Dmitry A Rodionov

List of Publications by Year
in descending order

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148 papers	15,084 citations	25423 59 h-index	22488 117 g-index
154 all docs	154 docs citations	154 times ranked	17752 citing authors

#	ARTICLE	IF	CITATIONS
1	Short-Chain Fatty Acids Modulate Healthy Gut Microbiota Composition and Functional Potential. Current Microbiology, 2022, 79, 128.	1.0	26
2	Genomics-Based Reconstruction and Predictive Profiling of Amino Acid Biosynthesis in the Human Gut Microbiome. Microorganisms, 2022, 10, 740.	1.6	15
3	<i>Bifidobacterium infantis</i> treatment promotes weight gain in Bangladeshi infants with severe acute malnutrition. Science Translational Medicine, 2022, 14, eabk1107.	5.8	61
4	Products of gut microbial Toll/interleukin-1 receptor domain NADase activities in gnotobiotic mice and Bangladeshi children with malnutrition. Cell Reports, 2022, 39, 110738.	2.9	13
5	A systems approach discovers the role and characteristics of seven LysR type transcription factors in Escherichia coli. Scientific Reports, 2022, 12, 7274.	1.6	5
6	Priority effects shape the structure of infant-type <i>Bifidobacterium</i> communities on human milk oligosaccharides. ISME Journal, 2022, 16, 2265-2279.	4.4	34
7	Microbial liberation of N-methylserotonin from orange fiber in gnotobiotic mice and humans. Cell, 2022, 185, 2495-2509.e11.	13.5	26
8	Carbohydrates great and small, from dietary fiber to sialic acids: How glycans influence the gut microbiome and affect human health. Gut Microbes, 2021, 13, 1-18.	4.3	41
9	Community Metabolic Interactions, Vitamin Production and Prebiotic Potential of Medicinal Herbs Used for Immunomodulation. Frontiers in Genetics, 2021, 12, 584197.	1.1	3
10	Binary Metabolic Phenotypes and Phenotype Diversity Metrics for the Functional Characterization of Microbial Communities. Frontiers in Microbiology, 2021, 12, 653314.	1.5	5
11	Evaluating microbiome-directed fibre snacks in gnotobiotic mice and humans. Nature, 2021, 595, 91-95.	13.7	70
12	Genome-Scale Metabolic Model of <i>Caldicellulosiruptor bescii</i> Reveals Optimal Metabolic Engineering Strategies for Bio-based Chemical Production. MSystems, 2021, 6, e0135120.	1.7	6
13	Transcriptional Regulation of Plant Biomass Degradation and Carbohydrate Utilization Genes in the Extreme Thermophile <i>Caldicellulosiruptor bescii</i>. MSystems, 2021, 6, e0134520.	1.7	10
14	Identification of a transcription factor, PunR, that regulates the purine and purine nucleoside transporter punC in E. coli. Communications Biology, 2021, 4, 991.	2.0	13
15	Duodenal Microbiota in Stunted Undernourished Children with Enteropathy. New England Journal of Medicine, 2020, 383, 321-333.	13.9	105
16	Lactose-reduced infant formula with added corn syrup solids is associated with a distinct gut microbiota in Hispanic infants. Gut Microbes, 2020, 12, 1813534.	4.3	18
17	B Vitamins and Their Role in Immune Regulation and Cancer. Nutrients, 2020, 12, 3380.	1.7	129
18	Combined Prebiotic and Microbial Intervention Improves Oral Cholera Vaccination Responses in a Mouse Model of Childhood Undernutrition. Cell Host and Microbe, 2020, 27, 899-908.e5.	5.1	38

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19	Dietary Emulsifier Sodium Stearoyl Lactylate Alters Gut Microbiota in vitro and Inhibits Bacterial Butyrate Producers. Frontiers in Microbiology, 2020, 11, 892.	1.5	23
