Dan Andersson

List of Publications by Year
in descending order

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	Prevalence of colistin heteroresistance in carbapenem-resistant <i>Pseudomonas aeruginosa</i> and association with clinical outcomes in patients: an observational study. Journal of Antimicrobial Chemotherapy, 2022, 77, 793-798.	1.3	12
2	The physiology and genetics of bacterial responses to antibiotic combinations. Nature Reviews Microbiology, 2022, 20, 478-490.	13.6	54
3	Potential risks of treating bacterial infections with a combination of Î²-lactam and aminoglycoside antibiotics: A systematic quantification of antibiotic interactions in E. coli blood stream infection isolates. EBioMedicine, 2022, 78, 103979.	2.7	8
4	A Microfluidic Chip for Studies of the Dynamics of Antibiotic Resistance Selection in Bacterial Biofilms. Frontiers in Cellular and Infection Microbiology, 2022, 12, .	1.8	15
5	Antibiotic Minimal Selective Concentrations and Fitness Costs during Biofilm and Planktonic Growth. MBio, 2022, 13, .	1.8	4
6	A novel type of colistin resistance genes selected from random sequence space. PLoS Genetics, 2021, 17, e1009227.	1.5	23
7	Structure and mechanism of a phage-encoded SAM lyase revises catalytic function of enzyme family. ELife, 2021, 10, .	2.8	15
8	A broad spectrum anti-bacterial peptide with an adjunct potential for tuberculosis chemotherapy. Scientific Reports, 2021, 11, 4201.	1.6	8
9	Selection of Resistant Bacteria in Mallards Exposed to Subinhibitory Concentrations of Ciprofloxacin in Their Water Environment. Antimicrobial Agents and Chemotherapy, 2021, 65, .	1.4	9
10	Metabolic fitness landscapes predict the evolution of antibiotic resistance. Nature Ecology and Evolution, 2021, 5, 677-687.	3.4	49
11	The highly dynamic nature of bacterial heteroresistance impairs its clinical detection. Communications Biology, 2021, 4, 521.	2.0	17
12	Mechanisms and therapeutic potential of collateral sensitivity to antibiotics. PLoS Pathogens, 2021, 17, e1009172.	2.1	28
13	Maximum levels of crossâ€contamination for 24 antimicrobial active substances in nonâ€target feed. Part 8: Pleuromutilins: tiamulin and valnemulin. EFSA Journal, 2021, 19, e06860.	0.9	8
14	Maximum levels of crossâ€contamination for 24 antimicrobial active substances in nonâ€target feed.â€¯Part 10: Quinolones: flumequine and oxolinic acid. EFSA Journal, 2021, 19, e06862.	0.9	8
15	Maximum levels of crossâ€contamination for 24 antimicrobial active substances in nonâ€target feed. Part 1: Methodology, general data gaps and uncertainties. EFSA Journal, 2021, 19, e06852.	0.9	11
16	Maximum levels of crossâ€contamination for 24 antimicrobial active substances in nonâ€target feed. Part 13: Diaminopyrimidines: trimethoprim. EFSA Journal, 2021, 19, e06865.	0.9	12
17	Maximum levels of crossâ€contamination for 24 antimicrobial active substances in nonâ€target feed.â€¯Part 9: Polymyxins: colistin. EFSA Journal, 2021, 19, e06861.	0.9	10
18	Maximum levels of crossâ€contamination for 24 antimicrobial active substances in nonâ€target feed. Part 7: Amphenicols: florfenicol and thiamphenicol. EFSA Journal, 2021, 19, e06859.	0.9	4

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19	Maximum levels of crossâ€contamination for 24 antimicrobial active substances in nonâ€target feed. Part 11: Sulfonamides. EFSA Journal, 2021, 19, e06863.	0.9	13
20	Maximum levels of crossâ€contamination for 24 antimicrobial active substances in nonâ€target feed.â€ Part 3: Amprolium. EFSA Journal, 2021, 19, e06854.	0.9	13
21	Maximum levels of crossâ€contamination for 24 antimicrobial active substances in nonâ€target feed. Part 12: Tetracyclines: tetracycline, chlortetracycline, oxytetracycline, and doxycycline. EFSA Journal, 2021, 19, e06864.	0.9	5
