

Adam P Arkin

List of Publications by Year in descending order

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367
papers

60,376
citations

3334

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1222

227
g-index

441
all docs

441
docs citations

441
times ranked

59511
citing authors

#	ARTICLE	IF	CITATIONS
1	FastTree 2 "Approximately Maximum-Likelihood Trees for Large Alignments. PLoS ONE, 2010, 5, e9490.	2.5	11,284
2	FastTree: Computing Large Minimum Evolution Trees with Profiles instead of a Distance Matrix. Molecular Biology and Evolution, 2009, 26, 1641-1650.	8.9	4,165
3	Repurposing CRISPR as an RNA-Guided Platform for Sequence-Specific Control of Gene Expression. Cell, 2013, 152, 1173-1183.	28.9	4,090
4	Functional profiling of the Saccharomyces cerevisiae genome. Nature, 2002, 418, 387-391.	27.8	3,938
5	The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models. Bioinformatics, 2003, 19, 524-531.	4.1	2,811
6	Stochastic mechanisms in gene expression. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 814-819.	7.1	1,617
7	Stochastic Kinetic Analysis of Developmental Pathway Bifurcation in Phage λ -Infected Escherichia coli Cells. Genetics, 1998, 149, 1633-1648.	2.9	1,272
8	KBase: The United States Department of Energy Systems Biology Knowledgebase. Nature Biotechnology, 2018, 36, 566-569.	17.5	955
9	Control, exploitation and tolerance of intracellular noise. Nature, 2002, 420, 231-237.	27.8	909
10	It's a noisy business! Genetic regulation at the nanomolar scale. Trends in Genetics, 1999, 15, 65-69.	6.7	791
11	Precise and reliable gene expression via standard transcription and translation initiation elements. Nature Methods, 2013, 10, 354-360.	19.0	653
12	Stochastic Gene Expression in a Lentiviral Positive-Feedback Loop: HIV-1 Tat Fluctuations Drive Phenotypic Diversity. Cell, 2005, 122, 169-182.	28.9	599
13	Stochasticity, succession, and environmental perturbations in a fluidic ecosystem. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E836-45.	7.1	595
14	Environmentally Controlled Invasion of Cancer Cells by Engineered Bacteria. Journal of Molecular Biology, 2006, 355, 619-627.	4.2	547
15	Stochastic chemical kinetics and the quasi-steady-state assumption: Application to the Gillespie algorithm. Journal of Chemical Physics, 2003, 118, 4999-5010.	3.0	542
16	Environmental Genomics Reveals a Single-Species Ecosystem Deep Within Earth. Science, 2008, 322, 275-278.	12.6	474
17	Chemogenomic profiling: Identifying the functional interactions of small molecules in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 793-798.	7.1	460
18	A genomic catalog of Earth's microbiomes. Nature Biotechnology, 2021, 39, 499-509.	17.5	457

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19	Mutant phenotypes for thousands of bacterial genes of unknown function. <i>Nature</i> , 2018, 557, 503-509.	27.8	433
20	A quantitative framework reveals ecological drivers of grassland microbial community assembly in response to warming. <i>Nature Communications</i> , 2020, 11, 4717.	12.8	417
21	MicrobesOnline: an integrated portal for comparative and functional genomics. <i>Nucleic Acids Research</i> , 2010, 38, D396-D400.	14.5	408
22	RegPrecise 3.0 – A resource for genome-scale exploration of transcriptional regulation in bacteria. <i>BMC Genomics</i> , 2013, 14, 745.	2.8	408
23	Contextualizing context for synthetic biology – identifying causes of failure of synthetic biological systems. <i>Biotechnology Journal</i> , 2012, 7, 856-866.	3.5	394
24	Rapid Quantification of Mutant Fitness in Diverse Bacteria by Sequencing Randomly Bar-Coded Transposons. <i>MBio</i> , 2015, 6, e00306-15.	4.1	380
25	Composability of regulatory sequences controlling transcription and translation in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14024-14029.	7.1	377
26	Deciphering microbial interactions in synthetic human gut microbiome communities. <i>Molecular Systems Biology</i> , 2018, 14, e8157.	7.2	361
27	BglBricks: A flexible standard for biological part assembly. <i>Journal of Biological Engineering</i> , 2010, 4, 1.	4.7	348
28	Multiplexed RNA structure characterization with selective 2'-hydroxyl acylation analyzed by primer extension sequencing (SHAPE-Seq). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11063-11068.	7.1	346
29	Interactive XCMS Online: Simplifying Advanced Metabolomic Data Processing and Subsequent Statistical Analyses. <i>Analytical Chemistry</i> , 2014, 86, 6931-6939.	6.5	332
30	A novel method for accurate operon predictions in all sequenced prokaryotes. <i>Nucleic Acids Research</i> , 2005, 33, 880-892.	14.5	316
31	Selection of chromosomal DNA libraries using a multiplex CRISPR system. <i>ELife</i> , 2014, 3, .	6.0	314
32	Environmental signal integration by a modular AND gate. <i>Molecular Systems Biology</i> , 2007, 3, 133.	7.2	306
33	Stochastic amplification and signaling in enzymatic futile cycles through noise-induced bistability with oscillations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2310-2315.	7.1	304
34	Biological networks. <i>Current Opinion in Structural Biology</i> , 2003, 13, 193-202.	5.7	298
35	Detailed Simulations of Cell Biology with Smoldyn 2.1. <i>PLoS Computational Biology</i> , 2010, 6, e1000705.	3.2	285
36	Motifs, modules and games in bacteria. <i>Current Opinion in Microbiology</i> , 2003, 6, 125-134.	5.1	280