20	Identifying determinants of bacterial fitness in a model of human gut microbial succession. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2622-2633.	3.3	29
21	Metabolic Phenotypes as Potential Biomarkers for Linking Gut Microbiome With Inflammatory Bowel Diseases. Frontiers in Molecular Biosciences, 2020, 7, 603740.	1.6	8
22	Genomic based prediction of amino acid metabolic pathways and phenotypes in human gut microbiome. , 2020, , .		0
23	Effects of microbiota-directed foods in gnotobiotic animals and undernourished children. Science, 2019, 365, .	6.0	305
24	A sparse covarying unit that describes healthy and impaired human gut microbiota development. Science, 2019, 365, .	6.0	136
25	Prebiotic Potential of Culinary Spices Used to Support Digestion and Bioabsorption. Evidence-based Complementary and Alternative Medicine, 2019, 2019, 1-11.	0.5	20
26	B-Vitamin Sharing Promotes Stability of Gut Microbial Communities. Frontiers in Microbiology, 2019, 10, 1485.	1.5	86
27	A Riboflavin Transporter in <i>Bdellovibrio exovorous</i> JSS. Journal of Molecular Microbiology and Biotechnology, 2019, 29, 27-34.	1.0	3
28	Bioremediation of a Common Product of Food Processing by a Human Gut Bacterium. Cell Host and Microbe, 2019, 26, 463-477.e8.	5.1	43
29	Micronutrient Requirements and Sharing Capabilities of the Human Gut Microbiome. Frontiers in Microbiology, 2019, 10, 1316.	1.5	113
30	16S rRNA gene profiling and genome reconstruction reveal community metabolic interactions and prebiotic potential of medicinal herbs used in neurodegenerative disease and as nootropics. PLoS ONE, 2019, 14, e0213869.	1.1	20
31	Transcriptional control of central carbon metabolic flux in Bifidobacteria by two functionally similar, yet distinct LacI-type regulators. Scientific Reports, 2019, 9, 17851.	1.6	13
32	Novel Metabolic Pathways and Regulons for Hexuronate Utilization in Proteobacteria. Journal of Bacteriology, 2019, 201, .	1.0	19
33	Prediction of enzymatic pathways by integrative pathway mapping. ELife, 2018, 7, .	2.8	30
34	Comparative Genomics Reveals the Regulatory Complexity of Bifidobacterial Arabinose and Arabino-Oligosaccharide Utilization. Frontiers in Microbiology, 2018, 9, 776.	1.5	45
35	Cpe1786/IscR of Clostridium perfringens represses expression of genes involved in Feâ€“S cluster biogenesis. Research in Microbiology, 2017, 168, 345-355.	1.0	4
36	Elucidation of roles for vitamin B ₁₂ in regulation of folate, ubiquinone, and methionine metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1205-E1214.	3.3	75

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37	Underlying mechanisms for syntrophic metabolism of essential enzyme cofactors in microbial communities. ISME Journal, 2017, 11, 1434-1446.	4.4	123
38	The effects of micronutrient deficiencies on bacterial species from the human gut microbiota. Science Translational Medicine, 2017, 9, .	5.8	190
39	A Novel Transcriptional Regulator Related to Thiamine Phosphate Synthase Controls Thiamine Metabolism Genes in Archaea. Journal of Bacteriology, 2017, 199, .	1.0	38
40	A novel bifunctional transcriptional regulator of riboflavin metabolism in Archaea. Nucleic Acids Research, 2017, 45, gkw1331.	6.5	44
41	Genomic Reconstruction of Carbohydrate Utilization Capacities in Microbial-Mat Derived Consortia. Frontiers in Microbiology, 2017, 8, 1304.	1.5	20
42	Transcriptional Regulation of Carbohydrate Utilization Pathways in the Bifidobacterium Genus. Frontiers in Microbiology, 2016, 7, 120.	1.5	50