22	Maximum levels of crossâ€contamination for 24 antimicrobial active substances in nonâ€target feed.â€ Part 6: Macrolides: tilmicosin, tylosin and tylvalosin. EFSA Journal, 2021, 19, e06858.	0.9	8
23	Maximum levels of crossâ€contamination for 24 antimicrobial active substances in nonâ€target feed.â€ Part 2: Aminoglycosides/aminocyclitols: apramycin, paromomycin, neomycin and spectinomycin. EFSA Journal, 2021, 19, e06853.	0.9	9
24	Maximum levels of crossâ€contamination for 24 antimicrobial active substances in nonâ€target feed.â€ Part 4: Î²â€Lactams: amoxicillin and penicillin V. EFSA Journal, 2021, 19, e06855.	0.9	3
25	Maximum levels of crossâ€contamination for 24 antimicrobial active substances in nonâ€target feed. Part 5: Lincosamides: lincomycin. EFSA Journal, 2021, 19, e06856.	0.9	14
26	An Effort Worth Making: A Qualitative Study of How Swedes Respond to Antibiotic Resistance. Public Health Ethics, 2021, 14, 1-11.	0.4	2
27	Modular 3D-Printed Peg Biofilm Device for Flexible Setup of Surface-Related Biofilm Studies. Frontiers in Cellular and Infection Microbiology, 2021, 11, 802303.	1.8	6
28	The chemotherapeutic drug methotrexate selects for antibiotic resistance. EBioMedicine, 2021, 74, 103742.	2.7	9
29	A novel type of colistin resistance genes selected from random sequence space. , 2021, 17, e1009227.		0
30	A novel type of colistin resistance genes selected from random sequence space. , 2021, 17, e1009227.		0
31	A novel type of colistin resistance genes selected from random sequence space. , 2021, 17, e1009227.		0
32	A novel type of colistin resistance genes selected from random sequence space. , 2021, 17, e1009227.		0
33	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.	1.3	16
34	Dynamics of Extensive Drug Resistance Evolution of Mycobacterium tuberculosis in a Single Patient During 9 Years of Disease and Treatment. Journal of Infectious Diseases, 2020, , .	1.9	12
35	Preferences regarding antibiotic treatment and the role of antibiotic resistance: A discrete choice experiment. International Journal of Antimicrobial Agents, 2020, 56, 106198.	1.1	12
36	Mutational Pathways and Trade-Offs Between HisA and TrpF Functions: Implications for Evolution via Gene Duplication and Divergence. Frontiers in Microbiology, 2020, 11, 588235.	1.5	5

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37	CombiANT: Antibiotic interaction testing made easy. PLoS Biology, 2020, 18, e3000856.	2.6	24
38	Synonymous Mutations in rpsT Lead to Ribosomal Assembly Defects That Can Be Compensated by Mutations in fis and rpoA. Frontiers in Microbiology, 2020, 11, 340.	1.5	3
39	Antibiotic resistance: turning evolutionary principles into clinical reality. FEMS Microbiology Reviews, 2020, 44, 171-188.	3.9	154
40	Evolution of a New Function by Fusion between Phage DNA and a Bacterial Gene. Molecular Biology and Evolution, 2020, 37, 1329-1341.	3.5	2
41	Molecular mechanisms of collateral sensitivity to the antibiotic nitrofurantoin. PLoS Biology, 2020, 18, e3000612.	2.6	53
42	Antimicrobial Peptide Exposure Selects for Resistant and Fit Stenotrophomonas maltophilia Mutants That Show Cross-Resistance to Antibiotics. MSphere, 2020, 5, .	1.3	9
43	A portable epigenetic switch for bistable gene expression in bacteria. Scientific Reports, 2019, 9, 11261.	1.6	15
44	Upregulation of PBP1B and LpoB in cysB Mutants Confers Mecillinam (Amdinocillin) Resistance in Escherichia coli. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	7
45	Inhibition of translation termination by small molecules targeting ribosomal release factors. Scientific Reports, 2019, 9, 15424.	1.6	6
