Morgan N Price

List of Publications by Year in descending order

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	FastTree 2 â€" Approximately Maximum-Likelihood Trees for Large Alignments. PLoS ONE, 2010, 5, e9490.	2.5	11,284
2	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
3	Mutant phenotypes for thousands of bacterial genes of unknown function. Nature, 2018, 557, 503-509.	27.8	433
4	MicrobesOnline: an integrated portal for comparative and functional genomics. Nucleic Acids Research, 2010, 38, D396-D400.	14.5	408
5	Rapid Quantification of Mutant Fitness in Diverse Bacteria by Sequencing Randomly Bar-Coded Transposons. MBio, 2015, 6, e00306-15.	4.1	380
6	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
7	Evidence-Based Annotation of Gene Function in Shewanella oneidensis MR-1 Using Genome-Wide Fitness Profiling across 121 Conditions. PLoS Genetics, 2011, 7, e1002385.	3.5	119
8	Horizontal gene transfer and the evolution of transcriptional regulation in Escherichia coli. Genome Biology, 2008, 9, R4.	9.6	116
9	Indirect and suboptimal control of gene expression is widespread in bacteria. Molecular Systems Biology, 2013, 9, 660.	7.2	111
10	PaperBLAST: Text Mining Papers for Information about Homologs. MSystems, 2017, 2, .	3.8	107
11	High-throughput mapping of the phage resistance landscape in E. coli. PLoS Biology, 2020, 18, e3000877.	5.6	91
12	Filling gaps in bacterial amino acid biosynthesis pathways with high-throughput genetics. PLoS Genetics, 2018, 14, e1007147.	3.5	90
13	Mechanisms of direct inhibition of the respiratory sulfate-reduction pathway by (per)chlorate and nitrate. ISME Journal, 2015, 9, 1295-1305.	9.8	87
14	Orthologous Transcription Factors in Bacteria Have Different Functions and Regulate Different Genes. PLoS Computational Biology, 2007, 3, e175.	3.2	86
15	A metabolic pathway for catabolizing levulinic acid in bacteria. Nature Microbiology, 2017, 2, 1624-1634.	13.3	86
16	Functional genetics of human gut commensal Bacteroides thetaiotaomicron reveals metabolic requirements for growth across environments. Cell Reports, 2021, 34, 108789.	6.4	82
17	The genetic basis of energy conservation in the sulfate-reducing bacterium Desulfovibrio alaskensis G20. Frontiers in Microbiology, 2014, 5, 577.	3.5	61
18	Selective carbon sources influence the end products of microbial nitrate respiration. ISME Journal, 2020, 14, 2034-2045.	9.8	61

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19	Towards an Informative Mutant Phenotype for Every Bacterial Gene. Journal of Bacteriology, 2014, 196, 3643-3655.	2.2	60
20	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
21	Conservation of Transcription Start Sites within Genes across a Bacterial Genus. MBio, 2014, 5, e01398-14.	4.1	56
22	The selective pressures on the microbial community in a metal-contaminated aquifer. ISME Journal, 2019, 13, 937-949.	9.8	56
23	A universal TagModule collection for parallel genetic analysis of microorganisms. Nucleic Acids Research, 2010, 38, e146-e146.	14.5	54
24	Systematic mapping of two component response regulators to gene targets in a model sulfate reducing bacterium. Genome Biology, 2011, 12, R99.	9.6	49
25	GapMind: Automated Annotation of Amino Acid Biosynthesis. MSystems, 2020, 5, .	3.8	40
26	The energyâ€conserving electron transfer system used by <scp><i>D</i></scp><i>esulfovibrio alaskensis</i></scp> strain <scp>G</scp>20 during pyruvate fermentation involves reduction of endogenously formed fumarate and cytoplasmic and membraneâ€bound complexes, <scp>Hdrâ€Flox</scp> and <scp>Rnf</scp>. Environmental Microbiology, 2014, 16, 3463-3486.	3.8	36
27	Metabolic Footprinting of Mutant Libraries to Map Metabolite Utilization to Genotype. ACS Chemical Biology, 2013, 8, 189-199.	3.4	34
28	Oxidative Pathways of Deoxyribose and Deoxyribonate Catabolism. MSystems, 2019, 4, .	3.8	34
29	Dual-barcoded shotgun expression library sequencing for high-throughput characterization of functional traits in bacteria. Nature Communications, 2019, 10, 308.	12.8	33
30	Magic Pools: Parallel Assessment of Transposon Delivery Vectors in Bacteria. MSystems, 2018, 3, .	3.8	31
31	Evidence-Based Annotation of Transcripts and Proteins in the Sulfate-Reducing Bacterium Desulfovibrio vulgaris Hildenborough. Journal of Bacteriology, 2011, 193, 5716-5727.	2.2	28
32	Systematic discovery of pseudomonad genetic factors involved in sensitivity to tailocins. ISME Journal, 2021, 15, 2289-2305.	9.8	27
33	A Comparison of the Costs and Benefits of Bacterial Gene Expression. PLoS ONE, 2016, 11, e0164314.	2.5	26
34	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
35	OpWise: operons aid the identification of differentially expressed genes in bacterial microarray experiments. BMC Bioinformatics, 2006, 7, 19.	2.6	19
36	Filling gaps in bacterial catabolic pathways with computation and high-throughput genetics. PLoS Genetics, 2022, 18, e1010156.	3.5	15

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37	FastBLAST: Homology Relationships for Millions of Proteins. PLoS ONE, 2008, 3, *e*3589.	2.5	14
38	Nitrate-Utilizing Microorganisms Resistant to Multiple Metals from the Heavily Contaminated Oak Ridge Reservation. Applied and Environmental Microbiology, 2019, 85, .	3.1	13
39	Curated BLAST for Genomes. MSystems, 2019, 4, .	3.8	13
40	A Theoretical Lower Bound for Selection on the Expression Levels of Proteins. Genome Biology and Evolution, 2016, 8, 1917-1928.	2.5	9
41	Validating regulatory predictions from diverse bacteria with mutant fitness data. PLoS ONE, 2017, 12, e0178258.	2.5	9
42	Four families of folate-independent methionine synthases. PLoS Genetics, 2021, 17, e1009342.	3.5	8
43	High-throughput mapping of the phage resistance landscape in E. coli. , 2020, 18, e3000877.		0
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48	High-throughput mapping of the phage resistance landscape in E. coli. , 2020, 18, e3000877.		0