43	Comparative genomics and evolution of transcriptional regulons in Proteobacteria. Microbial Genomics, 2016, 2, e000061.	1.0	18
44	Identification and Regulation of Genes for Cobalamin Transport in the Cyanobacterium Synechococcus sp. Strain PCC 7002. Journal of Bacteriology, 2016, 198, 2753-2761.	1.0	26
45	Complementation of Cobalamin Auxotrophy in Synechococcus sp. Strain PCC 7002 and Validation of a Putative Cobalamin Riboswitch <i>In Vivo</i>. Journal of Bacteriology, 2016, 198, 2743-2752.	1.0	25
46	Gut bacteria that prevent growth impairments transmitted by microbiota from malnourished children. Science, 2016, 351, .	6.0	580
47	Comparative genomics of pyridoxal 5â€²-phosphate-dependent transcription factor regulons in Bacteria. Microbial Genomics, 2016, 2, e000047.	1.0	21
48	Comparative Genomics and Functional Analysis of Carbohydrate Utilization Networks in Unicyanobacterial Consortia Derived from Hypersaline Lake Microbial Mats. FASEB Journal, 2016, 30, .	0.2	0
49	Two novel regulators of <i>N</i>â€acetylâ€galactosamine utilization pathway and distinct roles in bacterial infections. MicrobiologyOpen, 2015, 4, 983-1000.	1.2	22
50	Genomic distribution of <scp>B</scp>â€vitamin auxotrophy and uptake transporters in environmental bacteria from the <scp><i>C</i></scp><i>hloroflexi</i> phylum. Environmental Microbiology Reports, 2015, 7, 204-210.	1.0	71
51	Experimental Strategies for Functional Annotation and Metabolism Discovery: Targeted Screening of Solute Binding Proteins and Unbiased Panning of Metabolomes. Biochemistry, 2015, 54, 909-931.	1.2	95
52	Novel Transcriptional Regulons for Autotrophic Cycle Genes in Crenarchaeota. Journal of Bacteriology, 2015, 197, 2383-2391.	1.0	11
53	Genetic determinants of in vivo fitness and diet responsiveness in multiple human gut <i>Bacteroides</i>. Science, 2015, 350, aac5992.	6.0	229
54	A novel transcriptional regulator of L-arabinose utilization in human gut bacteria. Nucleic Acids Research, 2015, 43, gkv1005.	6.5	26

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55	Rex (Encoded by DVU_0916) in Desulfovibrio vulgaris Hildenborough Is a Repressor of Sulfate Adenylyl Transferase and Is Regulated by NADH. Journal of Bacteriology, 2015, 197, 29-39.	1.0	37
56	Comparative Genomics of DtxR Family Regulons for Metal Homeostasis in Archaea. Journal of Bacteriology, 2015, 197, 451-458.	1.0	25
57	Comparative Genomics of Transcriptional Regulation of Methionine Metabolism in Proteobacteria. PLoS ONE, 2014, 9, e113714.	1.1	20
58	Comparative genomics and evolution of regulons of the LacI-family transcription factors. Frontiers in Microbiology, 2014, 5, 294.	1.5	76
59	Transport of Magnesium by a Bacterial Nramp-Related Gene. PLoS Genetics, 2014, 10, e1004429.	1.5	31
60	Control of methionine metabolism by the <scp>SahR</scp> transcriptional regulator in <scp>P</scp>roteobacteria. Environmental Microbiology, 2014, 16, 1-8.	1.8	18
61	Computational analysis of riboswitch-based regulation. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 900-907.	0.9	9
62	Redox-Responsive Repressor Rex Modulates Alcohol Production and Oxidative Stress Tolerance in Clostridium acetobutylicum. Journal of Bacteriology, 2014, 196, 3949-3963.	1.0	60
63	Functional Metabolic Map of Faecalibacterium prausnitzii, a Beneficial Human Gut Microbe. Journal of Bacteriology, 2014, 196, 3289-3302.	1.0	173
