

Adam P Arkin

List of Publications by Year in descending order

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367
papers

60,376
citations

3325

91
h-index

1250

226
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.	1.1	11,284
2	FastTree: Computing Large Minimum Evolution Trees with Profiles instead of a Distance Matrix. Molecular Biology and Evolution, 2009, 26, 1641-1650.	3.5	4,165
3	Repurposing CRISPR as an RNA-Guided Platform for Sequence-Specific Control of Gene Expression. Cell, 2013, 152, 1173-1183.	13.5	4,090
4	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. Nature, 2002, 418, 387-391.	13.7	3,938
5	The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models. Bioinformatics, 2003, 19, 524-531.	1.8	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.	3.3	1,617
7	Stochastic Kinetic Analysis of Developmental Pathway Bifurcation in Phage λ -Infected <i>Escherichia coli</i> Cells. Genetics, 1998, 149, 1633-1648.	1.2	1,272
8	KBase: The United States Department of Energy Systems Biology Knowledgebase. Nature Biotechnology, 2018, 36, 566-569.	9.4	955
9	Control, exploitation and tolerance of intracellular noise. Nature, 2002, 420, 231-237.	13.7	909
10	It’s a noisy business! Genetic regulation at the nanomolar scale. Trends in Genetics, 1999, 15, 65-69.	2.9	791
11	Precise and reliable gene expression via standard transcription and translation initiation elements. Nature Methods, 2013, 10, 354-360.	9.0	653
12	Stochastic Gene Expression in a Lentiviral Positive-Feedback Loop: HIV-1 Tat Fluctuations Drive Phenotypic Diversity. Cell, 2005, 122, 169-182.	13.5	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.	3.3	595
14	Environmentally Controlled Invasion of Cancer Cells by Engineered Bacteria. Journal of Molecular Biology, 2006, 355, 619-627.	2.0	547
15	Stochastic chemical kinetics and the quasi-steady-state assumption: Application to the Gillespie algorithm. Journal of Chemical Physics, 2003, 118, 4999-5010.	1.2	542
16	Environmental Genomics Reveals a Single-Species Ecosystem Deep Within Earth. Science, 2008, 322, 275-278.	6.0	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.	3.3	460
18	A genomic catalog of Earth’s microbiomes. Nature Biotechnology, 2021, 39, 499-509.	9.4	457

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19	Mutant phenotypes for thousands of bacterial genes of unknown function. <i>Nature</i> , 2018, 557, 503-509.	13.7	433
20	A quantitative framework reveals ecological drivers of grassland microbial community assembly in response to warming. <i>Nature Communications</i> , 2020, 11, 4717.	5.8	417
21	MicrobesOnline: an integrated portal for comparative and functional genomics. <i>Nucleic Acids Research</i> , 2010, 38, D396-D400.	6.5	408
22	RegPrecise 3.0 – A resource for genome-scale exploration of transcriptional regulation in bacteria. <i>BMC Genomics</i> , 2013, 14, 745.	1.2	408
23	Contextualizing context for synthetic biology – identifying causes of failure of synthetic biological systems. <i>Biotechnology Journal</i> , 2012, 7, 856-866.	1.8	394
24	Rapid Quantification of Mutant Fitness in Diverse Bacteria by Sequencing Randomly Bar-Coded Transposons. <i>MBio</i> , 2015, 6, e00306-15.	1.8	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.	3.3	377
26	Deciphering microbial interactions in synthetic human gut microbiome communities. <i>Molecular Systems Biology</i> , 2018, 14, e8157.	3.2	361
27	BglBricks: A flexible standard for biological part assembly. <i>Journal of Biological Engineering</i> , 2010, 4, 1.	2.0	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.	3.3	346
29	Interactive XCMS Online: Simplifying Advanced Metabolomic Data Processing and Subsequent Statistical Analyses. <i>Analytical Chemistry</i> , 2014, 86, 6931-6939.	3.2	332
30	A novel method for accurate operon predictions in all sequenced prokaryotes. <i>Nucleic Acids Research</i> , 2005, 33, 880-892.	6.5	316
31	Selection of chromosomal DNA libraries using a multiplex CRISPR system. <i>ELife</i> , 2014, 3, .	2.8	314
32	Environmental signal integration by a modular AND gate. <i>Molecular Systems Biology</i> , 2007, 3, 133.	3.2	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.	3.3	304
34	Biological networks. <i>Current Opinion in Structural Biology</i> , 2003, 13, 193-202.	2.6	298
35	Detailed Simulations of Cell Biology with Smoldyn 2.1. <i>PLoS Computational Biology</i> , 2010, 6, e1000705.	1.5	285
36	Motifs, modules and games in bacteria. <i>Current Opinion in Microbiology</i> , 2003, 6, 125-134.	2.3	280

