Patricia J Kiley

List of Publications by Year
in descending order

86	6,087	71102 41	71685 76
papers	citations	h-index	g-index

92	92	92	4507
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Creation of Markerless Genome Modifications in a Nonmodel Bacterium by Fluorescence-Aided Recombineering. Methods in Molecular Biology, 2022, 2479, 53-70.	0.9	1
2	The essential Rhodobacter sphaeroides CenKR two-component system regulates cell division and envelope biosynthesis. PLoS Genetics, 2022, 18, e1010270.	3.5	7
3	Genome Scale Analysis Reveals IscR Directly and Indirectly Regulates Virulence Factor Genes in Pathogenic Yersinia. MBio, 2021, 12, e0063321.	4.1	4
4	Improving Mobilization of Foreign DNA into Zymomonas mobilis Strain ZM4 by Removal of Multiple Restriction Systems. Applied and Environmental Microbiology, 2021, 87, e0080821.	3.1	6
5	Minor Alterations in Core Promoter Element Positioning Reveal Functional Plasticity of a Bacterial Transcription Factor. MBio, 2021, 12, e0275321.	4.1	1
6	Elevated Expression of a Functional Suf Pathway in Escherichia coli BL21(DE3) Enhances Recombinant Production of an Iron-Sulfur Cluster-Containing Protein. Journal of Bacteriology, 2020, 202, .	2.2	22
7	Model-driven analysis of mutant fitness experiments improves genome-scale metabolic models of Zymomonas mobilis ZM4. PLoS Computational Biology, 2020, 16, e1008137.	3.2	12
8	Tailoring a Global Iron Regulon to a Uropathogen. MBio, 2020, 11, .	4.1	21
9	Identification and Unusual Properties of the Master Regulator FNR in the Extreme Acidophile Acidithiobacillus ferrooxidans. Frontiers in Microbiology, 2019, 10, 1642.	3.5	19
10	Systems Metabolic Engineering of <i>Escherichia coli</i> Improves Coconversion of Lignocelluloseâ€Derived Sugars. Biotechnology Journal, 2019, 14, e1800441.	3.5	9
11	A Markerless Method for Genome Engineering in Zymomonas mobilis ZM4. Frontiers in Microbiology, 2019, 10, 2216.	3.5	19
12	Iron availability and oxygen tension regulate the Yersinia Ysc type III secretion system to enable disseminated infection. PLoS Pathogens, 2019, 15, e1008001.	4.7	10
13	Phage integration alters the respiratory strategy of its host. ELife, 2019, 8, .	6.0	24
14	Title is missing!. , 2019, 15, e1008001.		0
15	Title is missing!. , 2019, 15, e1008001.		0
16	Title is missing!. , 2019, 15, e1008001.		0
17	Title is missing!. , 2019, 15, e1008001.		0
18	Regulated Stochasticity in a Bacterial Signaling Network Permits Tolerance to a Rapid Environmental Change. Cell, 2018, 173, 196-207.e14.	28.9	61

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19	Reassessing the Structure and Function Relationship of the O₂Sensing Transcription Factor FNR. Antioxidants and Redox Signaling, 2018, 29, 1830-1840.	5.4	34
20	Control of hmu Heme Uptake Genes in Yersinia pseudotuberculosis in Response to Iron Sources. Frontiers in Cellular and Infection Microbiology, 2018, 8, 47.	3.9	34
21	O ₂ availability impacts iron homeostasis in <i>Escherichia coli</i>. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12261-12266.	7.1	72
22	4 Sensing the cellular Fe-S cluster demand: a structural, functional, and phylogenetic overview of Escherichia coli IscR. , 2017, , 75-96.		0
23	Defining bacterial regulons using ChIP-seq. Methods, 2015, 86, 80-88.	3.8	32
24	Impact of Anaerobiosis on Expression of the Iron-Responsive Fur and RyhB Regulons. MBio, 2015, 6, e01947-15.	4.1	67
25	How Is Fe-S Cluster Formation Regulated?. Annual Review of Microbiology, 2015, 69, 505-526.	7.3	60
26	Design principles of a conditional futile cycle exploited for regulation. Molecular BioSystems, 2015, 11, 1841-1849.	2.9	10
27	Feâ€“S proteins that regulate gene expression. Biochimica Et Biophysica Acta - Molecular Cell Research, 2015, 1853, 1284-1293.	4.1	95
28	13. Sensing the cellular Fe-S cluster demand: a structural, functional, and phylogenetic overview of Escherichia coli IscR. , 2014, , 325-346.		3
29	Coordinate Regulation of the Suf and Isc Fe-S Cluster Biogenesis Pathways by IscR Is Essential for Viability of Escherichia coli. Journal of Bacteriology, 2014, 196, 4315-4323.	2.2	39
30	Aromatic inhibitors derived from ammonia-pretreated lignocellulose hinder bacterial ethanologenesis by activating regulatory circuits controlling inhibitor efflux and detoxification. Frontiers in Microbiology, 2014, 5, 402.	3.5	46
31	IscR Is Essential for Yersinia pseudotuberculosis Type III Secretion and Virulence. PLoS Pathogens, 2014, 10, e1004194.	4.7	53
32	The Influence of Repressor DNA Binding Site Architecture on Transcriptional Control. MBio, 2014, 5, e01684-14.	4.1	15
33	Correcting direct effects of ethanol on translation and transcription machinery confers ethanol tolerance in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2576-85.	7.1	126
34	Global Responses of Bacteria to Oxygen Deprivation. , 2014, , 175-189.		3
35	Regulation of ironâ€“sulphur cluster homeostasis through transcriptional control of the <scp>Isc</scp> pathway by [2<scp>Fe</scp>â€“2<scp>S</scp>]â€“<scp>IscR</scp> in <i><scp>E</scp>scherichia coli</i>. Molecular Microbiology, 2013, 87, 478-492.	2.5	112
36	Studies of IscR reveal a unique mechanism for metal-dependent regulation of DNA binding specificity. Nature Structural and Molecular Biology, 2013, 20, 740-747.	8.2	104

