

Olivier Tenaillon

List of Publications by Year in descending order

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88
papers

9,587
citations

57752

44
h-index

51602

86
g-index

100
all docs

100
docs citations

100
times ranked

10061
citing authors

#	ARTICLE	IF	CITATIONS
1	The population genetics of commensal <i>Escherichia coli</i> . <i>Nature Reviews Microbiology</i> , 2010, 8, 207-217.	28.6	1,104
2	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
3	The Molecular Diversity of Adaptive Convergence. <i>Science</i> , 2012, 335, 457-461.	12.6	688
4	Stress-Induced Mutagenesis in Bacteria. <i>Science</i> , 2003, 300, 1404-1409.	12.6	508
5	Costs and Benefits of High Mutation Rates: Adaptive Evolution of Bacteria in the Mouse Gut. <i>Science</i> , 2001, 291, 2606-2608.	12.6	447
6	Tempo and mode of genome evolution in a 50,000-generation experiment. <i>Nature</i> , 2016, 536, 165-170.	27.8	404
7	Selection Versus Demography: A Multilocus Investigation of the Domestication Process in Maize. <i>Molecular Biology and Evolution</i> , 2004, 21, 1214-1225.	8.9	251
8	Evolutionary Implications of the Frequent Horizontal Transfer of Mismatch Repair Genes. <i>Cell</i> , 2000, 103, 711-721.	28.9	246
9	Elucidating the molecular architecture of adaptation via evolve and resequence experiments. <i>Nature Reviews Genetics</i> , 2015, 16, 567-582.	16.3	236
10	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
11	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
12	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
13	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
14	Mutators, Population Size, Adaptive Landscape and the Adaptation of Asexual Populations of Bacteria. <i>Genetics</i> , 1999, 152, 485-493.	2.9	219
15	Understanding the Evolutionary Fate of Finite Populations: The Dynamics of Mutational Effects. <i>PLoS Biology</i> , 2007, 5, e94.	5.6	172
16	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
17	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
18	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

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19	Second-order selection in bacterial evolution: selection acting on mutation and recombination rates in the course of adaptation. <i>Research in Microbiology</i> , 2001, 152, 11-16.	2.1	116
20	Evolutionary significance of stress-induced mutagenesis in bacteria. <i>Trends in Microbiology</i> , 2004, 12, 264-270.	7.7	116
21	Evolution of Mutational Robustness in an RNA Virus. <i>PLoS Biology</i> , 2005, 3, e381.	5.6	116
22	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
23	Large Chromosomal Rearrangements during a Long-Term Evolution Experiment with <i>Escherichia coli</i> . <i>MBio</i> , 2014, 5, e01377-14.	4.1	109
24	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
25	Extensive Recombination among Human Immunodeficiency Virus Type 1 Quasispecies Makes an Important Contribution to Viral Diversity in Individual Patients. <i>Journal of Virology</i> , 2006, 80, 2472-2482.	3.4	102
26	The rule of declining adaptability in microbial evolution experiments. <i>Frontiers in Genetics</i> , 2015, 6, 99.	2.3	94
27	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
28	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
29	Mutators and sex in bacteria: Conflict between adaptive strategies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 10465-10470.	7.1	86
30	Evidence for a human-specific <i>Escherichia coli</i> clone. <i>Environmental Microbiology</i> , 2008, 10, 1000-1006.	3.8	86
31	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
32	Accumulation of Deleterious Mutations During Bacterial Range Expansions. <i>Genetics</i> , 2017, 207, 669-684.	2.9	74
33	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
34	Mutation rate and genome reduction in endosymbiotic and free-living bacteria. <i>Genetica</i> , 2008, 134, 205-210.	1.1	72
35	Quantifying Organismal Complexity using a Population Genetic Approach. <i>PLoS ONE</i> , 2007, 2, e217.	2.5	68
36	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

