

Jeffrey E Barrick

List of Publications by Year in descending order

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86
papers

12,723
citations

66343

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85
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docs citations

104
times ranked

11134
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of Mutations in Laboratory-Evolved Microbes from Next-Generation Sequencing Data Using breseq. <i>Methods in Molecular Biology</i> , 2014, 1151, 165-188.	0.9	1,200
2	Genome evolution and adaptation in a long-term experiment with <i>Escherichia coli</i> . <i>Nature</i> , 2009, 461, 1243-1247.	27.8	1,038
3	Riboswitches Control Fundamental Biochemical Pathways in <i>Bacillus subtilis</i> and Other Bacteria. <i>Cell</i> , 2003, 113, 577-586.	28.9	665
4	The dynamics of molecular evolution over 60,000 generations. <i>Nature</i> , 2017, 551, 45-50.	27.8	585
5	Genome dynamics during experimental evolution. <i>Nature Reviews Genetics</i> , 2013, 14, 827-839.	16.3	544
6	Genomic analysis of a key innovation in an experimental <i>Escherichia coli</i> population. <i>Nature</i> , 2012, 489, 513-518.	27.8	527
7	A Glycine-Dependent Riboswitch That Uses Cooperative Binding to Control Gene Expression. <i>Science</i> , 2004, 306, 275-279.	12.6	491
8	New RNA motifs suggest an expanded scope for riboswitches in bacterial genetic control. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 6421-6426.	7.1	432
9	The distributions, mechanisms, and structures of metabolite-binding riboswitches. <i>Genome Biology</i> , 2007, 8, R239.	9.6	414
10	An mRNA structure that controls gene expression by binding S-adenosylmethionine. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 701-707.	8.2	406
11	Tempo and mode of genome evolution in a 50,000-generation experiment. <i>Nature</i> , 2016, 536, 165-170.	27.8	404
12	Repeatability and Contingency in the Evolution of a Key Innovation in Phage Lambda. <i>Science</i> , 2012, 335, 428-432.	12.6	401
13	Metabolite-binding RNA domains are present in the genes of eukaryotes. <i>Rna</i> , 2003, 9, 644-647.	3.5	372
14	Second-Order Selection for Evolvability in a Large <i>Escherichia coli</i> Population. <i>Science</i> , 2011, 331, 1433-1436.	12.6	300
15	Coenzyme B12 riboswitches are widespread genetic control elements in prokaryotes. <i>Nucleic Acids Research</i> , 2004, 32, 143-150.	14.5	292
16	Identification of 22 candidate structured RNAs in bacteria using the CMfinder comparative genomics pipeline. <i>Nucleic Acids Research</i> , 2007, 35, 4809-4819.	14.5	292
17	Tandem Riboswitch Architectures Exhibit Complex Gene Control Functions. <i>Science</i> , 2006, 314, 300-304.	12.6	232
18	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

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19	Identifying structural variation in haploid microbial genomes from short-read resequencing data using breseq. <i>BMC Genomics</i> , 2014, 15, 1039.	2.8	228
20	A riboswitch selective for the queuosine precursor preQ1 contains an unusually small aptamer domain. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 308-317.	8.2	224
21	Evidence for a second class of S-adenosylmethionine riboswitches and other regulatory RNA motifs in alpha-proteobacteria. <i>Genome Biology</i> , 2005, 6, R70.	9.6	213
22	6S RNA is a widespread regulator of eubacterial RNA polymerase that resembles an open promoter. <i>Rna</i> , 2005, 11, 774-784.	3.5	210
23	Balancing Robustness and Evolvability. <i>PLoS Biology</i> , 2006, 4, e428.	5.6	171
24	Engineered symbionts activate honey bee immunity and limit pathogens. <i>Science</i> , 2020, 367, 573-576.	12.6	161
25	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
26	A widespread riboswitch candidate that controls bacterial genes involved in molybdenum cofactor and tungsten cofactor metabolism. <i>Molecular Microbiology</i> , 2008, 68, 918-932.	2.5	142
27	Adaptation, Clonal Interference, and Frequency-Dependent Interactions in a Long-Term Evolution Experiment with <i>Escherichia coli</i> . <i>Genetics</i> , 2015, 200, 619-631.	2.9	140
28	Nanostructured Hybrid Transparent Conductive Films with Antibacterial Properties. <i>ACS Nano</i> , 2012, 6, 5157-5163.	14.6	139
29	<i>Escherichia coli</i> rpoB Mutants Have Increased Evolvability in Proportion to Their Fitness Defects. <i>Molecular Biology and Evolution</i> , 2010, 27, 1338-1347.	8.9	130
30	Large Chromosomal Rearrangements during a Long-Term Evolution Experiment with <i>Escherichia coli</i> . <i>MBio</i> , 2014, 5, e01377-14.	4.1	109
31	Specificity of genome evolution in experimental populations of <i>Escherichia coli</i> evolved at different temperatures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1904-E1912.	7.1	105
32	The aptamer core of SAM-IV riboswitches mimics the ligand-binding site of SAM-I riboswitches. <i>Rna</i> , 2008, 14, 822-828.	3.5	103
33	Standing Genetic Variation in Contingency Loci Drives the Rapid Adaptation of <i>Campylobacter jejuni</i> to a Novel Host. <i>PLoS ONE</i> , 2011, 6, e16399.	2.5	97
34	Genetic Engineering of Bee Gut Microbiome Bacteria with a Toolkit for Modular Assembly of Broad-Host-Range Plasmids. <i>ACS Synthetic Biology</i> , 2018, 7, 1279-1290.	3.8	87
35	Engineering reduced evolutionary potential for synthetic biology. <i>Molecular BioSystems</i> , 2014, 10, 1668-1678.	2.9	83
36	Detecting rare structural variation in evolving microbial populations from new sequence junctions using breseq. <i>Frontiers in Genetics</i> , 2014, 5, 468.	2.3	82

