

Olivier Tenaillon

List of Publications by Year in descending order

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Version: 2024-02-01

88
papers

9,587
citations

57758

44
h-index

51608

86
g-index

100
all docs

100
docs citations

100
times ranked

10061
citing authors

#	ARTICLE	IF	CITATIONS
1	The interplay between anticancer challenges and the microbial communities from the gut. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2022, 41, 691-711.	2.9	1
2	Local and Global Protein Interactions Contribute to Residue Entrenchment in Beta-Lactamase TEM-1. <i>Antibiotics</i> , 2022, 11, 652.	3.7	3
3	Modeling the bacterial dynamics in the gut microbiota following an antibiotic-induced perturbation. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2022, 11, 906-918.	2.5	4
4	A Microbiota-Dependent Response to Anticancer Treatment in an In Vitro Human Microbiota Model: A Pilot Study With Hydroxycarbamide and Daunorubicin. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	3.9	0
5	Deciphering polymorphism in 61,157 <i>Escherichia coli</i> genomes via epistatic sequence landscapes. <i>Nature Communications</i> , 2022, 13, .	12.8	6
6	Insertion-sequence-mediated mutations both promote and constrain evolvability during a long-term experiment with bacteria. <i>Nature Communications</i> , 2021, 12, 980.	12.8	63
7	<i>Escherichia coli</i> Genomic Diversity within Extraintestinal Acute Infections Argues for Adaptive Evolution at Play. <i>MSphere</i> , 2021, 6, .	2.9	6
8	Success of prophylactic antiviral therapy for SARS-CoV-2: Predicted critical efficacies and impact of different drug-specific mechanisms of action. <i>PLoS Computational Biology</i> , 2021, 17, e1008752.	3.2	41
9	Dynamics of extended-spectrum beta-lactamase-producing Enterobacterales colonization in long-term carriers following travel abroad. <i>Microbial Genomics</i> , 2021, 7, .	2.0	11
10	Cross-resistance to cefiderocol and ceftazidime-avibactam in KPC β -lactamase mutants and the inoculum effect. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1172.e7-1172.e10.	6.0	57
11	Gut microbiota composition alterations are associated with the onset of diabetes in kidney transplant recipients. <i>PLoS ONE</i> , 2020, 15, e0227373.	2.5	18
12	KPC Beta-Lactamases Are Permissive to Insertions and Deletions Conferring Substrate Spectrum Modifications and Resistance to Ceftazidime-Avibactam. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	24
13	Flux, toxicity, and expression costs generate complex genetic interactions in a metabolic pathway. <i>Science Advances</i> , 2020, 6, eabb2236.	10.3	26
14	Genomic characterization of 16S rRNA methyltransferase-producing <i>Escherichia coli</i> isolates from the Parisian area, France. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1726-1735.	3.0	13
15	Impact of anticancer chemotherapy on the extension of beta-lactamase spectrum: an example with KPC-type carbapenemase activity towards ceftazidime-avibactam. <i>Scientific Reports</i> , 2020, 10, 589.	3.3	16
16	CRISPR/Cas9 recombineering-mediated deep mutational scanning of essential genes in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2020, 16, e9265.	7.2	28
17	Primary and promiscuous functions coexist during evolutionary innovation through whole protein domain acquisitions. <i>ELife</i> , 2020, 9, .	6.0	7
18	The Impact of Neutral Mutations on Genome Evolvability. <i>Current Biology</i> , 2020, 30, R527-R534.	3.9	9

