Jeffrey E Barrick

List of Publications by Year
in descending order

86 papers	12,723 citations	66315 42 h-index	53190 85 g-index
104 all docs	104 docs citations	104 times ranked	11134 citing authors

#	Article	IF	Citations
1	Engineering insects from the endosymbiont out. Trends in Microbiology, 2022, 30, 79-96.	3.5	22
2	Disentangling the Evolutionary History of Feo, the Major Ferrous Iron Transport System in Bacteria. MBio, 2022, 13, e0351221.	1.8	4
3	A road map for in vivo evolution experiments with blood‐borne parasitic microbes. Molecular Ecology Resources, 2022, 22, 2843-2859.	2.2	6
4	Engineering a Culturable Serratia symbiotica Strain for Aphid Paratransgenesis. Applied and Environmental Microbiology, 2021, 87, .	1.4	15
5	Global Transcriptional Response of Methylorubrum extorquens to Formaldehyde Stress Expands the Role of EfgA and Is Distinct from Antibiotic Translational Inhibition. Microorganisms, 2021, 9, 347.	1.6	4
6	Insertion-sequence-mediated mutations both promote and constrain evolvability during a long-term experiment with bacteria. Nature Communications, 2021, 12, 980.	5.8	63
7	Vertical Transmission at the Pathogen-Symbiont Interface: Serratia symbiotica and Aphids. MBio, 2021, 12, .	1.8	19
8	pLannotate: engineered plasmid annotation. Nucleic Acids Research, 2021, 49, W516-W522.	6.5	20
9	Coevolutionary phage training leads to greater bacterial suppression and delays the evolution of phage resistance. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	67
10	OSTIR: open source translation initiation rate prediction. Journal of Open Source Software, 2021, 6, 3362.	2.0	0
11	High-throughput characterization of mutations in genes that drive clonal evolution using multiplex adaptome capture sequencing. Cell Systems, 2021, 12, 1187-1200.e4.	2.9	5
12	Genomic evolution of antibiotic resistance is contingent on genetic background following a long-term experiment with *Escherichia coli*. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	39
13	Rates of gene conversions between *Escherichia coli* ribosomal operons. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	4
14	Engineered symbionts activate honey bee immunity and limit pathogens. Science, 2020, 367, 573-576.	6.0	161
15	Rapid and assured genetic engineering methods applied to Acinetobacter baylyi ADP1 genome streamlining. Nucleic Acids Research, 2020, 48, 4585-4600.	6.5	14
16	Genomic and phenotypic evolution of Escherichia coli in a novel citrate-only resource environment. ELife, 2020, 9, .	2.8	26
17	Limits to Predicting Evolution: Insights from a Long-Term Experiment with Escherichia coli. Genetic and Evolutionary Computation, 2020, , 63-76.	1.0	2
18	Bioassay for Determining the Concentrations of Caffeine and Individual Methylxanthines in Complex Samples. Applied and Environmental Microbiology, 2019, 85, .	1.4	3

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19	Synthetic Genome Defenses against Selfish DNA Elements Stabilize Engineered Bacteria against Evolutionary Failure. ACS Synthetic Biology, 2019, 8, 521-531.	1.9	34
20	Evolution of satellite plasmids can prolong the maintenance of newly acquired accessory genes in bacteria. Nature Communications, 2019, 10, 5809.	5.8	13
21	Genetic Engineering of Bee Gut Microbiome Bacteria with a Toolkit for Modular Assembly of Broad-Host-Range Plasmids. ACS Synthetic Biology, 2018, 7, 1279-1290.	1.9	87
22	Bacterial Production of Gellan Gum as a Do-It-Yourself Alternative to Agar. Journal of Microbiology and Biology Education, 2018, 19, .	0.5	8
23	Directed evolution of Escherichia coli with lower-than-natural plasmid mutation rates. Nucleic Acids Research, 2018, 46, 9236-9250.	6.5	33
24	Innovation in an E. coli evolution experiment is contingent on maintaining adaptive potential until competition subsides. PLoS Genetics, 2018, 14, e1007348.	1.5	33
25	Specificity of genome evolution in experimental populations of *Escherichia coli* evolved at different temperatures. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1904-E1912.	3.3	105
26	The E. coli molecular phenotype under different growth conditions. Scientific Reports, 2017, 7, 45303.	1.6	46
27	Arresting Evolution. Trends in Genetics, 2017, 33, 910-920.	2.9	34
28	The dynamics of molecular evolution over 60,000 generations. Nature, 2017, 551, 45-50.	13.7	585
29	Large-scale analysis of post-translational modifications in E. coli under glucose-limiting conditions. BMC Genomics, 2017, 18, 301.	1.2	55
30	Reduced Mutation Rate and Increased Transformability of Transposon-Free Acinetobacter baylyi ADP1-ISx. Applied and Environmental Microbiology, 2017, 83, .	1.4	28
31	Rapid and Inexpensive Evaluation of Nonstandard Amino Acid Incorporation in *Escherichia coli*. ACS Synthetic Biology, 2017, 6, 45-54.	1.9	32
32	Expanded Genetic Codes Create New Mutational Routes to Rifampicin Resistance in *Escherichia coli*. Molecular Biology and Evolution, 2016, 33, 2054-2063.	3.5	14
33	Emergence of a Competence-Reducing Filamentous Phage from the Genome of Acinetobacter baylyi ADP1. Journal of Bacteriology, 2016, 198, 3209-3219.	1.0	17
34	Tempo and mode of genome evolution in a 50,000-generation experiment. Nature, 2016, 536, 165-170.	13.7	404
35	Genome Instability Mediates the Loss of Key Traits by Acinetobacter baylyi ADP1 during Laboratory Evolution. Journal of Bacteriology, 2015, 197, 872-881.	1.0	31
36	Adaptation, Clonal Interference, and Frequency-Dependent Interactions in a Long-Term Evolution Experiment with *Escherichia coli*. Genetics, 2015, 200, 619-631.	1.2	140

