Julio Collado-Vides

List of Publications by Year
in descending order

129 papers	20,665 citations	47409 49 h-index	16186 128 g-index
138 all docs	138 docs citations	138 times ranked	19352 citing authors

#	Article	IF	Citations
1	Missing Links Between Gene Function and Physiology in Genomics. Frontiers in Physiology, 2022, 13, 815874.	1.3	1
2	Sensory Systems and Transcriptional Regulation in Escherichia coli. Frontiers in Bioengineering and Biotechnology, 2022, 10, 823240.	2.0	5
3	RegulonDB 11.0: Comprehensive high-throughput datasets on transcriptional regulation in Escherichia coli K-12. Microbial Genomics, 2022, 8, .	1.0	32
4	The EcoCyc Database in 2021. Frontiers in Microbiology, 2021, 12, 711077.	1.5	122
5	Lisen&Curate: A platform to facilitate gathering textual evidence for curation of regulation of transcription initiation in bacteria. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2021, 1864, 194753.	0.9	3
6	Redefining fundamental concepts of transcription initiation in bacteria. Nature Reviews Genetics, 2020, 21, 699-714.	7.7	100
7	PulmonDB: a curated lung disease gene expression database. Scientific Reports, 2020, 10, 514.	1.6	14
8	Knowledge extraction for assisted curation of summaries of bacterial transcription factor properties. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	2
9	In the pursuit of semantic similarity for literature on microbial transcriptional regulation. Journal of Intelligent and Fuzzy Systems, 2019, 36, 4777-4786.	0.8	3
10	Limits to a classic paradigm: most transcription factors in E. coli regulate genes involved in multiple biological processes. Nucleic Acids Research, 2019, 47, 6656-6667.	6.5	9
11	Similarity corpus on microbial transcriptional regulation. Journal of Biomedical Semantics, 2019, 10, 8.	0.9	8
12	Integrating Bacterial ChIPâ€seq and RNAâ€seq Data With SnakeChunks. Current Protocols in Bioinformatics, 2019, 66, e72.	25.8	3
13	RegulonDB v 10.5: tackling challenges to unify classic and high throughput knowledge of gene regulation in<i>E. coli</i>K-12. Nucleic Acids Research, 2019, 47, D212-D220.	6.5	322
14	The EcoCyc Database. EcoSal Plus, 2018, 8, .	2.1	75
15	A unified resource for transcriptional regulation in Escherichia coli K-12 incorporating high-throughput-generated binding data into RegulonDB version 10.0. BMC Biology, 2018, 16, 91.	1.7	42
16	Using RegulonDB, the <i>Escherichia coli</i> Kâ€12 Gene Regulatory Transcriptional Network Database. Current Protocols in Bioinformatics, 2018, 61, 1.32.1-1.32.30.	25.8	8
17	Strategies towards digital and semi-automated curation in RegulonDB. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	6
18	Improving biocuration of microRNAs in diseases: a case study in idiopathic pulmonary fibrosis. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	4