64	RegTransBase â€“ a database of regulatory sequences and interactions based on literature: a resource for investigating transcriptional regulation in prokaryotes. BMC Genomics, 2013, 14, 213.	1.2	69
65	Genomic reconstruction of transcriptional regulatory networks in lactic acid bacteria. BMC Genomics, 2013, 14, 94.	1.2	38
66	Comparative genomics of metabolic capacities of regulons controlled by cis-regulatory RNA motifs in bacteria. BMC Genomics, 2013, 14, 597.	1.2	39
67	Polysaccharides utilization in human gut bacterium Bacteroides thetaiotaomicron: comparative genomics reconstruction of metabolic and regulatory networks. BMC Genomics, 2013, 14, 873.	1.2	122
68	Crystal Structures of the First Condensation Domain of CDA Synthetase Suggest Conformational Changes during the Synthetic Cycle of Nonribosomal Peptide Synthetases. Journal of Molecular Biology, 2013, 425, 3137-3150.	2.0	79
69	Novel inositol catabolic pathway in <i><scp>T</scp>hermotoga maritima</i>. Environmental Microbiology, 2013, 15, 2254-2266.	1.8	23
70	The COMBREX Project: Design, Methodology, and Initial Results. PLoS Biology, 2013, 11, e1001638.	2.6	54
71	Functional diversification of ROK-family transcriptional regulators of sugar catabolism in the Thermotogae phylum. Nucleic Acids Research, 2013, 41, 790-803.	6.5	44
72	New Family of Tungstate-Responsive Transcriptional Regulators in Sulfate-Reducing Bacteria. Journal of Bacteriology, 2013, 195, 4466-4475.	1.0	16

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73	Transcription Factor Family-Based Reconstruction of Singleton Regulons and Study of the Crp/Fnr, ArsR, and GntR Families in Desulfovibrionales Genomes. Journal of Bacteriology, 2013, 195, 29-38.	1.0	15
74	Genomic Reconstruction of the Transcriptional Regulatory Network in Bacillus subtilis. Journal of Bacteriology, 2013, 195, 2463-2473.	1.0	54
75	RegPrecise 3.0 â€“ A resource for genome-scale exploration of transcriptional regulation in bacteria. BMC Genomics, 2013, 14, 745.	1.2	408
76	Transcriptional regulation of the carbohydrate utilization network in Thermotoga maritima. Frontiers in Microbiology, 2013, 4, 244.	1.5	48
77	Comparative genomics and functional analysis of rhamnose catabolic pathways and regulons in bacteria. Frontiers in Microbiology, 2013, 4, 407.	1.5	55
78	RegPrecise web services interface: programmatic access to the transcriptional regulatory interactions in bacteria reconstructed by comparative genomics. Nucleic Acids Research, 2012, 40, W604-W608.	6.5	24
79	N-Acetylgalactosamine Utilization Pathway and Regulon in Proteobacteria. Journal of Biological Chemistry, 2012, 287, 28047-28056.	1.6	30
80	Global transcriptional control by glucose and carbon regulator CcpA in Clostridium difficile. Nucleic Acids Research, 2012, 40, 10701-10718.	6.5	228
81	Transcriptional Regulation of Central Carbon and Energy Metabolism in Bacteria by Redox-Responsive Repressor Rex. Journal of Bacteriology, 2012, 194, 1145-1157.	1.0	120
82	Phenylacetic Acid Catabolism and Its Transcriptional Regulation in Corynebacterium glutamicum. Applied and Environmental Microbiology, 2012, 78, 5796-5804.	1.4	32
83	Diversity and Versatility of the Thermotoga maritima Sugar Kinome. Journal of Bacteriology, 2012, 194, 5552-5563.	1.0	25
84	Tagaturonateâ€“fructuronate epimerase <scp><scp>UxaE</scp></scp>, a novel enzyme in the hexuronate catabolic network in <i><scp>T</scp>hermotoga maritima</i>. Environmental Microbiology, 2012, 14, 2920-2934.	1.8	41
