Robert M Blumenthal

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Many paths to methyltransfer: a chronicle of convergence. Trends in Biochemical Sciences, 2003, 28, 329-335.	7.5	766
2	A nomenclature for restriction enzymes, DNA methyltransferases, homing endonucleases and their genes. Nucleic Acids Research, 2003, 31, 1805-1812.	14.5	634
3	Structure-guided Analysis Reveals Nine Sequence Motifs Conserved among DNA Amino-methyl-transferases, and Suggests a Catalytic Mechanism for these Enzymes. Journal of Molecular Biology, 1995, 253, 618-632.	4.2	457
4	Mammalian DNA Methyltransferases: A Structural Perspective. Structure, 2008, 16, 341-350.	3.3	349
5	Adaptation to famine: A family of stationary-phase genes revealed by microarray analysis. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13471-13476.	7.1	206
6	Coordinated Chromatin Control: Structural and Functional Linkage of DNA and Histone Methylation. Biochemistry, 2010, 49, 2999-3008.	2.5	199
7	The Isolation and Characterization of theEsherichia ColiDNA adenine methylase(dam)gene. Nucleic Acids Research, 1983, 11, 837-851.	14.5	187
8	Structure Prediction and Phylogenetic Analysis of a Functionally Diverse Family of Proteins Homologous to the MT-A70 Subunit of the Human mRNA:m6A Methyltransferase. Journal of Molecular Evolution, 2002, 55, 431-444.	1.8	186
9	Assignment of enzymic function to specific protein regions of cobalamin-dependent methionine synthase from Escherichia coli. Biochemistry, 1993, 32, 9290-9295.	2.5	121
10	Finding a basis for flipping bases. Structure, 1996, 4, 639-645.	3.3	114
11	A common mode of recognition for methylated CpG. Trends in Biochemical Sciences, 2013, 38, 177-183.	7.5	89
12	The effects of the relA gene on the synthesis of aminoacyl-tRNA synthetases and other transcription and translation proteins in Escherichia coli B. Molecular Genetics and Genomics, 1976, 149, 291-296.	2.4	86
13	Emergence, origin, and function of neutrophil–dendritic cell hybrids in experimentally induced inflammatory lesions in mice. Blood, 2013, 121, 1690-1700.	1.4	82
14	Structural basis for Klf4 recognition of methylated DNA. Nucleic Acids Research, 2014, 42, 4859-4867.	14.5	81
15	S-Adenosylmethionine-Dependent Methyltransferases. , 1999, , .		70
16	Role and Mechanism of Action of C · Pvu II, a Regulatory Protein Conserved among Restriction-Modification Systems. Journal of Bacteriology, 2000, 182, 477-487.	2.2	65
17	STRUCTURE AND EVOLUTION OF ADOMET-DEPENDENT METHYLTRANSFERASES. , 1999, , 1-38.		57
18	The COMBREX Project: Design, Methodology, and Initial Results. PLoS Biology, 2013, 11, e1001638.	5.6	54