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19	The EcoCyc database: reflecting new knowledge about *Escherichia coli* K-12. Nucleic Acids Research, 2017, 45, D543-D550.	6.5	541
20	Genome-Wide Mapping of Transcriptional Regulation and Metabolism Describes Information-Processing Units in Escherichia coli. Frontiers in Microbiology, 2017, 8, 1466.	1.5	17
21	First steps in automatic summarization of transcription factor properties for RegulonDB: classification of sentences about structural domains and regulated processes. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	6
22	Effect of genomic distance on coexpression of coregulated genes in E. coli. PLoS ONE, 2017, 12, e0174887.	1.1	28
23	In silico clustering of Salmonella global gene expression data reveals novel genes co-regulated with the SPI-1 virulence genes through HilD. Scientific Reports, 2016, 6, 37858.	1.6	19
24	RegulonDB version 9.0: high-level integration of gene regulation, coexpression, motif clustering and beyond. Nucleic Acids Research, 2016, 44, D133-D143.	6.5	450
25	COLOMBOS v3.0: leveraging gene expression compendia for cross-species analyses: Table 1.. Nucleic Acids Research, 2016, 44, D620-D623.	6.5	69
26	Mathematical modeling of the apo and holo transcriptional regulation in Escherichia coli. Molecular BioSystems, 2015, 11, 994-1003.	2.9	2
27	Structural Properties of Prokaryotic Promoter Regions Correlate with Functional Features. PLoS ONE, 2014, 9, e88717.	1.1	22
28	Assisted curation of regulatory interactions and growth conditions of OxyR in E. coli K-12. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau049-bau049.	1.4	15
29	COLOMBOS v2.0: an ever expanding collection of bacterial expression compendia: Table 1.. Nucleic Acids Research, 2014, 42, D649-D653.	6.5	38
30	In Silico Identification and Experimental Characterization of Regulatory Elements Controlling the Expression of the Salmonella csrB and csrC Genes. Journal of Bacteriology, 2014, 196, 325-336.	1.0	34
31	The EcoCyc Database. EcoSal Plus, 2014, 6, .	2.1	101
32	Evidence classification of high-throughput protocols and confidence integration in RegulonDB. Database: the Journal of Biological Databases and Curation, 2013, 2013, bas059.	1.4	23
33	RegulonDB v8.0: omics data sets, evolutionary conservation, regulatory phrases, cross-validated gold standards and more. Nucleic Acids Research, 2013, 41, D203-D213.	6.5	404
34	EcoCyc: fusing model organism databases with systems biology. Nucleic Acids Research, 2013, 41, D605-D612.	6.5	505
35	Transcription Factors in Escherichia coli Prefer the Holo Conformation. PLoS ONE, 2013, 8, e65723.	1.1	23
36	On the trail of EHEC/EAECâ€"unraveling the gene regulatory networks of human pathogenic *Escherichia coli* bacteria. Integrative Biology (United Kingdom), 2012, 4, 728-733.	0.6	9

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37	Extracting Regulatory Networks of Escherichia coli from RegulonDB. Methods in Molecular Biology, 2012, 804, 179-195.	0.4	15
38	RegulonDB version 7.0: transcriptional regulation of Escherichia coli K-12 integrated within genetic sensory response units (Gensor Units). Nucleic Acids Research, 2011, 39, D98-D105.	6.5	315
39	EcoCyc: a comprehensive database of Escherichia coli biology. Nucleic Acids Research, 2011, 39, D583-D590.	6.5	444
40	Theoretical and empirical quality assessment of transcription factor-binding motifs. Nucleic Acids Research, 2011, 39, 808-824.	6.5	70
41	The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942.	9.4	613
42	Report on the International Conference & Meetings EMBnet-RIBio 2009. EMBnet Journal, 2010, 16, 3.	0.2	0
43	EcoCyc: A comprehensive view of Escherichia coli biology. Nucleic Acids Research, 2009, 37, D464-D470.	6.5	320
44	Bioinformatics Resources for the Study of Gene Regulation in Bacteria. Journal of Bacteriology, 2009, 191, 23-31.	1.0	25
45	From sequence to dynamics: the effects of transcription factor and polymerase concentration changes on activated and repressed promoters. BMC Molecular Biology, 2009, 10, 92.	3.0	3
46	Regulation by transcription factors in bacteria: beyond description. FEMS Microbiology Reviews, 2009, 33, 133-151.	3.9	185
47	The Condition‐Dependent Transcriptional Network in <i>Escherichia coli</i>. Annals of the New York Academy of Sciences, 2009, 1158, 29-35.	1.8	4
48	DISTILLER: a data integration framework to reveal condition dependency of complex regulons in Escherichia coli. Genome Biology, 2009, 10, R27.	13.9	52
49	Structural and functional map of a bacterial nucleoid. Genome Biology, 2009, 10, 247.	13.9	13
50	Genome-Wide Identification of Transcription Start Sites, Promoters and Transcription Factor Binding Sites in E. coli. PLoS ONE, 2009, 4, e7526.	1.1	237
51	Impact of Transcription Units rearrangement on the evolution of the regulatory network of gamma-proteobacteria. BMC Genomics, 2008, 9, 128.	1.2	10
52	Prediction of TF target sites based on atomistic models of protein-DNA complexes. BMC Bioinformatics, 2008, 9, 436.	1.2	39
53	Functional architecture of Escherichia coli: new insights provided by a natural decomposition approach. Genome Biology, 2008, 9, R154.	13.9	56
54	The Role of DNA-binding Specificity in the Evolution of Bacterial Regulatory Networks. Journal of Molecular Biology, 2008, 379, 627-643.	2.0	36