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37	Fine-tuning citrate synthase flux potentiates and refines metabolic innovation in the Lenski evolution experiment. <i>ELife</i> , 2015, 4, .	6.0	79
38	Recursive genomewide recombination and sequencing reveals a key refinement step in the evolution of a metabolic innovation in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2217-2222.	7.1	75
39	Coevolutionary phage training leads to greater bacterial suppression and delays the evolution of phage resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	67
40	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
41	Predicting the Genetic Stability of Engineered DNA Sequences with the EFM Calculator. <i>ACS Synthetic Biology</i> , 2015, 4, 939-943.	3.8	55
42	Large-scale analysis of post-translational modifications in <i>E. coli</i> under glucose-limiting conditions. <i>BMC Genomics</i> , 2017, 18, 301.	2.8	55
43	The <i>E. coli</i> molecular phenotype under different growth conditions. <i>Scientific Reports</i> , 2017, 7, 45303.	3.3	46
44	Bacteriophages use an expanded genetic code on evolutionary paths to higher fitness. <i>Nature Chemical Biology</i> , 2014, 10, 178-180.	8.0	44
45	Controlled Measurement and Comparative Analysis of Cellular Components in <i>E. coli</i> Reveals Broad Regulatory Changes in Response to Glucose Starvation. <i>PLoS Computational Biology</i> , 2015, 11, e1004400.	3.2	42
46	Selection of RNA-Binding Peptides Using mRNA-Peptide Fusions. <i>Methods</i> , 2001, 23, 287-293.	3.8	40
47	The Power of Riboswitches. <i>Scientific American</i> , 2007, 296, 50-57.	1.0	40
48	Genomic evolution of antibiotic resistance is contingent on genetic background following a long-term experiment with <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	39
49	Identification of a large noncoding RNA in extremophilic eubacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 19490-19495.	7.1	34
50	Arresting Evolution. <i>Trends in Genetics</i> , 2017, 33, 910-920.	6.7	34
51	Synthetic Genome Defenses against Selfish DNA Elements Stabilize Engineered Bacteria against Evolutionary Failure. <i>ACS Synthetic Biology</i> , 2019, 8, 521-531.	3.8	34
52	Directed evolution of <i>Escherichia coli</i> with lower-than-natural plasmid mutation rates. <i>Nucleic Acids Research</i> , 2018, 46, 9236-9250.	14.5	33
53	Innovation in an <i>E. coli</i> evolution experiment is contingent on maintaining adaptive potential until competition subsides. <i>PLoS Genetics</i> , 2018, 14, e1007348.	3.5	33
54	The Molecular and Genetic Basis of Repeatable Coevolution between <i>Escherichia coli</i> and Bacteriophage T3 in a Laboratory Microcosm. <i>PLoS ONE</i> , 2015, 10, e0130639.	2.5	33

