

Adam P Arkin

List of Publications by Year in descending order

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367
papers

60,376
citations

3334

91
h-index

1222

227
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441
all docs

441
docs citations

441
times ranked

59511
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.	1.3	6
2	Systems-informed genome mining for electroautotrophic microbial production. <i>Bioelectrochemistry</i> , 2022, 145, 108054.	4.6	7
3	Global Analysis of Biomineralization Genes in <i>Magnetospirillum magneticum</i> AMB-1. <i>MSystems</i> , 2022, 7, e0103721.	3.8	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.	3.0	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, .	4.2	9
6	A Phage Foundry Framework to Systematically Develop Viral Countermeasures to Combat Antibiotic-Resistant Bacterial Pathogens. <i>IScience</i> , 2022, 25, 104121.	4.1	12
7	Filling gaps in bacterial catabolic pathways with computation and high-throughput genetics. <i>PLoS Genetics</i> , 2022, 18, e1010156.	3.5	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.	0.6	1
9	Photovoltaics-Driven Power Production Can Support Human Exploration on Mars. <i>Frontiers in Astronomy and Space Sciences</i> , 2022, 9, .	2.8	3
10	A Defined Medium for Cultivation and Exometabolite Profiling of Soil Bacteria. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	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, .	3.1	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.	17.5	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.	14.5	119
15	Four families of folate-independent methionine synthases. <i>PLoS Genetics</i> , 2021, 17, e1009342.	3.5	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, .	0.6	6
17	Molecular pharming to support human life on the moon, mars, and beyond. <i>Critical Reviews in Biotechnology</i> , 2021, 41, 849-864.	9.0	25
18	Systematic discovery of pseudomonad genetic factors involved in sensitivity to tailocins. <i>ISME Journal</i> , 2021, 15, 2289-2305.	9.8	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.	3.5	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.	6.4	82
21	A method for achieving complete microbial genomes and improving bins from metagenomics data. <i>PLoS Computational Biology</i> , 2021, 17, e1008972.	3.2	22
22	Ecogenomics of Groundwater Phages Suggests Niche Differentiation Linked to Specific Environmental Tolerance. <i>MSystems</i> , 2021, 6, e0053721.	3.8	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.	3.5	17
24	Towards a Biomanufactory on Mars. <i>Frontiers in Astronomy and Space Sciences</i> , 2021, 8, .	2.8	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.	3.1	3
26	A Simple, Cost-Effective, and Automation-Friendly Direct PCR Approach for Bacterial Community Analysis. <i>MSystems</i> , 2021, 6, e0022421.	3.8	6
27	Evaluating the Cost of Pharmaceutical Purification for a Long-Duration Space Exploration Medical Foundry. <i>Frontiers in Microbiology</i> , 2021, 12, 700863.	3.5	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, .	2.1	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.	4.7	4
30	The genetic basis of phage susceptibility, cross-resistance and host-range in <i>Salmonella</i> . <i>Microbiology (United Kingdom)</i> , 2021, 167, .	1.8	20
31	iVirus 2.0: Cyberinfrastructure-supported tools and data to power DNA virus ecology. <i>ISME Communications</i> , 2021, 1, .	4.2	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.	3.5	1
33	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . <i>PLoS Biology</i> , 2020, 18, e3000877.	5.6	91
34	Redefining fundamental concepts of transcription initiation in bacteria. <i>Nature Reviews Genetics</i> , 2020, 21, 699-714.	16.3	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.	3.5	11
36	GapMind: Automated Annotation of Amino Acid Biosynthesis. <i>MSystems</i> , 2020, 5, .	3.8	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.	12.8	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, .	4.1	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, .	0.6	0
40	Diverse Bacterial Genes Modulate Plant Root Association by Beneficial Bacteria. <i>MBio</i> , 2020, 11, .	4.1	15
41	Selective carbon sources influence the end products of microbial nitrate respiration. <i>ISME Journal</i> , 2020, 14, 2034-2045.	9.8	61
42	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. <i>Microbiome</i> , 2020, 8, 51.	11.1	205
43	Characterization of subsurface media from locations up- and down-gradient of a uranium-contaminated aquifer. <i>Chemosphere</i> , 2020, 255, 126951.	8.2	18
44	In-field bioreactors demonstrate dynamic shifts in microbial communities in response to geochemical perturbations. <i>PLoS ONE</i> , 2020, 15, e0232437.	2.5	5
45	The Role of Synthetic Biology in Atmospheric Greenhouse Gas Reduction: Prospects and Challenges. <i>Biodesign Research</i> , 2020, 2020, .	1.9	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.	1.3	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.	11.3	23
54	Nitrate-Utilizing Microorganisms Resistant to Multiple Metals from the Heavily Contaminated Oak Ridge Reservation. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	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.	5.5	24
56	Dual-barcoded shotgun expression library sequencing for high-throughput characterization of functional traits in bacteria. <i>Nature Communications</i> , 2019, 10, 308.	12.8	33
57	Principles of synthetic biology: a MOOC for an emerging field. <i>Synthetic Biology</i> , 2019, 4, ysz010.	2.2	10
58	Massively Parallel Fitness Profiling Reveals Multiple Novel Enzymes in <i>Pseudomonas putida</i> Lysine Metabolism. <i>MBio</i> , 2019, 10, .	4.1	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.	3.3	25
60	Multiplexed CRISPR-Cas9-Based Genome Editing of <i>Rhodospiridium toruloides</i> . <i>MSphere</i> , 2019, 4, .	2.9	47
61	A versatile platform strain for high-fidelity multiplex genome editing. <i>Nucleic Acids Research</i> , 2019, 47, 3244-3256.	14.5	16
62	Curated BLAST for Genomes. <i>MSystems</i> , 2019, 4, .	3.8	13
63	Oxidative Pathways of Deoxyribose and Deoxyribonate Catabolism. <i>MSystems</i> , 2019, 4, .	3.8	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, .	3.8	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.	0.6	38
66	CRISPR-Cas9 Circular Permutants as Programmable Scaffolds for Genome Modification. <i>Cell</i> , 2019, 176, 254-267.e16.	28.9	73
67	Designing Spatially Distributed Gene Regulatory Networks To Elicit Contrasting Patterns. <i>ACS Synthetic Biology</i> , 2019, 8, 119-126.	3.8	6
68	The selective pressures on the microbial community in a metal-contaminated aquifer. <i>ISME Journal</i> , 2019, 13, 937-949.	9.8	56
69	Iron- and aluminium-induced depletion of molybdenum in acidic environments impedes the nitrogen cycle. <i>Environmental Microbiology</i> , 2019, 21, 152-163.	3.8	22
70	Structural basis for AcrVA4 inhibition of specific CRISPR-Cas12a. <i>ELife</i> , 2019, 8, .	6.0	41
71	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. <i>MBio</i> , 2018, 9, .	4.1	57
72	Magic Pools: Parallel Assessment of Transposon Delivery Vectors in Bacteria. <i>MSystems</i> , 2018, 3, .	3.8	31