46	Mechanisms and clinical relevance of bacterial heteroresistance. Nature Reviews Microbiology, 2019, 17, 479-496.	13.6	264
47	<i>De Novo</i> Emergence of Peptides That Confer Antibiotic Resistance. MBio, 2019, 10, .	1.8	34
48	Selection for novel metabolic capabilities inSalmonella enterica. Evolution; International Journal of Organic Evolution, 2019, 73, 990-1000.	1.1	0
49	Definitions and guidelines for research on antibiotic persistence. Nature Reviews Microbiology, 2019, 17, 441-448.	13.6	748
50	Collateral sensitivity constrains resistance evolution of the CTX-M-15 Î^2-lactamase. Nature Communications, 2019, 10, 618.	5.8	64
51	The high prevalence of antibiotic heteroresistance in pathogenic bacteria is mainly caused by gene amplification. Nature Microbiology, 2019, 4, 504-514.	5.9	259
52	Selection and Transmission of Antibiotic-Resistant Bacteria. , 2019, , 117-137.		2
53	Evolution of high-level resistance during low-level antibiotic exposure. Nature Communications, 2018, 9, 1599.	5.8	300
54	Experimental Determination and Prediction of the Fitness Effects of Random Point Mutations in the Biosynthetic Enzyme HisA. Molecular Biology and Evolution, 2018, 35, 704-718.	3.5	21

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55	Pharmacokinetics and Pharmacodynamics of Fosfomycin and Its Activity against Extended-Spectrum-Î²-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
56	Predicting mutant selection in competition experiments with ciprofloxacin-exposed Escherichia coli. International Journal of Antimicrobial Agents, 2018, 51, 399-406.	1.1	4
57	Occurrence of<i>Yersinia rohdei</i>among feral reindeer (<i>Rangifer t. tarandus</i>) and kelp gulls (<i>Larus dominicanus</i>) on the Sub-Antarctic island South Georgia. Infection Ecology and Epidemiology, 2018, 8, 1517582.	0.5	1
58	Public awareness and individual responsibility needed for judicious use of antibiotics: a qualitative study of public beliefs and perceptions. BMC Public Health, 2018, 18, 1153.	1.2	49
59	Cellular hysteresis as a principle to maximize the efficacy of antibiotic therapy. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9767-9772.	3.3	81
60	A bacteriophage enzyme induces bacterial metabolic perturbation that confers a novel promiscuous function. Nature Ecology and Evolution, 2018, 2, 1321-1330.	3.4	19
61	Predictable Phenotypes of Antibiotic Resistance Mutations. MBio, 2018, 9, .	1.8	68
62	Different adaptive strategies in E. coli populations evolving under macronutrient limitation and metal ion limitation. BMC Evolutionary Biology, 2018, 18, 72.	3.2	16
63	Longâ€term carriage and rapid transmission of extended spectrum betaâ€lactamaseâ€producing <scp><i>E. coli</i></scp> within a flock of Mallards in the absence of antibiotic selection. Environmental Microbiology Reports, 2018, 10, 576-582.	1.0	20
64	Genetic Adaptation to Growth Under Laboratory Conditions in Escherichia coli and Salmonella enterica. Frontiers in Microbiology, 2018, 9, 756.	1.5	70
65	No beneficial fitness effects of random peptides. Nature Ecology and Evolution, 2018, 2, 1046-1047.	3.4	16
66	Environmental and genetic modulation of the phenotypic expression of antibiotic resistance. FEMS Microbiology Reviews, 2017, 41, 374-391.	3.9	112
67	Structural and functional innovations in the real-time evolution of new (Î²Î±) ₈ barrel enzymes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4727-4732.	3.3	26
68	Rapid Antibiotic Susceptibility Testing for Urinary Tract Infections. Methods in Molecular Biology, 2017, 1616, 147-153.	0.4	1
69	Resistance to the Cyclotide Cycloviolacin O2 in Salmonella enterica Caused by Different Mutations That Often Confer Cross-Resistance or Collateral Sensitivity to Other Antimicrobial Peptides. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	11
