

Enrique Morett

List of Publications by Year in descending order

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65
papers

5,038
citations

186265

28
h-index

128289

60
g-index

66
all docs

66
docs citations

66
times ranked

6131
citing authors

#	ARTICLE	IF	CITATIONS
1	Specialization of the Reiterated Copies of the Heterodimeric Integration Host Factor Genes in <i>Geobacter sulfurreducens</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 626443.	3.5	6
2	High-throughput transcriptome sequencing and comparative analysis of <i>Escherichia coli</i> and <i>Schizosaccharomyces pombe</i> in respiratory and fermentative growth. <i>PLoS ONE</i> , 2021, 16, e0248513.	2.5	1
3	Whole genome variation in 27 Mexican indigenous populations, demographic and biomedical insights. <i>PLoS ONE</i> , 2021, 16, e0249773.	2.5	8
4	Transcriptome Analysis Reveals Cr(VI) Adaptation Mechanisms in <i>Klebsiella</i> sp. Strain AqSCr. <i>Frontiers in Microbiology</i> , 2021, 12, 656589.	3.5	3
5	The unphosphorylated form of the PilR two-component system regulates pilA gene expression in <i>Geobacter sulfurreducens</i> . <i>Environmental Science and Pollution Research</i> , 2017, 24, 25693-25701.	5.3	19
6	Demographic history and biologically relevant genetic variation of Native Mexicans inferred from whole-genome sequencing. <i>Nature Communications</i> , 2017, 8, 1005.	12.8	44
7	Acetate biostimulation as an effective treatment for cleaning up alkaline soil highly contaminated with Cr(VI). <i>Environmental Science and Pollution Research</i> , 2017, 24, 25513-25521.	5.3	20
8	Global transcriptional start site mapping in <i>Geobacter sulfurreducens</i> during growth with two different electron acceptors. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw175.	1.8	3
9	Structural Properties of Prokaryotic Promoter Regions Correlate with Functional Features. <i>PLoS ONE</i> , 2014, 9, e88717.	2.5	22
10	Exopolyphosphatase of <i>Pseudomonas aeruginosa</i> is essential for the production of virulence factors, and its expression is controlled by NtrC and PhoB acting at two interspaced promoters. <i>Microbiology (United Kingdom)</i> , 2014, 160, 406-417.	1.8	24
11	The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , 2013, 496, 57-63.	27.8	603
12	Evidence classification of high-throughput protocols and confidence integration in RegulonDB. Database: the Journal of Biological Databases and Curation, 2013, 2013, bas059.	3.0	23
13	RegulonDB v8.0: omics data sets, evolutionary conservation, regulatory phrases, cross-validated gold standards and more. <i>Nucleic Acids Research</i> , 2013, 41, D203-D213.	14.5	404
14	Transcription Factors in <i>Escherichia coli</i> Prefer the Holo Conformation. <i>PLoS ONE</i> , 2013, 8, e65723.	2.5	23
15	Transcriptional Regulation of the <i>assT</i> - <i>dsbL</i> - <i>dsbL</i> Gene Cluster in <i>Salmonella enterica</i> Serovar Typhi IMSS-1 Depends on LeuO, H-NS, and Specific Growth Conditions. <i>Journal of Bacteriology</i> , 2012, 194, 2254-2264.	2.2	12
16	Evolution of a new function in an esterase: simple amino acid substitutions enable the activity present in the larger paralog, BioH. <i>Protein Engineering, Design and Selection</i> , 2012, 25, 387-395.	2.1	9
17	Evolutionary Walk between (1 ² /1 [±]) ₈ Barrels: Catalytic Migration from Triosephosphate Isomerase to Thiamin Phosphate Synthase. <i>Journal of Molecular Biology</i> , 2012, 416, 255-270.	4.2	17
18	Genetic changes during a laboratory adaptive evolution process that allowed fast growth in glucose to an <i>Escherichia coli</i> strain lacking the major glucose transport system. <i>BMC Genomics</i> , 2012, 13, 385.	2.8	45

