

Adam P Arkin

List of Publications by Year in descending order

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367
papers

60,376
citations

3874

91
h-index

1446

226
g-index

441
all docs

441
docs citations

441
times ranked

66518
citing authors

#	ARTICLE	IF	CITATIONS
1	Sustained Ability of a Natural Microbial Community to Remove Nitrate from Groundwater. <i>Ground Water</i> , 2022, 60, 99-111.	0.7	6
2	Systems-informed genome mining for electroautotrophic microbial production. <i>Bioelectrochemistry</i> , 2022, 145, 108054.	2.4	7
3	Global Analysis of Biomineralization Genes in <i>Magnetospirillum magneticum</i> AMB-1. <i>MSystems</i> , 2022, 7, e0103721.	1.7	2
4	Genomic Features and Pervasive Negative Selection in <i>Rhodanobacter</i> Strains Isolated from Nitrate and Heavy Metal Contaminated Aquifer. <i>Microbiology Spectrum</i> , 2022, 10, e0259121.	1.2	8
5	Genotype to ecotype in niche environments: adaptation of <i>Arthrobacter</i> to carbon availability and environmental conditions. <i>ISME Communications</i> , 2022, 2, .	1.7	9
6	A Phage Foundry Framework to Systematically Develop Viral Countermeasures to Combat Antibiotic-Resistant Bacterial Pathogens. <i>IScience</i> , 2022, 25, 104121.	1.9	12
7	Filling gaps in bacterial catabolic pathways with computation and high-throughput genetics. <i>PLoS Genetics</i> , 2022, 18, e1010156.	1.5	15
8	Complete Genome Sequence of <i>Bacillus cereus</i> Strain CPT56D-587-MTF, Isolated from a Nitrate- and Metal-Contaminated Subsurface Environment. <i>Microbiology Resource Announcements</i> , 2022, 11, e0014522.	0.3	1
9	Photovoltaics-Driven Power Production Can Support Human Exploration on Mars. <i>Frontiers in Astronomy and Space Sciences</i> , 2022, 9, .	1.1	3
10	A Defined Medium for Cultivation and Exometabolite Profiling of Soil Bacteria. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	11
11	Development of a Markerless Deletion Mutagenesis System in Nitrate-Reducing Bacterium <i>Rhodanobacter denitrificans</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	3
12	Space bioprocess engineering on the horizon. , 2022, 1, .		11
13	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
14	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
15	Four families of folate-independent methionine synthases. <i>PLoS Genetics</i> , 2021, 17, e1009342.	1.5	8
16	Deletion Mutants, Archived Transposon Library, and Tagged Protein Constructs of the Model Sulfate-Reducing Bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	6
17	Molecular pharming to support human life on the moon, mars, and beyond. <i>Critical Reviews in Biotechnology</i> , 2021, 41, 849-864.	5.1	25
18	Systematic discovery of pseudomonad genetic factors involved in sensitivity to tailocins. <i>ISME Journal</i> , 2021, 15, 2289-2305.	4.4	27

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19	Mechanism Across Scales: A Holistic Modeling Framework Integrating Laboratory and Field Studies for Microbial Ecology. <i>Frontiers in Microbiology</i> , 2021, 12, 642422.	1.5	12
20	Functional genetics of human gut commensal <i>Bacteroides thetaiotaomicron</i> reveals metabolic requirements for growth across environments. <i>Cell Reports</i> , 2021, 34, 108789.	2.9	82
21	A method for achieving complete microbial genomes and improving bins from metagenomics data. <i>PLoS Computational Biology</i> , 2021, 17, e1008972.	1.5	22
22	Ecogenomics of Groundwater Phages Suggests Niche Differentiation Linked to Specific Environmental Tolerance. <i>MSystems</i> , 2021, 6, e0053721.	1.7	8
23	Production of PHB From CO ₂ -Derived Acetate With Minimal Processing Assessed for Space Biomanufacturing. <i>Frontiers in Microbiology</i> , 2021, 12, 700010.	1.5	17
24	Towards a Biomanufactory on Mars. <i>Frontiers in Astronomy and Space Sciences</i> , 2021, 8, .	1.1	30
25	Deciphering Microbial Metal Toxicity Responses via Random Bar Code Transposon Site Sequencing and Activity-Based Metabolomics. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0103721.	1.4	3
26	A Simple, Cost-Effective, and Automation-Friendly Direct PCR Approach for Bacterial Community Analysis. <i>MSystems</i> , 2021, 6, e0022421.	1.7	6
27	Evaluating the Cost of Pharmaceutical Purification for a Long-Duration Space Exploration Medical Foundry. <i>Frontiers in Microbiology</i> , 2021, 12, 700863.	1.5	9
28	Bioinformatic Teaching Resources “ For Educators, by Educators “ Using KBase, a Free, User-Friendly, Open Source Platform. <i>Frontiers in Education</i> , 2021, 6, .	1.2	4
29	A KBase case study on genome-wide transcriptomics and plant primary metabolism in response to drought stress in <i>Sorghum</i> .. <i>Current Plant Biology</i> , 2021, 28, 100229.	2.3	4
30	The genetic basis of phage susceptibility, cross-resistance and host-range in <i>Salmonella</i> . <i>Microbiology (United Kingdom)</i> , 2021, 167, .	0.7	20
31	iVirus 2.0: Cyberinfrastructure-supported tools and data to power DNA virus ecology. <i>ISME Communications</i> , 2021, 1, .	1.7	13
32	Biofilm Interaction Mapping and Analysis (BIMA) of Interspecific Interactions in <i>Pseudomonas</i> Co-culture Biofilms. <i>Frontiers in Microbiology</i> , 2021, 12, 757856.	1.5	1
33	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . <i>PLoS Biology</i> , 2020, 18, e3000877.	2.6	91
34	Redefining fundamental concepts of transcription initiation in bacteria. <i>Nature Reviews Genetics</i> , 2020, 21, 699-714.	7.7	100
35	Characterization of a Metal-Resistant <i>Bacillus</i> Strain With a High Molybdate Affinity ModA From Contaminated Sediments at the Oak Ridge Reservation. <i>Frontiers in Microbiology</i> , 2020, 11, 587127.	1.5	11
36	GapMind: Automated Annotation of Amino Acid Biosynthesis. <i>MSystems</i> , 2020, 5, .	1.7	40