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37	Versatile RNA-sensing transcriptional regulators for engineering genetic networks. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 8617-8622.	3.3	277
38	Dissimilatory Metabolism of Nitrogen Oxides in Bacteria: Comparative Reconstruction of Transcriptional Networks. PLoS Computational Biology, 2005, 1, e55.	1.5	260
39	A Test Case of Correlation Metric Construction of a Reaction Pathway from Measurements. Science, 1997, 277, 1275-1279.	6.0	253
40	Diversity in times of adversity: probabilistic strategies in microbial survival games. Journal of Theoretical Biology, 2005, 234, 227-253.	0.8	251
41	SIMULATION OF PROKARYOTIC GENETIC CIRCUITS. Annual Review of Biophysics and Biomolecular Structure, 1998, 27, 199-224.	18.3	237
42	Computational functions in biochemical reaction networks. Biophysical Journal, 1994, 67, 560-578.	0.2	207
43	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. Microbiome, 2020, 8, 51.	4.9	205
44	Genetic basis for nitrate resistance in Desulfovibrio strains. Frontiers in Microbiology, 2014, 5, 153.	1.5	202
45	The Genome Project-Write. Science, 2016, 353, 126-127.	6.0	194
46	RNA processing enables predictable programming of gene expression. Nature Biotechnology, 2012, 30, 1002-1006.	9.4	184
47	Quantitative estimation of activity and quality for collections of functional genetic elements. Nature Methods, 2013, 10, 347-353.	9.0	183
48	Evaluation of 244,000 synthetic sequences reveals design principles to optimize translation in Escherichia coli. Nature Biotechnology, 2018, 36, 1005-1015.	9.4	182
49	The Evolution of Two-Component Systems in Bacteria Reveals Different Strategies for Niche Adaptation. PLoS Computational Biology, 2006, 2, e143.	1.5	181
50	The MicrobesOnline Web site for comparative genomics. Genome Research, 2005, 15, 1015-1022.	2.4	176
51	Global Transcriptome Analysis of the Heat Shock Response of Shewanella oneidensis. Journal of Bacteriology, 2004, 186, 7796-7803.	1.0	173
52	Rational and Evolutionary Engineering Approaches Uncover a Small Set of Genetic Changes Efficient for Rapid Xylose Fermentation in Saccharomyces cerevisiae. PLoS ONE, 2013, 8, e57048.	1.1	173
53	Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. MBio, 2015, 6, e00326-15.	1.8	173
54	RegPrecise: a database of curated genomic inferences of transcriptional regulatory interactions in prokaryotes. Nucleic Acids Research, 2010, 38, D111-D118.	6.5	172