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73	Engineering <i>Kluyveromyces marxianus</i> as a Robust Synthetic Biology Platform Host. <i>MBio</i> , 2018, 9, .	4.1	58
74	Genetic dissection of interspecific differences in yeast thermotolerance. <i>Nature Genetics</i> , 2018, 50, 1501-1504.	21.4	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.	17.5	182
76	Mutant phenotypes for thousands of bacterial genes of unknown function. <i>Nature</i> , 2018, 557, 503-509.	27.8	433
77	Functional genomics of lipid metabolism in the oleaginous yeast <i>Rhodospiridium toruloides</i> . <i>ELife</i> , 2018, 7, .	6.0	98
78	Deciphering microbial interactions in synthetic human gut microbiome communities. <i>Molecular Systems Biology</i> , 2018, 14, e8157.	7.2	361
79	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018, 36, 566-569.	17.5	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.	2.5	9
81	Filling gaps in bacterial amino acid biosynthesis pathways with high-throughput genetics. <i>PLoS Genetics</i> , 2018, 14, e1007147.	3.5	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.	7.0	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, .	3.1	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.	10.0	15
85	Programming mRNA decay to modulate synthetic circuit resource allocation. <i>Nature Communications</i> , 2017, 8, 15128.	12.8	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.	10.0	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, .	12.4	23
89	Quantitative Trait Loci (QTL)-Guided Metabolic Engineering of a Complex Trait. <i>ACS Synthetic Biology</i> , 2017, 6, 566-581.	3.8	26
90	Unintended Laboratory-Driven Evolution Reveals Genetic Requirements for Biofilm Formation by <i>Desulfovibrio vulgaris</i> Hildenborough. <i>MBio</i> , 2017, 8, .	4.1	18

