

# Dan Andersson

## List of Publications by Year in descending order

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212  
papers

21,298  
citations

14655

66  
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11607

135  
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221  
all docs

221  
docs citations

221  
times ranked

20611  
citing authors

#	ARTICLE	IF	CITATIONS
1	Antibiotic resistance and its cost: is it possible to reverse resistance?. Nature Reviews Microbiology, 2010, 8, 260-271.	28.6	1,855
2	Microbiological effects of sublethal levels of antibiotics. Nature Reviews Microbiology, 2014, 12, 465-478.	28.6	1,255
3	Selection of Resistant Bacteria at Very Low Antibiotic Concentrations. PLoS Pathogens, 2011, 7, e1002158.	4.7	1,248
4	Definitions and guidelines for research on antibiotic persistence. Nature Reviews Microbiology, 2019, 17, 441-448.	28.6	748
5	The biological cost of antibiotic resistance. Current Opinion in Microbiology, 1999, 2, 489-493.	5.1	747
6	Mechanisms and consequences of bacterial resistance to antimicrobial peptides. Drug Resistance Updates, 2016, 26, 43-57.	14.4	491
7	Selection of a Multidrug Resistance Plasmid by Sublethal Levels of Antibiotics and Heavy Metals. MBio, 2014, 5, e01918-14.	4.1	451
8	The biological cost of mutational antibiotic resistance: any practical conclusions?. Current Opinion in Microbiology, 2006, 9, 461-465.	5.1	397
9	Effects of Environment on Compensatory Mutations to Ameliorate Costs of Antibiotic Resistance. Science, 2000, 287, 1479-1482.	12.6	388
10	Persistence of antibiotic resistant bacteria. Current Opinion in Microbiology, 2003, 6, 452-456.	5.1	341
11	Persistence of antibiotic resistance in bacterial populations. FEMS Microbiology Reviews, 2011, 35, 901-911.	8.6	325
12	Ohno's dilemma: Evolution of new genes under continuous selection. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17004-17009.	7.1	313
13	Predicting antibiotic resistance. Nature Reviews Microbiology, 2007, 5, 958-965.	28.6	305
14	Evolution of high-level resistance during low-level antibiotic exposure. Nature Communications, 2018, 9, 1599.	12.8	300
15	Bacterial gene amplification: implications for the evolution of antibiotic resistance. Nature Reviews Microbiology, 2009, 7, 578-588.	28.6	299
16	Antibiotic susceptibility testing in less than 30 min using direct single-cell imaging. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9170-9175.	7.1	296
17	Mechanisms and clinical relevance of bacterial heteroresistance. Nature Reviews Microbiology, 2019, 17, 479-496.	28.6	264
18	Evolution of antibiotic resistance at non-lethal drug concentrations. Drug Resistance Updates, 2012, 15, 162-172.	14.4	262