85	Negative transcriptional control of biotin metabolism genes by the TetR-type regulator BioQ in biotin-auxotrophic Corynebacterium glutamicum ATCC 13032. Journal of Biotechnology, 2012, 159, 225-234.	1.9	32
86	Ribulokinase and Transcriptional Regulation of Arabinose Metabolism in Clostridium acetobutylicum. Journal of Bacteriology, 2012, 194, 1055-1064.	1.0	54
87	Comparative genomics and functional analysis of the NiaP family uncover nicotinate transporters from bacteria, plants, and mammals. Functional and Integrative Genomics, 2012, 12, 25-34.	1.4	25
88	Comparative genomic reconstruction of transcriptional networks controlling central metabolism in the Shewanella genus. BMC Genomics, 2011, 12, S3.	1.2	59
89	Role of a Zn-independent DksA in Zn homeostasis and stringent response. Molecular Microbiology, 2011, 79, 700-715.	1.2	68
90	Canonical and ECF-type ATP-binding cassette importers in prokaryotes: diversity in modular organization and cellular functions. FEMS Microbiology Reviews, 2011, 35, 3-67.	3.9	174

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91	Inference of the Transcriptional Regulatory Network in Staphylococcus aureus by Integration of Experimental and Genomics-Based Evidence. Journal of Bacteriology, 2011, 193, 3228-3240.	1.0	45
92	Control of Proteobacterial Central Carbon Metabolism by the HexR Transcriptional Regulator. Journal of Biological Chemistry, 2011, 286, 35782-35794.	1.6	51
93	Comparative Genomic Analysis of the Hexuronate Metabolism Genes and Their Regulation in Gammaproteobacteria. Journal of Bacteriology, 2011, 193, 3956-3963.	1.0	34
94	Identification of Nicotinamide Mononucleotide Deamidase of the Bacterial Pyridine Nucleotide Cycle Reveals a Novel Broadly Conserved Amidohydrolase Family. Journal of Biological Chemistry, 2011, 286, 40365-40375.	1.6	54
95	Genomics and Enzymology of NAD Biosynthesis. , 2010, , 213-257.		46
96	Evolution of Regulatory Motifs of Bacterial Transcription Factors. In Silico Biology, 2010, 10, 163-183.	0.4	5
97	The Zur regulon of Corynebacterium glutamicum ATCC 13032. BMC Genomics, 2010, 11, 12.	1.2	63
98	Reconstruction of xylose utilization pathway and regulons in Firmicutes. BMC Genomics, 2010, 11, 255.	1.2	100
99	Genomic encyclopedia of sugar utilization pathways in the Shewanella genus. BMC Genomics, 2010, 11, 494.	1.2	89
100	A Eubacterial Riboswitch Class That Senses the Coenzyme Tetrahydrofolate. Chemistry and Biology, 2010, 17, 681-685.	6.2	86
101	The Use of Subsystems to Encode Biosynthesis of Vitamins and Cofactors. , 2010, , 141-159.		35
102	RegPrecise: a database of curated genomic inferences of transcriptional regulatory interactions in prokaryotes. Nucleic Acids Research, 2010, 38, D111-D118.	6.5	172
103	RegPredict: an integrated system for regulon inference in prokaryotes by comparative genomics approach. Nucleic Acids Research, 2010, 38, W299-W307.	6.5	130
104	Genomic reconstruction of <i>Shewanella oneidensis</i> MR-1 metabolism reveals a previously uncharacterized machinery for lactate utilization. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2874-2879.	3.3	140
105	Engineering transcription factors with novel DNA-binding specificity using comparative genomics. Nucleic Acids Research, 2009, 37, 2493-2503.	6.5	39
106	Zinc-Independent Folate Biosynthesis: Genetic, Biochemical, and Structural Investigations Reveal New Metal Dependence for GTP Cyclohydrolase IB. Journal of Bacteriology, 2009, 191, 6936-6949.	1.0	61
