

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	The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , 2013, 496, 57-63.	27.8	603
2	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
3	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
4	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
5	Insights on the evolution of trehalose biosynthesis. <i>BMC Evolutionary Biology</i> , 2006, 6, 109.	3.2	391
6	Compilation and analysis of σ 54-dependent promoter sequences. <i>Nucleic Acids Research</i> , 1999, 27, 4305-4313.	14.5	333
7	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
8	In vivo studies on the interaction of RNA polymerase- σ 54 with the <i>Klebsiella pneumoniae</i> and <i>Rhizobium meliloti</i> nifH promoters. <i>Journal of Molecular Biology</i> , 1989, 210, 65-77.	4.2	259
9	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
10	A novel transactivation domain in parkin. <i>Trends in Biochemical Sciences</i> , 1999, 24, 229-231.	7.5	145
11	NifA-dependent in vivo protection demonstrates that the upstream activator sequence of nif promoters is a protein binding site.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1988, 85, 9401-9405.	7.1	136
12	Systematic discovery of analogous enzymes in thiamin biosynthesis. <i>Nature Biotechnology</i> , 2003, 21, 790-795.	17.5	121
13	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
14	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. <i>Nucleic Acids Research</i> , 1988, 16, 11469-11488.	14.5	93
15	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
16	GeConT: gene context analysis. <i>Bioinformatics</i> , 2004, 20, 2307-2308.	4.1	59
17	Influence of oxygen on DNA binding, positive control, and stability of the <i>Bradyrhizobium japonicum</i> NifA regulatory protein. <i>Journal of Bacteriology</i> , 1991, 173, 3478-3487.	2.2	54
18	The genome project of <i>Taenia solium</i> . <i>Parasitology International</i> , 2006, 55, S127-S130.	1.3	49

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19	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
20	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
21	Selection for Unequal Densities of λ 70 Promoter-Like Signals in Different Regions of Large Bacterial Genomes. <i>PLoS Genetics</i> , 2006, 2, e185.	3.5	43
22	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
23	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
24	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
25	Omega-amidase pathway in the degradation of glutamine in <i>Neurospora crassa</i> . <i>Journal of Bacteriology</i> , 1985, 161, 807-809.	2.2	40
26	Activation of the <i>Klebsiella pneumoniae</i> nifU promoter: identification of multiple and overlapping upstream NifA binding sites. <i>Nucleic Acids Research</i> , 1990, 18, 1693-1701.	14.5	38
27	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
28	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
29	The influence of the <i>Klebsiella pneumoniae</i> regulatory gene nifL upon the transcriptional activator protein NifA. <i>Molecular Microbiology</i> , 1990, 4, 1253-1258.	2.5	28
30	Communication between λ 54, promoter DNA and the conserved threonine residue in the GAFTGA motif of the PspF λ 54-dependent activator during transcription activation. <i>Molecular Microbiology</i> , 2004, 54, 489-506.	2.5	26
31	Transcription Analysis of Central Metabolism Genes in <i>Escherichia coli</i> . Possible Roles of λ 38 in Their Expression, as a Response to Carbon Limitation. <i>PLoS ONE</i> , 2009, 4, e7466.	2.5	26
32	Did cyclodextrin glycosyltransferases evolve from α -amylases?. <i>FEBS Letters</i> , 1997, 416, 221-224.	2.8	25
33	Bioinformatics Resources for the Study of Gene Regulation in Bacteria. <i>Journal of Bacteriology</i> , 2009, 191, 23-31.	2.2	25
34	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
35	Evidence classification of high-throughput protocols and confidence integration in RegulonDB. Database: the <i>Journal of Biological Databases and Curation</i> , 2013, 2013, bas059.	3.0	23
36	Transcription Factors in <i>Escherichia coli</i> Prefer the Holo Conformation. <i>PLoS ONE</i> , 2013, 8, e65723.	2.5	23

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37	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
38	Structural Properties of Prokaryotic Promoter Regions Correlate with Functional Features. <i>PLoS ONE</i> , 2014, 9, e88717.	2.5	22
39	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
40	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
41	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
42	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
43	Evolutionary Walk between (12/1±)8 Barrels: Catalytic Migration from Triosephosphate Isomerase to Thiamin Phosphate Synthase. <i>Journal of Molecular Biology</i> , 2012, 416, 255-270.	4.2	17
44	Impaired nitrogen fixation and glutamine synthesis in methionine sulfoximine sensitive (MSs) mutants of <i>Rhizobium phaseoli</i> . <i>Molecular Genetics and Genomics</i> , 1985, 200, 229-234.	2.4	14
45	Transcription analysis of the three nifH genes of <i>Rhizobium phaseoli</i> with gene fusions. <i>Molecular Genetics and Genomics</i> , 1988, 213, 499-504.	2.4	14
46	Inferring modules of functionally interacting proteins using the Bond Energy Algorithm. <i>BMC Bioinformatics</i> , 2008, 9, 285.	2.6	13
47	Transcriptional Regulation of the <i>assT</i> - <i>dsbL</i> - <i>dsbI</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
48	A Clustering Genetic Algorithm for Genomic Data Mining. <i>Studies in Computational Intelligence</i> , 2009, , 249-275.	0.9	12
49	Effect of Naturally Occurring <i>nif</i> Reiterations on Symbiotic Effectiveness in <i>Rhizobium phaseoli</i> . <i>Applied and Environmental Microbiology</i> , 1988, 54, 848-850.	3.1	12
50	Choline catabolism, γ 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
51	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
52	Whole genome variation in 27 Mexican indigenous populations, demographic and biomedical insights. <i>PLoS ONE</i> , 2021, 16, e0249773.	2.5	8
53	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
54	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

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55	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
56	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
57	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
58	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
59	Complex Regulatory Network for <i>nif</i> and <i>fix</i> Gene Expression in <i>Bradyrhizobium Japonicum</i> . <i>Current Plant Science and Biotechnology in Agriculture</i> , 1991, , 203-210.	0.0	3
60	Fuzzy C-means for inferring functional coupling of proteins from their phylogenetic profiles. , 2006, , .		1
61	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
62	Improving Random Mutagenesis by Purification of the Oligonucleotide Variants. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2005, 8, 537-544.	1.1	0
63	Inferring functional coupling of proteins using the Evolutionary Bond Energy Algorithm. , 2006, , .		0
64	MOCEA. , 2009, , .		0
65	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