

Morgan N Price

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

18,731
citations

201674

27
h-index

265206

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. PLoS Genetics, 2022, 18, e1010156.	3.5	15
2	Four families of folate-independent methionine synthases. PLoS Genetics, 2021, 17, e1009342.	3.5	8
3	Systematic discovery of pseudomonad genetic factors involved in sensitivity to tailocins. ISME Journal, 2021, 15, 2289-2305.	9.8	27
4	Functional genetics of human gut commensal Bacteroides thetaiotaomicron reveals metabolic requirements for growth across environments. Cell Reports, 2021, 34, 108789.	6.4	82
5	High-throughput mapping of the phage resistance landscape in E. coli. PLoS Biology, 2020, 18, e3000877.	5.6	91
6	GapMind: Automated Annotation of Amino Acid Biosynthesis. MSystems, 2020, 5, .	3.8	40
7	Selective carbon sources influence the end products of microbial nitrate respiration. ISME Journal, 2020, 14, 2034-2045.	9.8	61
8	High-throughput mapping of the phage resistance landscape in E. coli. , 2020, 18, e3000877.		0
9	High-throughput mapping of the phage resistance landscape in E. coli. , 2020, 18, e3000877.		0
10	High-throughput mapping of the phage resistance landscape in E. coli. , 2020, 18, e3000877.		0
11	High-throughput mapping of the phage resistance landscape in E. coli. , 2020, 18, e3000877.		0
12	High-throughput mapping of the phage resistance landscape in E. coli. , 2020, 18, e3000877.		0
13	High-throughput mapping of the phage resistance landscape in E. coli. , 2020, 18, e3000877.		0
14	Nitrate-Utilizing Microorganisms Resistant to Multiple Metals from the Heavily Contaminated Oak Ridge Reservation. Applied and Environmental Microbiology, 2019, 85, .	3.1	13
15	Dual-barcoded shotgun expression library sequencing for high-throughput characterization of functional traits in bacteria. Nature Communications, 2019, 10, 308.	12.8	33
16	Curated BLAST for Genomes. MSystems, 2019, 4, .	3.8	13
17	Oxidative Pathways of Deoxyribose and Deoxyribonate Catabolism. MSystems, 2019, 4, .	3.8	34
18	The selective pressures on the microbial community in a metal-contaminated aquifer. ISME Journal, 2019, 13, 937-949.	9.8	56

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19	Magic Pools: Parallel Assessment of Transposon Delivery Vectors in Bacteria. MSystems, 2018, 3, .	3.8	31
20	Mutant phenotypes for thousands of bacterial genes of unknown function. Nature, 2018, 557, 503-509.	27.8	433
21	Filling gaps in bacterial amino acid biosynthesis pathways with high-throughput genetics. PLoS Genetics, 2018, 14, e1007147.	3.5	90
22	A metabolic pathway for catabolizing levulinic acid in bacteria. Nature Microbiology, 2017, 2, 1624-1634.	13.3	86
23	PaperBLAST: Text Mining Papers for Information about Homologs. MSystems, 2017, 2, .	3.8	107
24	Validating regulatory predictions from diverse bacteria with mutant fitness data. PLoS ONE, 2017, 12, e0178258.	2.5	9
25	A Theoretical Lower Bound for Selection on the Expression Levels of Proteins. Genome Biology and Evolution, 2016, 8, 1917-1928.	2.5	9
26	A Comparison of the Costs and Benefits of Bacterial Gene Expression. PLoS ONE, 2016, 11, e0164314.	2.5	26
27	Rapid Quantification of Mutant Fitness in Diverse Bacteria by Sequencing Randomly Bar-Coded Transposons. MBio, 2015, 6, e00306-15.	4.1	380
28	Weakly Deleterious Mutations and Low Rates of Recombination Limit the Impact of Natural Selection on Bacterial Genomes. MBio, 2015, 6, e01302-15.	4.1	22
29	The essential gene set of a photosynthetic organism. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6634-43.	7.1	166
30	Mechanisms of direct inhibition of the respiratory sulfate-reduction pathway by (per)chlorate and nitrate. ISME Journal, 2015, 9, 1295-1305.	9.8	87
31	Functional Genomics with a Comprehensive Library of Transposon Mutants for the Sulfate-Reducing Bacterium Desulfovibrio alaskensis G20. MBio, 2014, 5, e01041-14.	4.1	56
32	The genetic basis of energy conservation in the sulfate-reducing bacterium Desulfovibrio alaskensis G20. Frontiers in Microbiology, 2014, 5, 577.	3.5	61
33	Towards an Informative Mutant Phenotype for Every Bacterial Gene. Journal of Bacteriology, 2014, 196, 3643-3655.	2.2	60
34	Conservation of Transcription Start Sites within Genes across a Bacterial Genus. MBio, 2014, 5, e01398-14.	4.1	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, HdrFlox and Rnf. Environmental Microbiology, 2014, 16, 3463-3486.	3.8	36
36	Indirect and suboptimal control of gene expression is widespread in bacteria. Molecular Systems Biology, 2013, 9, 660.	7.2	111

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37	Metabolic Footprinting of Mutant Libraries to Map Metabolite Utilization to Genotype. ACS Chemical Biology, 2013, 8, 189-199.	3.4	34
38	Systematic mapping of two component response regulators to gene targets in a model sulfate reducing bacterium. Genome Biology, 2011, 12, R99.	9.6	49
39	Evidence-Based Annotation of Transcripts and Proteins in the Sulfate-Reducing Bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. Journal of Bacteriology, 2011, 193, 5716-5727.	2.2	28
40	Evidence-Based Annotation of Gene Function in <i>Shewanella oneidensis</i> MR-1 Using Genome-Wide Fitness Profiling across 121 Conditions. PLoS Genetics, 2011, 7, e1002385.	3.5	119
41	MicrobesOnline: an integrated portal for comparative and functional genomics. Nucleic Acids Research, 2010, 38, D396-D400.	14.5	408
42	A universal TagModule collection for parallel genetic analysis of microorganisms. Nucleic Acids Research, 2010, 38, e146-e146.	14.5	54
43	FastTree 2 “Approximately Maximum-Likelihood Trees for Large Alignments. PLoS ONE, 2010, 5, e9490.	2.5	11,284
44	FastTree: Computing Large Minimum Evolution Trees with Profiles instead of a Distance Matrix. Molecular Biology and Evolution, 2009, 26, 1641-1650.	8.9	4,165
45	Horizontal gene transfer and the evolution of transcriptional regulation in <i>Escherichia coli</i> . Genome Biology, 2008, 9, R4.	9.6	116
46	FastBLAST: Homology Relationships for Millions of Proteins. PLoS ONE, 2008, 3, e3589.	2.5	14
47	Orthologous Transcription Factors in Bacteria Have Different Functions and Regulate Different Genes. PLoS Computational Biology, 2007, 3, e175.	3.2	86
48	OpWise: operons aid the identification of differentially expressed genes in bacterial microarray experiments. BMC Bioinformatics, 2006, 7, 19.	2.6	19