#	ARTICLE	IF	CITATIONS
37	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
38	Effects of Genetic and Physiological Divergence on the Evolution of a Sulfate-Reducing Bacterium under Conditions of Elevated Temperature. <i>MBio</i> , 2020, 11, .	1.8	5
39	Draft Genome Sequence of <i>Bacillus</i> sp. Strain EB106-08-02-XG196, Isolated from High-Nitrate-Contaminated Sediment. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
40	Diverse Bacterial Genes Modulate Plant Root Association by Beneficial Bacteria. <i>MBio</i> , 2020, 11, .	1.8	15
41	Selective carbon sources influence the end products of microbial nitrate respiration. <i>ISME Journal</i> , 2020, 14, 2034-2045.	4.4	61
42	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. <i>Microbiome</i> , 2020, 8, 51.	4.9	205
43	Characterization of subsurface media from locations up- and down-gradient of a uranium-contaminated aquifer. <i>Chemosphere</i> , 2020, 255, 126951.	4.2	18
44	In-field bioreactors demonstrate dynamic shifts in microbial communities in response to geochemical perturbations. <i>PLoS ONE</i> , 2020, 15, e0232437.	1.1	5
45	The Role of Synthetic Biology in Atmospheric Greenhouse Gas Reduction: Prospects and Challenges. <i>Biodesign Research</i> , 2020, 2020, .	0.8	24
46	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . , 2020, 18, e3000877.		0
47	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . , 2020, 18, e3000877.		0
48	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . , 2020, 18, e3000877.		0
49	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . , 2020, 18, e3000877.		0
50	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . , 2020, 18, e3000877.		0
51	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . , 2020, 18, e3000877.		0
52	Improved Method for Estimating Reaction Rates During Push–Pull Tests. <i>Ground Water</i> , 2019, 57, 292-302.	0.7	8
53	High spatiotemporal variability of bacterial diversity over short time scales with unique hydrochemical associations within a shallow aquifer. <i>Water Research</i> , 2019, 164, 114917.	5.3	23
54	Nitrate-Utilizing Microorganisms Resistant to Multiple Metals from the Heavily Contaminated Oak Ridge Reservation. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	13

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55	Transposon insertional mutagenesis in <i>Saccharomyces uvarum</i> reveals trans-acting effects influencing species-dependent essential genes. <i>Genome Research</i> , 2019, 29, 396-406.	2.4	24
56	Dual-barcoded shotgun expression library sequencing for high-throughput characterization of functional traits in bacteria. <i>Nature Communications</i> , 2019, 10, 308.	5.8	33
57	Principles of synthetic biology: a MOOC for an emerging field. <i>Synthetic Biology</i> , 2019, 4, ysz010.	1.2	10
58	Massively Parallel Fitness Profiling Reveals Multiple Novel Enzymes in <i>Pseudomonas putida</i> Lysine Metabolism. <i>MBio</i> , 2019, 10, .	1.8	60
59	Iterative screening methodology enables isolation of strains with improved properties for a FACS-based screen and increased L-DOPA production. <i>Scientific Reports</i> , 2019, 9, 5815.	1.6	25
60	Multiplexed CRISPR-Cas9-Based Genome Editing of <i>Rhodospiridium toruloides</i> . <i>MSphere</i> , 2019, 4, .	1.3	47
61	A versatile platform strain for high-fidelity multiplex genome editing. <i>Nucleic Acids Research</i> , 2019, 47, 3244-3256.	6.5	16
62	Curated BLAST for Genomes. <i>MSystems</i> , 2019, 4, .	1.7	13
63	Oxidative Pathways of Deoxyribose and Deoxyribonate Catabolism. <i>MSystems</i> , 2019, 4, .	1.7	34
64	Genomewide and Enzymatic Analysis Reveals Efficient D -Galacturonic Acid Metabolism in the Basidiomycete Yeast <i>Rhodospiridium toruloides</i> . <i>MSystems</i> , 2019, 4, .	1.7	20
65	Older Blood Is Associated With Increased Mortality and Adverse Events in Massively Transfused Trauma Patients: Secondary Analysis of the PROPPR Trial. <i>Annals of Emergency Medicine</i> , 2019, 73, 650-661.	0.3	38
66	CRISPR-Cas9 Circular Permutants as Programmable Scaffolds for Genome Modification. <i>Cell</i> , 2019, 176, 254-267.e16.	13.5	73
67	Designing Spatially Distributed Gene Regulatory Networks To Elicit Contrasting Patterns. <i>ACS Synthetic Biology</i> , 2019, 8, 119-126.	1.9	6
68	The selective pressures on the microbial community in a metal-contaminated aquifer. <i>ISME Journal</i> , 2019, 13, 937-949.	4.4	56
69	Iron- and aluminium-induced depletion of molybdenum in acidic environments impedes the nitrogen cycle. <i>Environmental Microbiology</i> , 2019, 21, 152-163.	1.8	22
70	Structural basis for AcrVA4 inhibition of specific CRISPR-Cas12a. <i>ELife</i> , 2019, 8, .	2.8	41
71	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. <i>MBio</i> , 2018, 9, .	1.8	57
72	Magic Pools: Parallel Assessment of Transposon Delivery Vectors in Bacteria. <i>MSystems</i> , 2018, 3, .	1.7	31

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73	Engineering <i>Kluyveromyces marxianus</i> as a Robust Synthetic Biology Platform Host. <i>MBio</i> , 2018, 9, .	1.8	58
74	Genetic dissection of interspecific differences in yeast thermotolerance. <i>Nature Genetics</i> , 2018, 50, 1501-1504.	9.4	43
75	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.	9.4	182
76	Mutant phenotypes for thousands of bacterial genes of unknown function. <i>Nature</i> , 2018, 557, 503-509.	13.7	433
77	Functional genomics of lipid metabolism in the oleaginous yeast <i>Rhodospiridium toruloides</i> . <i>ELife</i> , 2018, 7, .	2.8	98
78	Deciphering microbial interactions in synthetic human gut microbiome communities. <i>Molecular Systems Biology</i> , 2018, 14, e8157.	3.2	361
79	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018, 36, 566-569.	9.4	955
80	Use of in-field bioreactors demonstrate groundwater filtration influences planktonic bacterial community assembly, but not biofilm composition. <i>PLoS ONE</i> , 2018, 13, e0194663.	1.1	9
81	Filling gaps in bacterial amino acid biosynthesis pathways with high-throughput genetics. <i>PLoS Genetics</i> , 2018, 14, e1007147.	1.5	90
82	Metabolic engineering of a haploid strain derived from a triploid industrial yeast for producing cellulosic ethanol. <i>Metabolic Engineering</i> , 2017, 40, 176-185.	3.6	27
83	A Highly Expressed High-Molecular-Weight S-Layer Complex of <i>Pelosinus</i> sp. Strain UFO1 Binds Uranium. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	17
84	Temporal Dynamics of In-Field Bioreactor Populations Reflect the Groundwater System and Respond Predictably to Perturbation. <i>Environmental Science & Technology</i> , 2017, 51, 2879-2889.	4.6	15
85	Programming mRNA decay to modulate synthetic circuit resource allocation. <i>Nature Communications</i> , 2017, 8, 15128.	5.8	50
86	Dynamic Succession of Groundwater Sulfate-Reducing Communities during Prolonged Reduction of Uranium in a Contaminated Aquifer. <i>Environmental Science & Technology</i> , 2017, 51, 3609-3620.	4.6	22
87	Complete genome sequence of <i>Pseudomonas stutzeri</i> strain RCH2 isolated from a Hexavalent Chromium [Cr(VI)] contaminated site. <i>Standards in Genomic Sciences</i> , 2017, 12, 23.	1.5	12
88	Targeted clinical control of trauma patient coagulation through a thrombin dynamics model. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	23
89	Quantitative Trait Loci (QTL)-Guided Metabolic Engineering of a Complex Trait. <i>ACS Synthetic Biology</i> , 2017, 6, 566-581.	1.9	26
90	Unintended Laboratory-Driven Evolution Reveals Genetic Requirements for Biofilm Formation by <i>Desulfovibrio vulgaris</i> Hildenborough. <i>MBio</i> , 2017, 8, .	1.8	18