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55	Rapid and Inexpensive Evaluation of Nonstandard Amino Acid Incorporation in <i>Escherichia coli</i> . ACS Synthetic Biology, 2017, 6, 45-54.	3.8	32
56	Genome Instability Mediates the Loss of Key Traits by <i>Acinetobacter baylyi</i> ADP1 during Laboratory Evolution. Journal of Bacteriology, 2015, 197, 872-881.	2.2	31
57	Caffeine Junkie: an Unprecedented Glutathione S-Transferase-Dependent Oxygenase Required for Caffeine Degradation by <i>Pseudomonas putida</i> CBB5. Journal of Bacteriology, 2013, 195, 3933-3939.	2.2	28
58	Reduced Mutation Rate and Increased Transformability of Transposon-Free <i>Acinetobacter baylyi</i> ADP1-ISx. Applied and Environmental Microbiology, 2017, 83, .	3.1	28
59	Synonymous Genetic Variation in Natural Isolates of <i>Escherichia coli</i> Does Not Predict Where Synonymous Substitutions Occur in a Long-Term Experiment. Molecular Biology and Evolution, 2015, 32, 2897-2904.	8.9	27
60	Genomic and phenotypic evolution of <i>Escherichia coli</i> in a novel citrate-only resource environment. ELife, 2020, 9, .	6.0	26
61	Physical model of the immune response of bacteria against bacteriophage through the adaptive CRISPR-Cas immune system. Physical Biology, 2013, 10, 025004.	1.8	24
62	Engineering insects from the endosymbiont out. Trends in Microbiology, 2022, 30, 79-96.	7.7	22
63	Stock culture heterogeneity rather than new mutational variation complicates short-term cell physiology studies of <i>Escherichia coli</i> K-12 MG1655 in continuous culture. Microbiology (United Kingdom), 2021, 157, 1000-1008.	1.0	20
64	pLannotate: engineered plasmid annotation. Nucleic Acids Research, 2021, 49, W516-W522.	14.5	20
65	Vertical Transmission at the Pathogen-Symbiont Interface: <i>Serratia symbiotica</i> and Aphids. MBio, 2021, 12, .	4.1	19
66	Predicting Growth Conditions from Internal Metabolic Fluxes in an In-Silico Model of <i>E. coli</i> . PLoS ONE, 2014, 9, e114608.	2.5	17
67	Emergence of a Competence-Reducing Filamentous Phage from the Genome of <i>Acinetobacter baylyi</i> ADP1. Journal of Bacteriology, 2016, 198, 3209-3219.	2.2	17
68	Sequence analysis of an artificial family of RNA-binding peptides. Protein Science, 2009, 11, 2688-2696.	7.6	16
69	Decaffeination and Measurement of Caffeine Content by Addicted <i>Escherichia coli</i> with a Refactored N-Demethylation Operon from <i>Pseudomonas putida</i> CBB5. ACS Synthetic Biology, 2013, 2, 301-307.	3.8	15
70	Engineering a Culturable <i>Serratia symbiotica</i> Strain for Aphid Paratransgenesis. Applied and Environmental Microbiology, 2021, 87, .	3.1	15
71	Expanded Genetic Codes Create New Mutational Routes to Rifampicin Resistance in <i>Escherichia coli</i> . Molecular Biology and Evolution, 2016, 33, 2054-2063.	8.9	14
72	Rapid and assured genetic engineering methods applied to <i>Acinetobacter baylyi</i> ADP1 genome streamlining. Nucleic Acids Research, 2020, 48, 4585-4600.	14.5	14

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73	Evolution of satellite plasmids can prolong the maintenance of newly acquired accessory genes in bacteria. <i>Nature Communications</i> , 2019, 10, 5809.	12.8	13
74	Achieving Specificity in Selected and Wild-Type N Peptide~RNA Complexes: The Importance of Discrimination against Noncognate RNA Targets. <i>Biochemistry</i> , 2003, 42, 12998-13007.	2.5	8
75	Bacterial Production of Gellan Gum as a Do-It-Yourself Alternative to Agar. <i>Journal of Microbiology and Biology Education</i> , 2018, 19, .	1.0	8
76	The case for decoupling assembly and submission standards to maintain a more flexible registry of biological parts. <i>Journal of Biological Engineering</i> , 2014, 8, 28.	4.7	7
77	Draft Genome Sequence of the Bacterium <i>Pseudomonas putida</i> CBB5, Which Can Utilize Caffeine as a Sole Carbon and Nitrogen Source. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
78	A road map for in vivo evolution experiments with blood-borne parasitic microbes. <i>Molecular Ecology Resources</i> , 2022, 22, 2843-2859.	4.8	6
79	High-throughput characterization of mutations in genes that drive clonal evolution using multiplex adaptome capture sequencing. <i>Cell Systems</i> , 2021, 12, 1187-1200.e4.	6.2	5
80	Global Transcriptional Response of <i>Methylorubrum extorquens</i> to Formaldehyde Stress Expands the Role of EfgA and Is Distinct from Antibiotic Translational Inhibition. <i>Microorganisms</i> , 2021, 9, 347.	3.6	4
81	Rates of gene conversions between <i>Escherichia coli</i> ribosomal operons. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	4
82	Disentangling the Evolutionary History of Feo, the Major Ferrous Iron Transport System in Bacteria. <i>MBio</i> , 2022, 13, e0351221.	4.1	4
83	Bioassay for Determining the Concentrations of Caffeine and Individual Methylxanthines in Complex Samples. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	3
84	Limits to Predicting Evolution: Insights from a Long-Term Experiment with <i>Escherichia coli</i> . <i>Genetic and Evolutionary Computation</i> , 2020, , 63-76.	1.0	2
85	Draft Genome Sequences of Two <i>Campylobacter jejuni</i> Clinical Isolates, NW and D2600. <i>Journal of Bacteriology</i> , 2012, 194, 5707-5708.	2.2	1
86	OSTIR: open source translation initiation rate prediction. <i>Journal of Open Source Software</i> , 2021, 6, 3362.	4.6	0