

# Robert M Blumenthal

## List of Publications by Year in descending order

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73  
papers

4,905  
citations

159358

30  
h-index

102304

66  
g-index

75  
all docs

75  
docs citations

75  
times ranked

5541  
citing authors

#	ARTICLE	IF	CITATIONS
1	Repurposing epigenetic inhibitors to target the <i>Clostridioides difficile</i> -specific DNA adenine methyltransferase and sporulation regulator CamA. <i>Epigenetics</i> , 2022, 17, 970-981.	1.3	8
2	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. <i>DNA Repair</i> , 2022, 113, 103306.	1.3	1
3	A Role for N6-Methyladenine in DNA Damage Repair. <i>Trends in Biochemical Sciences</i> , 2021, 46, 175-183.	3.7	14
4	Enzymatic characterization of three human RNA adenosine methyltransferases reveals diverse substrate affinities and reaction optima. <i>Journal of Biological Chemistry</i> , 2021, 296, 100270.	1.6	21
5	<i>Clostridioides difficile</i> specific DNA adenine methyltransferase CamA squeezes and flips adenine out of DNA helix. <i>Nature Communications</i> , 2021, 12, 3436.	5.8	16
6	Detection of DNA Modifications by Sequence-Specific Transcription Factors. <i>Journal of Molecular Biology</i> , 2020, 432, 1661-1673.	2.0	15
7	Biochemical and structural basis for YTH domain of human YTHDC1 binding to methylated adenine in DNA. <i>Nucleic Acids Research</i> , 2020, 48, 10329-10341.	6.5	26
8	Beta class amino methyltransferases from bacteria to humans: evolution and structural consequences. <i>Nucleic Acids Research</i> , 2020, 48, 10034-10044.	6.5	21
9	Distribution of RecBCD and AddAB recombination-associated genes among bacteria in 33 phyla. <i>Microbiology (United Kingdom)</i> , 2020, 166, 1047-1064.	0.7	5
10	Structural basis for preferential binding of human TCF4 to DNA containing 5-carboxylcytosine. <i>Nucleic Acids Research</i> , 2019, 47, 8375-8387.	6.5	19
11	Structural basis for effects of CpA modifications on C/EBP $\beta$ binding of DNA. <i>Nucleic Acids Research</i> , 2019, 47, 1774-1785.	6.5	23
12	Role for first zinc finger of WT1 in DNA sequence specificity: Denysâ€Drash syndrome-associated WT1 mutant in ZF1 enhances affinity for a subset of WT1 binding sites. <i>Nucleic Acids Research</i> , 2018, 46, 3864-3877.	6.5	20
13	Detecting and interpreting DNA methylation marks. <i>Current Opinion in Structural Biology</i> , 2018, 53, 88-99.	2.6	39
14	Structural basis of human PR/SET domain 9 (PRDM9) allele Câ€specific recognition of its cognate DNA sequence. <i>Journal of Biological Chemistry</i> , 2017, 292, 15994-16002.	1.6	15
15	Methyl-dependent and spatial-specific DNA recognition by the orthologous transcription factors human AP-1 and Epstein-Barr virus Zta. <i>Nucleic Acids Research</i> , 2017, 45, 2503-2515.	6.5	38
16	Complementation of a metK-deficient <i>E. coli</i> strain with heterologous AdoMet synthetase genes. <i>Microbiology (United Kingdom)</i> , 2017, 163, 1812-1821.	0.7	7
17	Distinctive Klf4 mutants determine preference for DNA methylation status. <i>Nucleic Acids Research</i> , 2016, 44, gkw774.	6.5	19
18	Evolution of a global regulator: Lrp in four orders of $\hat{3}$ -Proteobacteria. <i>BMC Evolutionary Biology</i> , 2016, 16, 111.	3.2	17

