

Dan Andersson

List of Publications by Year in descending order

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212
papers

21,298
citations

14614

66
h-index

11581

135
g-index

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?. <i>Nature Reviews Microbiology</i> , 2010, 8, 260-271.	13.6	1,855
2	Microbiological effects of sublethal levels of antibiotics. <i>Nature Reviews Microbiology</i> , 2014, 12, 465-478.	13.6	1,255
3	Selection of Resistant Bacteria at Very Low Antibiotic Concentrations. <i>PLoS Pathogens</i> , 2011, 7, e1002158.	2.1	1,248
4	Definitions and guidelines for research on antibiotic persistence. <i>Nature Reviews Microbiology</i> , 2019, 17, 441-448.	13.6	748
5	The biological cost of antibiotic resistance. <i>Current Opinion in Microbiology</i> , 1999, 2, 489-493.	2.3	747
6	Mechanisms and consequences of bacterial resistance to antimicrobial peptides. <i>Drug Resistance Updates</i> , 2016, 26, 43-57.	6.5	491
7	Selection of a Multidrug Resistance Plasmid by Sublethal Levels of Antibiotics and Heavy Metals. <i>MBio</i> , 2014, 5, e01918-14.	1.8	451
8	The biological cost of mutational antibiotic resistance: any practical conclusions?. <i>Current Opinion in Microbiology</i> , 2006, 9, 461-465.	2.3	397
9	Effects of Environment on Compensatory Mutations to Ameliorate Costs of Antibiotic Resistance. <i>Science</i> , 2000, 287, 1479-1482.	6.0	388
10	Persistence of antibiotic resistant bacteria. <i>Current Opinion in Microbiology</i> , 2003, 6, 452-456.	2.3	341
11	Persistence of antibiotic resistance in bacterial populations. <i>FEMS Microbiology Reviews</i> , 2011, 35, 901-911.	3.9	325
12	Ohno's dilemma: Evolution of new genes under continuous selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17004-17009.	3.3	313
13	Predicting antibiotic resistance. <i>Nature Reviews Microbiology</i> , 2007, 5, 958-965.	13.6	305
14	Evolution of high-level resistance during low-level antibiotic exposure. <i>Nature Communications</i> , 2018, 9, 1599.	5.8	300
15	Bacterial gene amplification: implications for the evolution of antibiotic resistance. <i>Nature Reviews Microbiology</i> , 2009, 7, 578-588.	13.6	299
16	Antibiotic susceptibility testing in less than 30 min using direct single-cell imaging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9170-9175.	3.3	296
17	Mechanisms and clinical relevance of bacterial heteroresistance. <i>Nature Reviews Microbiology</i> , 2019, 17, 479-496.	13.6	264
18	Evolution of antibiotic resistance at non-lethal drug concentrations. <i>Drug Resistance Updates</i> , 2012, 15, 162-172.	6.5	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.	5.9	259
20	Gene Amplification and Adaptive Evolution in Bacteria. <i>Annual Review of Genetics</i> , 2009, 43, 167-195.	3.2	247
21	Effect of rpoB Mutations Conferring Rifampin Resistance on Fitness of <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2004, 48, 1289-1294.	1.4	221
22	Prediction of antibiotic resistance: time for a new preclinical paradigm?. <i>Nature Reviews Microbiology</i> , 2017, 15, 689-696.	13.6	221
23	Biological cost and compensatory evolution in fusidic acid-resistant <i>Staphylococcus aureus</i> . <i>Molecular Microbiology</i> , 2001, 40, 433-439.	1.2	217
24	Adaptation to the deleterious effects of antimicrobial drug resistance mutations by compensatory evolution. <i>Research in Microbiology</i> , 2004, 155, 360-369.	1.0	216
25	Biological Costs and Mechanisms of Fosfomycin Resistance in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 2850-2858.	1.4	213
26	Selection-Driven Gene Loss in Bacteria. <i>PLoS Genetics</i> , 2012, 8, e1002787.	1.5	206
27	Compensatory adaptation to the deleterious effect of antibiotic resistance in <i>Salmonella typhimurium</i> . <i>Molecular Microbiology</i> , 2002, 46, 355-366.	1.2	205
28	Real-Time Evolution of New Genes by Innovation, Amplification, and Divergence. <i>Science</i> , 2012, 338, 384-387.	6.0	202
29	Evolutionary consequences of drug resistance: shared principles across diverse targets and organisms. <i>Nature Reviews Genetics</i> , 2015, 16, 459-471.	7.7	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.	1.3	179
31	Evolutionary Trajectories to Antibiotic Resistance. <i>Annual Review of Microbiology</i> , 2017, 71, 579-596.	2.9	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.	3.3	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.	3.3	172
34	Amplification-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.	3.3	159
35	Origin of Mutations Under Selection: The Adaptive Mutation Controversy. <i>Annual Review of Microbiology</i> , 2006, 60, 477-501.	2.9	158
36	Nitrofurantoin resistance mechanism and fitness cost in <i>Escherichia coli</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2008, 62, 495-503.	1.3	157