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37	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
38	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
39	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
40	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
41	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
42	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
43	Recent insights into the genotype-phenotype relationship from massively parallel genetic assays. <i>Evolutionary Applications</i> , 2019, 12, 1721-1742.	3.1	52
44	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
45	Intermediate Mutation Frequencies Favor Evolution of Multidrug Resistance in <i>Escherichia coli</i> . <i>Genetics</i> , 2005, 171, 825-827.	2.9	47
46	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
47	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
48	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
49	Selection Acts on DNA Secondary Structures to Decrease Transcriptional Mutagenesis. <i>PLoS Genetics</i> , 2006, 2, e176.	3.5	39
50	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
51	Fitness, Stress Resistance, and Extraintestinal Virulence in <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2013, 81, 2733-2742.	2.2	33
52	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
53	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
54	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

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55	<sc>CRISPR</sc> /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
56	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
57	Flux, toxicity, and expression costs generate complex genetic interactions in a metabolic pathway. <i>Science Advances</i> , 2020, 6, eabb2236.	10.3	26
58	Polymorphism of genes encoding SOS polymerases in natural populations of <i>Escherichia coli</i> . <i>DNA Repair</i> , 2003, 2, 417-426.	2.8	24
59	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
60	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
61	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
62	High Recombinant Frequency in Extraintestinal Pathogenic <i>Escherichia coli</i> Strains. <i>Molecular Biology and Evolution</i> , 2015, 32, 1708-1716.	8.9	21
63	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
64	The emergence of complexity and restricted pleiotropy in adapting networks. <i>BMC Evolutionary Biology</i> , 2011, 11, 326.	3.2	19
65	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
66	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
67	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
68	Electrophoretic mobility confirms reassortment bias among geographic isolates of segmented RNA phages. <i>BMC Evolutionary Biology</i> , 2013, 13, 206.	3.2	17
69	Mutation bias and GC content shape antimutator invasions. <i>Nature Communications</i> , 2019, 10, 3114.	12.8	17
70	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
71	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
72	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

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73	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
74	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
75	Dynamics of extended-spectrum beta-lactamase-producing <i>Enterobacterales</i> colonization in long-term carriers following travel abroad. <i>Microbial Genomics</i> , 2021, 7, .	2.0	11
76	FROM METABOLISM TO POLYMORPHISM IN BACTERIAL POPULATIONS: A THEORETICAL STUDY. <i>Evolution; International Journal of Organic Evolution</i> , 2001, 55, 2181-2193.	2.3	10
77	The Impact of Neutral Mutations on Genome Evolvability. <i>Current Biology</i> , 2020, 30, R527-R534.	3.9	9
78	Primary and promiscuous functions coexist during evolutionary innovation through whole protein domain acquisitions. <i>ELife</i> , 2020, 9, .	6.0	7
79	<i>Escherichia coli</i> Genomic Diversity within Extraintestinal Acute Infections Argues for Adaptive Evolution at Play. <i>MSphere</i> , 2021, 6, .	2.9	6
80	Deciphering polymorphism in 61,157 <i>Escherichia coli</i> genomes via epistatic sequence landscapes. <i>Nature Communications</i> , 2022, 13, .	12.8	6
81	How Fitch-Margoliash Algorithm can Benefit from Multi Dimensional Scaling. <i>Evolutionary Bioinformatics</i> , 2011, 7, EBO.S7048.	1.2	4
82	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
83	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
84	Local and Global Protein Interactions Contribute to Residue Entrenchment in Beta-Lactamase TEM-1. <i>Antibiotics</i> , 2022, 11, 652.	3.7	3
85	Horizontal Transfer of Mismatch Repair Genes and the Variable Speed of Bacterial Evolution. , 2002, , 147-155.		2
86	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
87	Quand les bactéries modulent leur vitesse d'évolution selon l'environnement.. <i>Medecine/Sciences</i> , 2001, 17, 514.	0.2	0
88	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