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19	Structures of <i>Escherichia coli</i> DNA adenine methyltransferase (Dam) in complex with a non-GATC sequence: potential implications for methylation-independent transcriptional repression. <i>Nucleic Acids Research</i> , 2015, 43, 4296-4308.	6.5	11
20	A surprising range of modified-methionyl S-adenosylmethionine analogues support bacterial growth. <i>Microbiology (United Kingdom)</i> , 2015, 161, 674-682.	0.7	8
21	Structural basis for Klf4 recognition of methylated DNA. <i>Nucleic Acids Research</i> , 2014, 42, 4859-4867.	6.5	81
22	Producing Proficient Methyl Donors from Alternative Substrates of S-Adenosylmethionine Synthetase. <i>Biochemistry</i> , 2014, 53, 1521-1526.	1.2	9
23	Naturally-occurring, dually-functional fusions between restriction endonucleases and regulatory proteins. <i>BMC Evolutionary Biology</i> , 2013, 13, 218.	3.2	4
24	Emergence, origin, and function of neutrophil-dendritic cell hybrids in experimentally induced inflammatory lesions in mice. <i>Blood</i> , 2013, 121, 1690-1700.	0.6	82
25	Response to Mackay et al.. <i>Trends in Biochemical Sciences</i> , 2013, 38, 423.	3.7	1
26	A common mode of recognition for methylated CpG. <i>Trends in Biochemical Sciences</i> , 2013, 38, 177-183.	3.7	89
27	The COMBREX Project: Design, Methodology, and Initial Results. <i>PLoS Biology</i> , 2013, 11, e1001638.	2.6	54
28	A bistable hysteretic switch in an activator-repressor regulated restriction-modification system. <i>Nucleic Acids Research</i> , 2013, 41, 6045-6057.	6.5	19
29	Introduction Epiphanies in Epigenetics. <i>Progress in Molecular Biology and Translational Science</i> , 2011, 101, 1-21.	0.9	18
30	Higher incidence of perineal community acquired MRSA infections among toddlers. <i>BMC Pediatrics</i> , 2011, 11, 96.	0.7	18
31	Preface. <i>Progress in Molecular Biology and Translational Science</i> , 2011, 101, xiii-xiv.	0.9	0
32	Unexpected Coregulator Range for the Global Regulator Lrp of <i>Escherichia coli</i> and <i>Proteus mirabilis</i> . <i>Journal of Bacteriology</i> , 2011, 193, 1054-1064.	1.0	39
33	Recognition of DNA by the Helix-Turn-Helix Global Regulatory Protein Lrp Is Modulated by the Amino Terminus. <i>Journal of Bacteriology</i> , 2011, 193, 3794-3803.	1.0	13
34	Translational independence between overlapping genes for a restriction endonuclease and its transcriptional regulator. <i>BMC Molecular Biology</i> , 2010, 11, 87.	3.0	7
35	Coordinated Chromatin Control: Structural and Functional Linkage of DNA and Histone Methylation. <i>Biochemistry</i> , 2010, 49, 2999-3008.	1.2	199
36	Tuning the relative affinities for activating and repressing operators of a temporally regulated restriction-modification system. <i>Nucleic Acids Research</i> , 2009, 37, 983-998.	6.5	37

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37	Structural and Biochemical Advances in Mammalian DNA Methylation. , 2009, , 85-100.		0
38	Limited functional conservation of a global regulator among related bacterial genera: Lrp in Escherichia, Proteus and Vibrio. BMC Microbiology, 2008, 8, 60.	1.3	32
39	Mammalian DNA Methyltransferases: A Structural Perspective. Structure, 2008, 16, 341-350.	1.6	349
40	Real-time kinetics of restrictionâ€“modification gene expression after entry into a new host cell. Nucleic Acids Research, 2008, 36, 2581-2593.	6.5	44
41	Regulatory circuit based on autogenous activation-repression: roles of C-boxes and spacer sequences in control of the PvuII restriction-modification system. Nucleic Acids Research, 2007, 35, 6935-6952.	6.5	31
42	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.	1.3	41
43	1 Protein Methyltransferases: Their Distribution Among the Five Structural Classes of AdoMet-Dependent Methyltransferases. The Enzymes, 2006, 24, 3-28.	0.7	17
44	Nature of the Promoter Activated by C.PvuII, an Unusual Regulatory Protein Conserved among Restriction-Modification Systems. Journal of Bacteriology, 2005, 187, 488-497.	1.0	43
45	Many paths to methyltransfer: a chronicle of convergence. Trends in Biochemical Sciences, 2003, 28, 329-335.	3.7	766
46	A nomenclature for restriction enzymes, DNA methyltransferases, homing endonucleases and their genes. Nucleic Acids Research, 2003, 31, 1805-1812.	6.5	634
47	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.	3.3	206
48	Mobility of a Restriction-Modification System Revealed by Its Genetic Contexts in Three Hosts. Journal of Bacteriology, 2002, 184, 2411-2419.	1.0	35
49	Cytosines Do It, Thymines Do It, Even Pseudouridines Do Itâ€“Base Flipping by an Enzyme that Acts on RNA. Structure, 2002, 10, 127-129.	1.6	11
50	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.	0.8	186
51	A Taq attack displaces bases. , 2001, 8, 101-103.		10
52	Activation from a Distance: Roles of Lrp and Integration Host Factor in Transcriptional Activation of gltBDF. Journal of Bacteriology, 2001, 183, 3910-3918.	1.0	26
53	Role and Mechanism of Action of C $\hat{\cdot}$ Pvu II, a Regulatory Protein Conserved among Restriction-Modification Systems. Journal of Bacteriology, 2000, 182, 477-487.	1.0	65
54	Mapping regulatory networks in microbial cells. Trends in Microbiology, 1999, 7, 320-328.	3.5	47