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19	Mutation bias and GC content shape antimutator invasions. <i>Nature Communications</i> , 2019, 10, 3114.	12.8	17
20	Advantage of the F2:A1:B- IncF Pandemic Plasmid over IncC Plasmids in <i>In Vitro</i> Acquisition and Evolution of <i>bla</i> _{CTX-M} Gene-Bearing Plasmids in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	26
21	Recent insights into the genotype–phenotype relationship from massively parallel genetic assays. <i>Evolutionary Applications</i> , 2019, 12, 1721-1742.	3.1	52
22	Long-term evolution of the natural isolate of <i>Escherichia coli</i> 536 in the mouse gut colonized after maternal transmission reveals convergence in the constitutive expression of the lactose operon. <i>Molecular Ecology</i> , 2019, 28, 4470-4485.	3.9	23
23	Ceftriaxone and Cefotaxime Have Similar Effects on the Intestinal Microbiota in Human Volunteers Treated by Standard-Dose Regimens. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	41
24	Successful Treatment of Bacteremia Due to NDM-1-Producing <i>Morganella morganii</i> with Aztreonam and Ceftazidime-Avibactam Combination in a Pediatric Patient with Hematologic Malignancy. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	42
25	Experimental evolution heals the scars of genome-scale recoding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2853-2855.	7.1	3
26	Evolution of a Dominant Natural Isolate of <i>Escherichia coli</i> in the Human Gut over the Course of a Year Suggests a Neutral Evolution with Reduced Effective Population Size. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	58
27	Extended-spectrum β -lactamase-encoding genes are spreading on a wide range of <i>Escherichia coli</i> plasmids existing prior to the use of third-generation cephalosporins. <i>Microbial Genomics</i> , 2018, 4, .	2.0	33
28	Molecular epidemiology of penicillinase-producing <i>Neisseria gonorrhoeae</i> isolates in France. <i>Clinical Microbiology and Infection</i> , 2017, 23, 968-973.	6.0	13
29	Mutator genomes decay, despite sustained fitness gains, in a long-term experiment with bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9026-E9035.	7.1	87
30	Accumulation of Deleterious Mutations During Bacterial Range Expansions. <i>Genetics</i> , 2017, 207, 669-684.	2.9	74
31	Using long-term experimental evolution to uncover the patterns and determinants of molecular evolution of an <i>Escherichia coli</i> natural isolate in the streptomycin-treated mouse gut. <i>Molecular Ecology</i> , 2017, 26, 1802-1817.	3.9	63
32	Tempo and mode of genome evolution in a 50,000-generation experiment. <i>Nature</i> , 2016, 536, 165-170.	27.8	404
33	Links between Transcription, Environmental Adaptation and Gene Variability in <i>Escherichia coli</i> : Correlations between Gene Expression and Gene Variability Reflect Growth Efficiencies. <i>Molecular Biology and Evolution</i> , 2016, 33, 2515-2529.	8.9	31
34	Emergence of Antimicrobial-Resistant <i>Escherichia coli</i> of Animal Origin Spreading in Humans. <i>Molecular Biology and Evolution</i> , 2016, 33, 898-914.	8.9	65
35	First-Step Mutations during Adaptation Restore the Expression of Hundreds of Genes. <i>Molecular Biology and Evolution</i> , 2016, 33, 25-39.	8.9	60
36	Coevolutionary Landscape Inference and the Context-Dependence of Mutations in Beta-Lactamase TEM-1. <i>Molecular Biology and Evolution</i> , 2016, 33, 268-280.	8.9	233