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37	Draft Genome Sequence of the Bacterium Pseudomonas putida CBB5, Which Can Utilize Caffeine as a Sole Carbon and Nitrogen Source. Genome Announcements, 2015, 3, .	0.8	6
38	Predicting the Genetic Stability of Engineered DNA Sequences with the EFM Calculator. ACS Synthetic Biology, 2015, 4, 939-943.	1.9	55
39	Synonymous Genetic Variation in Natural Isolates of *Escherichia coli* Does Not Predict Where Synonymous Substitutions Occur in a Long-Term Experiment. Molecular Biology and Evolution, 2015, 32, 2897-2904.	3.5	27
40	Controlled Measurement and Comparative Analysis of Cellular Components in E. coli Reveals Broad Regulatory Changes in Response to Glucose Starvation. PLoS Computational Biology, 2015, 11, e1004400.	1.5	42
41	The Molecular and Genetic Basis of Repeatable Coevolution between Escherichia coli and Bacteriophage T3 in a Laboratory Microcosm. PLoS ONE, 2015, 10, e0130639.	1.1	33
42	Fine-tuning citrate synthase flux potentiates and refines metabolic innovation in the Lenski evolution experiment. ELife, 2015, 4, .	2.8	79
43	Predicting Growth Conditions from Internal Metabolic Fluxes in an In-Silico Model of E. coli. PLoS ONE, 2014, 9, e114608.	1.1	17
44	Large Chromosomal Rearrangements during a Long-Term Evolution Experiment with Escherichia coli. MBio, 2014, 5, e01377-14.	1.8	109
45	Identifying structural variation in haploid microbial genomes from short-read resequencing data using breseq. BMC Genomics, 2014, 15, 1039.	1.2	228
46	The case for decoupling assembly and submission standards to maintain a more flexible registry of biological parts. Journal of Biological Engineering, 2014, 8, 28.	2.0	7
47	Bacteriophages use an expanded genetic code on evolutionary paths to higher fitness. Nature Chemical Biology, 2014, 10, 178-180.	3.9	44
48	Engineering reduced evolutionary potential for synthetic biology. Molecular BioSystems, 2014, 10, 1668-1678.	2.9	83
49	Recursive genomewide recombination and sequencing reveals a key refinement step in the evolution of a metabolic innovation in *Escherichia coli*. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2217-2222.	3.3	75
50	Detecting rare structural variation in evolving microbial populations from new sequence junctions using breseq. Frontiers in Genetics, 2014, 5, 468.	1.1	82
51	Identification of Mutations in Laboratory-Evolved Microbes from Next-Generation Sequencing Data Using breseq. Methods in Molecular Biology, 2014, 1151, 165-188.	0.4	1,200
52	Genome dynamics during experimental evolution. Nature Reviews Genetics, 2013, 14, 827-839.	7.7	544
53	Mutation rate dynamics in a bacterial population reflect tension between adaptation and genetic load. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 222-227.	3.3	231
54	Physical model of the immune response of bacteria against bacteriophage through the adaptive CRISPR-Cas immune system. Physical Biology, 2013, 10, 025004.	0.8	24