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37	Versatile RNA-sensing transcriptional regulators for engineering genetic networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 8617-8622.	7.1	277
38	Dissimilatory Metabolism of Nitrogen Oxides in Bacteria: Comparative Reconstruction of Transcriptional Networks. <i>PLoS Computational Biology</i> , 2005, 1, e55.	3.2	260
39	A Test Case of Correlation Metric Construction of a Reaction Pathway from Measurements. <i>Science</i> , 1997, 277, 1275-1279.	12.6	253
40	Diversity in times of adversity: probabilistic strategies in microbial survival games. <i>Journal of Theoretical Biology</i> , 2005, 234, 227-253.	1.7	251
41	SIMULATION OF PROKARYOTIC GENETIC CIRCUITS. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1998, 27, 199-224.	18.3	237
42	Computational functions in biochemical reaction networks. <i>Biophysical Journal</i> , 1994, 67, 560-578.	0.5	207
43	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. <i>Microbiome</i> , 2020, 8, 51.	11.1	205
44	Genetic basis for nitrate resistance in <i>Desulfovibrio</i> strains. <i>Frontiers in Microbiology</i> , 2014, 5, 153.	3.5	202
45	The Genome Project-Write. <i>Science</i> , 2016, 353, 126-127.	12.6	194
46	RNA processing enables predictable programming of gene expression. <i>Nature Biotechnology</i> , 2012, 30, 1002-1006.	17.5	184
47	Quantitative estimation of activity and quality for collections of functional genetic elements. <i>Nature Methods</i> , 2013, 10, 347-353.	19.0	183
48	Evaluation of 244,000 synthetic sequences reveals design principles to optimize translation in <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2018, 36, 1005-1015.	17.5	182
49	The Evolution of Two-Component Systems in Bacteria Reveals Different Strategies for Niche Adaptation. <i>PLoS Computational Biology</i> , 2006, 2, e143.	3.2	181
50	The MicrobesOnline Web site for comparative genomics. <i>Genome Research</i> , 2005, 15, 1015-1022.	5.5	176
51	Global Transcriptome Analysis of the Heat Shock Response of <i>Shewanella oneidensis</i> . <i>Journal of Bacteriology</i> , 2004, 186, 7796-7803.	2.2	173
52	Rational and Evolutionary Engineering Approaches Uncover a Small Set of Genetic Changes Efficient for Rapid Xylose Fermentation in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2013, 8, e57048.	2.5	173
53	Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. <i>MBio</i> , 2015, 6, e00326-15.	4.1	173
54	RegPrecise: a database of curated genomic inferences of transcriptional regulatory interactions in prokaryotes. <i>Nucleic Acids Research</i> , 2010, 38, D111-D118.	14.5	172