107	Nicotinamide mononucleotide synthetase is the key enzyme for an alternative route of NAD biosynthesis in <i>Francisella tularensis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3083-3088.	3.3	70
108	Structure and Function of an ADP-Ribose-Dependent Transcriptional Regulator of NAD Metabolism. Structure, 2009, 17, 939-951.	1.6	41

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109	A subset of the diverse COG0523 family of putative metal chaperones is linked to zinc homeostasis in all kingdoms of life. BMC Genomics, 2009, 10, 470.	1.2	141
110	Comparative genomic analyses of nickel, cobalt and vitamin B12 utilization. BMC Genomics, 2009, 10, 78.	1.2	260
111	A Novel Class of Modular Transporters for Vitamins in Prokaryotes. Journal of Bacteriology, 2009, 191, 42-51.	1.0	280
112	Comparative Genomics of Regulation of Fatty Acid and Branched-Chain Amino Acid Utilization in Proteobacteria. Journal of Bacteriology, 2009, 191, 52-64.	1.0	115
113	Evolution of Regulatory Systems in Bacteria (Invited Keynote Talk). Lecture Notes in Computer Science, 2009, , 1-4.	1.0	0
114	Comparative genomics and functional annotation of bacterial transporters. Physics of Life Reviews, 2008, 5, 22-49.	1.5	25
115	Towards environmental systems biology of Shewanella. Nature Reviews Microbiology, 2008, 6, 592-603.	13.6	829
116	New substrates for TonB-dependent transport: do we only see the â€˜tip of the icebergâ€™?. Trends in Biochemical Sciences, 2008, 33, 330-338.	3.7	323
117	Transcriptional regulation of NAD metabolism in bacteria: genomic reconstruction of NiaR (YrxA) regulon. Nucleic Acids Research, 2008, 36, 2032-2046.	6.5	67
118	Identification of Genes Encoding the Folate- and Thiamine-Binding Membrane Proteins in Firmicutes. Journal of Bacteriology, 2008, 190, 7591-7594.	1.0	51
119	Glycerate 2-Kinase of <i>Thermotoga maritima</i> and Genomic Reconstruction of Related Metabolic Pathways. Journal of Bacteriology, 2008, 190, 1773-1782.	1.0	30
120	Transcriptional regulation of NAD metabolism in bacteria: NrtR family of Nudix-related regulators. Nucleic Acids Research, 2008, 36, 2047-2059.	6.5	72
121	The National Microbial Pathogen Database Resource (NMPDR): a genomics platform based on subsystem annotation. Nucleic Acids Research, 2007, 35, D347-D353.	6.5	87
122	Biotin uptake in prokaryotes by solute transporters with an optional ATP-binding cassette-containing module. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2909-2914.	3.3	134
123	Genomic identification and in vitro reconstitution of a complete biosynthetic pathway for the osmolyte di-myo-inositol-phosphate. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 4279-4284.	3.3	36
124	Comparative Genomic Reconstruction of Transcriptional Regulatory Networks in Bacteria. Chemical Reviews, 2007, 107, 3467-3497.	23.0	193
125	Crystal structure of TM1030 from Thermotoga maritima at 2.3 Ã… resolution reveals molecular details of its transcription repressor function. Proteins: Structure, Function and Bioinformatics, 2007, 68, 418-424.	1.5	5
126	Living without Fur: the subtlety and complexity of iron-responsive gene regulation in the symbiotic bacterium Rhizobium and other Î±-proteobacteria. BioMetals, 2007, 20, 501-511.	1.8	92

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127	Computational identification of BioR, a transcriptional regulator of biotin metabolism inAlphaproteobacteria, and of its binding signal. FEMS Microbiology Letters, 2006, 255, 102-107.	0.7	27