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55	Transcriptional regulation constrains the organization of genes on eukaryotic chromosomes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15761-15766.	3.3	72
56	COMPARATIVE MECHANISMS FOR TRANSCRIPTION AND REGULATORY SIGNALS IN ARCHAEA AND BACTERIA. Series on Advances in Bioinformatics and Computational Biology, 2008, , 185-208.	0.2	1
57	Metabolic Reconstruction and Modeling of Nitrogen Fixation in Rhizobium etli. PLoS Computational Biology, 2007, 3, e192.	1.5	85
58	Development of Genomic Sciences in Mexico: A Good Start and a Long Way to Go. PLoS Computational Biology, 2007, 3, e143.	1.5	12
59	RegulonDB (version 6.0): gene regulation model of Escherichia coli K-12 beyond transcription, active (experimental) annotated promoters and Textpresso navigation. Nucleic Acids Research, 2007, 36, D120-D124.	6.5	395
60	Tractor_DB (version 2.0): a database of regulatory interactions in gamma-proteobacterial genomes. Nucleic Acids Research, 2007, 35, D132-D136.	6.5	26
61	Multidimensional annotation of the Escherichia coli K-12 genome. Nucleic Acids Research, 2007, 35, 7577-7590.	6.5	168
62	Coordination logic of the sensing machinery in the transcriptional regulatory network of Escherichia coli. Nucleic Acids Research, 2007, 35, 6963-6972.	6.5	21
63	Structure and evolution of gene regulatory networks in microbial genomes. Research in Microbiology, 2007, 158, 787-794.	1.0	47
64	Internal Versus External Effector and Transcription Factor Gene Pairs Differ in Their Relative Chromosomal Position in Escherichia coli. Journal of Molecular Biology, 2007, 368, 263-272.	2.0	15
65	TFmodeller: comparative modelling of protein–DNA complexes. Bioinformatics, 2007, 23, 1694-1696.	1.8	23
66	Automatic reconstruction of a bacterial regulatory network using Natural Language Processing. BMC Bioinformatics, 2007, 8, 293.	1.2	43
67	Identification of regulatory network topological units coordinating the genome-wide transcriptional response to glucose in Escherichia coli. BMC Microbiology, 2007, 7, 53.	1.3	59
68	Internal-sensing machinery directs the activity of the regulatory network in Escherichia coli. Trends in Microbiology, 2006, 14, 22-27.	3.5	78
69	The comprehensive updated regulatory network of Escherichia coli K-12. BMC Bioinformatics, 2006, 7, 5.	1.2	63
70	Selection for Unequal Densities of Ïƒ70 Promoter-Like Signals in Different Regions of Large Bacterial Genomes. PLoS Genetics, 2006, 2, e185.	1.5	43
71	Bacterial regulatory networks are extremely flexible in evolution. Nucleic Acids Research, 2006, 34, 3434-3445.	6.5	207
72	Positional Conservation of Clusters of Overlapping Promoter-Like Sequences in Enterobacterial Genomes. Molecular Biology and Evolution, 2006, 23, 997-1010.	3.5	4