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55	Setting the standard in synthetic biology. <i>Nature Biotechnology</i> , 2008, 26, 771-774.	17.5	171
56	How sulphate-reducing microorganisms cope with stress: lessons from systems biology. <i>Nature Reviews Microbiology</i> , 2011, 9, 452-466.	28.6	169
57	The essential gene set of a photosynthetic organism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E6634-43.	7.1	166
58	Reconstruction of regulatory and metabolic pathways in metal-reducing delta-proteobacteria. <i>Genome Biology</i> , 2004, 5, R90.	9.6	162
59	Rationally designed families of orthogonal RNA regulators of translation. <i>Nature Chemical Biology</i> , 2012, 8, 447-454.	8.0	157
60	Salt Stress in <i>Desulfovibrio vulgaris</i> Hildenborough: an Integrated Genomics Approach. <i>Journal of Bacteriology</i> , 2006, 188, 4068-4078.	2.2	155
61	Measurement and modeling of intrinsic transcription terminators. <i>Nucleic Acids Research</i> , 2013, 41, 5139-5148.	14.5	155
62	<i>Rhodospiridium toruloides</i> : a new platform organism for conversion of lignocellulose into terpene biofuels and bioproducts. <i>Biotechnology for Biofuels</i> , 2017, 10, 241.	6.2	150
63	The Life-Cycle of Operons. <i>PLoS Genetics</i> , 2006, 2, e96.	3.5	146
64	Genome-Wide Requirements for Resistance to Functionally Distinct DNA-Damaging Agents. <i>PLoS Genetics</i> , 2005, 1, e24.	3.5	144
65	Engineering <i>Rhodospiridium toruloides</i> for increased lipid production. <i>Biotechnology and Bioengineering</i> , 2016, 113, 1056-1066.	3.3	143
66	Rapid and Efficient One-Step Metabolic Pathway Integration in <i>E. coli</i> . <i>ACS Synthetic Biology</i> , 2016, 5, 561-568.	3.8	143
67	The evolution of genetic regulatory systems in bacteria. <i>Nature Reviews Genetics</i> , 2004, 5, 169-178.	16.3	140
68	Overview of the Alliance for Cellular Signaling. <i>Nature</i> , 2002, 420, 703-706.	27.8	134
69	The Electron Transfer System of Syntrophically Grown <i>Desulfovibrio vulgaris</i> . <i>Journal of Bacteriology</i> , 2009, 191, 5793-5801.	2.2	133
70	Operon formation is driven by co-regulation and not by horizontal gene transfer. <i>Genome Research</i> , 2005, 15, 809-819.	5.5	131
71	Design and Diversity in Bacterial Chemotaxis: A Comparative Study in <i>Escherichia coli</i> and <i>Bacillus subtilis</i> . <i>PLoS Biology</i> , 2004, 2, e49.	5.6	130
72	RegPredict: an integrated system for regulon inference in prokaryotes by comparative genomics approach. <i>Nucleic Acids Research</i> , 2010, 38, W299-W307.	14.5	130

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73	A versatile framework for microbial engineering using synthetic non-coding RNAs. <i>Nature Reviews Microbiology</i> , 2014, 12, 341-354.	28.6	126
74	Design and Construction of a Double Inversion Recombination Switch for Heritable Sequential Genetic Memory. <i>PLoS ONE</i> , 2008, 3, e2815.	2.5	123
75	Evidence-Based Annotation of Gene Function in <i>Shewanella oneidensis</i> MR-1 Using Genome-Wide Fitness Profiling across 121 Conditions. <i>PLoS Genetics</i> , 2011, 7, e1002385.	3.5	119
76	The ModelSEED Biochemistry Database for the integration of metabolic annotations and the reconstruction, comparison and analysis of metabolic models for plants, fungi and microbes. <i>Nucleic Acids Research</i> , 2021, 49, D575-D588.	14.5	119
77	Statistical Construction of Chemical Reaction Mechanisms from Measured Time-Series. <i>The Journal of Physical Chemistry</i> , 1995, 99, 970-979.	2.9	118
78	Horizontal gene transfer and the evolution of transcriptional regulation in <i>Escherichia coli</i> . <i>Genome Biology</i> , 2008, 9, R4.	9.6	116
79	Memory in Microbes: Quantifying History-Dependent Behavior in a Bacterium. <i>PLoS ONE</i> , 2008, 3, e1700.	2.5	115
80	Comparative Genomics of Regulation of Fatty Acid and Branched-Chain Amino Acid Utilization in Proteobacteria. <i>Journal of Bacteriology</i> , 2009, 191, 52-64.	2.2	115
81	Deviant effects in molecular reaction pathways. <i>Nature Biotechnology</i> , 2006, 24, 1235-1240.	17.5	113
82	Control Motifs for Intracellular Regulatory Networks. <i>Annual Review of Biomedical Engineering</i> , 2001, 3, 391-419.	12.3	112
83	Indirect and suboptimal control of gene expression is widespread in bacteria. <i>Molecular Systems Biology</i> , 2013, 9, 660.	7.2	111
84	Modeling and automation of sequencing-based characterization of RNA structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11069-11074.	7.1	109
85	From Fluctuations to Phenotypes: The Physiology of Noise. <i>Science's STKE: Signal Transduction Knowledge Environment</i> , 2006, 2006, re17-re17.	3.9	108
86	PaperBLAST: Text Mining Papers for Information about Homologs. <i>MSystems</i> , 2017, 2, .	3.8	107
87	Global Analysis of Heat Shock Response in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Journal of Bacteriology</i> , 2006, 188, 1817-1828.	2.2	106
88	Toward scalable parts families for predictable design of biological circuits. <i>Current Opinion in Microbiology</i> , 2008, 11, 567-573.	5.1	106
89	Lateral Gene Transfer in a Heavy Metal-Contaminated-Groundwater Microbial Community. <i>MBio</i> , 2016, 7, e02234-15.	4.1	105
90	Dissecting a complex chemical stress: chemogenomic profiling of plant hydrolysates. <i>Molecular Systems Biology</i> , 2013, 9, 674.	7.2	103