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55	Setting the standard in synthetic biology. <i>Nature Biotechnology</i> , 2008, 26, 771-774.	9.4	171
56	How sulphate-reducing microorganisms cope with stress: lessons from systems biology. <i>Nature Reviews Microbiology</i> , 2011, 9, 452-466.	13.6	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.	3.3	166
58	Reconstruction of regulatory and metabolic pathways in metal-reducing delta-proteobacteria. <i>Genome Biology</i> , 2004, 5, R90.	13.9	162
59	Rationally designed families of orthogonal RNA regulators of translation. <i>Nature Chemical Biology</i> , 2012, 8, 447-454.	3.9	157
60	Salt Stress in <i>Desulfovibrio vulgaris</i> Hildenborough: an Integrated Genomics Approach. <i>Journal of Bacteriology</i> , 2006, 188, 4068-4078.	1.0	155
61	Measurement and modeling of intrinsic transcription terminators. <i>Nucleic Acids Research</i> , 2013, 41, 5139-5148.	6.5	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.	1.5	146
64	Genome-Wide Requirements for Resistance to Functionally Distinct DNA-Damaging Agents. <i>PLoS Genetics</i> , 2005, 1, e24.	1.5	144
65	Engineering <i>Rhodospiridium toruloides</i> for increased lipid production. <i>Biotechnology and Bioengineering</i> , 2016, 113, 1056-1066.	1.7	143
66	Rapid and Efficient One-Step Metabolic Pathway Integration in <i>E. coli</i> . <i>ACS Synthetic Biology</i> , 2016, 5, 561-568.	1.9	143
67	The evolution of genetic regulatory systems in bacteria. <i>Nature Reviews Genetics</i> , 2004, 5, 169-178.	7.7	140
68	Overview of the Alliance for Cellular Signaling. <i>Nature</i> , 2002, 420, 703-706.	13.7	134
69	The Electron Transfer System of Syntrophically Grown <i>Desulfovibrio vulgaris</i> . <i>Journal of Bacteriology</i> , 2009, 191, 5793-5801.	1.0	133
70	Operon formation is driven by co-regulation and not by horizontal gene transfer. <i>Genome Research</i> , 2005, 15, 809-819.	2.4	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.	2.6	130
72	RegPredict: an integrated system for regulon inference in prokaryotes by comparative genomics approach. <i>Nucleic Acids Research</i> , 2010, 38, W299-W307.	6.5	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.	13.6	126
74	Design and Construction of a Double Inversion Recombination Switch for Heritable Sequential Genetic Memory. <i>PLoS ONE</i> , 2008, 3, e2815.	1.1	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.	1.5	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.	6.5	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.	13.9	116
79	Memory in Microbes: Quantifying History-Dependent Behavior in a Bacterium. <i>PLoS ONE</i> , 2008, 3, e1700.	1.1	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.	1.0	115
81	Deviant effects in molecular reaction pathways. <i>Nature Biotechnology</i> , 2006, 24, 1235-1240.	9.4	113
82	Control Motifs for Intracellular Regulatory Networks. <i>Annual Review of Biomedical Engineering</i> , 2001, 3, 391-419.	5.7	112
83	Indirect and suboptimal control of gene expression is widespread in bacteria. <i>Molecular Systems Biology</i> , 2013, 9, 660.	3.2	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.	3.3	109
85	From Fluctuations to Phenotypes: The Physiology of Noise. <i>Science's STKE: Signal Transduction Knowledge Environment</i> , 2006, 2006, re17-re17.	4.1	108
86	PaperBLAST: Text Mining Papers for Information about Homologs. <i>MSystems</i> , 2017, 2, .	1.7	107
87	Global Analysis of Heat Shock Response in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Journal of Bacteriology</i> , 2006, 188, 1817-1828.	1.0	106
88	Toward scalable parts families for predictable design of biological circuits. <i>Current Opinion in Microbiology</i> , 2008, 11, 567-573.	2.3	106
89	Lateral Gene Transfer in a Heavy Metal-Contaminated-Groundwater Microbial Community. <i>MBio</i> , 2016, 7, e02234-15.	1.8	105
90	Dissecting a complex chemical stress: chemogenomic profiling of plant hydrolysates. <i>Molecular Systems Biology</i> , 2013, 9, 674.	3.2	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.	1.7	101
92	Towards synthetic biological approaches to resource utilization on space missions. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20140715.	1.5	100
93	Redefining fundamental concepts of transcription initiation in bacteria. <i>Nature Reviews Genetics</i> , 2020, 21, 699-714.	7.7	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.	3.3	98
95	Control of Stochastic Gene Expression by Host Factors at the HIV Promoter. <i>PLoS Pathogens</i> , 2009, 5, e1000260.	2.1	98
96	Functional genomics of lipid metabolism in the oleaginous yeast <i>Rhodospiridium toruloides</i> . <i>ELife</i> , 2018, 7, .	2.8	98
97	Combinatorial Latency Reactivation for HIV-1 Subtypes and Variants. <i>Journal of Virology</i> , 2010, 84, 5958-5974.	1.5	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.	6.5	95
99	HIV Promoter Integration Site Primarily Modulates Transcriptional Burst Size Rather Than Frequency. <i>PLoS Computational Biology</i> , 2010, 6, e1000952.	1.5	95
100	Orthogonal control of expression mean and variance by epigenetic features at different genomic loci. <i>Molecular Systems Biology</i> , 2015, 11, 806.	3.2	95
101	Cell-Wide Responses to Low-Oxygen Exposure in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Journal of Bacteriology</i> , 2007, 189, 5996-6010.	1.0	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.	1.4	92
103	Gene regulation: Towards a circuit engineering discipline. <i>Current Biology</i> , 2000, 10, R318-R320.	1.8	91
104	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . <i>PLoS Biology</i> , 2020, 18, e3000877.	2.6	91
105	Filling gaps in bacterial amino acid biosynthesis pathways with high-throughput genetics. <i>PLoS Genetics</i> , 2018, 14, e1007147.	1.5	90
106	Signal Processing by Simple Chemical Systems. <i>Journal of Physical Chemistry A</i> , 2002, 106, 10205-10221.	1.1	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.	3.3	88
108	Engineering naturally occurring trans-acting non-coding RNAs to sense molecular signals. <i>Nucleic Acids Research</i> , 2012, 40, 5775-5786.	6.5	87