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55	Decaffeination and Measurement of Caffeine Content by Addicted Escherichia coli with a Refactored N-Demethylation Operon from Pseudomonas putida CBB5. ACS Synthetic Biology, 2013, 2, 301-307.	1.9	15
56	Caffeine Junkie: an Unprecedented Glutathione S-Transferase-Dependent Oxygenase Required for Caffeine Degradation by Pseudomonas putida CBB5. Journal of Bacteriology, 2013, 195, 3933-3939.	1.0	28
57	Draft Genome Sequences of Two Campylobacter jejuni Clinical Isolates, NW and D2600. Journal of Bacteriology, 2012, 194, 5707-5708.	1.0	1
58	Repeatability and Contingency in the Evolution of a Key Innovation in Phage Lambda. Science, 2012, 335, 428-432.	6.0	401
59	Genomic analysis of a key innovation in an experimental Escherichia coli population. Nature, 2012, 489, 513-518.	13.7	527
60	Nanostructured Hybrid Transparent Conductive Films with Antibacterial Properties. ACS Nano, 2012, 6, 5157-5163.	7.3	139
61	Mutation Rate Inferred From Synonymous Substitutions in a Long-Term Evolution Experiment With <i>Escherichia coli</i>. G3: Genes, Genomes, Genetics, 2011, 1, 183-186.	0.8	157
62	Second-Order Selection for Evolvability in a Large <i>Escherichia coli</i> Population. Science, 2011, 331, 1433-1436.	6.0	300
63	Standing Genetic Variation in Contingency Loci Drives the Rapid Adaptation of Campylobacter jejuni to a Novel Host. PLoS ONE, 2011, 6, e16399.	1.1	97
64	Stock culture heterogeneity rather than new mutational variation complicates short-term cell physiology studies of Escherichia coli K-12 MG1655 in continuous culture. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	1.0	21
65	Escherichia coli rpoB Mutants Have Increased Evolvability in Proportion to Their Fitness Defects. Molecular Biology and Evolution, 2010, 27, 1338-1347.	3.5	130
66	Genome evolution and adaptation in a long-term experiment with Escherichia coli. Nature, 2009, 461, 1243-1247.	13.7	1,038
67	Sequence analysis of an artificial family of RNA-binding peptides. Protein Science, 2009, 11, 2688-2696.	3.1	16
68	A widespread riboswitch candidate that controls bacterial genes involved in molybdenum cofactor and tungsten cofactor metabolism. Molecular Microbiology, 2008, 68, 918-932.	1.2	142
69	The aptamer core of SAM-IV riboswitches mimics the ligand-binding site of SAM-I riboswitches. Rna, 2008, 14, 822-828.	1.6	103
70	Identification of 22 candidate structured RNAs in bacteria using the CMfinder comparative genomics pipeline. Nucleic Acids Research, 2007, 35, 4809-4819.	6.5	292
71	The distributions, mechanisms, and structures of metabolite-binding riboswitches. Genome Biology, 2007, 8, R239.	13.9	414
72	A riboswitch selective for the queuosine precursor preQ1 contains an unusually small aptamer domain. Nature Structural and Molecular Biology, 2007, 14, 308-317.	3.6	224

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73	The Power of Riboswitches. Scientific American, 2007, 296, 50-57.	1.0	40
74	Tandem Riboswitch Architectures Exhibit Complex Gene Control Functions. Science, 2006, 314, 300-304.	6.0	232
75	Balancing Robustness and Evolvability. PLoS Biology, 2006, 4, e428.	2.6	171
76	Identification of a large noncoding RNA in extremophilic eubacteria. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 19490-19495.	3.3	34
77	6S RNA is a widespread regulator of eubacterial RNA polymerase that resembles an open promoter. Rna, 2005, 11, 774-784.	1.6	210
78	Evidence for a second class of S-adenosylmethionine riboswitches and other regulatory RNA motifs in alpha-proteobacteria. Genome Biology, 2005, 6, R70.	13.9	213
79	New RNA motifs suggest an expanded scope for riboswitches in bacterial genetic control. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 6421-6426.	3.3	432
80	Coenzyme B12 riboswitches are widespread genetic control elements in prokaryotes. Nucleic Acids Research, 2004, 32, 143-150.	6.5	292
81	A Glycine-Dependent Riboswitch That Uses Cooperative Binding to Control Gene Expression. Science, 2004, 306, 275-279.	6.0	491
82	An mRNA structure that controls gene expression by binding S-adenosylmethionine. Nature Structural and Molecular Biology, 2003, 10, 701-707.	3.6	406
83	Achieving Specificity in Selected and Wild-Type N Peptideâ'RNA Complexes: The Importance of Discrimination against Noncognate RNA Targetsâ€. Biochemistry, 2003, 42, 12998-13007.	1.2	8
84	Riboswitches Control Fundamental Biochemical Pathways in Bacillus subtilis and Other Bacteria. Cell, 2003, 113, 577-586.	13.5	665
85	Metabolite-binding RNA domains are present in the genes of eukaryotes. Rna, 2003, 9, 644-647.	1.6	372
86	Selection of RNA-Binding Peptides Using mRNA-Peptide Fusions. Methods, 2001, 23, 287-293.	1.9	40