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91	Metabolic engineering of the oleaginous yeast <i>Rhodospiridium toruloides</i> IFO0880 for lipid overproduction during high-density fermentation. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 9393-9405.	3.6	101
92	Towards synthetic biological approaches to resource utilization on space missions. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20140715.	3.4	100
93	Redefining fundamental concepts of transcription initiation in bacteria. <i>Nature Reviews Genetics</i> , 2020, 21, 699-714.	16.3	100
94	Determination of causal connectivities of species in reaction networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 5816-5821.	7.1	98
95	Control of Stochastic Gene Expression by Host Factors at the HIV Promoter. <i>PLoS Pathogens</i> , 2009, 5, e1000260.	4.7	98
96	Functional genomics of lipid metabolism in the oleaginous yeast <i>Rhodospiridium toruloides</i> . <i>ELife</i> , 2018, 7, .	6.0	98
97	Combinatorial Latency Reactivation for HIV-1 Subtypes and Variants. <i>Journal of Virology</i> , 2010, 84, 5958-5974.	3.4	97
98	RegTransBase—a database of regulatory sequences and interactions in a wide range of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2007, 35, D407-D412.	14.5	95
99	HIV Promoter Integration Site Primarily Modulates Transcriptional Burst Size Rather Than Frequency. <i>PLoS Computational Biology</i> , 2010, 6, e1000952.	3.2	95
100	Orthogonal control of expression mean and variance by epigenetic features at different genomic loci. <i>Molecular Systems Biology</i> , 2015, 11, 806.	7.2	95
101	Cell-Wide Responses to Low-Oxygen Exposure in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Journal of Bacteriology</i> , 2007, 189, 5996-6010.	2.2	94
102	Energetic Consequences of Nitrite Stress in <i>Desulfovibrio vulgaris</i> Hildenborough, Inferred from Global Transcriptional Analysis. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4370-4381.	3.1	92
103	Gene regulation: Towards a circuit engineering discipline. <i>Current Biology</i> , 2000, 10, R318-R320.	3.9	91
104	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . <i>PLoS Biology</i> , 2020, 18, e3000877.	5.6	91
105	Filling gaps in bacterial amino acid biosynthesis pathways with high-throughput genetics. <i>PLoS Genetics</i> , 2018, 14, e1007147.	3.5	90
106	Signal Processing by Simple Chemical Systems. <i>Journal of Physical Chemistry A</i> , 2002, 106, 10205-10221.	2.5	88
107	Complexity in bacterial cell-cell communication: Quorum signal integration and subpopulation signaling in the <i>Bacillus subtilis</i> phosphorelay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6459-6464.	7.1	88
108	Engineering naturally occurring trans-acting non-coding RNAs to sense molecular signals. <i>Nucleic Acids Research</i> , 2012, 40, 5775-5786.	14.5	87