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91	A metabolic pathway for catabolizing levulinic acid in bacteria. <i>Nature Microbiology</i> , 2017, 2, 1624-1634.	5.9	86
92	PaperBLAST: Text Mining Papers for Information about Homologs. <i>MSystems</i> , 2017, 2, .	1.7	107
93	Environmental Selection, Dispersal, and Organism Interactions Shape Community Assembly in High-Throughput Enrichment Culturing. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	12
94	Key Metabolites and Mechanistic Changes for Salt Tolerance in an Experimentally Evolved Sulfate-Reducing Bacterium, <i>Desulfovibrio vulgaris</i> . <i>MBio</i> , 2017, 8, .	1.8	13
95	The JBEI quantitative metabolic modeling library (jQMM): a python library for modeling microbial metabolism. <i>BMC Bioinformatics</i> , 2017, 18, 205.	1.2	19
96	Draft Genome Sequences of Two <i>Janthinobacterium lividum</i> Strains, Isolated from Pristine Groundwater Collected from the Oak Ridge Field Research Center. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
97	Mechanisms of Chromium and Uranium Toxicity in <i>Pseudomonas stutzeri</i> RCH2 Grown under Anaerobic Nitrate-Reducing Conditions. <i>Frontiers in Microbiology</i> , 2017, 8, 1529.	1.5	45
98	<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
99	Genetic interaction mapping with microfluidic-based single cell sequencing. <i>PLoS ONE</i> , 2017, 12, e0171302.	1.1	9
100	Validating regulatory predictions from diverse bacteria with mutant fitness data. <i>PLoS ONE</i> , 2017, 12, e0178258.	1.1	9
101	An Interventional Soylent Diet Increases the Bacteroidetes to Firmicutes Ratio in Human Gut Microbiome Communities. <i>American Journal of Gastroenterology</i> , 2017, 112, S67-S69.	0.2	0
102	A Theoretical Lower Bound for Selection on the Expression Levels of Proteins. <i>Genome Biology and Evolution</i> , 2016, 8, 1917-1928.	1.1	9
103	A Comparison of the Costs and Benefits of Bacterial Gene Expression. <i>PLoS ONE</i> , 2016, 11, e0164314.	1.1	26
104	System-Wide Adaptations of <i>Desulfovibrio alaskensis</i> G20 to Phosphate-Limited Conditions. <i>PLoS ONE</i> , 2016, 11, e0168719.	1.1	15
105	Engineering <i>Rhodospiridium toruloides</i> for increased lipid production. <i>Biotechnology and Bioengineering</i> , 2016, 113, 1056-1066.	1.7	143
106	Lateral Gene Transfer in a Heavy Metal-Contaminated-Groundwater Microbial Community. <i>MBio</i> , 2016, 7, e02234-15.	1.8	105
107	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
108	Rapid and efficient galactose fermentation by engineered <i>Saccharomyces cerevisiae</i> . <i>Journal of Biotechnology</i> , 2016, 229, 13-21.	1.9	24

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109	Gene Amplification on Demand Accelerates Cellobiose Utilization in Engineered <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 3631-3639.	1.4	24
110	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
111	Novel Metal Cation Resistance Systems from Mutant Fitness Analysis of Denitrifying <i>Pseudomonas stutzeri</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 6046-6056.	1.4	21
112	The Genome Project-Write. <i>Science</i> , 2016, 353, 126-127.	6.0	194
113	Exometabolomics Assisted Design and Validation of Synthetic Obligate Mutualism. <i>ACS Synthetic Biology</i> , 2016, 5, 569-576.	1.9	23
114	Towards Engineering Biological Systems in a Broader Context. <i>Journal of Molecular Biology</i> , 2016, 428, 928-944.	2.0	30
115	Determining Roles of Accessory Genes in Denitrification by Mutant Fitness Analyses. <i>Applied and Environmental Microbiology</i> , 2016, 82, 51-61.	1.4	31
116	Grand challenges in space synthetic biology. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150803.	1.5	55
117	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
118	Complete Genome Sequences of Four <i>Escherichia coli</i> ST95 Isolates from Bloodstream Infections. <i>Genome Announcements</i> , 2015, 3, .	0.8	18
119	Complete Genome Sequence of <i>Pelosinus fermentans</i> JBW45, a Member of a Remarkably Competitive Group of <i>Negativicutes</i> in the <i>Firmicutes</i> Phylum. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
120	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. <i>Frontiers in Microbiology</i> , 2015, 6, 1205.	1.5	77
121	Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. <i>MBio</i> , 2015, 6, e00326-15.	1.8	173
122	Rapid Quantification of Mutant Fitness in Diverse Bacteria by Sequencing Randomly Bar-Coded Transposons. <i>MBio</i> , 2015, 6, e00306-15.	1.8	380
123	Molybdenum Availability Is Key to Nitrate Removal in Contaminated Groundwater Environments. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4976-4983.	1.4	49
124	High-Quality Draft Genome Sequence of <i>Desulfovibrio carbinoliphilus</i> FW-101-2B, an Organic Acid-Oxidizing Sulfate-Reducing Bacterium Isolated from Uranium(VI)-Contaminated Groundwater. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
125	Weakly Deleterious Mutations and Low Rates of Recombination Limit the Impact of Natural Selection on Bacterial Genomes. <i>MBio</i> , 2015, 6, e01302-15.	1.8	22
126	Avoidance of Truncated Proteins from Unintended Ribosome Binding Sites within Heterologous Protein Coding Sequences. <i>ACS Synthetic Biology</i> , 2015, 4, 249-257.	1.9	30