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55	STRUCTURE AND EVOLUTION OF ADOMET-DEPENDENT METHYLTRANSFERASES. , 1999, , 1-38.		57
56	S-Adenosylmethionine-Dependent Methyltransferases. , 1999, , .		70
57	The PvuII DNA (Cytosine-N4)-methyltransferase Comprises Two Trypsin-Defined Domains, Each of Which Binds a Molecule of S-Adenosyl-l-methionine. <i>Biochemistry</i> , 1997, 36, 8284-8292.	1.2	31
58	A nucleoprotein activation complex between the leucine-responsive regulatory protein and DNA upstream of the <i>gltBDF</i> operon in <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1997, 270, 152-168.	2.0	45
59	Expression, Purification, Mass Spectrometry, Crystallization and Multiwavelength Anomalous Diffraction of Selenomethionyl PvuII DNA Methyltransferase (cytosine-N4-specific). <i>FEBS Journal</i> , 1997, 247, 1009-1018.	0.2	9
60	Finding a basis for flipping bases. <i>Structure</i> , 1996, 4, 639-645.	1.6	114
61	Experimental Analysis of Global Gene Regulation in <i>Escherichia coli</i> . <i>Progress in Molecular Biology and Translational Science</i> , 1996, 55, 1-86.	1.9	6
62	Characterization of pPvu1, the autonomous plasmid from <i>proteus vulgaris</i> that carries the genes of the PvuII restriction-modification system. <i>Gene</i> , 1995, 157, 73-79.	1.0	20
63	Gene <i>pvuIIW</i> : A possible modulator of PvuII endonuclease subunit association. <i>Gene</i> , 1995, 157, 193-199.	1.0	20
64	Structure-guided Analysis Reveals Nine Sequence Motifs Conserved among DNA Amino-methyl-transferases, and Suggests a Catalytic Mechanism for these Enzymes. <i>Journal of Molecular Biology</i> , 1995, 253, 618-632.	2.0	457
65	Assignment of enzymic function to specific protein regions of cobalamin-dependent methionine synthase from <i>Escherichia coli</i> . <i>Biochemistry</i> , 1993, 32, 9290-9295.	1.2	121
66	The M <sup>h</sup> -AluI DNA-(cytosineC5)-methyltransferase has an unusually large, partially dispensable, variable region. <i>Nucleic Acids Research</i> , 1993, 21, 905-911.	6.5	23
67	Sequence, internal homology and high-level expression of the gene for a DNA-(cytosineN4)-methyltransferase, M-PvuII. <i>Nucleic Acids Research</i> , 1989, 17, 4161-4175.	6.5	48
68	Skewed genomic libraries revisited. <i>Trends in Biotechnology</i> , 1988, 6, 35.	4.9	0
69	Isolation of mutants in a DNA methyltransferase through <i>mcrB</i> -mediated restriction. <i>Gene</i> , 1988, 74, 269-273.	1.0	4
70	The Isolation and Characterization of the <i>Escherichia coli</i> DNA adenine methylase ( <i>dam</i> ) gene. <i>Nucleic Acids Research</i> , 1983, 11, 837-851.	6.5	187
71	Gene expression in <i>Escherichia coli</i> B/r during partial rifampicin-mediated restrictions of transcription initiation. <i>Molecular Genetics and Genomics</i> , 1978, 165, 79-86.	2.4	34
72	The effects of the <i>relA</i> gene on the synthesis of aminoacyl-tRNA synthetases and other transcription and translation proteins in <i>Escherichia coli</i> B. <i>Molecular Genetics and Genomics</i> , 1976, 149, 291-296.	2.4	86

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73	Restriction-Modification Systems. , 0, , 177-225.		17