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37	dPeak: High Resolution Identification of Transcription Factor Binding Sites from PET and SET ChIP-Seq Data. PLoS Computational Biology, 2013, 9, e1003246.	3.2	15
38	Genome-scale Analysis of Escherichia coli FNR Reveals Complex Features of Transcription Factor Binding. PLoS Genetics, 2013, 9, e1003565.	3.5	158
39	The Bacterial Response Regulator ArcA Uses a Diverse Binding Site Architecture to Regulate Carbon Oxidation Globally. PLoS Genetics, 2013, 9, e1003839.	3.5	132
40	Transcriptome Changes Associated with Anaerobic Growth in Yersinia intermedia (ATCC29909). PLoS ONE, 2013, 8, e76567.	2.5	8
41	Complex Physiology and Compound Stress Responses during Fermentation of Alkali-Pretreated Corn Stover Hydrolysate by an Escherichia coli Ethanologen. Applied and Environmental Microbiology, 2012, 78, 3442-3457.	3.1	57
42	Characterization of the [2Fe-2S] Cluster of <i>Escherichia coli</i> Transcription Factor IscR. Biochemistry, 2012, 51, 4453-4462.	2.5	85
43	Evolution of the metabolic and regulatory networks associated with oxygen availability in two phytopathogenic enterobacteria. BMC Genomics, 2012, 13, 110.	2.8	39
44	A shared mechanism of SoxR activation by redoxâ€cycling compounds. Molecular Microbiology, 2011, 79, 1119-1122.	2.5	35
45	Iron-containing transcription factors and their roles as sensors. Current Opinion in Chemical Biology, 2011, 15, 335-341.	6.1	92
46	Global Approaches for Finding Small RNA and Small Open Reading Frame Functions. Journal of Bacteriology, 2010, 192, 26-28.	2.2	4
47	Reconstruction of the Core and Extended Regulons of Global Transcription Factors. PLoS Genetics, 2010, 6, e1001027.	3.5	62
48	Sequence-Specific Binding to a Subset of IscR-Regulated Promoters Does Not Require IscR Feâ€"S Cluster Ligation. Journal of Molecular Biology, 2009, 387, 28-41.	4.2	105
49	Chapter 42 Techniques to Isolate O2-Sensitive Proteins. Methods in Enzymology, 2009, 463, 787-805.	1.0	16
50	The Impact of O2 on the Feâ€"S Cluster Biogenesis Requirements of Escherichia coli FNR. Journal of Molecular Biology, 2008, 384, 798-811.	4.2	57
51	Bridges and Chasms: Summary of the IMAGE 2 Meeting in Montreal, Canada, 30 April to 3 May 2007. Journal of Bacteriology, 2008, 190, 792-797.	2.2	1
52	Dissecting the Role of the N-Terminal Region of the <i>Escherichia coli</i> Global Transcription Factor FNR. Journal of Bacteriology, 2008, 190, 8230-8233.	2.2	6
53	Contributions of [4Fe-4S]-FNR and Integration Host Factor to fnr Transcriptional Regulation. Journal of Bacteriology, 2007, 189, 3036-3043.	2.2	32
54	Two-pronged survival strategy for the major cystic fibrosis pathogen, Pseudomonas aeruginosa, lacking the capacity to degrade nitric oxide during anaerobic respiration. EMBO Journal, 2007, 26, 3662-3672.	7.8	63