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73	RegulonDB (version 5.0): Escherichia coli K-12 transcriptional regulatory network, operon organization, and growth conditions. Nucleic Acids Research, 2006, 34, D394-D397.	6.5	325
74	Comparative footprinting of DNA-binding proteins. Bioinformatics, 2006, 22, e74-e80.	1.8	19
75	The partitioned Rhizobium etli genome: Genetic and metabolic redundancy in seven interacting replicons. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3834-3839.	3.3	365
76	Minimum information requested in the annotation of biochemical models (MIRIAM). Nature Biotechnology, 2005, 23, 1509-1515.	9.4	553
77	Modular analysis of the transcriptional regulatory network of E. coli. Trends in Genetics, 2005, 21, 16-20.	2.9	99
78	Diversification of DNA Sequences in the Symbiotic Genome of Rhizobium etli. Journal of Bacteriology, 2005, 187, 7185-7192.	1.0	27
79	Nebulon: a system for the inference of functional relationships of gene products from the rearrangement of predicted operons. Nucleic Acids Research, 2005, 33, 2521-2530.	6.5	44
80	The Network of Transcriptional Interactions Imposes Linear Constrains in the Genome. OMICS A Journal of Integrative Biology, 2005, 9, 139-145.	1.0	4
81	Comparative Studies of Transcriptional Regulation Mechanisms in a Group of Eight Gamma-proteobacterial Genomes. Journal of Molecular Biology, 2005, 354, 184-199.	2.0	17
82	Complementing computationally predicted regulatory sites in Tractor_DB using a pattern matching approach. In Silico Biology, 2005, 5, 209-19.	0.4	6
83	Successful Lateral Transfer Requires Codon Usage Compatibility Between Foreign Genes and Recipient Genomes. Molecular Biology and Evolution, 2004, 21, 1884-1894.	3.5	75
84	RegulonDB (version 4.0): transcriptional regulation, operon organization and growth conditions in Escherichia coli K-12. Nucleic Acids Research, 2004, 32, 303D-306.	6.5	231
85	TRACTOR_DB: a database of regulatory networks in gamma-proteobacterial genomes. Nucleic Acids Research, 2004, 33, D98-D102.	6.5	22
86	EcoCyc: a comprehensive database resource for Escherichia coli. Nucleic Acids Research, 2004, 33, D334-D337.	6.5	597
87	The growth of random networks as a diffusion process. Physica A: Statistical Mechanics and Its Applications, 2004, 342, 551-560.	1.2	0
88	Phylogenetic distribution of DNA-binding transcription factors in bacteria and archaea. Computational Biology and Chemistry, 2004, 28, 341-350.	1.1	94
89	Distribution of minigenes in the bacteriophage lambda chromosome. Gene, 2004, 329, 115-124.	1.0	3
90	Environmental conditions and transcriptional regulation inEscherichia coli: a physiological integrative approach. Biotechnology and Bioengineering, 2003, 84, 743-749.	1.7	15

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91	Identifying global regulators in transcriptional regulatory networks in bacteria. Current Opinion in Microbiology, 2003, 6, 482-489.	2.3	511
92	Sigma70 Promoters in Escherichia coli: Specific Transcription in Dense Regions of Overlapping Promoter-like Signals. Journal of Molecular Biology, 2003, 333, 261-278.	2.0	205
93	The mosaic structure of the symbiotic plasmid of Rhizobium etli CFN42 and its relation to other symbiotic genome compartments. Genome Biology, 2003, 4, R36.	13.9	167
94	Conservation of DNA curvature signals in regulatory regions of prokaryotic genes. Nucleic Acids Research, 2003, 31, 6770-6777.	6.5	54
95	Regulatory Network of Escherichia coli: Consistency Between Literature Knowledge and Microarray Profiles. Genome Research, 2003, 13, 2435-2443.	2.4	104
96	A powerful non-homology method for the prediction of operons in prokaryotes. Bioinformatics, 2002, 18, S329-S336.	1.8	173
97	The EcoCyc Database. Nucleic Acids Research, 2002, 30, 56-58.	6.5	386
98	Microbial computational genomics of gene regulation. Pure and Applied Chemistry, 2002, 74, 899-905.	0.9	3
99	Evaluation of thresholds for the detection of binding sites for regulatory proteins in Escherichia coli K12 DNA. Genome Biology, 2002, 3, research0013.1.	13.9	24
100	GETools: gene expression tool for analysis of transcriptome experiments in E. coli. Trends in Genetics, 2002, 18, 217-218.	2.9	10
101	Analysis of the Cellular Functions of Escherichia coli Operons and Their Conservation in Bacillus subtilis. Journal of Molecular Evolution, 2002, 55, 211-221.	0.8	35
102	Operon conservation from the point of view of Escherichia coli, and inference of functional interdependence of gene products from genome context. In Silico Biology, 2002, 2, 87-95.	0.4	15
103	Towards a bioinformatics network for Latin America and the Caribbean (LACBioNet). Applied Bioinformatics, 2002, 1, 53-6.	1.7	6
104	RegulonDB (version 3.2): transcriptional regulation and operon organization in Escherichia coli K-12. Nucleic Acids Research, 2001, 29, 72-74.	6.5	201
105	Common History at the Origin of the Position-Function Correlation in Transcriptional Regulators in Archaea and Bacteria. Journal of Molecular Evolution, 2001, 53, 172-179.	0.8	69
106	Transcription unit conservation in the three domains of life: a perspective from Escherichia coli. Trends in Genetics, 2001, 17, 175-177.	2.9	46
107	A Comparative Genomics Approach to Prediction of New Members of Regulons. Genome Research, 2001, 11, 566-584.	2.4	113
108	A web site for the computational analysis of yeast regulatory sequences. Yeast, 2000, 16, 177-187.	0.8	166