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127	Independence of Nitrate and Nitrite Inhibition of <i>Desulfovibrio vulgaris</i> Hildenborough and Use of Nitrite as a Substrate for Growth. <i>Environmental Science & Technology</i> , 2015, 49, 924-931.	4.6	28
128	Monofluorophosphate Is a Selective Inhibitor of Respiratory Sulfate-Reducing Microorganisms. <i>Environmental Science & Technology</i> , 2015, 49, 3727-3736.	4.6	69
129	Dynamic Succession of Groundwater Functional Microbial Communities in Response to Emulsified Vegetable Oil Amendment during Sustained <i>In Situ</i> U(VI) Reduction. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4164-4172.	1.4	24
130	A Slow-Release Substrate Stimulates Groundwater Microbial Communities for Long-Term <i>In Situ</i> Cr(VI) Reduction. <i>Environmental Science & Technology</i> , 2015, 49, 12922-12931.	4.6	19
131	Rapid selective sweep of pre-existing polymorphisms and slow fixation of new mutations in experimental evolution of <i>Desulfovibrio vulgaris</i> . <i>ISME Journal</i> , 2015, 9, 2360-2372.	4.4	24
132	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
133	Genome-Wide Tuning of Protein Expression Levels to Rapidly Engineer Microbial Traits. <i>ACS Synthetic Biology</i> , 2015, 4, 1244-1253.	1.9	22
134	Complete Genome Sequence of <i>Cupriavidus basilensis</i> 4G11, Isolated from the Oak Ridge Field Research Center Site. <i>Genome Announcements</i> , 2015, 3, .	0.8	23
135	Novel Mechanism for Scavenging of Hypochlorite Involving a Periplasmic Methionine-Rich Peptide and Methionine Sulfoxide Reductase. <i>MBio</i> , 2015, 6, e00233-15.	1.8	50
136	Towards synthetic biological approaches to resource utilization on space missions. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20140715.	1.5	100
137	Rex (Encoded by DVU_0916) in <i>Desulfovibrio vulgaris</i> Hildenborough Is a Repressor of Sulfate Adenylyl Transferase and Is Regulated by NADH. <i>Journal of Bacteriology</i> , 2015, 197, 29-39.	1.0	37
138	Mechanisms of direct inhibition of the respiratory sulfate-reduction pathway by (per)chlorate and nitrate. <i>ISME Journal</i> , 2015, 9, 1295-1305.	4.4	87
139	A Method to Constrain Genome-Scale Models with ¹³ C Labeling Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004363.	1.5	53
140	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
141	Transcript level and sequence determinants of protein abundance and noise in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2014, 42, 4791-4799.	6.5	79
142	D-Tailor: automated analysis and design of DNA sequences. <i>Bioinformatics</i> , 2014, 30, 1087-1094.	1.8	31
143	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
144	Pattern formation with a compartmental lateral inhibition system. , 2014, , .		2

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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	Conservation of Transcription Start Sites within Genes across a Bacterial Genus. <i>MBio</i> , 2014, 5, e01398-14.	1.8	56
147	Control of methionine metabolism by the <i>SahR</i> transcriptional regulator in <i>Proteobacteria</i> . <i>Environmental Microbiology</i> , 2014, 16, 1-8.	1.8	18
148	A versatile framework for microbial engineering using synthetic non-coding RNAs. <i>Nature Reviews Microbiology</i> , 2014, 12, 341-354.	13.6	126
149	The energy-conserving electron transfer system used by <i>Desulfovibrio alaskensis</i> strain <i>G</i> 20 during pyruvate fermentation involves reduction of endogenously formed fumarate and cytoplasmic and membrane-bound complexes, <i>Hdr</i> _{Flox} and <i>Rnf</i> . <i>Environmental Microbiology</i> , 2014, 16, 3463-3486.	1.8	36
150	Stochasticity, succession, and environmental perturbations in a fluidic ecosystem. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E836-45.	3.3	595
151	Interactive XCMS Online: Simplifying Advanced Metabolomic Data Processing and Subsequent Statistical Analyses. <i>Analytical Chemistry</i> , 2014, 86, 6931-6939.	3.2	332
152	Fermentation of hydrolysate detoxified by pervaporation through block copolymer membranes. <i>Green Chemistry</i> , 2014, 16, 4206-4213.	4.6	22
153	Metabolomic data streaming for biology-dependent data acquisition. <i>Nature Biotechnology</i> , 2014, 32, 524-527.	9.4	45
154	Genetic basis for nitrate resistance in <i>Desulfovibrio</i> strains. <i>Frontiers in Microbiology</i> , 2014, 5, 153.	1.5	202
155	Selection of chromosomal DNA libraries using a multiplex CRISPR system. <i>ELife</i> , 2014, 3, .	2.8	314
156	Characterization of Wastewater Treatment Plant Microbial Communities and the Effects of Carbon Sources on Diversity in Laboratory Models. <i>PLoS ONE</i> , 2014, 9, e105689.	1.1	7
157	Changes in microbial dynamics during long-term decomposition in tropical forests. <i>Soil Biology and Biochemistry</i> , 2013, 66, 60-68.	4.2	47
158	Dissecting a complex chemical stress: chemogenomic profiling of plant hydrolysates. <i>Molecular Systems Biology</i> , 2013, 9, 674.	3.2	103
159	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
160	Correction: Global analysis of host response to induction of a latent bacteriophage. <i>BMC Microbiology</i> , 2013, 13, 183.	1.3	0
161	From Biological Parts to Circuit Design. , 2013, , 63-78.		2
162	Synthetic biology. <i>Current Opinion in Chemical Biology</i> , 2013, 17, 869-870.	2.8	1

#	ARTICLE	IF	CITATIONS
163	Composability of regulatory sequences controlling transcription and translation in <i>Escherichia coli</i> . Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14024-14029.	3.3	377
164	Indirect and suboptimal control of gene expression is widespread in bacteria. Molecular Systems Biology, 2013, 9, 660.	3.2	111
165	Variation among <i>Desulfovibrio</i> Species in Electron Transfer Systems Used for Syntrophic Growth. Journal of Bacteriology, 2013, 195, 990-1004.	1.0	77
166	Effects of Genetic Variation on the <i>E. coli</i> Host-Circuit Interface. Cell Reports, 2013, 4, 231-237.	2.9	75
167	A wise consistency: engineering biology for conformity, reliability, predictability. Current Opinion in Chemical Biology, 2013, 17, 893-901.	2.8	50
168	Modular Design of a Synthetic Payload Delivery Device. ACS Synthetic Biology, 2013, 2, 418-424.	1.9	16
169	Repurposing CRISPR as an RNA-Guided Platform for Sequence-Specific Control of Gene Expression. Cell, 2013, 152, 1173-1183.	13.5	4,090
170	Precise and reliable gene expression via standard transcription and translation initiation elements. Nature Methods, 2013, 10, 354-360.	9.0	653
171	Quantitative estimation of activity and quality for collections of functional genetic elements. Nature Methods, 2013, 10, 347-353.	9.0	183
172	Characterization of NaCl tolerance in <i>Desulfovibrio vulgaris</i> Hildenborough through experimental evolution. ISME Journal, 2013, 7, 1790-1802.	4.4	46
173	Replica-Extraction-Transfer Nanostructure-Initiator Mass Spectrometry Imaging of Acoustically Printed Bacteria. Analytical Chemistry, 2013, 85, 10856-10862.	3.2	43
174	StressChip as a High-Throughput Tool for Assessing Microbial Community Responses to Environmental Stresses. Environmental Science & Technology, 2013, 47, 9841-9849.	4.6	17
175	Metabolic Footprinting of Mutant Libraries to Map Metabolite Utilization to Genotype. ACS Chemical Biology, 2013, 8, 189-199.	1.6	34
176	Draft Genome Sequence for <i>Desulfovibrio africanus</i> Strain PCS. Genome Announcements, 2013, 1, e0014413.	0.8	5
177	Flexibility of Syntrophic Enzyme Systems in <i>Desulfovibrio</i> Species Ensures Their Adaptation Capability to Environmental Changes. Journal of Bacteriology, 2013, 195, 4900-4914.	1.0	37
178	Inference of gene regulatory networks from genome-wide knockout fitness data. Bioinformatics, 2013, 29, 338-346.	1.8	10
179	Genetic Selection for Context-Dependent Stochastic Phenotypes: Sp1 and TATA Mutations Increase Phenotypic Noise in HIV-1 Gene Expression. PLoS Computational Biology, 2013, 9, e1003135.	1.5	30
180	New Family of Tungstate-Responsive Transcriptional Regulators in Sulfate-Reducing Bacteria. Journal of Bacteriology, 2013, 195, 4466-4475.	1.0	16