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19	The high prevalence of antibiotic heteroresistance in pathogenic bacteria is mainly caused by gene amplification. <i>Nature Microbiology</i> , 2019, 4, 504-514.	13.3	259
20	Gene Amplification and Adaptive Evolution in Bacteria. <i>Annual Review of Genetics</i> , 2009, 43, 167-195.	7.6	247
21	Effect of <i>rpoB</i> Mutations Conferring Rifampin Resistance on Fitness of <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2004, 48, 1289-1294.	3.2	221
22	Prediction of antibiotic resistance: time for a new preclinical paradigm?. <i>Nature Reviews Microbiology</i> , 2017, 15, 689-696.	28.6	221
23	Biological cost and compensatory evolution in fusidic acid-resistant <i>Staphylococcus aureus</i> . <i>Molecular Microbiology</i> , 2001, 40, 433-439.	2.5	217
24	Adaptation to the deleterious effects of antimicrobial drug resistance mutations by compensatory evolution. <i>Research in Microbiology</i> , 2004, 155, 360-369.	2.1	216
25	Biological Costs and Mechanisms of Fosfomycin Resistance in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 2850-2858.	3.2	213
26	Selection-Driven Gene Loss in Bacteria. <i>PLoS Genetics</i> , 2012, 8, e1002787.	3.5	206
27	Compensatory adaptation to the deleterious effect of antibiotic resistance in <i>Salmonella typhimurium</i> . <i>Molecular Microbiology</i> , 2002, 46, 355-366.	2.5	205
28	Real-Time Evolution of New Genes by Innovation, Amplification, and Divergence. <i>Science</i> , 2012, 338, 384-387.	12.6	202
29	Evolutionary consequences of drug resistance: shared principles across diverse targets and organisms. <i>Nature Reviews Genetics</i> , 2015, 16, 459-471.	16.3	201
30	The cyclotide cycloviolacin O2 from <i>Viola odorata</i> has potent bactericidal activity against Gram-negative bacteria. <i>Journal of Antimicrobial Chemotherapy</i> , 2010, 65, 1964-1971.	3.0	179
31	Evolutionary Trajectories to Antibiotic Resistance. <i>Annual Review of Microbiology</i> , 2017, 71, 579-596.	7.3	179
32	Whole-genome mutational biases in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17878-17883.	7.1	177
33	Muller's ratchet decreases fitness of a DNA-based microbe.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 906-907.	7.1	172
34	Amplification-induced mutagenesis: Evidence that directed adaptive mutation and general hypermutability result from growth with a selected gene amplification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 2164-2169.	7.1	159
35	Origin of Mutations Under Selection: The Adaptive Mutation Controversy. <i>Annual Review of Microbiology</i> , 2006, 60, 477-501.	7.3	158
36	Nitrofurantoin resistance mechanism and fitness cost in <i>Escherichia coli</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2008, 62, 495-503.	3.0	157

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37	Antibiotic resistance: turning evolutionary principles into clinical reality. FEMS Microbiology Reviews, 2020, 44, 171-188.	8.6	154
38	Establishment of a Superficial Skin Infection Model in Mice by Using Staphylococcus aureus and Streptococcus pyogenes. Antimicrobial Agents and Chemotherapy, 2005, 49, 3435-3441.	3.2	149
39	Comparative proteome analysis of Mycobacterium tuberculosis grown under aerobic and anaerobic conditions. Microbiology (United Kingdom), 2004, 150, 3821-3829.	1.8	144
40	Genomic buffering mitigates the effects of deleterious mutations in bacteria. Nature Genetics, 2005, 37, 1376-1379.	21.4	142
41	Selection of resistance at lethal and non-lethal antibiotic concentrations. Current Opinion in Microbiology, 2012, 15, 555-560.	5.1	141
42	Long-Term Persistence of Resistant <i>Enterococcus</i> Species after Antibiotics To Eradicate <i>Helicobacter pylori</i> . Annals of Internal Medicine, 2003, 139, 483.	3.9	140
43	The cost of antibiotic resistance from a bacterial perspective. Drug Resistance Updates, 2000, 3, 237-245.	14.4	137
44	Translation rates and misreading characteristics of rpsD mutants in Escherichia coli. Molecular Genetics and Genomics, 1982, 187, 467-472.	2.4	134
45	Transfer of an Escherichia coli ST131 multiresistance cassette has created a Klebsiella pneumoniae-specific plasmid associated with a major nosocomial outbreak. Journal of Antimicrobial Chemotherapy, 2012, 67, 74-83.	3.0	133
46	Novel ribosomal mutations affecting translational accuracy, antibiotic resistance and virulence of Salmonella typhimurium. Molecular Microbiology, 1999, 31, 53-58.	2.5	130
47	Evolution of New Functions De Novo and from Preexisting Genes. Cold Spring Harbor Perspectives in Biology, 2015, 7, a017996.	5.5	129
48	Potential of Tetracycline Resistance Proteins To Evolve Tigecycline Resistance. Antimicrobial Agents and Chemotherapy, 2016, 60, 789-796.	3.2	127
49	Reduction of the fitness burden of quinolone resistance in Pseudomonas aeruginosa. Journal of Antimicrobial Chemotherapy, 2005, 55, 22-30.	3.0	116
50	Reducing the fitness cost of antibiotic resistance by amplification of initiator tRNA genes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6976-6981.	7.1	116
51	Environmental and genetic modulation of the phenotypic expression of antibiotic resistance. FEMS Microbiology Reviews, 2017, 41, 374-391.	8.6	112
52	Genetic Analysis of Colistin Resistance in <i>Salmonella enterica</i> Serovar Typhimurium. Antimicrobial Agents and Chemotherapy, 2009, 53, 2298-2305.	3.2	107
53	Compensatory gene amplification restores fitness after inter-species gene replacements. Molecular Microbiology, 2010, 75, 1078-1089.	2.5	106
54	Mutational Robustness of Ribosomal Protein Genes. Science, 2010, 330, 825-827.	12.6	105