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19	Choline catabolism, σ^{54} factor and NtrC are required for the full expression of the <i>Pseudomonas aeruginosa</i> phosphorylcholine phosphatase gene. <i>Microbiological Research</i> , 2011, 166, 380-390.	5.3	10
20	RegulonDB version 7.0: transcriptional regulation of <i>Escherichia coli</i> K-12 integrated within genetic sensory response units (Gensor Units). <i>Nucleic Acids Research</i> , 2011, 39, D98-D105.	14.5	315
21	Transcription Analysis of Central Metabolism Genes in <i>Escherichia coli</i> . Possible Roles of σ^{38} in Their Expression, as a Response to Carbon Limitation. <i>PLoS ONE</i> , 2009, 4, e7466.	2.5	26
22	Bioinformatics Resources for the Study of Gene Regulation in Bacteria. <i>Journal of Bacteriology</i> , 2009, 191, 23-31.	2.2	25
23	MOCEA. , 2009, , .		0
24	A Clustering Genetic Algorithm for Genomic Data Mining. <i>Studies in Computational Intelligence</i> , 2009, , 249-275.	0.9	12
25	Genome-Wide Identification of Transcription Start Sites, Promoters and Transcription Factor Binding Sites in <i>E. coli</i> . <i>PLoS ONE</i> , 2009, 4, e7526.	2.5	237
26	Inferring modules of functionally interacting proteins using the Bond Energy Algorithm. <i>BMC Bioinformatics</i> , 2008, 9, 285.	2.6	13
27	Sensitive Genome-Wide Screen for Low Secondary Enzymatic Activities: The YjbQ Family Shows Thiamin Phosphate Synthase Activity. <i>Journal of Molecular Biology</i> , 2008, 376, 839-853.	4.2	22
28	A Role for the Conserved GAFTGA Motif of AAA+ Transcription Activators in Sensing Promoter DNA Conformation. <i>Journal of Biological Chemistry</i> , 2007, 282, 1087-1097.	3.4	21
29	RegulonDB (version 6.0): gene regulation model of <i>Escherichia coli</i> K-12 beyond transcription, active (experimental) annotated promoters and Textpresso navigation. <i>Nucleic Acids Research</i> , 2007, 36, D120-D124.	14.5	395
30	The genome project of <i>Taenia solium</i> . <i>Parasitology International</i> , 2006, 55, S127-S130.	1.3	49
31	Multiple regulators of the Flavohaemoglobin (hmp) gene of <i>Salmonella enterica</i> serovar Typhimurium include RamA, a transcriptional regulator conferring the multidrug resistance phenotype. <i>Archives of Microbiology</i> , 2006, 187, 67-77.	2.2	31
32	Insights on the evolution of trehalose biosynthesis. <i>BMC Evolutionary Biology</i> , 2006, 6, 109.	3.2	391
33	Selection for Unequal Densities of σ^{70} Promoter-Like Signals in Different Regions of Large Bacterial Genomes. <i>PLoS Genetics</i> , 2006, 2, e185.	3.5	43
34	Fuzzy C-means for inferring functional coupling of proteins from their phylogenetic profiles. , 2006, , .		1
35	Inferring functional coupling of proteins using the Evolutionary Bond Energy Algorithm. , 2006, , .		0
36	Improving Random Mutagenesis by Purification of the Oligonucleotide Variants. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2005, 8, 537-544.	1.1	0

