolism and coordination with the TCA cycle via a processed small RNA. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1043-1052.	7.1	55
20	Toxin-Antitoxin Systems and Persistence. , 2019, , 181-202.		4
21	Mechanism of regulation and neutralization of the AtaRâ€™AtaT toxinâ€™antitoxin system. Nature Chemical Biology, 2019, 15, 285-294.	8.0	33
22	Growth-dependent recombinant product formation kinetics can be reproduced through engineering of glucose transport and is prone to phenotypic heterogeneity. Microbial Cell Factories, 2019, 18, 26.	4.0	13
23	Messing up translation from the start: How AtaT inhibits translation initiation in E. coli. RNA Biology, 2018, 15, 303-307.	3.1	11
24	Reply to Holden and Errington, â€™Type II Toxin-Antitoxin Systems and Persister Cellsâ€™ MBio, 2018, 9, .	4.1	10
25	Crystallization and X-ray analysis of all of the players in the autoregulation of the <i>ataRT</i> toxinâ€™antitoxin system. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 391-401.	0.8	5
26	Reassessing the Role of Type II Toxin-Antitoxin Systems in Formation of Escherichia coli Type II Persister Cells. MBio, 2018, 9, .	4.1	174
27	AtaT blocks translation initiation by N-acetylation of the initiator tRNA <sup>fMet</sup> . Nature Chemical Biology, 2017, 13, 640-646.	8.0	71
28	Novel toxins from type II toxin-antitoxin systems with acetyltransferase activity. Plasmid, 2017, 93, 30-35.	1.4	38
29	Commentary: What Is the Link between Stringent Response, Endoribonuclease Encoding Type II Toxin-Antitoxin Systems and Persistence?. Frontiers in Microbiology, 2017, 8, 191.	3.5	31
30	Escherichia coli mazEF 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
31	A unique hetero-hexameric architecture displayed by the Escherichia coli O157 PaaA2â€™ParE2 antitoxinâ€™toxin complex. Journal of Molecular Biology, 2016, 428, 1589-1603.	4.2	41
32	Optimized Method for Measuring Persistence in Escherichia coli with Improved Reproducibility. Methods in Molecular Biology, 2016, 1333, 43-52.	0.9	9
33	Regulatory crosstalk between type I and type II toxin-antitoxin systems in the human pathogen <i>Enterococcus faecalis</i> . RNA Biology, 2015, 12, 1099-1108.	3.1	49
34	Toxin-Antitoxin Systems as Multilevel Interaction Systems. Toxins, 2014, 6, 304-324.	3.4	205
35	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
36	A Systematic and Functional Classification of Streptococcus pyogenes That Serves as a New Tool for Molecular Typing and Vaccine Development. Journal of Infectious Diseases, 2014, 210, 1325-1338.	4.0	257

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37	Crystallization and preliminary X-ray analysis of two variants of the <i>Escherichia coli</i> O157 ParE2-“PaaA2 toxin-antitoxin complex. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1284-1291.	0.8	2
38	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. <i>Extremophiles</i> , 2013, 17, 565-573.	2.3	5
39	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
40	Relaxed Cleavage Specificity within the RelE Toxin Family. <i>Journal of Bacteriology</i> , 2013, 195, 2541-2549.	2.2	34
41	Type II Toxin-Antitoxin Loci: The <i>ccdAB</i> and <i>parDE</i> Families. , 2013, , 45-67.		3
42	Updated model of group A <i>Streptococcus</i> M proteins based on a comprehensive worldwide study. <i>Clinical Microbiology and Infection</i> , 2013, 19, E222-E229.	6.0	135
43	The Ribonucleoprotein Csr Network. <i>International Journal of Molecular Sciences</i> , 2013, 14, 22117-22131.	4.1	19
44	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
45	Carriage-Associated <i>Streptococcus pneumoniae</i> Serotype 1 in Brussels, Belgium. <i>Pediatric Infectious Disease Journal</i> , 2013, 32, 86-87.	2.0	5
46	Group A <i>Streptococcus</i> Colonies From a Single Throat Swab Can Have Heterogeneous Antimicrobial Susceptibility Patterns. <i>Pediatric Infectious Disease Journal</i> , 2013, 32, 296-298.	2.0	3
47	The Staphylococci Phages Family: An Overview. <i>Viruses</i> , 2012, 4, 3316-3335.	3.3	163
48	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
49	GhoSTly bacterial persists. <i>Nature Chemical Biology</i> , 2012, 8, 812-813.	8.0	1
50	The ParE2-“PaaA2 toxin-antitoxin complex from <i>Escherichia coli</i> O157 forms a heterodoecamer in solution and in the crystal. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 724-729.	0.7	9
51	Bacterial toxin-antitoxin systems. <i>Mobile Genetic Elements</i> , 2011, 1, 283-306.	1.8	74
52	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
53	Differences in nasopharyngeal bacterial carriage in preschool children from different socio-economic origins. <i>Clinical Microbiology and Infection</i> , 2011, 17, 907-914.	6.0	76
54	Toxins-antitoxins: diversity, evolution and function. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2011, 46, 386-408.	5.2	254