#	ARTICLE	IF	CITATIONS
181	Measurement and modeling of intrinsic transcription terminators. <i>Nucleic Acids Research</i> , 2013, 41, 5139-5148.	6.5	155
182	Transcription Factor Family-Based Reconstruction of Singleton Regulons and Study of the Crp/Fnr, ArsR, and GntR Families in <i>Desulfovibrionales</i> Genomes. <i>Journal of Bacteriology</i> , 2013, 195, 29-38.	1.0	15
183	RegPrecise 3.0 – A resource for genome-scale exploration of transcriptional regulation in bacteria. <i>BMC Genomics</i> , 2013, 14, 745.	1.2	408
184	Metallochaperones Regulate Intracellular Copper Levels. <i>PLoS Computational Biology</i> , 2013, 9, e1002880.	1.5	26
185	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.	1.1	173
186	Hexavalent Chromium Reduction under Fermentative Conditions with Lactate Stimulated Native Microbial Communities. <i>PLoS ONE</i> , 2013, 8, e83909.	1.1	36
187	Metagenomes of tropical soil-derived anaerobic switchgrass-adapted consortia with and without iron. <i>Standards in Genomic Sciences</i> , 2013, 7, 382-398.	1.5	12
188	RegPrecise web services interface: programmatic access to the transcriptional regulatory interactions in bacteria reconstructed by comparative genomics. <i>Nucleic Acids Research</i> , 2012, 40, W604-W608.	6.5	24
189	Microbial Community Succession during Lactate Amendment and Electron Acceptor Limitation Reveals a Predominance of Metal-Reducing <i>Pelosinus</i> spp. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2082-2091.	1.4	42
190	Functional responses of methanogenic archaea to syntrophic growth. <i>ISME Journal</i> , 2012, 6, 2045-2055.	4.4	66
191	Tracing Determinants of Dual Substrate Specificity in Glycoside Hydrolase Family 5. <i>Journal of Biological Chemistry</i> , 2012, 287, 25335-25343.	1.6	39
192	Draft Genome Sequences for Two Metal-Reducing <i>Pelosinus fermentans</i> Strains Isolated from a Cr(VI)-Contaminated Site and for Type Strain R7. <i>Journal of Bacteriology</i> , 2012, 194, 5147-5148.	1.0	24
193	Draft Genome Sequence of <i>Pelosinus fermentans</i> JBW45, Isolated during <i>In Situ</i> Stimulation for Cr(VI) Reduction. <i>Journal of Bacteriology</i> , 2012, 194, 5456-5457.	1.0	16
194	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.	3.3	79
195	Engineering naturally occurring trans-acting non-coding RNAs to sense molecular signals. <i>Nucleic Acids Research</i> , 2012, 40, 5775-5786.	6.5	87
196	Functional Characterization of Crp/Fnr-Type Global Transcriptional Regulators in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1168-1177.	1.4	32
197	Mutual Information Analysis Reveals Coevolving Residues in Tat That Compensate for Two Distinct Functions in HIV-1 Gene Expression. <i>Journal of Biological Chemistry</i> , 2012, 287, 7945-7955.	1.6	10
198	metaMicrobesOnline: phylogenomic analysis of microbial communities. <i>Nucleic Acids Research</i> , 2012, 41, D648-D654.	6.5	17

#	ARTICLE	IF	CITATIONS
199	Chromatin accessibility at the HIV LTR promoter sets a threshold for NF- κ B mediated viral gene expression. <i>Integrative Biology (United Kingdom)</i> , 2012, 4, 661.	0.6	27
200	An adaptor from translational to transcriptional control enables predictable assembly of complex regulation. <i>Nature Methods</i> , 2012, 9, 1088-1094.	9.0	67
201	RNA processing enables predictable programming of gene expression. <i>Nature Biotechnology</i> , 2012, 30, 1002-1006.	9.4	184
202	Deletion of the <i>Desulfovibrio vulgaris</i> Carbon Monoxide Sensor Invokes Global Changes in Transcription. <i>Journal of Bacteriology</i> , 2012, 194, 5783-5793.	1.0	20
203	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
204	Manipulation of the carbon storage regulator system for metabolite remodeling and biofuel production in <i>Escherichia coli</i> . <i>Microbial Cell Factories</i> , 2012, 11, 79.	1.9	53
205	Sequestration-based bistability enables tuning of the switching boundaries and design of a latch. <i>Molecular Systems Biology</i> , 2012, 8, 620.	3.2	83
206	Rationally designed families of orthogonal RNA regulators of translation. <i>Nature Chemical Biology</i> , 2012, 8, 447-454.	3.9	157
207	Contextualizing context for synthetic biology – identifying causes of failure of synthetic biological systems. <i>Biotechnology Journal</i> , 2012, 7, 856-866.	1.8	394
208	The hunt for the biological transistor. <i>IEEE Spectrum</i> , 2011, 48, 38-43.	0.5	9
209	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
210	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
211	Systematic mapping of two component response regulators to gene targets in a model sulfate reducing bacterium. <i>Genome Biology</i> , 2011, 12, R99.	13.9	49
212	Network News: Innovations in 21st Century Systems Biology. <i>Cell</i> , 2011, 144, 844-849.	13.5	57
213	Microfluidic fluorescence in situ hybridization and flow cytometry (1/4FlowFISH). <i>Lab on A Chip</i> , 2011, 11, 2673.	3.1	58
214	Toward rational design of bacterial genomes. <i>Current Opinion in Microbiology</i> , 2011, 14, 624-630.	2.3	34
215	How sulphate-reducing microorganisms cope with stress: lessons from systems biology. <i>Nature Reviews Microbiology</i> , 2011, 9, 452-466.	13.6	169
216	Comparative Genomics of the Dormancy Regulons in Mycobacteria. <i>Journal of Bacteriology</i> , 2011, 193, 3446-3452.	1.0	48