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55	Directed mutagenesis of <i>Mycobacterium smegmatis</i> 16S rRNA to reconstruct the <i>in vivo</i> evolution of aminoglycoside resistance in <i>Mycobacterium tuberculosis</i> . <i>Molecular Microbiology</i> , 2010, 77, 830-840.	2.5	97
56	Contribution of Gene Amplification to Evolution of Increased Antibiotic Resistance in <i>Salmonella typhimurium</i> . <i>Genetics</i> , 2009, 182, 1183-1195.	2.9	96
57	Multiple pathways of selected gene amplification during adaptive mutation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17319-17324.	7.1	89
58	The Fitness Cost of Streptomycin Resistance Depends on <i>rpsL</i> Mutation, Carbon Source and RpoS (Ifs). <i>Genetics</i> , 2009, 183, 539-546.	2.9	88
59	Activation of cryptic aminoglycoside resistance in <i>Salmonella enterica</i> . <i>Molecular Microbiology</i> , 2011, 80, 1464-1478.	2.5	84
60	The first major extended-spectrum $\beta$ -lactamase outbreak in Scandinavia was caused by clonal spread of a multiresistant <i>Klebsiella pneumoniae</i> producing CTX-M-15. <i>Apmis</i> , 2008, 116, 302-8.	2.0	83
61	Adaptive mutation: General mutagenesis is not a programmed response to stress but results from rare coamplification of <i>dinB</i> with <i>lac</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12847-12852.	7.1	82
62	High Fitness Costs and Instability of Gene Duplications Reduce Rates of Evolution of New Genes by Duplication-Divergence Mechanisms. <i>Molecular Biology and Evolution</i> , 2014, 31, 1526-1535.	8.9	82
63	Cellular hysteresis as a principle to maximize the efficacy of antibiotic therapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 9767-9772.	7.1	81
64	Beyond serial passages: new methods for predicting the emergence of resistance to novel antibiotics. <i>Current Opinion in Pharmacology</i> , 2011, 11, 439-445.	3.5	80
65	<i>Salmonella typhimurium</i> mutants that downregulate phagocyte nitric oxide production. <i>Cellular Microbiology</i> , 2000, 2, 239-250.	2.1	78
66	Amdinocillin (Mecillinam) Resistance Mutations in Clinical Isolates and Laboratory-Selected Mutants of <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 1718-1727.	3.2	78
67	Mechanisms and fitness costs of tigecycline resistance in <i>Escherichia coli</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 2809-2819.	3.0	77
68	Polymorphic Mutation Frequencies in <i>Escherichia coli</i> : Emergence of Weak Mutators in Clinical Isolates. <i>Journal of Bacteriology</i> , 2004, 186, 5538-5542.	2.2	74
69	Antimicrobial peptide exposure selects for <i>Staphylococcus aureus</i> resistance to human defence peptides. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 115-127.	3.0	74
70	Evolution of Antibiotic Resistance without Antibiotic Exposure. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	73
71	Genetic Adaptation to Growth Under Laboratory Conditions in <i>Escherichia coli</i> and <i>Salmonella enterica</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 756.	3.5	70
72	Experimental Adaptation of <i>Salmonella typhimurium</i> to Mice. <i>Genetics</i> , 2004, 168, 1119-1130.	2.9	68