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109	Mechanisms of direct inhibition of the respiratory sulfate-reduction pathway by (per)chlorate and nitrate. <i>ISME Journal</i> , 2015, 9, 1295-1305.	9.8	87
110	Orthologous Transcription Factors in Bacteria Have Different Functions and Regulate Different Genes. <i>PLoS Computational Biology</i> , 2007, 3, e175.	3.2	86
111	A metabolic pathway for catabolizing levulinic acid in bacteria. <i>Nature Microbiology</i> , 2017, 2, 1624-1634.	13.3	86
112	Synthetic cell biology. <i>Current Opinion in Biotechnology</i> , 2001, 12, 638-644.	6.6	85
113	Sequestration-based bistability enables tuning of the switching boundaries and design of a latch. <i>Molecular Systems Biology</i> , 2012, 8, 620.	7.2	83
114	Fast, cheap and somewhat in control. <i>Genome Biology</i> , 2006, 7, 114.	9.6	82
115	Functional genetics of human gut commensal <i>Bacteroides thetaiotaomicron</i> reveals metabolic requirements for growth across environments. <i>Cell Reports</i> , 2021, 34, 108789.	6.4	82
116	Identification of Genes Involved in the Toxic Response of <i>Saccharomyces cerevisiae</i> against Iron and Copper Overload by Parallel Analysis of Deletion Mutants. <i>Toxicological Sciences</i> , 2008, 101, 140-151.	3.1	81
117	Sequencing of Multiple Clostridial Genomes Related to Biomass Conversion and Biofuel Production. <i>Journal of Bacteriology</i> , 2010, 192, 6494-6496.	2.2	81
118	GENETIC CODE: Representations and Dynamical Models of Genetic Components and Networks. <i>Annual Review of Genomics and Human Genetics</i> , 2002, 3, 341-369.	6.2	80
119	Engineering robust control of two-component system phosphotransfer using modular scaffolds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18090-18095.	7.1	79
120	Transcript level and sequence determinants of protein abundance and noise in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2014, 42, 4791-4799.	14.5	79
121	Variation among <i>Desulfovibrio</i> Species in Electron Transfer Systems Used for Syntrophic Growth. <i>Journal of Bacteriology</i> , 2013, 195, 990-1004.	2.2	77
122	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. <i>Frontiers in Microbiology</i> , 2015, 6, 1205.	3.5	77
123	Complete genome sequence of <i>Enterobacter lignolyticus</i> -SCF1. <i>Standards in Genomic Sciences</i> , 2011, 5, 69-85.	1.5	76
124	Effects of Genetic Variation on the <i>E. coli</i> Host-Circuit Interface. <i>Cell Reports</i> , 2013, 4, 231-237.	6.4	75
125	Transcriptome Analysis of <i>Shewanella oneidensis</i> MR-1 in Response to Elevated Salt Conditions. <i>Journal of Bacteriology</i> , 2005, 187, 2501-2507.	2.2	74
126	Efficient stochastic sensitivity analysis of discrete event systems. <i>Journal of Computational Physics</i> , 2007, 221, 724-738.	3.8	73

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127	CRISPR-Cas9 Circular Permutants as Programmable Scaffolds for Genome Modification. <i>Cell</i> , 2019, 176, 254-267.e16.	28.9	73
128	On the deduction of chemical reaction pathways from measurements of time series of concentrations. <i>Chaos</i> , 2001, 11, 108.	2.5	71
129	A tightly regulated inducible expression system utilizing the <i>fim</i> inversion recombination switch. <i>Biotechnology and Bioengineering</i> , 2006, 94, 1-4.	3.3	70
130	Analysis of a Ferric Uptake Regulator (Fur) Mutant of <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5389-5400.	3.1	70
131	RegTransBase – a database of regulatory sequences and interactions based on literature: a resource for investigating transcriptional regulation in prokaryotes. <i>BMC Genomics</i> , 2013, 14, 213.	2.8	69
132	Monofluorophosphate Is a Selective Inhibitor of Respiratory Sulfate-Reducing Microorganisms. <i>Environmental Science & Technology</i> , 2015, 49, 3727-3736.	10.0	69
133	Impact of elevated nitrate on sulfate-reducing bacteria: a comparative Study of <i>Desulfovibrio vulgaris</i> . <i>ISME Journal</i> , 2010, 4, 1386-1397.	9.8	67
134	An adaptor from translational to transcriptional control enables predictable assembly of complex regulation. <i>Nature Methods</i> , 2012, 9, 1088-1094.	19.0	67
135	Transcriptomic and proteomic analyses of <i>Desulfovibrio vulgaris</i> biofilms: Carbon and energy flow contribute to the distinct biofilm growth state. <i>BMC Genomics</i> , 2012, 13, 138.	2.8	67
136	Functional responses of methanogenic archaea to syntrophic growth. <i>ISME Journal</i> , 2012, 6, 2045-2055.	9.8	66
137	Interruptions in gene expression drive highly expressed operons to the leading strand of DNA replication. <i>Nucleic Acids Research</i> , 2005, 33, 3224-3234.	14.5	64
138	Global Transcriptional, Physiological, and Metabolite Analyses of the Responses of <i>Desulfovibrio vulgaris</i> Hildenborough to Salt Adaptation. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1574-1586.	3.1	64
139	Genomics for environmental microbiology. <i>Current Opinion in Biotechnology</i> , 2006, 17, 229-235.	6.6	63
140	Transcriptome Profiling of <i>Shewanella oneidensis</i> Gene Expression following Exposure to Acidic and Alkaline pH. <i>Journal of Bacteriology</i> , 2006, 188, 1633-1642.	2.2	62
141	Response of <i>Desulfovibrio vulgaris</i> to Alkaline Stress. <i>Journal of Bacteriology</i> , 2007, 189, 8944-8952.	2.2	62
142	The genetic basis of energy conservation in the sulfate-reducing bacterium <i>Desulfovibrio alaskensis</i> G20. <i>Frontiers in Microbiology</i> , 2014, 5, 577.	3.5	61
143	Selective carbon sources influence the end products of microbial nitrate respiration. <i>ISME Journal</i> , 2020, 14, 2034-2045.	9.8	61
144	Theoretical Design of a Gene Therapy To Prevent AIDS but Not Human Immunodeficiency Virus Type 1 Infection. <i>Journal of Virology</i> , 2003, 77, 10028-10036.	3.4	60