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37	GeConT: gene context analysis. <i>Bioinformatics</i> , 2004, 20, 2307-2308.	4.1	59
38	Communication between σ 54, promoter DNA and the conserved threonine residue in the GAFTGA motif of the PspF σ 54-dependent activator during transcription activation. <i>Molecular Microbiology</i> , 2004, 54, 489-506.	2.5	26
39	Systematic discovery of analogous enzymes in thiamin biosynthesis. <i>Nature Biotechnology</i> , 2003, 21, 790-795.	17.5	121
40	In vivo studies on the positive control function of NifA: a conserved hydrophobic amino acid patch at the central domain involved in transcriptional activation. <i>Molecular Microbiology</i> , 2002, 28, 55-67.	2.5	40
41	Binding of transcriptional activators to sigma 54 in the presence of the transition state analog ADP-aluminum fluoride: insights into activator mechanochemical action. <i>Genes and Development</i> , 2001, 15, 2282-2294.	5.9	118
42	Reciprocal domain evolution within a transactivator in a restricted sequence space. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 3314-3318.	7.1	6
43	Reciprocal domain evolution within a transactivator in a restricted sequence space. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 3314-3318.	7.1	5
44	Compilation and analysis of σ 54-dependent promoter sequences. <i>Nucleic Acids Research</i> , 1999, 27, 4305-4313.	14.5	333
45	A novel transactivation domain in parkin. <i>Trends in Biochemical Sciences</i> , 1999, 24, 229-231.	7.5	145
46	Suppression analysis of positive control mutants of NifA reveals two overlapping promoters for <i>Klebsiella pneumoniae</i> rpoN. <i>Journal of Molecular Biology</i> , 1999, 294, 291-298.	4.2	7
47	Evolution of new protein function: recombinational enhancer Fis originated by horizontal gene transfer from the transcriptional regulator NtrC. <i>FEBS Letters</i> , 1998, 433, 108-112.	2.8	34
48	In vivo genomic footprinting analysis reveals that the complex <i>Bradyrhizobium japonicum</i> fixRnifA promoter region is differently occupied by two distinct RNA polymerase holoenzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 1014-1019.	7.1	20
49	Enhancing Nitrogen Fixation Gene Expression by Modifying the DNA-Binding Function of <i>Rhizobium meliloti</i> NifA. <i>Current Plant Science and Biotechnology in Agriculture</i> , 1998, , 133-134.	0.0	0
50	Did cyclodextrin glycosyltransferases evolve from α -amylases?. <i>FEBS Letters</i> , 1997, 416, 221-224.	2.8	25
51	A proposed architecture for the central domain of the bacterial enhancer-binding proteins based on secondary structure prediction and fold recognition. <i>Protein Science</i> , 1997, 6, 543-555.	7.6	60
52	Regulatory proteins and cis-acting elements involved in the transcriptional control of <i>Rhizobium etli</i> reiterated nifH genes. <i>Journal of Bacteriology</i> , 1996, 178, 3119-3126.	2.2	40
53	Overlapping promoters for two different RNA polymerase holoenzymes control <i>Bradyrhizobium japonicum</i> nifA expression. <i>Journal of Bacteriology</i> , 1995, 177, 1760-1765.	2.2	40
54	The sigma 54 bacterial enhancer-binding protein family: mechanism of action and phylogenetic relationship of their functional domains. <i>Journal of Bacteriology</i> , 1993, 175, 6067-6074.	2.2	391

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55	Influence of oxygen on DNA binding, positive control, and stability of the Bradyrhizobium japonicum NifA regulatory protein. Journal of Bacteriology, 1991, 173, 3478-3487.	2.2	54
56	Complex Regulatory Network for nif and fix Gene Expression in Bradyrhizobium Japonicum. Current Plant Science and Biotechnology in Agriculture, 1991, , 203-210.	0.0	3
57	The influence of the Klebsiella pneumoniae regulatory gene nifL upon the transcriptional activator protein NifA. Molecular Microbiology, 1990, 4, 1253-1258.	2.5	28
58	Activation of the Klebsiella pneumoniae nifU promoter: identification of multiple and overlapping upstream NifA binding sites. Nucleic Acids Research, 1990, 18, 1693-1701.	14.5	38
59	In vivo studies on the interaction of RNA polymerase- σ^{54} with the Klebsiella pneumoniae and Rhizobium meliloti nifH promoters. Journal of Molecular Biology, 1989, 210, 65-77.	4.2	259
60	Transcription analysis of the three nifH genes of Rhizobium phaseoli with gene fusions. Molecular Genetics and Genomics, 1988, 213, 499-504.	2.4	14
61	The DNA-binding domain of the transcriptional activator protein NifA resides in its carboxy terminus, recognises the upstream activator sequences of nif promoters and can be separated from the positive control function of NifA. Nucleic Acids Research, 1988, 16, 11469-11488.	14.5	93
62	NifA-dependent in vivo protection demonstrates that the upstream activator sequence of nif promoters is a protein binding site.. Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 9401-9405.	7.1	136
63	Effect of Naturally Occurring <i>nif</i> Reiterations on Symbiotic Effectiveness in <i>Rhizobium phaseoli</i> . Applied and Environmental Microbiology, 1988, 54, 848-850.	3.1	12
64	Impaired nitrogen fixation and glutamine synthesis in methionine sulfoximine sensitive (MSs) mutants of Rhizobium phaseoli. Molecular Genetics and Genomics, 1985, 200, 229-234.	2.4	14
65	Omega-amidase pathway in the degradation of glutamine in Neurospora crassa. Journal of Bacteriology, 1985, 161, 807-809.	2.2	40