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73	A General Method for Rapid Determination of Antibiotic Susceptibility and Species in Bacterial Infections. <i>Journal of Clinical Microbiology</i> , 2015, 53, 425-432.	3.9	68
74	Combinations of mutations in <i>envZ</i> , <i>ftsL</i> , <i>mrdA</i> , <i>acrB</i> and <i>acrR</i> can cause high-level carbapenem resistance in <i>Escherichia coli</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 1188-1198.	3.0	68
75	Predictable Phenotypes of Antibiotic Resistance Mutations. <i>MBio</i> , 2018, 9, .	4.1	68
76	Mechanism and Fitness Costs of PR-39 Resistance in <i>Salmonella enterica</i> Serovar Typhimurium LT2. <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 2734-2741.	3.2	67
77	Unstable tandem gene amplification generates heteroresistance (variation in resistance within a) Tj ETQq1 1 0.784314 rgBT /Overlock 1	2.5	67
78	Mechanisms and Fitness Costs of Resistance to Antimicrobial Peptides LL-37, CNY100HL and Wheat Germ Histones. <i>PLoS ONE</i> , 2013, 8, e68875.	2.5	66
79	Indirect resistance to several classes of antibiotics in cocultures with resistant bacteria expressing antibiotic-modifying or -degrading enzymes. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 100-110.	3.0	64
80	Collateral sensitivity constrains resistance evolution of the CTX-M-15 $\beta$ -lactamase. <i>Nature Communications</i> , 2019, 10, 618.	12.8	64
81	Transfer and Persistence of a Multi-Drug Resistance Plasmid in situ of the Infant Gut Microbiota in the Absence of Antibiotic Treatment. <i>Frontiers in Microbiology</i> , 2017, 8, 1852.	3.5	63
82	An adenosyl-cobalamin (coenzyme-B12)-repressed translational enhancer in the <i>cob</i> mRNA of <i>Salmonella typhimurium</i> . <i>Molecular Microbiology</i> , 2001, 39, 1585-1594.	2.5	61
83	Multiple mechanisms to ameliorate the fitness burden of mupirocin resistance in <i>Salmonella typhimurium</i> . <i>Molecular Microbiology</i> , 2007, 64, 1038-1048.	2.5	60
84	Persistence of Resistant <i>Staphylococcus epidermidis</i> after Single Course of Clarithromycin. <i>Emerging Infectious Diseases</i> , 2005, 11, 1389-1393.	4.3	59
85	<i>Lon</i> protease inactivation, or translocation of the <i>lon</i> gene, potentiate bacterial evolution to antibiotic resistance. <i>Molecular Microbiology</i> , 2013, 90, 1233-1248.	2.5	59
86	Selection of Orphan Rhs Toxin Expression in Evolved <i>Salmonella enterica</i> Serovar Typhimurium. <i>PLoS Genetics</i> , 2014, 10, e1004255.	3.5	56
87	Compensatory Evolution Reveals Functional Interactions between Ribosomal Proteins S12, L14 and L19. <i>Journal of Molecular Biology</i> , 2007, 366, 207-215.	4.2	55
88	Selection and Transmission of Antibiotic-Resistant Bacteria. <i>Microbiology Spectrum</i> , 2017, 5, .	3.0	55
89	Regulating General Mutation Rates: Examination of the Hypermutable State Model for Cairnsian Adaptive Mutation. <i>Genetics</i> , 2003, 163, 1483-1496.	2.9	55
90	Suboptimal growth with hyper-accurate ribosomes. <i>Archives of Microbiology</i> , 1986, 144, 96-101.	2.2	54