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109	Promoter Interference in a Bacteriophage Lambda Control Region: Effects of a Range of Interpromoter Distances. Journal of Bacteriology, 2000, 182, 216-220.	1.0	16
110	Operons in Escherichia coli: Genomic analyses and predictions. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 6652-6657.	3.3	314
111	Modeling and simulation of gene regulation and metabolic pathways. BioSystems, 1999, 49, 79-82.	0.9	3
112	RegulonDB (version 2.0): a database on transcriptional regulation in Escherichia coli. Nucleic Acids Research, 1999, 27, 59-60.	6.5	38
113	From specific gene regulation to genomic networks: a global analysis of transcriptional regulation in Escherichia coli. BioEssays, 1998, 20, 433-440.	1.2	421
114	Networks of transcriptional regulation encoded in a grammatical model. BioSystems, 1998, 47, 103-118.	0.9	14
115	Genomic position analyses and the transcription machinery 1 1Edited by M. Yahiv. Journal of Molecular Biology, 1998, 275, 165-170.	2.0	34
116	Extracting regulatory sites from the upstream region of yeast genes by computational analysis of oligonucleotide frequencies 1 1Edited by G. von Heijne. Journal of Molecular Biology, 1998, 281, 827-842.	2.0	660
117	RegulonDB: a database on transcriptional regulation in Escherichia coli. Nucleic Acids Research, 1998, 26, 55-59.	6.5	176
118	The Complete Genome Sequence of Escherichia coli K-12. Science, 1997, 277, 1453-1462.	6.0	7,145
119	Towards a unified grammatical model of σ70 and σ54 bacterial promoters. Biochimie, 1996, 78, 351-363.	1.3	9
120	Three models of gene regulation in E. coli. Lecture Notes in Computer Science, 1996, , 72-78.	1.0	0
121	Syntactic recognition of regulatory regions in Escherichia coli. Bioinformatics, 1996, 12, 415-422.	1.8	8
122	The Elements for a Classification of Units of Genetic Information with a Combinatorial Component. Journal of Theoretical Biology, 1993, 163, 527-548.	0.8	9
123	A linguistic representation of the regulation of transcription initiation. I. An ordered array of complex symbols with distinctive features. BioSystems, 1993, 29, 87-104.	0.9	16
124	A linguistic representation of the regulation of transcription initiation. II. Distinctive features of sigma 70 promoters and their regulatory binding sites. BioSystems, 1993, 29, 105-128.	0.9	13
125	A LINGUISTIC INTEGRATION OF A BIOLOGICAL DATABASE. , 1993, , .		0
126	Grammatical model of the regulation of gene expression.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 9405-9409.	3.3	41

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127	A syntactic representation of units of genetic information—A syntax of units of genetic information. Journal of Theoretical Biology, 1991, 148, 401-429.	0.8	21
128	The search for a grammatical theory of gene regulation is formally justified by showing the inadequacy of context-free grammars. Bioinformatics, 1991, 7, 321-326.	1.8	18
129	A transformational-grammar approach to the study of the regulation of gene expression. Journal of Theoretical Biology, 1989, 136, 403-425.	0.8	42