#	ARTICLE	IF	CITATIONS
217	Meta-analysis of global metabolomics and proteomics data to link alterations with phenotype. <i>Spectroscopy</i> , 2011, 26, 151-154.	0.8	0
218	Complete genome sequence of <i>Enterobacter lignolyticus</i> SCF1. <i>Standards in Genomic Sciences</i> , 2011, 5, 69-85.	1.5	76
219	Regulation of transcription by unnatural amino acids. <i>Nature Biotechnology</i> , 2011, 29, 164-168.	9.4	32
220	Varying virulence: epigenetic control of expression noise and disease processes. <i>Trends in Biotechnology</i> , 2011, 29, 517-525.	4.9	57
221	Joint DAC/IWBDA special session design and synthesis of biological circuits. , 2011, , .		0
222	Evidence-Based Annotation of Transcripts and Proteins in the Sulfate-Reducing Bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Journal of Bacteriology</i> , 2011, 193, 5716-5727.	1.0	28
223	Modeling sporulation decisions in <i>Bacillus subtilis</i> as optimal evolutionary decision-making. , 2011, , .		1
224	GLAMM: Genome-Linked Application for Metabolic Maps. <i>Nucleic Acids Research</i> , 2011, 39, W400-W405.	6.5	26
225	WIST: toolkit for rapid, customized LIMS development. <i>Bioinformatics</i> , 2011, 27, 437-438.	1.8	9
226	Bayesian multiple-instance motif discovery with BAMBI: inference of recombinase and transcription factor binding sites. <i>Nucleic Acids Research</i> , 2011, 39, e146-e146.	6.5	12
227	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
228	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.	3.3	277
229	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
230	Towards a Rigorous Network of Protein-Protein Interactions of the Model Sulfate Reducer <i>Desulfovibrio vulgaris</i> Hildenborough. <i>PLoS ONE</i> , 2011, 6, e21470.	1.1	12
231	Simulated niche partitioning by bacteria. , 2011, , 10-22.		0
232	Design and Construction of a Double Inversion Recombination Switch for Heritable Sequential Genetic Memory. , 2011, , 175-196.		0
233	BglBricks: A flexible standard for biological part assembly. <i>Journal of Biological Engineering</i> , 2010, 4, 1.	2.0	348
234	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

#	ARTICLE	IF	CITATIONS
235	Hydrogen peroxide-induced oxidative stress responses in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Environmental Microbiology</i> , 2010, 12, 2645-2657.	1.8	46
236	Combinatorial Latency Reactivation for HIV-1 Subtypes and Variants. <i>Journal of Virology</i> , 2010, 84, 5958-5974.	1.5	97
237	MicrobesOnline: an integrated portal for comparative and functional genomics. <i>Nucleic Acids Research</i> , 2010, 38, D396-D400.	6.5	408
238	RegPrecise: a database of curated genomic inferences of transcriptional regulatory interactions in prokaryotes. <i>Nucleic Acids Research</i> , 2010, 38, D111-D118.	6.5	172
239	A universal TagModule collection for parallel genetic analysis of microorganisms. <i>Nucleic Acids Research</i> , 2010, 38, e146-e146.	6.5	54
240	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
241	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
242	Detailed Simulations of Cell Biology with Smoldyn 2.1. <i>PLoS Computational Biology</i> , 2010, 6, e1000705.	1.5	285
243	HIV Promoter Integration Site Primarily Modulates Transcriptional Burst Size Rather Than Frequency. <i>PLoS Computational Biology</i> , 2010, 6, e1000952.	1.5	95
244	Computational Models of HIV-1 Resistance to Gene Therapy Elucidate Therapy Design Principles. <i>PLoS Computational Biology</i> , 2010, 6, e1000883.	1.5	14
245	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
246	The Case for RNA. <i>Science</i> , 2010, 330, 1185-1186.	6.0	14
247	Sequencing of Multiple Clostridial Genomes Related to Biomass Conversion and Biofuel Production. <i>Journal of Bacteriology</i> , 2010, 192, 6494-6496.	1.0	81
248	Inference of binding sites with a Bayesian multiple-instance motif discovery method. , 2010, , .		0
249	FastTree 2 "Approximately Maximum-Likelihood Trees for Large Alignments. <i>PLoS ONE</i> , 2010, 5, e9490.	1.1	11,284
250	Engineering mRNA structural regulation of transcription using an RNA-sensing riboregulator. <i>FASEB Journal</i> , 2010, 24, .	0.2	0
251	FastTree: Computing Large Minimum Evolution Trees with Profiles instead of a Distance Matrix. <i>Molecular Biology and Evolution</i> , 2009, 26, 1641-1650.	3.5	4,165
252	The Electron Transfer System of Syntrophically Grown <i>Desulfovibrio vulgaris</i> . <i>Journal of Bacteriology</i> , 2009, 191, 5793-5801.	1.0	133

#	ARTICLE	IF	CITATIONS
253	Expression profiling of hypothetical genes in <i>Desulfovibrio vulgaris</i> leads to improved functional annotation. <i>Nucleic Acids Research</i> , 2009, 37, 2926-2939.	6.5	22
254	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
255	Control of Stochastic Gene Expression by Host Factors at the HIV Promoter. <i>PLoS Pathogens</i> , 2009, 5, e1000260.	2.1	98
256	Novel insights into iron metabolism by integrating deletome and transcriptome analysis in an iron deficiency model of the yeast <i>Saccharomyces cerevisiae</i> . <i>BMC Genomics</i> , 2009, 10, 130.	1.2	35
257	Snapshot of iron response in <i>Shewanella oneidensis</i> by gene network reconstruction. <i>BMC Genomics</i> , 2009, 10, 131.	1.2	56
258	Metabolic flux analysis of <i>Shewanella</i> spp. reveals evolutionary robustness in central carbon metabolism. <i>Biotechnology and Bioengineering</i> , 2009, 102, 1161-1169.	1.7	49
259	Invariability of central metabolic flux distribution in <i>Shewanella oneidensis</i> under environmental or genetic perturbations. <i>Biotechnology Progress</i> , 2009, 25, 1254-1259.	1.3	34
260	Contribution of mobile genetic elements to <i>Desulfovibrio vulgaris</i> genome plasticity. <i>Environmental Microbiology</i> , 2009, 11, 2244-2252.	1.8	20
261	Evolution, ecology and the engineered organism: lessons for synthetic biology. <i>Genome Biology</i> , 2009, 10, 114.	13.9	7
262	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
263	Complex Systems: From chemistry to systems biology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6433-6434.	3.3	44
264	Stochastic Models of Biological Processes. , 2009, , 8730-8749.		24
265	Environmental Genomics Reveals a Single-Species Ecosystem Deep Within Earth. <i>Science</i> , 2008, 322, 275-278.	6.0	474
266	Setting the standard in synthetic biology. <i>Nature Biotechnology</i> , 2008, 26, 771-774.	9.4	171
267	Horizontal gene transfer and the evolution of transcriptional regulation in <i>Escherichia coli</i> . <i>Genome Biology</i> , 2008, 9, R4.	13.9	116
268	Toward scalable parts families for predictable design of biological circuits. <i>Current Opinion in Microbiology</i> , 2008, 11, 567-573.	2.3	106
269	Modularity of stress response evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7500-7505.	3.3	53
270	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.	1.4	81