70	Can a pharmacokinetic/pharmacodynamic (PKPD) model be predictive across bacterial densities and strains? External evaluation of a PKPD model describing longitudinal in vitro data. Journal of Antimicrobial Chemotherapy, 2017, 72, 3108-3116.	1.3	23
71	Functional Constraints on Replacing an Essential Gene with Its Ancient and Modern Homologs. MBio, 2017, 8, .	1.8	42
72	Evolution of Antibiotic Resistance without Antibiotic Exposure. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	73

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73	Reversion of High-level Mecillinam Resistance to Susceptibility in Escherichia coli During Growth in Urine. EBioMedicine, 2017, 23, 111-118.	2.7	21
74	Prediction of antibiotic resistance: time for a new preclinical paradigm?. Nature Reviews Microbiology, 2017, 15, 689-696.	13.6	221
75	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.	3.3	296
76	Evolutionary Trajectories to Antibiotic Resistance. Annual Review of Microbiology, 2017, 71, 579-596.	2.9	179
77	Antimicrobial peptide exposure selects for<i>Staphylococcus aureus</i>resistance to human defence peptides. Journal of Antimicrobial Chemotherapy, 2017, 72, 115-127.	1.3	74
78	Genome Dynamics of Escherichia coli during Antibiotic Treatment: Transfer, Loss, and Persistence of Genetic Elements In situ of the Infant Gut. Frontiers in Cellular and Infection Microbiology, 2017, 7, 126.	1.8	46
79	Transfer and Persistence of a Multi-Drug Resistance Plasmid in situ of the Infant Gut Microbiota in the Absence of Antibiotic Treatment. Frontiers in Microbiology, 2017, 8, 1852.	1.5	63
80	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
81	Selection and Transmission of Antibiotic-Resistant Bacteria. Microbiology Spectrum, 2017, 5, .	1.2	55
82	Compensating the Fitness Costs of Synonymous Mutations. Molecular Biology and Evolution, 2016, 33, 1461-1477.	3.5	45
83	Fitness of<i>Escherichia coli</i>mutants with reduced susceptibility to tigecycline. Journal of Antimicrobial Chemotherapy, 2016, 71, 1307-1313.	1.3	18
84	Mechanisms and consequences of bacterial resistance to antimicrobial peptides. Drug Resistance Updates, 2016, 26, 43-57.	6.5	491
85	Nonmutational compensation of the fitness cost of antibiotic resistance in mycobacteria by overexpression of <i>tlyA</i> rRNA methylase. Rna, 2016, 22, 1836-1843.	1.6	40
86	Unstable tandem gene amplification generates heteroresistance (variation in resistance within a) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2	1.2	67
87	Variation in Mutational Robustness between Different Proteins and the Predictability of Fitness Effects. Molecular Biology and Evolution, 2016, 34, msw239.	3.5	24
88	Combinations of mutations in<i>envZ</i>,<i>ftsI</i>,<i>mrdA</i>,<i>acrB</i>and<i>acrR</i>can cause high-level carbapenem resistance in<i>Escherichia coli</i>. Journal of Antimicrobial Chemotherapy, 2016, 71, 1188-1198.	1.3	68
89	Potential of Tetracycline Resistance Proteins To Evolve Tigecycline Resistance. Antimicrobial Agents and Chemotherapy, 2016, 60, 789-796.	1.4	127
90	Indirect resistance to several classes of antibiotics in cocultures with resistant bacteria expressing antibiotic-modifying or -degrading enzymes. Journal of Antimicrobial Chemotherapy, 2016, 71, 100-110.	1.3	64

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91	Structure of AadA from<i>Salmonella enterica</i>: a monomeric aminoglycoside (3â€²â€²)(9) adenyltransferase. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2267-2277.	2.5	16
92	Intestinal spirochaetes (genus<i>Brachyspira</i>) colonise wild birds in the southern Atlantic region and Antarctica. Infection Ecology and Epidemiology, 2015, 5, 29296.	0.5	5