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145	Towards an Informative Mutant Phenotype for Every Bacterial Gene. <i>Journal of Bacteriology</i> , 2014, 196, 3643-3655.	2.2	60
146	Massively Parallel Fitness Profiling Reveals Multiple Novel Enzymes in <i>Pseudomonas putida</i> Lysine Metabolism. <i>MBio</i> , 2019, 10, .	4.1	60
147	The <i>Bacillus subtilis</i> <i>sin</i> Operon. <i>Genetics</i> , 2005, 169, 1187-1202.	2.9	59
148	Comparative genomic reconstruction of transcriptional networks controlling central metabolism in the <i>Shewanella</i> genus. <i>BMC Genomics</i> , 2011, 12, S3.	2.8	59
149	Development of a Low Bias Method for Characterizing Viral Populations Using Next Generation Sequencing Technology. <i>PLoS ONE</i> , 2010, 5, e13564.	2.5	58
150	Microfluidic fluorescence in situ hybridization and flow cytometry (¼FlowFISH). <i>Lab on A Chip</i> , 2011, 11, 2673.	6.0	58
151	Engineering <i>Kluyveromyces marxianus</i> as a Robust Synthetic Biology Platform Host. <i>MBio</i> , 2018, 9, .	4.1	58
152	Network News: Innovations in 21st Century Systems Biology. <i>Cell</i> , 2011, 144, 844-849.	28.9	57
153	Varying virulence: epigenetic control of expression noise and disease processes. <i>Trends in Biotechnology</i> , 2011, 29, 517-525.	9.3	57
154	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. <i>MBio</i> , 2018, 9, .	4.1	57
155	Snapshot of iron response in <i>Shewanella oneidensis</i> by gene network reconstruction. <i>BMC Genomics</i> , 2009, 10, 131.	2.8	56
156	Functional Genomics with a Comprehensive Library of Transposon Mutants for the Sulfate-Reducing Bacterium <i>Desulfovibrio alaskensis</i> G20. <i>MBio</i> , 2014, 5, e01041-14.	4.1	56
157	Conservation of Transcription Start Sites within Genes across a Bacterial Genus. <i>MBio</i> , 2014, 5, e01398-14.	4.1	56
158	The selective pressures on the microbial community in a metal-contaminated aquifer. <i>ISME Journal</i> , 2019, 13, 937-949.	9.8	56
159	Model Discrimination Using Data Collaboration. <i>Journal of Physical Chemistry A</i> , 2006, 110, 6803-6813.	2.5	55
160	Grand challenges in space synthetic biology. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150803.	3.4	55
161	A universal TagModule collection for parallel genetic analysis of microorganisms. <i>Nucleic Acids Research</i> , 2010, 38, e146-e146.	14.5	54
162	A latent variable model for chemogenomic profiling. <i>Bioinformatics</i> , 2005, 21, 3286-3293.	4.1	53

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163	Modularity of stress response evolution. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7500-7505.	7.1	53
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165	A Method to Constrain Genome-Scale Models with 13C Labeling Data. PLoS Computational Biology, 2015, 11, e1004363.	3.2	53
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