#	ARTICLE	IF	CITATIONS
271	A Dual Receptor Crosstalk Model of G-Protein-Coupled Signal Transduction. <i>PLoS Computational Biology</i> , 2008, 4, e1000185.	1.5	38
272	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, 102, 205-205.	1.4	7
273	Appreciation of the Machinations of the Blind Watchmaker. <i>IEEE Transactions on Automatic Control</i> , 2008, 53, 8-9.	3.6	3
274	Memory in Microbes: Quantifying History-Dependent Behavior in a Bacterium. <i>PLoS ONE</i> , 2008, 3, e1700.	1.1	115
275	Design and Construction of a Double Inversion Recombination Switch for Heritable Sequential Genetic Memory. <i>PLoS ONE</i> , 2008, 3, e2815.	1.1	123
276	FastBLAST: Homology Relationships for Millions of Proteins. <i>PLoS ONE</i> , 2008, 3, e3589.	1.1	14
277	Genetics and Genomics of Sulfate Respiration in <i>Desulfovibrio</i> . , 2008, , 1-12.		13
278	Environmental signal integration by a modular AND gate. <i>Molecular Systems Biology</i> , 2007, 3, 133.	3.2	306
279	Orthologous Transcription Factors in Bacteria Have Different Functions and Regulate Different Genes. <i>PLoS Computational Biology</i> , 2007, 3, e175.	1.5	86
280	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
281	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
282	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
283	Response of <i>Desulfovibrio vulgaris</i> to Alkaline Stress. <i>Journal of Bacteriology</i> , 2007, 189, 8944-8952.	1.0	62
284	Modeling and Network Organization. , 2007, , 47-81.		1
285	Processing Single-Cell Single-Molecule Genomic Information: New Methods for New Data. <i>Conference Record of the Asilomar Conference on Signals, Systems and Computers</i> , 2007, , .	0.0	0
286	A Mechanical Explanation for Cytoskeletal Rings and Helices in Bacteria. <i>Biophysical Journal</i> , 2007, 93, 1872-1884.	0.2	34
287	Efficient stochastic sensitivity analysis of discrete event systems. <i>Journal of Computational Physics</i> , 2007, 221, 724-738.	1.9	73
288	Global analysis of host response to induction of a latent bacteriophage. <i>BMC Microbiology</i> , 2007, 7, 82.	1.3	44

#	ARTICLE	IF	CITATIONS
289	Systems Biology: A Switch for Sex. <i>Current Biology</i> , 2007, 17, R410-R412.	1.8	3
290	Fast, cheap and somewhat in control. <i>Genome Biology</i> , 2006, 7, 114.	13.9	82
291	From Fluctuations to Phenotypes: The Physiology of Noise. <i>Science's STKE: Signal Transduction Knowledge Environment</i> , 2006, 2006, re17-re17.	4.1	108
292	Salt Stress in <i>Desulfovibrio vulgaris</i> Hildenborough: an Integrated Genomics Approach. <i>Journal of Bacteriology</i> , 2006, 188, 4068-4078.	1.0	155
293	Averaging Methods for Stochastic Dynamics of Complex Reaction Networks: Description of Multiscale Couplings. <i>Multiscale Modeling and Simulation</i> , 2006, 5, 497-513.	0.6	3
294	Model Discrimination Using Data Collaboration. <i>Journal of Physical Chemistry A</i> , 2006, 110, 6803-6813.	1.1	55
295	Environmentally Controlled Invasion of Cancer Cells by Engineered Bacteria. <i>Journal of Molecular Biology</i> , 2006, 355, 619-627.	2.0	547
296	Deviant effects in molecular reaction pathways. <i>Nature Biotechnology</i> , 2006, 24, 1235-1240.	9.4	113
297	Genomics for environmental microbiology. <i>Current Opinion in Biotechnology</i> , 2006, 17, 229-235.	3.3	63
298	The Histidine Operon Is Ancient. <i>Journal of Molecular Evolution</i> , 2006, 62, 807-808.	0.8	9
299	Simulating cell biology. <i>Current Biology</i> , 2006, 16, R523-R527.	1.8	29
300	OpWise: operons aid the identification of differentially expressed genes in bacterial microarray experiments. <i>BMC Bioinformatics</i> , 2006, 7, 19.	1.2	19
301	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
302	The Evolution of Two-Component Systems in Bacteria Reveals Different Strategies for Niche Adaptation. <i>PLoS Computational Biology</i> , 2006, 2, e143.	1.5	181
303	The Life-Cycle of Operons. <i>PLoS Genetics</i> , 2006, 2, e96.	1.5	146
304	Cellular Response of <i>Shewanella oneidensis</i> to Strontium Stress. <i>Applied and Environmental Microbiology</i> , 2006, 72, 890-900.	1.4	44
305	Morphology matters in immune cell chemotaxis: membrane asymmetry affects amplification. <i>Physical Biology</i> , 2006, 3, 190-199.	0.8	22
306	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

#	ARTICLE	IF	CITATIONS
307	Global Analysis of Heat Shock Response in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Journal of Bacteriology</i> , 2006, 188, 1817-1828.	1.0	106
308	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
309	Autonomous Mobile Robot Control Based on White Blood Cell Chemotaxis. <i>Lecture Notes in Computer Science</i> , 2005, , 9-19.	1.0	3
310	Diversity in times of adversity: probabilistic strategies in microbial survival games. <i>Journal of Theoretical Biology</i> , 2005, 234, 227-253.	0.8	251
311	A microbial modified prisoner's dilemma game: how frequency-dependent selection can lead to random phase variation. <i>Journal of Theoretical Biology</i> , 2005, 234, 255-262.	0.8	39
312	A latent variable model for chemogenomic profiling. <i>Bioinformatics</i> , 2005, 21, 3286-3293.	1.8	53
313	Genome-Wide Requirements for Resistance to Functionally Distinct DNA-Damaging Agents. <i>PLoS Genetics</i> , 2005, 1, e24.	1.5	144
314	Dissimilatory Metabolism of Nitrogen Oxides in Bacteria: Comparative Reconstruction of Transcriptional Networks. <i>PLoS Computational Biology</i> , 2005, 1, e55.	1.5	260
315	Operon formation is driven by co-regulation and not by horizontal gene transfer. <i>Genome Research</i> , 2005, 15, 809-819.	2.4	131
316	Transcriptome Analysis of <i>Shewanella oneidensis</i> MR-1 in Response to Elevated Salt Conditions. <i>Journal of Bacteriology</i> , 2005, 187, 2501-2507.	1.0	74
317	The MicrobesOnline Web site for comparative genomics. <i>Genome Research</i> , 2005, 15, 1015-1022.	2.4	176
318	Numerical computation of diffusion on a surface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11151-11156.	3.3	43
319	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
320	The <i>Bacillus subtilis</i> sin Operon. <i>Genetics</i> , 2005, 169, 1187-1202.	1.2	59
321	Phosphatase localization in bacterial chemotaxis: divergent mechanisms, convergent principles. <i>Physical Biology</i> , 2005, 2, 148-158.	0.8	27
322	A novel method for accurate operon predictions in all sequenced prokaryotes. <i>Nucleic Acids Research</i> , 2005, 33, 880-892.	6.5	316
323	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
324	Stochastic Gene Expression in a Lentiviral Positive-Feedback Loop: HIV-1 Tat Fluctuations Drive Phenotypic Diversity. <i>Cell</i> , 2005, 122, 169-182.	13.5	599