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37	Antibiotic resistance: turning evolutionary principles into clinical reality. <i>FEMS Microbiology Reviews</i> , 2020, 44, 171-188.	3.9	154
38	Establishment of a Superficial Skin Infection Model in Mice by Using <i>Staphylococcus aureus</i> and <i>Streptococcus pyogenes</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 3435-3441.	1.4	149
39	Comparative proteome analysis of <i>Mycobacterium tuberculosis</i> grown under aerobic and anaerobic conditions. <i>Microbiology (United Kingdom)</i> , 2004, 150, 3821-3829.	0.7	144
40	Genomic buffering mitigates the effects of deleterious mutations in bacteria. <i>Nature Genetics</i> , 2005, 37, 1376-1379.	9.4	142
41	Selection of resistance at lethal and non-lethal antibiotic concentrations. <i>Current Opinion in Microbiology</i> , 2012, 15, 555-560.	2.3	141
42	Long-Term Persistence of Resistant <i>Enterococcus</i> Species after Antibiotics To Eradicate <i>Helicobacter pylori</i> . <i>Annals of Internal Medicine</i> , 2003, 139, 483.	2.0	140
43	The cost of antibiotic resistance from a bacterial perspective. <i>Drug Resistance Updates</i> , 2000, 3, 237-245.	6.5	137
44	Translation rates and misreading characteristics of rpsD mutants in <i>Escherichia coli</i> . <i>Molecular Genetics and Genomics</i> , 1982, 187, 467-472.	2.4	134
45	Transfer of an <i>Escherichia coli</i> ST131 multiresistance cassette has created a <i>Klebsiella pneumoniae</i> -specific plasmid associated with a major nosocomial outbreak. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 74-83.	1.3	133
46	Novel ribosomal mutations affecting translational accuracy, antibiotic resistance and virulence of <i>Salmonella typhimurium</i> . <i>Molecular Microbiology</i> , 1999, 31, 53-58.	1.2	130
47	Evolution of New Functions De Novo and from Preexisting Genes. <i>Cold Spring Harbor Perspectives in Biology</i> , 2015, 7, a017996.	2.3	129
48	Potential of Tetracycline Resistance Proteins To Evolve Tigecycline Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 789-796.	1.4	127
49	Reduction of the fitness burden of quinolone resistance in <i>Pseudomonas aeruginosa</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2005, 55, 22-30.	1.3	116
50	Reducing the fitness cost of antibiotic resistance by amplification of initiator tRNA genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6976-6981.	3.3	116
51	Environmental and genetic modulation of the phenotypic expression of antibiotic resistance. <i>FEMS Microbiology Reviews</i> , 2017, 41, 374-391.	3.9	112
52	Genetic Analysis of Colistin Resistance in <i>Salmonella enterica</i> Serovar Typhimurium. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 2298-2305.	1.4	107
53	Compensatory gene amplification restores fitness after inter-species gene replacements. <i>Molecular Microbiology</i> , 2010, 75, 1078-1089.	1.2	106
54	Mutational Robustness of Ribosomal Protein Genes. <i>Science</i> , 2010, 330, 825-827.	6.0	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.	1.2	97
56	Contribution of Gene Amplification to Evolution of Increased Antibiotic Resistance in <i>Salmonella typhimurium</i> . <i>Genetics</i> , 2009, 182, 1183-1195.	1.2	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.	3.3	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.	1.2	88
59	Activation of cryptic aminoglycoside resistance in <i>Salmonella enterica</i> . <i>Molecular Microbiology</i> , 2011, 80, 1464-1478.	1.2	84
60	The first major extended-spectrum β -lactamase outbreak in Scandinavia was caused by clonal spread of a multiresistant <i>Klebsiella pneumoniae</i> producing CTX-M β 15. <i>Apmis</i> , 2008, 116, 302-8.	0.9	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.	3.3	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.	3.5	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.	3.3	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.	1.7	80
65	<i>Salmonella typhimurium</i> mutants that downregulate phagocyte nitric oxide production. <i>Cellular Microbiology</i> , 2000, 2, 239-250.	1.1	78