93	Improving predictions of the risk of resistance development against new and old antibiotics. Clinical Microbiology and Infection, 2015, 21, 894-898.	2.8	38
94	A General Method for Rapid Determination of Antibiotic Susceptibility and Species in Bacterial Infections. Journal of Clinical Microbiology, 2015, 53, 425-432.	1.8	68
95	Evolutionary consequences of drug resistance: shared principles across diverse targets and organisms. Nature Reviews Genetics, 2015, 16, 459-471.	7.7	201
96	Amdinocillin (Mecillinam) Resistance Mutations in Clinical Isolates and Laboratory-Selected Mutants of Escherichia coli. Antimicrobial Agents and Chemotherapy, 2015, 59, 1718-1727.	1.4	78
97	Amelioration of the Fitness Costs of Antibiotic Resistance Due To Reduced Outer Membrane Permeability by Upregulation of Alternative Porins. Molecular Biology and Evolution, 2015, 32, msv195.	3.5	45
98	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
99	Evolution of New Functions De Novo and from Preexisting Genes. Cold Spring Harbor Perspectives in Biology, 2015, 7, a017996.	2.3	129
100	Fitness of Salmonella mutants resistant to antimicrobial peptides. Journal of Antimicrobial Chemotherapy, 2015, 70, 432-440.	1.3	14
101	Effects of Antibiotic Resistance on Bacterial Fitness, Virulence, and Transmission. , 2014, , 307-318.		2
102	Selection of Orphan Rhs Toxin Expression in Evolved Salmonella enterica Serovar Typhimurium. PLoS Genetics, 2014, 10, e1004255.	1.5	56
103	Selection of a Multidrug Resistance Plasmid by Sublethal Levels of Antibiotics and Heavy Metals. MBio, 2014, 5, e01918-14.	1.8	451
104	Minor Fitness Costs in an Experimental Model of Horizontal Gene Transfer in Bacteria. Molecular Biology and Evolution, 2014, 31, 1220-1227.	3.5	45
105	High Fitness Costs and Instability of Gene Duplications Reduce Rates of Evolution of New Genes by Duplication-Divergence Mechanisms. Molecular Biology and Evolution, 2014, 31, 1526-1535.	3.5	82
106	Microbiological effects of sublethal levels of antibiotics. Nature Reviews Microbiology, 2014, 12, 465-478.	13.6	1,255
107	Resistance to Î²-Lactam Antibiotics Conferred by Point Mutations in Penicillin-Binding Proteins PBP3, PBP4 and PBP6 in Salmonella enterica. PLoS ONE, 2014, 9, e97202.	1.1	40
108	Mechanisms and fitness costs of tigecycline resistance in Escherichia coli. Journal of Antimicrobial Chemotherapy, 2013, 68, 2809-2819.	1.3	77

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109	Influence of acquired Â-lactamases on the evolution of spontaneous carbapenem resistance in Escherichia coli. Journal of Antimicrobial Chemotherapy, 2013, 68, 51-59.	1.3	49
110	<scp>Lon</scp> protease inactivation, or translocation of the <scp><i>lon</i></scp> gene, potentiate bacterial evolution to antibiotic resistance. Molecular Microbiology, 2013, 90, 1233-1248.	1.2	59
111	Fitness Costs of Synonymous Mutations in the rpsT Gene Can Be Compensated by Restoring mRNA Base Pairing. PLoS ONE, 2013, 8, e63373.	1.1	19
112	Mechanisms and Fitness Costs of Resistance to Antimicrobial Peptides LL-37, CNY100HL and Wheat Germ Histones. PLoS ONE, 2013, 8, e68875.	1.1	66
113	Pathoadaptive Mutations in Salmonella enterica Isolated after Serial Passage in Mice. PLoS ONE, 2013, 8, e70147.	1.1	16
114	VIII.3. Evolution of Antibiotic Resistance. , 2013, , 747-753.		0
115	Selection-Driven Gene Loss in Bacteria. PLoS Genetics, 2012, 8, e1002787.	1.5	206
116	Compensatory mutations in agrC partly restore fitness in vitro to peptide deformylase inhibitor-resistant Staphylococcus aureus. Journal of Antimicrobial Chemotherapy, 2012, 67, 1835-1842.	1.3	13
117	Selection of resistance at lethal and non-lethal antibiotic concentrations. Current Opinion in Microbiology, 2012, 15, 555-560.	2.3	141