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91	The physiology and genetics of bacterial responses to antibiotic combinations. <i>Nature Reviews Microbiology</i> , 2022, 20, 478-490.	28.6	54
92	Molecular mechanisms of collateral sensitivity to the antibiotic nitrofurantoin. <i>PLoS Biology</i> , 2020, 18, e3000612.	5.6	53
93	Cobalamin (vitamin B12) repression of the Cob operon in <i>Salmonella typhimurium</i> requires sequences within the leader and the first translated open reading frame. <i>Molecular Microbiology</i> , 1992, 6, 743-749.	2.5	52
94	Bacteria with increased mutation frequency and antibiotic resistance are enriched in the commensal flora of patients with high antibiotic usage. <i>Journal of Antimicrobial Chemotherapy</i> , 2003, 52, 645-650.	3.0	52
95	Functional interactions between mutated forms of ribosomal proteins S4, S5 and S12. <i>Biochimie</i> , 1986, 68, 705-713.	2.6	51
96	Influence of acquired $\beta$ -lactamases on the evolution of spontaneous carbapenem resistance in <i>Escherichia coli</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 51-59.	3.0	49
97	Public awareness and individual responsibility needed for judicious use of antibiotics: a qualitative study of public beliefs and perceptions. <i>BMC Public Health</i> , 2018, 18, 1153.	2.9	49
98	Metabolic fitness landscapes predict the evolution of antibiotic resistance. <i>Nature Ecology and Evolution</i> , 2021, 5, 677-687.	7.8	49
99	Fitness of antibiotic resistant <i>Staphylococcus epidermidis</i> assessed by competition on the skin of human volunteers. <i>Journal of Antimicrobial Chemotherapy</i> , 2003, 52, 258-263.	3.0	46
100	Genome Dynamics of <i>Escherichia coli</i> during Antibiotic Treatment: Transfer, Loss, and Persistence of Genetic Elements In situ of the Infant Gut. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 126.	3.9	46
101	Minor Fitness Costs in an Experimental Model of Horizontal Gene Transfer in Bacteria. <i>Molecular Biology and Evolution</i> , 2014, 31, 1220-1227.	8.9	45
102	Amelioration of the Fitness Costs of Antibiotic Resistance Due To Reduced Outer Membrane Permeability by Upregulation of Alternative Porins. <i>Molecular Biology and Evolution</i> , 2015, 32, msv195.	8.9	45
103	Compensating the Fitness Costs of Synonymous Mutations. <i>Molecular Biology and Evolution</i> , 2016, 33, 1461-1477.	8.9	45
104	The Tandem Inversion Duplication in <i>Salmonella enterica</i> : Selection Drives Unstable Precursors to Final Mutation Types. <i>Genetics</i> , 2010, 185, 65-80.	2.9	43
105	Functional Constraints on Replacing an Essential Gene with Its Ancient and Modern Homologs. <i>MBio</i> , 2017, 8, .	4.1	42
106	Evolution of new gene functions: simulation and analysis of the amplification model. <i>Genetica</i> , 2009, 135, 309-324.	1.1	40
107	Nonmutational compensation of the fitness cost of antibiotic resistance in mycobacteria by overexpression of <i>tlyA</i> rRNA methylase. <i>Rna</i> , 2016, 22, 1836-1843.	3.5	40
108	Resistance to $\beta$ -Lactam Antibiotics Conferred by Point Mutations in Penicillin-Binding Proteins PBP3, PBP4 and PBP6 in <i>Salmonella enterica</i> . <i>PLoS ONE</i> , 2014, 9, e97202.	2.5	40

