

Morgan N Price

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

18,731
citations

201385

27
h-index

264894

42
g-index

62
all docs

62
docs citations

62
times ranked

28099
citing authors

#	ARTICLE	IF	CITATIONS
1	Filling gaps in bacterial catabolic pathways with computation and high-throughput genetics. <i>PLoS Genetics</i> , 2022, 18, e1010156.	1.5	15
2	Four families of folate-independent methionine synthases. <i>PLoS Genetics</i> , 2021, 17, e1009342.	1.5	8
3	Systematic discovery of pseudomonad genetic factors involved in sensitivity to tailocins. <i>ISME Journal</i> , 2021, 15, 2289-2305.	4.4	27
4	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
5	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . <i>PLoS Biology</i> , 2020, 18, e3000877.	2.6	91
6	GapMind: Automated Annotation of Amino Acid Biosynthesis. <i>MSystems</i> , 2020, 5, .	1.7	40
7	Selective carbon sources influence the end products of microbial nitrate respiration. <i>ISME Journal</i> , 2020, 14, 2034-2045.	4.4	61
8	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . , 2020, 18, e3000877.		0
9	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . , 2020, 18, e3000877.		0
10	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . , 2020, 18, e3000877.		0
11	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . , 2020, 18, e3000877.		0
12	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . , 2020, 18, e3000877.		0
13	High-throughput mapping of the phage resistance landscape in <i>E. coli</i> . , 2020, 18, e3000877.		0
14	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
15	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
16	Curated BLAST for Genomes. <i>MSystems</i> , 2019, 4, .	1.7	13
17	Oxidative Pathways of Deoxyribose and Deoxyribonate Catabolism. <i>MSystems</i> , 2019, 4, .	1.7	34
18	The selective pressures on the microbial community in a metal-contaminated aquifer. <i>ISME Journal</i> , 2019, 13, 937-949.	4.4	56

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19	Magic Pools: Parallel Assessment of Transposon Delivery Vectors in Bacteria. <i>MSystems</i> , 2018, 3, .	1.7	31
20	Mutant phenotypes for thousands of bacterial genes of unknown function. <i>Nature</i> , 2018, 557, 503-509.	13.7	433
21	Filling gaps in bacterial amino acid biosynthesis pathways with high-throughput genetics. <i>PLoS Genetics</i> , 2018, 14, e1007147.	1.5	90
22	A metabolic pathway for catabolizing levulinic acid in bacteria. <i>Nature Microbiology</i> , 2017, 2, 1624-1634.	5.9	86
23	PaperBLAST: Text Mining Papers for Information about Homologs. <i>MSystems</i> , 2017, 2, .	1.7	107
24	Validating regulatory predictions from diverse bacteria with mutant fitness data. <i>PLoS ONE</i> , 2017, 12, e0178258.	1.1	9
25	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
26	A Comparison of the Costs and Benefits of Bacterial Gene Expression. <i>PLoS ONE</i> , 2016, 11, e0164314.	1.1	26
27	Rapid Quantification of Mutant Fitness in Diverse Bacteria by Sequencing Randomly Bar-Coded Transposons. <i>MBio</i> , 2015, 6, e00306-15.	1.8	380
28	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
29	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
30	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
31	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
32	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
33	Towards an Informative Mutant Phenotype for Every Bacterial Gene. <i>Journal of Bacteriology</i> , 2014, 196, 3643-3655.	1.0	60
34	Conservation of Transcription Start Sites within Genes across a Bacterial Genus. <i>MBio</i> , 2014, 5, e01398-14.	1.8	56
35	The energy-conserving electron transfer system used by <i>Desulfovibrio alaskensis</i> strain G20 during pyruvate fermentation involves reduction of endogenously formed fumarate and cytoplasmic and membrane-bound complexes, HdrF and Rnf. <i>Environmental Microbiology</i> , 2014, 16, 3463-3486.	1.8	36
36	Indirect and suboptimal control of gene expression is widespread in bacteria. <i>Molecular Systems Biology</i> , 2013, 9, 660.	3.2	111

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37	Metabolic Footprinting of Mutant Libraries to Map Metabolite Utilization to Genotype. <i>ACS Chemical Biology</i> , 2013, 8, 189-199.	1.6	34
38	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
39	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
40	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
41	MicrobesOnline: an integrated portal for comparative and functional genomics. <i>Nucleic Acids Research</i> , 2010, 38, D396-D400.	6.5	408
42	A universal TagModule collection for parallel genetic analysis of microorganisms. <i>Nucleic Acids Research</i> , 2010, 38, e146-e146.	6.5	54
43	FastTree 2 "Approximately Maximum-Likelihood Trees for Large Alignments. <i>PLoS ONE</i> , 2010, 5, e9490.	1.1	11,284
44	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
45	Horizontal gene transfer and the evolution of transcriptional regulation in <i>Escherichia coli</i> . <i>Genome Biology</i> , 2008, 9, R4.	13.9	116
46	FastBLAST: Homology Relationships for Millions of Proteins. <i>PLoS ONE</i> , 2008, 3, e3589.	1.1	14
47	Orthologous Transcription Factors in Bacteria Have Different Functions and Regulate Different Genes. <i>PLoS Computational Biology</i> , 2007, 3, e175.	1.5	86
48	OpWise: operons aid the identification of differentially expressed genes in bacterial microarray experiments. <i>BMC Bioinformatics</i> , 2006, 7, 19.	1.2	19