128	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.	1.2	264
129	The Rhizobium leguminosarum regulator IrrA affects the transcription of a wide range of genes in response to Fe availability. Molecular Genetics and Genomics, 2006, 275, 564-577.	1.0	45
130	Computational Reconstruction of Iron- and Manganese-Responsive Transcriptional Networks in Î±-Proteobacteria. PLoS Computational Biology, 2006, 2, e163.	1.5	138
131	Comparative Genomics and Experimental Characterization of N-Acetylglucosamine Utilization Pathway of Shewanella oneidensis. Journal of Biological Chemistry, 2006, 281, 29872-29885.	1.6	120
132	Comparative and Functional Genomic Analysis of Prokaryotic Nickel and Cobalt Uptake Transporters: Evidence for a Novel Group of ATP-Binding Cassette Transporters. Journal of Bacteriology, 2006, 188, 317-327.	1.0	269
133	Identification of a bacterial regulatory system for ribonucleotide reductases by phylogenetic profiling. Trends in Genetics, 2005, 21, 385-389.	2.9	68
134	Dissimilatory Metabolism of Nitrogen Oxides in Bacteria: Comparative Reconstruction of Transcriptional Networks. PLoS Computational Biology, 2005, 1, e55.	1.5	260
135	The Subsystems Approach to Genome Annotation and its Use in the Project to Annotate 1000 Genomes. Nucleic Acids Research, 2005, 33, 5691-5702.	6.5	1,806
136	Definition of a Consensus DNA-binding Site for PecS, a Global Regulator of Virulence Gene Expression in Erwinia chrysanthemi and Identification of New Members of the PecS Regulon. Journal of Biological Chemistry, 2004, 279, 30158-30167.	1.6	51
137	Comparative genomics of the KdgR regulon in Erwinia chrysanthemi 3937 and other gamma-proteobacteria. Microbiology (United Kingdom), 2004, 150, 3571-3590.	0.7	108
138	Comparative genomics of the methionine metabolism in Gram-positive bacteria: a variety of regulatory systems. Nucleic Acids Research, 2004, 32, 3340-3353.	6.5	159
139	Riboswitches: the oldest mechanism for the regulation of gene expression?. Trends in Genetics, 2004, 20, 44-50.	2.9	274
140	Reconstruction of regulatory and metabolic pathways in metal-reducing delta-proteobacteria. Genome Biology, 2004, 5, R90.	13.9	162
141	Regulation of the vitamin B12 metabolism and transport in bacteria by a conserved RNA structural element. Rna, 2003, 9, 1084-1097.	1.6	170
142	Regulation of lysine biosynthesis and transport genes in bacteria: yet another RNA riboswitch?. Nucleic Acids Research, 2003, 31, 6748-6757.	6.5	170
143	Comparative Genomics of the Vitamin B12 Metabolism and Regulation in Prokaryotes. Journal of Biological Chemistry, 2003, 278, 41148-41159.	1.6	417
144	Comparative Genomics of Thiamin Biosynthesis in Procaryotes. Journal of Biological Chemistry, 2002, 277, 48949-48959.	1.6	326

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145	Regulation of riboflavin biosynthesis and transport genes in bacteria by transcriptional and translational attenuation. Nucleic Acids Research, 2002, 30, 3141-3151.	6.5	308
146	Conservation of the Biotin Regulon and the BirA Regulatory Signal in Eubacteria and Archaea. Genome Research, 2002, 12, 1507-1516.	2.4	196
147	Transcriptional regulation of pentose utilisation systems in the Bacillus/Clostridium group of bacteria. FEMS Microbiology Letters, 2001, 205, 305-314.	0.7	76
148	Transcriptional regulation of transport and utilization systems for hexuronides, hexuronates and hexonates in gamma purple bacteria. Molecular Microbiology, 2000, 38, 673-683.	1.2	56