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109	Dynamics of Antibiotic Resistant Mycobacterium tuberculosis during Long-Term Infection and Antibiotic Treatment. PLoS ONE, 2011, 6, e21147.	2.5	38
110	Escape from growth restriction in small colony variants of <i>Salmonella typhimurium</i> by gene amplification and mutation. Molecular Microbiology, 2011, 79, 305-315.	2.5	38
111	Improving predictions of the risk of resistance development against new and old antibiotics. Clinical Microbiology and Infection, 2015, 21, 894-898.	6.0	38
112	Fusidic Acid-Resistant Mutants of Salmonella enterica Serovar Typhimurium with Low Fitness In Vivo Are Defective in RpoS Induction. Antimicrobial Agents and Chemotherapy, 2003, 47, 3743-3749.	3.2	37
113	Pharmacodynamic Model To Describe the Concentration-Dependent Selection of Cefotaxime-Resistant Escherichia coli. Antimicrobial Agents and Chemotherapy, 2005, 49, 5081-5091.	3.2	36
114	Adaptive Mutation: How Growth under Selection Stimulates Lac+ Reversion by Increasing Target Copy Number. Journal of Bacteriology, 2004, 186, 4855-4860.	2.2	35
115	Amplification “mutagenesis” how growth under selection contributes to the origin of genetic diversity and explains the phenomenon of adaptive mutation. Research in Microbiology, 2004, 155, 342-351.	2.1	35
116	A mechanism-based pharmacokinetic/pharmacodynamic model allows prediction of antibiotic killing from MIC values for WT and mutants. Journal of Antimicrobial Chemotherapy, 2015, 70, 3051-3060.	3.0	35
117	Duplication-Insertion Recombineering: a fast and scar-free method for efficient transfer of multiple mutations in bacteria. Nucleic Acids Research, 2017, 45, e33-e33.	14.5	35
118	Genome-Wide Detection of Spontaneous Chromosomal Rearrangements in Bacteria. PLoS ONE, 2012, 7, e42639.	2.5	35
119	<i>De Novo</i> Emergence of Peptides That Confer Antibiotic Resistance. MBio, 2019, 10, .	4.1	34
120	Mechanisms and physiological effects of protamine resistance in Salmonella enterica serovar Typhimurium LT2. Journal of Antimicrobial Chemotherapy, 2010, 65, 876-887.	3.0	33
121	Evidence That Selected Amplification of a Bacterial <i>lac</i> Frameshift Allele Stimulates Lac+ Reversion (Adaptive Mutation) With or Without General Hypermutability. Genetics, 2002, 161, 945-956.	2.9	33
122	Caenorhabditis elegans as a Model To Determine Fitness of Antibiotic-Resistant Salmonella enterica Serovar Typhimurium. Antimicrobial Agents and Chemotherapy, 2007, 51, 766-769.	3.2	31
123	Pharmacokinetics and Pharmacodynamics of Fosfomycin and Its Activity against Extended-Spectrum-β-Lactamase-, Plasmid-Mediated AmpC-, and Carbapenemase-Producing Escherichia coli in a Murine Urinary Tract Infection Model. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	31
124	The effect of genomic position on reversion of a <i>lac</i> frameshift mutation ( <i>lacZ33</i> ) during nonlethal selection (adaptive mutation). Molecular Microbiology, 2002, 44, 1017-1032.	2.5	30
125	Ribosomes Lacking Protein S20 Are Defective in mRNA Binding and Subunit Association. Journal of Molecular Biology, 2010, 397, 767-776.	4.2	28
126	Mechanisms and therapeutic potential of collateral sensitivity to antibiotics. PLoS Pathogens, 2021, 17, e1009172.	4.7	28