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19	Sequence, internal homology and high-level expression of the gene for a DNA-(cytosineN4)-methyltransferase, M-Pvull. Nucleic Acids Research, 1989, 17, 4161-4175.	14.5	48
20	Mapping regulatory networks in microbial cells. Trends in Microbiology, 1999, 7, 320-328.	7.7	47
21	A nucleoprotein activation complex between the leucine-responsive regulatory protein and DNA upstream of the gltBDF operon in Escherichia coli. Journal of Molecular Biology, 1997, 270, 152-168.	4.2	45
22	Real-time kinetics of restriction–modification gene expression after entry into a new host cell. Nucleic Acids Research, 2008, 36, 2581-2593.	14.5	44
23	Nature of the Promoter Activated by C.Pvull, an Unusual Regulatory Protein Conserved among Restriction-Modification Systems. Journal of Bacteriology, 2005, 187, 488-497.	2.2	43
24	Integration of regulatory signals through involvement of multiple global regulators: control of the Escherichia coli gltBDF operon by Lrp, IHF, Crp, and ArgR. BMC Microbiology, 2007, 7, 2.	3.3	41
25	Unexpected Coregulator Range for the Global Regulator Lrp of <i>Escherichia coli</i> and <i>Proteus mirabilis</i> . Journal of Bacteriology, 2011, 193, 1054-1064.	2.2	39
26	Detecting and interpreting DNA methylation marks. Current Opinion in Structural Biology, 2018, 53, 88-99.	5.7	39
27	Methyl-dependent and spatial-specific DNA recognition by the orthologous transcription factors human AP-1 and Epstein-Barr virus Zta. Nucleic Acids Research, 2017, 45, 2503-2515.	14.5	38
28	Tuning the relative affinities for activating and repressing operators of a temporally regulated restriction-modification system. Nucleic Acids Research, 2009, 37, 983-998.	14.5	37
29	Mobility of a Restriction-Modification System Revealed by Its Genetic Contexts in Three Hosts. Journal of Bacteriology, 2002, 184, 2411-2419.	2.2	35
30	Gene expression in Escherichia coli B/r during partial rifampicin-mediated restrictions of transcription initiation. Molecular Genetics and Genomics, 1978, 165, 79-86.	2.4	34
31	Limited functional conservation of a global regulator among related bacterial genera: Lrp in Escherichia, Proteus and Vibrio. BMC Microbiology, 2008, 8, 60.	3.3	32
32	The Pvull DNA (Cytosine-N4)-methyltransferase Comprises Two Trypsin-Defined Domains, Each of Which Binds a Molecule of S-Adenosyl-l-methionine. Biochemistry, 1997, 36, 8284-8292.	2.5	31
33	Regulatory circuit based on autogenous activation-repression: roles of C-boxes and spacer sequences in control of the Pvull restriction-modification system. Nucleic Acids Research, 2007, 35, 6935-6952.	14.5	31
34	Activation from a Distance: Roles of Lrp and Integration Host Factor in Transcriptional Activation of gltBDF. Journal of Bacteriology, 2001, 183, 3910-3918.	2.2	26
35	Biochemical and structural basis for YTH domain of human YTHDC1 binding to methylated adenine in DNA. Nucleic Acids Research, 2020, 48, 10329-10341.	14.5	26
36	The M·Alul DNA-(cytosineC5)-methyltransferase has an unusually large, partially dispensable, variable region. Nucleic Acids Research, 1993, 21, 905-911.	14.5	23

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37	Structural basis for effects of CpA modifications on C/EBPβ binding of DNA. Nucleic Acids Research, 2019, 47, 1774-1785.	14.5	23
38	Beta class amino methyltransferases from bacteria to humans: evolution and structural consequences. Nucleic Acids Research, 2020, 48, 10034-10044.	14.5	21
39	Enzymatic characterization of three human RNA adenosine methyltransferases reveals diverse substrate affinities and reaction optima. Journal of Biological Chemistry, 2021, 296, 100270.	3.4	21
40	Characterization of pPvu1, the autonomous plasmid from proteus vulgaris that carries the genes of the Pvull restriction-modification system. Gene, 1995, 157, 73-79.	2.2	20
41	Gene pvullW: A possible modulator of Pvull endonuclease subunit association. Gene, 1995, 157, 193-199.	2.2	20
42	Role for first zinc finger of WT1 in DNA sequence specificity: Denys–Drash syndrome-associated WT1 mutant in ZF1 enhances affinity for a subset of WT1 binding sites. Nucleic Acids Research, 2018, 46, 3864-3877.	14.5	20
43	A bistable hysteretic switch in an activator–repressor regulated restriction–modification system. Nucleic Acids Research, 2013, 41, 6045-6057.	14.5	19
44	Distinctive Klf4 mutants determine preference for DNA methylation status. Nucleic Acids Research, 2016, 44, gkw774.	14.5	19
45	Structural basis for preferential binding of human TCF4 to DNA containing 5-carboxylcytosine. Nucleic Acids Research, 2019, 47, 8375-8387.	14.5	19
46	Introduction—Epiphanies in Epigenetics. Progress in Molecular Biology and Translational Science, 2011, 101, 1-21.	1.7	18
47	Higher incidence of perineal community acquired MRSA infections among toddlers. BMC Pediatrics, 2011, 11, 96.	1.7	18
48	Restriction-Modification Systems. , 0, , 177-225.		17
49	1 Protein Methyltransferases: Their Distribution Among the Five Structural Classes of AdoMet-Dependent Methyltransferases. The Enzymes, 2006, 24, 3-28.	1.7	17
50	Evolution of a global regulator: Lrp in four orders of γ-Proteobacteria. BMC Evolutionary Biology, 2016, 16, 111.	3.2	17
51	Clostridioides difficile specific DNA adenine methyltransferase CamA squeezes and flips adenine out of DNA helix. Nature Communications, 2021, 12, 3436.	12.8	16
52	Structural basis of human PR/SET domain 9 (PRDM9) allele C–specific recognition of its cognate DNA sequence. Journal of Biological Chemistry, 2017, 292, 15994-16002.	3.4	15
53	Detection of DNA Modifications by Sequence-Specific Transcription Factors. Journal of Molecular Biology, 2020, 432, 1661-1673.	4.2	15
54	A Role for N6-Methyladenine in DNA Damage Repair. Trends in Biochemical Sciences, 2021, 46, 175-183.	7.5	14