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37	The rule of declining adaptability in microbial evolution experiments. <i>Frontiers in Genetics</i> , 2015, 6, 99.	2.3	94
38	High Recombinant Frequency in Extraintestinal Pathogenic <i>Escherichia coli</i> Strains. <i>Molecular Biology and Evolution</i> , 2015, 32, 1708-1716.	8.9	21
39	Elucidating the molecular architecture of adaptation via evolve and resequence experiments. <i>Nature Reviews Genetics</i> , 2015, 16, 567-582.	16.3	236
40	The Conserved <i>nhaAR</i> Operon Is Drastically Divergent between B2 and Non-B2 <i>Escherichia coli</i> and Is Involved in Extra-Intestinal Virulence. <i>PLoS ONE</i> , 2014, 9, e108738.	2.5	13
41	Properties of selected mutations and genotypic landscapes under Fisher's geometric model. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 3537-3554.	2.3	73
42	Large Chromosomal Rearrangements during a Long-Term Evolution Experiment with <i>Escherichia coli</i> . <i>MBio</i> , 2014, 5, e01377-14.	4.1	109
43	Epistasis and Allele Specificity in the Emergence of a Stable Polymorphism in <i>Escherichia coli</i> . <i>Science</i> , 2014, 343, 1366-1369.	12.6	125
44	The Reproducibility of Adaptation in the Light of Experimental Evolution with Whole Genome Sequencing. <i>Advances in Experimental Medicine and Biology</i> , 2014, 781, 211-231.	1.6	32
45	Evolution of <i>Escherichia coli</i> rifampicin resistance in an antibiotic-free environment during thermal stress. <i>BMC Evolutionary Biology</i> , 2013, 13, 50.	3.2	116
46	A case of adaptation through a mutation in a tandem duplication during experimental evolution in <i>Escherichia coli</i> . <i>BMC Genomics</i> , 2013, 14, 441.	2.8	18
47	Fitness, Stress Resistance, and Extraintestinal Virulence in <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2013, 81, 2733-2742.	2.2	33
48	Electrophoretic mobility confirms reassortment bias among geographic isolates of segmented RNA phages. <i>BMC Evolutionary Biology</i> , 2013, 13, 206.	3.2	17
49	Mutation rate dynamics in a bacterial population reflect tension between adaptation and genetic load. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 222-227.	7.1	231
50	Capturing the mutational landscape of the beta-lactamase TEM-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13067-13072.	7.1	228
51	The Molecular Diversity of Adaptive Convergence. <i>Science</i> , 2012, 335, 457-461.	12.6	688
52	Mutation Rate Inferred From Synonymous Substitutions in a Long-Term Evolution Experiment With <i>Escherichia coli</i> . <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 183-186.	1.8	157
53	The emergence of complexity and restricted pleiotropy in adapting networks. <i>BMC Evolutionary Biology</i> , 2011, 11, 326.	3.2	19
54	Complete Nucleotide Sequence of Plasmid pTN48, Encoding the CTX-M-14 Extended-Spectrum β -Lactamase from an <i>Escherichia coli</i> O102-ST405 Strain. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 1270-1273.	3.2	17

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55	The interaction between a non-pathogenic and a pathogenic strain synergistically enhances extra-intestinal virulence in <i>Escherichia coli</i> . <i>Microbiology (United Kingdom)</i> , 2011, 157, 774-785.	1.8	11
56	How Fitch-Margoliash Algorithm can Benefit from Multi Dimensional Scaling. <i>Evolutionary Bioinformatics</i> , 2011, 7, EBO.S7048.	1.2	4
57	The population genetics of commensal <i>Escherichia coli</i> . <i>Nature Reviews Microbiology</i> , 2010, 8, 207-217.	28.6	1,104
58	Molecular and Evolutionary Bases of Within-Patient Genotypic and Phenotypic Diversity in <i>Escherichia coli</i> Extraintestinal Infections. <i>PLoS Pathogens</i> , 2010, 6, e1001125.	4.7	68
59	Bacteriophage PhiX174's Ecological Niche and the Flexibility of Its <i>Escherichia coli</i> Lipopolysaccharide Receptor. <i>Applied and Environmental Microbiology</i> , 2010, 76, 7310-7313.	3.1	51
60	A unique virus release mechanism in the Archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11306-11311.	7.1	126
61	Selection for Chaperone-Like Mediated Genetic Robustness at Low Mutation Rate: Impact of Drift, Epistasis and Complexity. <i>Genetics</i> , 2009, 182, 555-564.	2.9	23
62	A Module Located at a Chromosomal Integration Hot Spot Is Responsible for the Multidrug Resistance of a Reference Strain from <i>Escherichia coli</i> Clonal Group A. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 2283-2288.	3.2	33
63	The Evolution of Epistasis and Its Links With Genetic Robustness, Complexity and Drift in a Phenotypic Model of Adaptation. <i>Genetics</i> , 2009, 182, 277-293.	2.9	84
64	Organised Genome Dynamics in the <i>Escherichia coli</i> Species Results in Highly Diverse Adaptive Paths. <i>PLoS Genetics</i> , 2009, 5, e1000344.	3.5	1,005
65	Role of Intraspecies Recombination in the Spread of Pathogenicity Islands within the <i>Escherichia coli</i> Species. <i>PLoS Pathogens</i> , 2009, 5, e1000257.	4.7	93
66	Mutation rate and genome reduction in endosymbiotic and free-living bacteria. <i>Genetica</i> , 2008, 134, 205-210.	1.1	72
67	Evidence for a human-specific <i>Escherichia coli</i> clone. <i>Environmental Microbiology</i> , 2008, 10, 1000-1006.	3.8	86
68	Apparent mutational hotspots and long distance linkage disequilibrium resulting from a bottleneck. <i>Journal of Evolutionary Biology</i> , 2008, 21, 541-550.	1.7	20
69	Contribution of Recombination to the Evolution of Human Immunodeficiency Viruses Expressing Resistance to Antiretroviral Treatment. <i>Journal of Virology</i> , 2007, 81, 7620-7628.	3.4	103
70	Extraintestinal Virulence Is a Coincidental By-Product of Commensalism in B2 Phylogenetic Group <i>Escherichia coli</i> Strains. <i>Molecular Biology and Evolution</i> , 2007, 24, 2373-2384.	8.9	225
71	Understanding the Evolutionary Fate of Finite Populations: The Dynamics of Mutational Effects. <i>PLoS Biology</i> , 2007, 5, e94.	5.6	172
72	Quantifying Organismal Complexity using a Population Genetic Approach. <i>PLoS ONE</i> , 2007, 2, e217.	2.5	68