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127	Amplification of the Gene for Isoleucyl-tRNA Synthetase Facilitates Adaptation to the Fitness Cost of Mupirocin Resistance in <i>Salmonella enterica</i> . <i>Genetics</i> , 2010, 185, 305-312.	2.9	27
128	Structural and functional innovations in the real-time evolution of new (12±) <sub>8</sub> barrel enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4727-4732.	7.1	26
129	Involvement of the Arc system in redox regulation of the Cob operon in <i>Salmonella typhimurium</i> . <i>Molecular Microbiology</i> , 1992, 6, 1491-1494.	2.5	25
130	The Amplification Model for Adaptive Mutation. <i>Genetics</i> , 2005, 169, 1105-1115.	2.9	25
131	Activation of initiation factor 2 by ligands and mutations for rapid docking of ribosomal subunits. <i>EMBO Journal</i> , 2011, 30, 289-301.	7.8	25
132	Variation in Mutational Robustness between Different Proteins and the Predictability of Fitness Effects. <i>Molecular Biology and Evolution</i> , 2016, 34, msw239.	8.9	24
133	CombiANT: Antibiotic interaction testing made easy. <i>PLoS Biology</i> , 2020, 18, e3000856.	5.6	24
134	Biological roles of translesion synthesis DNA polymerases in eubacteria. <i>Molecular Microbiology</i> , 2010, 77, 540-548.	2.5	23
135	Can a pharmacokinetic/pharmacodynamic (PKPD) model be predictive across bacterial densities and strains? External evaluation of a PKPD model describing longitudinal in vitro data. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 3108-3116.	3.0	23
136	A novel type of colistin resistance genes selected from random sequence space. <i>PLoS Genetics</i> , 2021, 17, e1009227.	3.5	23
137	Antibiotic treatment in vitro of phenotypically tolerant bacterial populations. <i>Journal of Antimicrobial Chemotherapy</i> , 2007, 59, 254-263.	3.0	22
138	Error-prone initiation factor 2 mutations reduce the fitness cost of antibiotic resistance. <i>Molecular Microbiology</i> , 2010, 75, 1299-1313.	2.5	22
139	Restored fitness leads to long-term persistence of resistant <i>Bacteroides</i> strains in the human intestine. <i>Anaerobe</i> , 2008, 14, 157-160.	2.1	21
140	Reversion of High-level Mecillinam Resistance to Susceptibility in <i>Escherichia coli</i> During Growth in Urine. <i>EBioMedicine</i> , 2017, 23, 111-118.	6.1	21
141	Experimental Determination and Prediction of the Fitness Effects of Random Point Mutations in the Biosynthetic Enzyme HisA. <i>Molecular Biology and Evolution</i> , 2018, 35, 704-718.	8.9	21
142	Long-term carriage and rapid transmission of extended spectrum beta-lactamase-producing <i>E. coli</i> within a flock of Mallards in the absence of antibiotic selection. <i>Environmental Microbiology Reports</i> , 2018, 10, 576-582.	2.4	20
143	Fitness Costs of Synonymous Mutations in the rpsT Gene Can Be Compensated by Restoring mRNA Base Pairing. <i>PLoS ONE</i> , 2013, 8, e63373.	2.5	19
144	A bacteriophage enzyme induces bacterial metabolic perturbation that confers a novel promiscuous function. <i>Nature Ecology and Evolution</i> , 2018, 2, 1321-1330.	7.8	19

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145	Fitness of <i>Escherichia coli</i> mutants with reduced susceptibility to tigecycline. Journal of Antimicrobial Chemotherapy, 2016, 71, 1307-1313.	3.0	18
146	Salmonella typhimurium cobmutants are not hyper-virulent. FEMS Microbiology Letters, 1996, 139, 121-126.	1.8	17
147	The highly dynamic nature of bacterial heteroresistance impairs its clinical detection. Communications Biology, 2021, 4, 521.	4.4	17
148	Pathoadaptive Mutations in Salmonella enterica Isolated after Serial Passage in Mice. PLoS ONE, 2013, 8, e70147.	2.5	16
149	Structure of AadA from <i>Salmonella enterica</i> : a monomeric aminoglycoside (3'-phosphotransferase) adenylyltransferase. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2267-2277.	2.5	16
150	Different adaptive strategies in E. coli populations evolving under macronutrient limitation and metal ion limitation. BMC Evolutionary Biology, 2018, 18, 72.	3.2	16
151	No beneficial fitness effects of random peptides. Nature Ecology and Evolution, 2018, 2, 1046-1047.	7.8	16
152	Mutations that increase expression of the EmrAB-TolC efflux pump confer increased resistance to nitroxoline in Escherichia coli. Journal of Antimicrobial Chemotherapy, 2020, 75, 300-308.	3.0	16
153	Translesion DNA polymerases are required for spontaneous deletion formation in <i>Salmonella typhimurium</i> . Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10248-10253.	7.1	15
154	Effect of Translesion DNA Polymerases, Endonucleases and RpoS on Mutation Rates in <i>Salmonella typhimurium</i> . Genetics, 2010, 185, 783-795.	2.9	15
155	A portable epigenetic switch for bistable gene expression in bacteria. Scientific Reports, 2019, 9, 11261.	3.3	15
156	Structure and mechanism of a phage-encoded SAM lyase revises catalytic function of enzyme family. ELife, 2021, 10, .	6.0	15
157	A Microfluidic Chip for Studies of the Dynamics of Antibiotic Resistance Selection in Bacterial Biofilms. Frontiers in Cellular and Infection Microbiology, 2022, 12, .	3.9	15
158	Fitness of Salmonella mutants resistant to antimicrobial peptides. Journal of Antimicrobial Chemotherapy, 2015, 70, 432-440.	3.0	14
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