118	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.	1.3	133
119	Real-Time Evolution of New Genes by Innovation, Amplification, and Divergence. Science, 2012, 338, 384-387.	6.0	202
120	Evolution of antibiotic resistance at non-lethal drug concentrations. Drug Resistance Updates, 2012, 15, 162-172.	6.5	262
121	Genome-Wide Detection of Spontaneous Chromosomal Rearrangements in Bacteria. PLoS ONE, 2012, 7, e42639.	1.1	35
122	Beyond serial passages: new methods for predicting the emergence of resistance to novel antibiotics. Current Opinion in Pharmacology, 2011, 11, 439-445.	1.7	80
123	Dynamics of Antibiotic Resistant Mycobacterium tuberculosis during Long-Term Infection and Antibiotic Treatment. PLoS ONE, 2011, 6, e21147.	1.1	38
124	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
125	Activation of cryptic aminoglycoside resistance in <i>Salmonella enterica</i>. Molecular Microbiology, 2011, 80, 1464-1478.	1.2	84
126	Persistence of antibiotic resistance in bacterial populations. FEMS Microbiology Reviews, 2011, 35, 901-911.	3.9	325

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127	Activation of initiation factor 2 by ligands and mutations for rapid docking of ribosomal subunits. EMBO Journal, 2011, 30, 289-301.	3.5	25
128	Evolving promiscuously. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1199-1200.	3.3	7
129	Selection of Resistant Bacteria at Very Low Antibiotic Concentrations. PLoS Pathogens, 2011, 7, e1002158.	2.1	1,248
130	The Origin of Mutants under Selection: Interactions of Mutation, Growth, and Selection. EcoSal Plus, 2011, 4, .	2.1	13
131	Antibiotic resistance and its cost: is it possible to reverse resistance?. Nature Reviews Microbiology, 2010, 8, 260-271.	13.6	1,855
132	Compensatory gene amplification restores fitness after interâ€species gene replacements. Molecular Microbiology, 2010, 75, 1078-1089.	1.2	106
133	Errorâ€prone initiation factor 2 mutations reduce the fitness cost of antibiotic resistance. Molecular Microbiology, 2010, 75, 1299-1313.	1.2	22
134	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>. Molecular Microbiology, 2010, 77, 830-840.	1.2	97
135	Biological roles of translesion synthesis DNA polymerases in eubacteria. Molecular Microbiology, 2010, 77, 540-548.	1.2	23
136	The cyclotide cycloviolacin O2 from Viola odorata has potent bactericidal activity against Gram-negative bacteria. Journal of Antimicrobial Chemotherapy, 2010, 65, 1964-1971.	1.3	179
137	Effect of Translesion DNA Polymerases, Endonucleases and RpoS on Mutation Rates in<i>Salmonella typhimurium</i>. Genetics, 2010, 185, 783-795.	1.2	15
138	The Tandem Inversion Duplication in<i>Salmonella enterica</i>: Selection Drives Unstable Precursors to Final Mutation Types. Genetics, 2010, 185, 65-80.	1.2	43
139	Mutational Robustness of Ribosomal Protein Genes. Science, 2010, 330, 825-827.	6.0	105
140	Amplification of the Gene for Isoleucylâ€"tRNA Synthetase Facilitates Adaptation to the Fitness Cost of Mupirocin Resistance in<i>Salmonella enterica</i>. Genetics, 2010, 185, 305-312.	1.2	27
141	Mechanisms and physiological effects of protamine resistance in Salmonella enterica serovar Typhimurium LT2. Journal of Antimicrobial Chemotherapy, 2010, 65, 876-887.	1.3	33
142	Ribosomes Lacking Protein S20 Are Defective in mRNA Binding and Subunit Association. Journal of Molecular Biology, 2010, 397, 767-776.	2.0	28
143	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.	3.3	15
144	The Fitness Cost of Streptomycin Resistance Depends on <i>rpsL</i> Mutation, Carbon Source and RpoS (ÏƒS). Genetics, 2009, 183, 539-546.	1.2	88