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55	IscR-dependent gene expression links iron-sulphur cluster assembly to the control of O2-regulated genes in Escherichia coli. Molecular Microbiology, 2006, 60, 1058-1075.	2.5	264
56	Regulation of FNR Dimerization by Subunit Charge Repulsion. Journal of Biological Chemistry, 2006, 281, 33268-33275.	3.4	39
57	Genome-Wide Expression Analysis Indicates that FNR of<i>Escherichia coli</i>K-12 Regulates a Large Number of Genes of Unknown Function. Journal of Bacteriology, 2005, 187, 1135-1160.	2.2	238
58	Additional Determinants within Escherichia coli FNR Activating Region 1 and RNA Polymerase Î± Subunit Required for Transcription Activation. Journal of Bacteriology, 2005, 187, 1724-1731.	2.2	16
59	ClpXP-dependent Proteolysis of FNR upon Loss of its O2-sensing [4Feâ€“4S] Cluster. Journal of Molecular Biology, 2005, 354, 220-232.	4.2	65
60	Kinetic Analysis of the Oxidative Conversion of the [4Fe-4S]2+ Cluster of FNR to a [2Fe-2S]2+ Cluster. Journal of Bacteriology, 2004, 186, 8018-8025.	2.2	96
61	Exploiting Thiol Modifications. PLoS Biology, 2004, 2, e400.	5.6	89
62	Superoxide Destroys the [2Fe-2S]2+Cluster of FNR fromEscherichia coliâ€. Biochemistry, 2004, 43, 791-798.	2.5	69
63	The role of Feâ€“S proteins in sensing and regulation in bacteria. Current Opinion in Microbiology, 2003, 6, 181-185.	5.1	331
64	Techniques for Studying the Oxygen-Sensitive Transcription Factor FNR from Escherichia coli. Methods in Enzymology, 2003, 370, 300-312.	1.0	20
65	Characterization of activating region 3 from Escherichia coli FNR. Journal of Molecular Biology, 2002, 315, 275-283.	4.2	24
66	IscR, an Fe-S cluster-containing transcription factor, represses expression of Escherichia coli genes encoding Fe-S cluster assembly proteins. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 14895-14900.	7.1	382
67	Characterization of the Dimerization Domain in the FNR Transcription Factor. Journal of Biological Chemistry, 2001, 276, 45744-45750.	3.4	67
68	FNR-dependent activation of the class II dmsA and narG promoters of Escherichia coli requires FNR-activating regions 1 and 3. Molecular Microbiology, 2000, 38, 817-827.	2.5	40
69	Substitution of Leucine 28 with Histidine in theEscherichia coli Transcription Factor FNR Results in Increased Stability of the [4Fe-4S]2+ Cluster to Oxygen. Journal of Biological Chemistry, 2000, 275, 6234-6240.	3.4	75
70	The cysteine desulfurase, IscS, has a major role in in vivo Fe-S cluster formation in Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 9009-9014.	7.1	274
71	Fe-S proteins in sensing and regulatory functions. Current Opinion in Chemical Biology, 1999, 3, 152-157.	6.1	195
72	Oxygen sensing by the global regulator, FNR: the role of the iron-sulfur cluster. FEMS Microbiology Reviews, 1998, 22, 341-352.	8.6	294

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73	Identification of a contact site for different transcription activators in region 4 of the Escherichia coli RNA polymerase Ïƒ70 subunit 1 1Edited by R. Ebright. Journal of Molecular Biology, 1998, 284, 1353-1365.	4.2	153
74	Mossbauer spectroscopy as a tool for the study of activation/inactivation of the transcription regulator FNR in whole cells of Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 13431-13435.	7.1	108
75	Oxygen sensing by the global regulator, FNR: the role of the iron-sulfur cluster. FEMS Microbiology Reviews, 1998, 22, 341-352.	8.6	19
76	Fnr, NarP, and NarL Regulation of Escherichia coli K-12 napF (Periplasmic Nitrate Reductase) Operon Transcription In Vitro. Journal of Bacteriology, 1998, 180, 4192-4198.	2.2	65
77	Iron-sulfur cluster disassembly in the FNR protein of Escherichia coli by O2: [4Fe-4S] to [2Fe-2S] conversion with loss of biological activity. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 6087-6092.	7.1	323
78	Redox control of gene expression involving iron-sulfur proteins. Change of oxidation-state or assembly/disassembly of Fe-S clusters?. FEBS Letters, 1996, 382, 218-219.	2.8	49
79	DNA Binding and Dimerization of the Feâ"S-containing FNR Protein from Escherichia coli Are Regulated by Oxygen. Journal of Biological Chemistry, 1996, 271, 2762-2768.	3.4	284
80	Association of a polynuclear iron-sulfur center with a mutant FNR protein enhances DNA binding.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 2499-2503.	7.1	200
81	In vitroAnalysis of a Constitutively Active Mutant Form of theEscherichia coliGlobal Transcription Factor FNR. Journal of Molecular Biology, 1995, 245, 351-361.	4.2	59
82	The puf operon region of Rhodobacter sphaeroides. Photosynthesis Research, 1988, 19, 39-61.	2.9	30
83	The puf operon region of Rhodobacter sphaeroides. , 1988, , 137-159.		0
84	On the role of the light-harvesting B880 in the correct insertion of the reaction center ofRhodobacter capsulatusandRhodobacter sphaeroides. FEBS Letters, 1987, 215, 171-174.	2.8	22
85	Characterization of light-harvesting mutants of Rhodopseudomonas sphaeroides. I. Measurement of the efficiency of energy transfer from light-harvesting complexes to the reaction center. Archives of Biochemistry and Biophysics, 1985, 236, 130-139.	3.0	90
86	MÃ¶ssbauer studies of the FNR transcription factor in wholeEscherichia coli cells. , 0, , 153-160.		0