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109	Mechanisms of direct inhibition of the respiratory sulfate-reduction pathway by (per)chlorate and nitrate. ISME Journal, 2015, 9, 1295-1305.	4.4	87
110	Orthologous Transcription Factors in Bacteria Have Different Functions and Regulate Different Genes. PLoS Computational Biology, 2007, 3, e175.	1.5	86
111	A metabolic pathway for catabolizing levulinic acid in bacteria. Nature Microbiology, 2017, 2, 1624-1634.	5.9	86
112	Synthetic cell biology. Current Opinion in Biotechnology, 2001, 12, 638-644.	3.3	85
113	Sequestration-based bistability enables tuning of the switching boundaries and design of a latch. Molecular Systems Biology, 2012, 8, 620.	3.2	83
114	Fast, cheap and somewhat in control. Genome Biology, 2006, 7, 114.	13.9	82
115	Functional genetics of human gut commensal Bacteroides thetaiotaomicron reveals metabolic requirements for growth across environments. Cell Reports, 2021, 34, 108789.	2.9	82
116	Identification of Genes Involved in the Toxic Response of Saccharomyces cerevisiae against Iron and Copper Overload by Parallel Analysis of Deletion Mutants. Toxicological Sciences, 2008, 101, 140-151.	1.4	81
117	Sequencing of Multiple Clostridial Genomes Related to Biomass Conversion and Biofuel Production. Journal of Bacteriology, 2010, 192, 6494-6496.	1.0	81
118	GENETIC CODE: Representations and Dynamical Models of Genetic Components and Networks. Annual Review of Genomics and Human Genetics, 2002, 3, 341-369.	2.5	80
119	Engineering robust control of two-component system phosphotransfer using modular scaffolds. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18090-18095.	3.3	79
120	Transcript level and sequence determinants of protein abundance and noise in Escherichia coli. Nucleic Acids Research, 2014, 42, 4791-4799.	6.5	79
121	Variation among Desulfovibrio Species in Electron Transfer Systems Used for Syntrophic Growth. Journal of Bacteriology, 2013, 195, 990-1004.	1.0	77
122	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. Frontiers in Microbiology, 2015, 6, 1205.	1.5	77
123	Complete genome sequence of Enterobacter lignolyticus SCF1. Standards in Genomic Sciences, 2011, 5, 69-85.	1.5	76
124	Effects of Genetic Variation on the E. coli Host-Circuit Interface. Cell Reports, 2013, 4, 231-237.	2.9	75
125	Transcriptome Analysis of Shewanella oneidensis MR-1 in Response to Elevated Salt Conditions. Journal of Bacteriology, 2005, 187, 2501-2507.	1.0	74
126	Efficient stochastic sensitivity analysis of discrete event systems. Journal of Computational Physics, 2007, 221, 724-738.	1.9	73

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127	CRISPR-Cas9 Circular Permutants as Programmable Scaffolds for Genome Modification. <i>Cell</i> , 2019, 176, 254-267.e16.	13.5	73
128	On the deduction of chemical reaction pathways from measurements of time series of concentrations. <i>Chaos</i> , 2001, 11, 108.	1.0	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.	1.7	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.	1.4	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.	1.2	69
132	Monofluorophosphate Is a Selective Inhibitor of Respiratory Sulfate-Reducing Microorganisms. <i>Environmental Science & Technology</i> , 2015, 49, 3727-3736.	4.6	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.	4.4	67
134	An adaptor from translational to transcriptional control enables predictable assembly of complex regulation. <i>Nature Methods</i> , 2012, 9, 1088-1094.	9.0	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.	1.2	67
136	Functional responses of methanogenic archaea to syntrophic growth. <i>ISME Journal</i> , 2012, 6, 2045-2055.	4.4	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.	6.5	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.	1.4	64
139	Genomics for environmental microbiology. <i>Current Opinion in Biotechnology</i> , 2006, 17, 229-235.	3.3	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.	1.0	62
141	Response of <i>Desulfovibrio vulgaris</i> to Alkaline Stress. <i>Journal of Bacteriology</i> , 2007, 189, 8944-8952.	1.0	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.	1.5	61
143	Selective carbon sources influence the end products of microbial nitrate respiration. <i>ISME Journal</i> , 2020, 14, 2034-2045.	4.4	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.	1.5	60