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55	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
56	Evidence for an evolutionary antagonism between Mrr and Type III modification systems. <i>Nucleic Acids Research</i> , 2011, 39, 5991-6001.	14.5	21
57	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
58	Post-transcriptional global regulation by CsrA in bacteria. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 2897-2908.	5.4	157
59	New toxins homologous to ParE belonging to three-component toxin-antitoxin systems in <i>Escherichia coli</i> O157:H7. <i>Molecular Microbiology</i> , 2010, 76, 719-732.	2.5	110
60	Toxin-antitoxin systems: why so many, what for?. <i>Current Opinion in Microbiology</i> , 2010, 13, 781-785.	5.1	291
61	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
62	Group A <i>Streptococcus</i> 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
63	Nosocomial transmission of necrotising fasciitis. <i>Lancet, The</i> , 2010, 375, 1052.	13.7	19
64	Polyclonal dissemination of tetracycline resistance among <i>Streptococcus pyogenes</i> paediatric isolates from Brazil. <i>Journal of Infection in Developing Countries</i> , 2010, 4, 704-711.	1.2	9
65	Conditional Essentiality of the <i>csrA</i> Gene in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2009, 191, 1722-1724.	2.2	64
66	Bacterial Toxin-Antitoxin Systems: More Than Selfish Entities?. <i>PLoS Genetics</i> , 2009, 5, e1000437.	3.5	440
67	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
68	Sequence-specific 1H, 15N and 13C resonance assignments of the 23.7-kDa homodimeric toxin CcdB from <i>Vibrio fischeri</i> . <i>Biomolecular NMR Assignments</i> , 2009, 3, 145-147.	0.8	1
69	Regulation and quality control by Lon-dependent proteolysis. <i>Research in Microbiology</i> , 2009, 160, 645-651.	2.1	110
70	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
71	Genetic diversity of Group A <i>Streptococcus</i> M protein: Implications for typing and vaccine development. <i>Vaccine</i> , 2008, 26, 5835-5842.	3.8	57
72	Chromosomal Toxin-Antitoxin Systems May Act as Antiaddiction Modules. <i>Journal of Bacteriology</i> , 2008, 190, 4603-4609.	2.2	128

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73	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
74	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
75	Purification and crystallization of <i>Vibrio fischeri</i> CcdB and its complexes with fragments of gyrase and CcdA. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 356-360.	0.7	5
76	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
77	Structural Basis for Nucleic Acid and Toxin Recognition of the Bacterial Antitoxin CcdA. <i>Journal of Molecular Biology</i> , 2006, 364, 170-185.	4.2	119
78	Biological roles of the Lon ATP-dependent protease. <i>Research in Microbiology</i> , 2006, 157, 701-713.	2.1	189
79	Differences between Belgian and Brazilian Group A <i>Streptococcus</i> Epidemiologic Landscape. <i>PLoS ONE</i> , 2006, 1, e10.	2.5	60
80	Pharyngitis in Low-Resources Settings: A Pragmatic Clinical Approach to Reduce Unnecessary Antibiotic Use. <i>Pediatrics</i> , 2006, 118, e1607-e1611.	2.1	37
81	Molecular Basis of Gyrase Poisoning by the Addiction Toxin CcdB. <i>Journal of Molecular Biology</i> , 2005, 348, 1091-1102.	4.2	130
82	Crystallization of CcdB in complex with a GyrA fragment. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1132-1134.	2.5	20
83	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
84	The Highly Conserved TldD and TldE Proteins of <i>Escherichia coli</i> Are Involved in Microcin B17 Processing and in CcdA Degradation. <i>Journal of Bacteriology</i> , 2002, 184, 3224-3231.	2.2	64
85	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
86	The ratio between CcdA and CcdB modulates the transcriptional repression of the ccd poison-antidote system. <i>Molecular Microbiology</i> , 2001, 41, 73-82.	2.5	137
87	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
88	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
89	Bacterial death by DNA gyrase poisoning. <i>Trends in Microbiology</i> , 1998, 6, 269-275.	7.7	127
90	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

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91	ATP-dependent Degradation of CcdA by Lon Protease. <i>Journal of Biological Chemistry</i> , 1996, 271, 27730-27738.	3.4	191
92	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
93	The antidote and autoregulatory functions of the F plasmid CcdA protein: a genetic and biochemical survey. <i>Molecular Genetics and Genomics</i> , 1994, 244, 530-538.	2.4	59
94	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
95	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
96	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