66	Aminocillin (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.	1.4	78
67	Mechanisms and fitness costs of tigecycline resistance in <i>Escherichia coli</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 2809-2819.	1.3	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.	1.0	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.	1.3	74
70	Evolution of Antibiotic Resistance without Antibiotic Exposure. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	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.	1.5	70
72	Experimental Adaptation of <i>Salmonella typhimurium</i> to Mice. <i>Genetics</i> , 2004, 168, 1119-1130.	1.2	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.	1.8	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.	1.3	68
75	Predictable Phenotypes of Antibiotic Resistance Mutations. <i>MBio</i> , 2018, 9, .	1.8	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.	1.4	67
77	Unstable tandem gene amplification generates heteroresistance (variation in resistance within a) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.2	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.	1.1	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.	1.3	64
80	Collateral sensitivity constrains resistance evolution of the CTX-M-15 β -lactamase. <i>Nature Communications</i> , 2019, 10, 618.	5.8	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.	1.5	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.	1.2	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.	1.2	60
84	Persistence of Resistant <i>Staphylococcus epidermidis</i> after Single Course of Clarithromycin. <i>Emerging Infectious Diseases</i> , 2005, 11, 1389-1393.	2.0	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.	1.2	59
86	Selection of Orphan Rhs Toxin Expression in Evolved <i>Salmonella enterica</i> Serovar Typhimurium. <i>PLoS Genetics</i> , 2014, 10, e1004255.	1.5	56
87	Compensatory Evolution Reveals Functional Interactions between Ribosomal Proteins S12, L14 and L19. <i>Journal of Molecular Biology</i> , 2007, 366, 207-215.	2.0	55
88	Selection and Transmission of Antibiotic-Resistant Bacteria. <i>Microbiology Spectrum</i> , 2017, 5, .	1.2	55
89	Regulating General Mutation Rates: Examination of the Hypermutable State Model for Cairnsian Adaptive Mutation. <i>Genetics</i> , 2003, 163, 1483-1496.	1.2	55
90	Suboptimal growth with hyper-accurate ribosomes. <i>Archives of Microbiology</i> , 1986, 144, 96-101.	1.0	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.	13.6	54
92	Molecular mechanisms of collateral sensitivity to the antibiotic nitrofurantoin. <i>PLoS Biology</i> , 2020, 18, e3000612.	2.6	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.	1.2	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.	1.3	52
95	Functional interactions between mutated forms of ribosomal proteins S4, S5 and S12. <i>Biochimie</i> , 1986, 68, 705-713.	1.3	51
96	Influence of acquired β -lactamases on the evolution of spontaneous carbapenem resistance in <i>Escherichia coli</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 51-59.	1.3	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.	1.2	49
98	Metabolic fitness landscapes predict the evolution of antibiotic resistance. <i>Nature Ecology and Evolution</i> , 2021, 5, 677-687.	3.4	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.	1.3	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.	1.8	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.	3.5	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.	3.5	45
103	Compensating the Fitness Costs of Synonymous Mutations. <i>Molecular Biology and Evolution</i> , 2016, 33, 1461-1477.	3.5	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.	1.2	43
105	Functional Constraints on Replacing an Essential Gene with Its Ancient and Modern Homologs. <i>MBio</i> , 2017, 8, .	1.8	42
106	Evolution of new gene functions: simulation and analysis of the amplification model. <i>Genetica</i> , 2009, 135, 309-324.	0.5	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.	1.6	40
108	Resistance to β -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.	1.1	40