#	ARTICLE	IF	CITATIONS
325	Dissimilatory Metabolism of Nitrogen Oxides in Bacteria: Comparative Reconstruction of Transcriptional Networks. <i>PLoS Computational Biology</i> , 2005, preprint, e55.	1.5	4
326	Global Transcriptome Analysis of the Heat Shock Response of <i>Shewanella oneidensis</i> . <i>Journal of Bacteriology</i> , 2004, 186, 7796-7803.	1.0	173
327	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
328	The evolution of genetic regulatory systems in bacteria. <i>Nature Reviews Genetics</i> , 2004, 5, 169-178.	7.7	140
329	The old switcheroo: new tricks revealed in "Phage Lambda Revisited" TM . <i>Current Biology</i> , 2004, 14, R543-R544.	1.8	0
330	Response experiments for nonlinear systems with application to reaction kinetics and genetics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7223-7228.	3.3	27
331	Chemogenomic profiling: Identifying the functional interactions of small molecules in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 793-798.	3.3	460
332	Reconstruction of regulatory and metabolic pathways in metal-reducing delta-proteobacteria. <i>Genome Biology</i> , 2004, 5, R90.	13.9	162
333	An Allosteric Model for Transmembrane Signaling in Bacterial Chemotaxis. <i>Journal of Molecular Biology</i> , 2004, 343, 291-303.	2.0	32
334	Biological networks. <i>Current Opinion in Structural Biology</i> , 2003, 13, 193-202.	2.6	298
335	The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models. <i>Bioinformatics</i> , 2003, 19, 524-531.	1.8	2,811
336	Motifs, modules and games in bacteria. <i>Current Opinion in Microbiology</i> , 2003, 6, 125-134.	2.3	280
337	Stochastic chemical kinetics and the quasi-steady-state assumption: Application to the Gillespie algorithm. <i>Journal of Chemical Physics</i> , 2003, 118, 4999-5010.	1.2	542
338	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
339	Motifs and modules in cellular signal processing. , 2002, , .		0
340	GENETICâ€œCODEâ€œ Representations and Dynamical Models of Genetic Components and Networks. <i>Annual Review of Genomics and Human Genetics</i> , 2002, 3, 341-369.	2.5	80
341	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
342	Signal Processing by Simple Chemical Systems. <i>Journal of Physical Chemistry A</i> , 2002, 106, 10205-10221.	1.1	88

#	ARTICLE	IF	CITATIONS
343	Fifteen Minutes offim: Control of Type 1 Plii Expression inE. coli. OMICS A Journal of Integrative Biology, 2002, 6, 91-114.	1.0	39
344	Functional profiling of the Saccharomyces cerevisiae genome. Nature, 2002, 418, 387-391.	13.7	3,938
345	Control, exploitation and tolerance of intracellular noise. Nature, 2002, 420, 231-237.	13.7	909
346	Overview of the Alliance for Cellular Signaling. Nature, 2002, 420, 703-706.	13.7	134
347	Motifs and modules in cellular signal processing. , 2002, , .		0
348	Control Motifs for Intracellular Regulatory Networks. Annual Review of Biomedical Engineering, 2001, 3, 391-419.	5.7	112
349	Synthetic cell biology. Current Opinion in Biotechnology, 2001, 12, 638-644.	3.3	85
350	On the deduction of chemical reaction pathways from measurements of time series of concentrations. Chaos, 2001, 11, 108.	1.0	71
351	Signal processing by biochemical reaction networks. , 2000, , 112-144.		21
352	Gene regulation: Towards a circuit engineering discipline. Current Biology, 2000, 10, R318-R320.	1.8	91
353	Itâ€™s a noisy business! Genetic regulation at the nanomolar scale. Trends in Genetics, 1999, 15, 65-69.	2.9	791
354	SIMULATION OF PROKARYOTIC GENETIC CIRCUITS. Annual Review of Biophysics and Biomolecular Structure, 1998, 27, 199-224.	18.3	237
355	Stochastic Kinetic Analysis of Developmental Pathway Bifurcation in Phage Î»-Infected Escherichia coli Cells. Genetics, 1998, 149, 1633-1648.	1.2	1,272
356	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
357	Steady-State Measurements on the Fructose 6-Phosphate/Fructose 1,6-Bisphosphate Interconversion Cycle. Journal of Physical Chemistry B, 1997, 101, 3872-3876.	1.2	11
358	A Test Case of Correlation Metric Construction of a Reaction Pathway from Measurements. Science, 1997, 277, 1275-1279.	6.0	253
359	Experimental Evidence for Turing Structures. The Journal of Physical Chemistry, 1995, 99, 10417-10419.	2.9	23
360	Statistical Construction of Chemical Reaction Mechanisms from Measured Time-Series. The Journal of Physical Chemistry, 1995, 99, 970-979.	2.9	118

#	ARTICLE	IF	CITATIONS
361	Computational functions in biochemical reaction networks. Biophysical Journal, 1994, 67, 560-578.	0.2	207
362	Digital Imaging Spectroscopy. , 1993, , 133-155.		5
363	An algorithm for protein engineering: simulations of recursive ensemble mutagenesis.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 7811-7815.	3.3	28
364	Optimizing Nucleotide Mixtures to Encode Specific Subsets of Amino Acids for Semi-Random Mutagenesis. Nature Biotechnology, 1992, 10, 297-300.	9.4	36
365	Applications of Imaging Spectroscopy in Molecular Biology II. Colony Screening Based on Absorption Spectra. Nature Biotechnology, 1990, 8, 746-749.	9.4	17
366	Playing practical games with bacteria and viruses: exploring the molecular mechanisms behind clever cellular stratagems. , 0, , .		2
367	Motifs and modules in cellular signal processing: applications to microbial stress response pathways. , 0, , .		0