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73	Selection Acts on DNA Secondary Structures to Decrease Transcriptional Mutagenesis. PLoS Genetics, 2006, 2, e176.	3.5	39
74	Extensive Recombination among Human Immunodeficiency Virus Type 1 Quasispecies Makes an Important Contribution to Viral Diversity in Individual Patients. Journal of Virology, 2006, 80, 2472-2482.	3.4	102
75	Evolution of Mutational Robustness in an RNA Virus. PLoS Biology, 2005, 3, e381.	5.6	116
76	Intermediate Mutation Frequencies Favor Evolution of Multidrug Resistance in Escherichia coli. Genetics, 2005, 171, 825-827.	2.9	47
77	Selection Versus Demography: A Multilocus Investigation of the Domestication Process in Maize. Molecular Biology and Evolution, 2004, 21, 1214-1225.	8.9	251
78	Evolutionary significance of stress-induced mutagenesis in bacteria. Trends in Microbiology, 2004, 12, 264-270.	7.7	116
79	Polymorphism of genes encoding SOS polymerases in natural populations of Escherichia coli. DNA Repair, 2003, 2, 417-426.	2.8	24
80	Stress-Induced Mutagenesis in Bacteria. Science, 2003, 300, 1404-1409.	12.6	508
81	Horizontal Transfer of Mismatch Repair Genes and the Variable Speed of Bacterial Evolution. , 2002, , 147-155.		2
82	Second-order selection in bacterial evolution: selection acting on mutation and recombination rates in the course of adaptation. Research in Microbiology, 2001, 152, 11-16.	2.1	116
83	FROM METABOLISM TO POLYMORPHISM IN BACTERIAL POPULATIONS: A THEORETICAL STUDY. Evolution; International Journal of Organic Evolution, 2001, 55, 2181-2193.	2.3	10
84	Costs and Benefits of High Mutation Rates: Adaptive Evolution of Bacteria in the Mouse Gut. Science, 2001, 291, 2606-2608.	12.6	447
85	Quand les bactéries modulent leur vitesse d'évolution selon l'environnement.. Medecine/Sciences, 2001, 17, 514.	0.2	0
86	Mutators and sex in bacteria: Conflict between adaptive strategies. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 10465-10470.	7.1	86
87	Evolutionary Implications of the Frequent Horizontal Transfer of Mismatch Repair Genes. Cell, 2000, 103, 711-721.	28.9	246
88	Mutators, Population Size, Adaptive Landscape and the Adaptation of Asexual Populations of Bacteria. Genetics, 1999, 152, 485-493.	2.9	219