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109	Dynamics of Antibiotic Resistant Mycobacterium tuberculosis during Long-Term Infection and Antibiotic Treatment. PLoS ONE, 2011, 6, e21147.	1.1	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.	1.2	38
111	Improving predictions of the risk of resistance development against new and old antibiotics. Clinical Microbiology and Infection, 2015, 21, 894-898.	2.8	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.	1.4	37
113	Pharmacodynamic Model To Describe the Concentration-Dependent Selection of Cefotaxime-Resistant Escherichia coli. Antimicrobial Agents and Chemotherapy, 2005, 49, 5081-5091.	1.4	36
114	Adaptive Mutation: How Growth under Selection Stimulates Lac+ Reversion by Increasing Target Copy Number. Journal of Bacteriology, 2004, 186, 4855-4860.	1.0	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.	1.0	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.	1.3	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.	6.5	35
118	Genome-Wide Detection of Spontaneous Chromosomal Rearrangements in Bacteria. PLoS ONE, 2012, 7, e42639.	1.1	35
119	<i>De Novo</i> Emergence of Peptides That Confer Antibiotic Resistance. MBio, 2019, 10, .	1.8	34
120	Mechanisms and physiological effects of protamine resistance in Salmonella enterica serovar Typhimurium LT2. Journal of Antimicrobial Chemotherapy, 2010, 65, 876-887.	1.3	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.	1.2	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.	1.4	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, .	1.4	31
124	The effect of genomic position on reversion of a lac frameshift mutation (lacZ33) during non-lethal selection (adaptive mutation). Molecular Microbiology, 2002, 44, 1017-1032.	1.2	30
125	Ribosomes Lacking Protein S20 Are Defective in mRNA Binding and Subunit Association. Journal of Molecular Biology, 2010, 397, 767-776.	2.0	28
126	Mechanisms and therapeutic potential of collateral sensitivity to antibiotics. PLoS Pathogens, 2021, 17, e1009172.	2.1	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.	1.2	27
128	Structural and functional innovations in the real-time evolution of new (12±) ₈ barrel enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4727-4732.	3.3	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.	1.2	25
130	The Amplification Model for Adaptive Mutation. <i>Genetics</i> , 2005, 169, 1105-1115.	1.2	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.	3.5	25
132	Variation in Mutational Robustness between Different Proteins and the Predictability of Fitness Effects. <i>Molecular Biology and Evolution</i> , 2016, 34, msw239.	3.5	24
133	CombiANT: Antibiotic interaction testing made easy. <i>PLoS Biology</i> , 2020, 18, e3000856.	2.6	24
134	Biological roles of translesion synthesis DNA polymerases in eubacteria. <i>Molecular Microbiology</i> , 2010, 77, 540-548.	1.2	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.	1.3	23
136	A novel type of colistin resistance genes selected from random sequence space. <i>PLoS Genetics</i> , 2021, 17, e1009227.	1.5	23
137	Antibiotic treatment in vitro of phenotypically tolerant bacterial populations. <i>Journal of Antimicrobial Chemotherapy</i> , 2007, 59, 254-263.	1.3	22
138	Error-prone initiation factor 2 mutations reduce the fitness cost of antibiotic resistance. <i>Molecular Microbiology</i> , 2010, 75, 1299-1313.	1.2	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.	1.0	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.	2.7	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.	3.5	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.	1.0	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.	1.1	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.	3.4	19

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145	Fitness of <i>Escherichia coli</i> mutants with reduced susceptibility to tigecycline. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 1307-1313.	1.3	18
146	<i>Salmonella typhimurium</i> cobmutants are not hyper-virulent. <i>FEMS Microbiology Letters</i> , 1996, 139, 121-126.	0.7	17
147	The highly dynamic nature of bacterial heteroresistance impairs its clinical detection. <i>Communications Biology</i> , 2021, 4, 521.	2.0	17
148	Pathoadaptive Mutations in <i>Salmonella enterica</i> Isolated after Serial Passage in Mice. <i>PLoS ONE</i> , 2013, 8, e70147.	1.1	16
149	Structure of AadA from <i>Salmonella enterica</i> : a monomeric aminoglycoside (3-aminoglycoside)(9) adenylyltransferase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2267-2277.	2.5	16
150	Different adaptive strategies in <i>E. coli</i> populations evolving under macronutrient limitation and metal ion limitation. <i>BMC Evolutionary Biology</i> , 2018, 18, 72.	3.2	16
151	No beneficial fitness effects of random peptides. <i>Nature Ecology and Evolution</i> , 2018, 2, 1046-1047.	3.4	16
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