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91	A metabolic pathway for catabolizing levulinic acid in bacteria. <i>Nature Microbiology</i> , 2017, 2, 1624-1634.	13.3	86
92	PaperBLAST: Text Mining Papers for Information about Homologs. <i>MSystems</i> , 2017, 2, .	3.8	107
93	Environmental Selection, Dispersal, and Organism Interactions Shape Community Assembly in High-Throughput Enrichment Culturing. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	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, .	4.1	13
95	The JBEI quantitative metabolic modeling library (jQMM): a python library for modeling microbial metabolism. <i>BMC Bioinformatics</i> , 2017, 18, 205.	2.6	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.	3.5	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.	2.5	9
100	Validating regulatory predictions from diverse bacteria with mutant fitness data. <i>PLoS ONE</i> , 2017, 12, e0178258.	2.5	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.	0.4	0
102	A Theoretical Lower Bound for Selection on the Expression Levels of Proteins. <i>Genome Biology and Evolution</i> , 2016, 8, 1917-1928.	2.5	9
103	A Comparison of the Costs and Benefits of Bacterial Gene Expression. <i>PLoS ONE</i> , 2016, 11, e0164314.	2.5	26
104	System-Wide Adaptations of <i>Desulfovibrio alaskensis</i> G20 to Phosphate-Limited Conditions. <i>PLoS ONE</i> , 2016, 11, e0168719.	2.5	15
105	Engineering <i>Rhodospiridium toruloides</i> for increased lipid production. <i>Biotechnology and Bioengineering</i> , 2016, 113, 1056-1066.	3.3	143
106	Lateral Gene Transfer in a Heavy Metal-Contaminated-Groundwater Microbial Community. <i>MBio</i> , 2016, 7, e02234-15.	4.1	105
107	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
108	Rapid and efficient galactose fermentation by engineered <i>Saccharomyces cerevisiae</i> . <i>Journal of Biotechnology</i> , 2016, 229, 13-21.	3.8	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.	3.1	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.	3.6	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.	3.1	21
112	The Genome Project-Write. <i>Science</i> , 2016, 353, 126-127.	12.6	194
113	Exometabolomics Assisted Design and Validation of Synthetic Obligate Mutualism. <i>ACS Synthetic Biology</i> , 2016, 5, 569-576.	3.8	23
114	Towards Engineering Biological Systems in a Broader Context. <i>Journal of Molecular Biology</i> , 2016, 428, 928-944.	4.2	30
115	Determining Roles of Accessory Genes in Denitrification by Mutant Fitness Analyses. <i>Applied and Environmental Microbiology</i> , 2016, 82, 51-61.	3.1	31
116	Grand challenges in space synthetic biology. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150803.	3.4	55
117	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
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.	3.5	77
121	Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. <i>MBio</i> , 2015, 6, e00326-15.	4.1	173
122	Rapid Quantification of Mutant Fitness in Diverse Bacteria by Sequencing Randomly Bar-Coded Transposons. <i>MBio</i> , 2015, 6, e00306-15.	4.1	380
123	Molybdenum Availability Is Key to Nitrate Removal in Contaminated Groundwater Environments. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4976-4983.	3.1	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.	4.1	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.	3.8	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.	10.0	28
128	Monofluorophosphate Is a Selective Inhibitor of Respiratory Sulfate-Reducing Microorganisms. <i>Environmental Science & Technology</i> , 2015, 49, 3727-3736.	10.0	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.	3.1	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.	10.0	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.	9.8	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.	7.1	166
133	Genome-Wide Tuning of Protein Expression Levels to Rapidly Engineer Microbial Traits. <i>ACS Synthetic Biology</i> , 2015, 4, 1244-1253.	3.8	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.	4.1	50
136	Towards synthetic biological approaches to resource utilization on space missions. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20140715.	3.4	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.	2.2	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.	9.8	87
139	A Method to Constrain Genome-Scale Models with ¹³ C Labeling Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004363.	3.2	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.	4.1	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.	14.5	79
142	D-Tailor: automated analysis and design of DNA sequences. <i>Bioinformatics</i> , 2014, 30, 1087-1094.	4.1	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.	3.5	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.	2.2	60
146	Conservation of Transcription Start Sites within Genes across a Bacterial Genus. <i>MBio</i> , 2014, 5, e01398-14.	4.1	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.	3.8	18
148	A versatile framework for microbial engineering using synthetic non-coding RNAs. <i>Nature Reviews Microbiology</i> , 2014, 12, 341-354.	28.6	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>HdrFlox</i> and <i>Rnf</i> . <i>Environmental Microbiology</i> , 2014, 16, 3463-3486.	3.8	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.	7.1	595
151	Interactive XCMS Online: Simplifying Advanced Metabolomic Data Processing and Subsequent Statistical Analyses. <i>Analytical Chemistry</i> , 2014, 86, 6931-6939.	6.5	332
152	Fermentation of hydrolysate detoxified by pervaporation through block copolymer membranes. <i>Green Chemistry</i> , 2014, 16, 4206-4213.	9.0	22
153	Metabolomic data streaming for biology-dependent data acquisition. <i>Nature Biotechnology</i> , 2014, 32, 524-527.	17.5	45
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