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55	Recognition of DNA by the Helix-Turn-Helix Global Regulatory Protein Lrp Is Modulated by the Amino Terminus. Journal of Bacteriology, 2011, 193, 3794-3803.	2.2	13
56	Cytosines Do It, Thymines Do It, Even Pseudouridines Do It—Base Flipping by an Enzyme that Acts on RNA. Structure, 2002, 10, 127-129.	3.3	11
57	Structures of Escherichia coli DNA adenine methyltransferase (Dam) in complex with a non-GATC sequence: potential implications for methylation-independent transcriptional repression. Nucleic Acids Research, 2015, 43, 4296-4308.	14.5	11
58	A Taq attack displaces bases. , 2001, 8, 101-103.		10
59	Expression, Purification, Mass Spectrometry, Crystallization and Multiwavelength Anomalous Diffraction of Selenomethionyl Pvull DNA Methyltransferase (cytosine-N4-specific). FEBS Journal, 1997, 247, 1009-1018.	0.2	9
60	Producing Proficient Methyl Donors from Alternative Substrates of <i>S</i> -Adenosylmethionine Synthetase. Biochemistry, 2014, 53, 1521-1526.	2.5	9
61	A surprising range of modified-methionyl S-adenosylmethionine analogues support bacterial growth. Microbiology (United Kingdom), 2015, 161, 674-682.	1.8	8
62	Repurposing epigenetic inhibitors to target the <i>Clostridioides difficile-</i> specific DNA adenine methyltransferase and sporulation regulator CamA. Epigenetics, 2022, 17, 970-981.	2.7	8
63	Translational independence between overlapping genes for a restriction endonuclease and its transcriptional regulator. BMC Molecular Biology, 2010, 11, 87.	3.0	7
64	Complementation of a metK-deficient E. coli strain with heterologous AdoMet synthetase genes. Microbiology (United Kingdom), 2017, 163, 1812-1821.	1.8	7
65	Experimental Analysis of Global Gene Regulation in Escherichia coli. Progress in Molecular Biology and Translational Science, 1996, 55, 1-86.	1.9	6
66	Distribution of RecBCD and AddAB recombination-associated genes among bacteria in 33 phyla. Microbiology (United Kingdom), 2020, 166, 1047-1064.	1.8	5
67	Isolation of mutants in a DNA methyltransferase through mcrB-mediated restriction. Gene, 1988, 74, 269-273.	2.2	4
68	Naturally-occurring, dually-functional fusions between restriction endonucleases and regulatory proteins. BMC Evolutionary Biology, 2013, 13, 218.	3.2	4
69	Response to Mackay et al Trends in Biochemical Sciences, 2013, 38, 423.	7.5	1
70	Differential ETS1 binding to T:G mismatches within a CpG dinucleotide contributes to C-to-T somatic mutation rate of the IDH2 hotspot at codon Arg140. DNA Repair, 2022, 113, 103306.	2.8	1
71	Skewed genomic libraries revisited. Trends in Biotechnology, 1988, 6, 35.	9.3	0
72	Preface. Progress in Molecular Biology and Translational Science, 2011, 101, xiii-xiv.	1.7	0

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73	Structural and Biochemical Advances in Mammalian DNA Methylation. , 2009, , 85-100.		0