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145	Genetic Analysis of Colistin Resistance in <i>Salmonella enterica</i> Serovar Typhimurium. Antimicrobial Agents and Chemotherapy, 2009, 53, 2298-2305.	1.4	107
146	A multi-type branching model with varying environment for bacterial dynamics with postantibiotic effect. Journal of Theoretical Biology, 2009, 256, 58-64.	0.8	4
147	Evolution of new gene functions: simulation and analysis of the amplification model. Genetica, 2009, 135, 309-324.	0.5	40
148	Bacterial gene amplification: implications for the evolution of antibiotic resistance. Nature Reviews Microbiology, 2009, 7, 578-588.	13.6	299
149	Gene Amplification and Adaptive Evolution in Bacteria. Annual Review of Genetics, 2009, 43, 167-195.	3.2	247
150	Contribution of Gene Amplification to Evolution of Increased Antibiotic Resistance in<i>Salmonella typhimurium</i>. Genetics, 2009, 182, 1183-1195.	1.2	96
151	The first major extendedâ€spectrum Î²â€lactamase outbreak in Scandinavia was caused by clonal spread of a multiresistant <i>Klebsiella pneumoniae</i> producing CTXâ€Mâ€15. Apmis, 2008, 116, 302-8.	0.9	83
152	Restored fitness leads to long-term persistence of resistant Bacteroides strains in the human intestine. Anaerobe, 2008, 14, 157-160.	1.0	21
153	Nitrofurantoin resistance mechanism and fitness cost in Escherichia coli. Journal of Antimicrobial Chemotherapy, 2008, 62, 495-503.	1.3	157
154	Whole-genome mutational biases in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17878-17883.	3.3	177
155	Mechanism and Fitness Costs of PR-39 Resistance in <i>Salmonella enterica</i> Serovar Typhimurium LT2. Antimicrobial Agents and Chemotherapy, 2008, 52, 2734-2741.	1.4	67
156	Antibiotic treatment in vitro of phenotypically tolerant bacterial populations. Journal of Antimicrobial Chemotherapy, 2007, 59, 254-263.	1.3	22
157	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.	3.3	313
158	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
159	Compensatory Evolution Reveals Functional Interactions between Ribosomal Proteins S12, L14 and L19. Journal of Molecular Biology, 2007, 366, 207-215.	2.0	55
160	Predicting antibiotic resistance. Nature Reviews Microbiology, 2007, 5, 958-965.	13.6	305
161	Multiple mechanisms to ameliorate the fitness burden of mupirocin resistance in Salmonella typhimurium. Molecular Microbiology, 2007, 64, 1038-1048.	1.2	60
162	Origin of Mutations Under Selection: The Adaptive Mutation Controversy. Annual Review of Microbiology, 2006, 60, 477-501.	2.9	158

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163	The biological cost of mutational antibiotic resistance: any practical conclusions?. Current Opinion in Microbiology, 2006, 9, 461-465.	2.3	397
164	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.	3.3	116
165	Multiple pathways of selected gene amplification during adaptive mutation. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17319-17324.	3.3	89
166	Genomic buffering mitigates the effects of deleterious mutations in bacteria. Nature Genetics, 2005, 37, 1376-1379.	9.4	142
167	Persistence of Resistant<i>Staphylococcus epidermidis</i>after Single Course of Clarithromycin. Emerging Infectious Diseases, 2005, 11, 1389-1393.	2.0	59
168	Reduction of the fitness burden of quinolone resistance in Pseudomonas aeruginosa. Journal of Antimicrobial Chemotherapy, 2005, 55, 22-30.	1.3	116
169	Pharmacodynamic Model To Describe the Concentration-Dependent Selection of Cefotaxime-Resistant Escherichia coli. Antimicrobial Agents and Chemotherapy, 2005, 49, 5081-5091.	1.4	36
170	Establishment of a Superficial Skin Infection Model in Mice by Using Staphylococcus aureus and Streptococcus pyogenes. Antimicrobial Agents and Chemotherapy, 2005, 49, 3435-3441.	1.4	149
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