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145	Towards an Informative Mutant Phenotype for Every Bacterial Gene. <i>Journal of Bacteriology</i> , 2014, 196, 3643-3655.	1.0	60
146	Massively Parallel Fitness Profiling Reveals Multiple Novel Enzymes in <i>Pseudomonas putida</i> Lysine Metabolism. <i>MBio</i> , 2019, 10, .	1.8	60
147	The <i>Bacillus subtilis</i> <i>sin</i> Operon. <i>Genetics</i> , 2005, 169, 1187-1202.	1.2	59
148	Comparative genomic reconstruction of transcriptional networks controlling central metabolism in the <i>Shewanella</i> genus. <i>BMC Genomics</i> , 2011, 12, S3.	1.2	59
149	Development of a Low Bias Method for Characterizing Viral Populations Using Next Generation Sequencing Technology. <i>PLoS ONE</i> , 2010, 5, e13564.	1.1	58
150	Microfluidic fluorescence in situ hybridization and flow cytometry (1/4FlowFISH). <i>Lab on A Chip</i> , 2011, 11, 2673.	3.1	58
151	Engineering <i>Kluyveromyces marxianus</i> as a Robust Synthetic Biology Platform Host. <i>MBio</i> , 2018, 9, .	1.8	58
152	Network News: Innovations in 21st Century Systems Biology. <i>Cell</i> , 2011, 144, 844-849.	13.5	57
153	Varying virulence: epigenetic control of expression noise and disease processes. <i>Trends in Biotechnology</i> , 2011, 29, 517-525.	4.9	57
154	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. <i>MBio</i> , 2018, 9, .	1.8	57
155	Snapshot of iron response in <i>Shewanella oneidensis</i> by gene network reconstruction. <i>BMC Genomics</i> , 2009, 10, 131.	1.2	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.	1.8	56
157	Conservation of Transcription Start Sites within Genes across a Bacterial Genus. <i>MBio</i> , 2014, 5, e01398-14.	1.8	56
158	The selective pressures on the microbial community in a metal-contaminated aquifer. <i>ISME Journal</i> , 2019, 13, 937-949.	4.4	56
159	Model Discrimination Using Data Collaboration. <i>Journal of Physical Chemistry A</i> , 2006, 110, 6803-6813.	1.1	55
160	Grand challenges in space synthetic biology. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150803.	1.5	55
161	A universal TagModule collection for parallel genetic analysis of microorganisms. <i>Nucleic Acids Research</i> , 2010, 38, e146-e146.	6.5	54
162	A latent variable model for chemogenomic profiling. <i>Bioinformatics</i> , 2005, 21, 3286-3293.	1.8	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.	3.3	53
164	Manipulation of the carbon storage regulator system for metabolite remodeling and biofuel production in Escherichia coli. Microbial Cell Factories, 2012, 11, 79.	1.9	53
165	A Method to Constrain Genome-Scale Models with 13C Labeling Data. PLoS Computational Biology, 2015, 11, e1004363.	1.5	53
166	A wise consistency: engineering biology for conformity, reliability, predictability. Current Opinion in Chemical Biology, 2013, 17, 893-901.	2.8	50
167	Novel Mechanism for Scavenging of Hypochlorite Involving a Periplasmic Methionine-Rich Peptide and Methionine Sulfoxide Reductase. MBio, 2015, 6, e00233-15.	1.8	50
168	Programming mRNA decay to modulate synthetic circuit resource allocation. Nature Communications, 2017, 8, 15128.	5.8	50
169	Metabolic flux analysis of <i>Shewanella</i> spp. reveals evolutionary robustness in central carbon metabolism. Biotechnology and Bioengineering, 2009, 102, 1161-1169.	1.7	49
170	Systematic mapping of two component response regulators to gene targets in a model sulfate reducing bacterium. Genome Biology, 2011, 12, R99.	13.9	49
171	Molybdenum Availability Is Key to Nitrate Removal in Contaminated Groundwater Environments. Applied and Environmental Microbiology, 2015, 81, 4976-4983.	1.4	49
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