

# Richard J Roberts

## List of Publications by Year in descending order

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119  
papers

11,529  
citations

81434

41  
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33145

104  
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127  
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127  
docs citations

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times ranked

9678  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Sequence of the Early 20th-Century Extreme Halophile <i>Halobacterium</i> sp. Strain NRC-34001. <i>Microbiology Resource Announcements</i> , 2022, 11, e0118121.	0.3	1
2	Metagenomic methylation patterns resolve bacterial genomes of unusual size and structural complexity. <i>ISME Journal</i> , 2022, 16, 1921-1931.	4.4	11
3	Genome-wide methylome analysis of two strains belonging to the hypervirulent <i>Neisseria meningitidis</i> serogroup W ST-11 clonal complex. <i>Scientific Reports</i> , 2021, 11, 6239.	1.6	0
4	Genome-wide identification of 5-methylcytosine sites in bacterial genomes by high-throughput sequencing of <i>MspI</i> restriction fragments. <i>PLoS ONE</i> , 2021, 16, e0247541.	1.1	8
5	Genome Sequence and Methylation Pattern of <i>Haloterrigena salifodinae</i> BOL5-1, an Extremely Halophilic Archaeon from a Bolivian Salt Mine. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	4
6	Structural and functional diversity among Type III restriction-modification systems that confer host DNA protection via methylation of the N4 atom of cytosine. <i>PLoS ONE</i> , 2021, 16, e0253267.	1.1	6
7	Production and Characterization of the exopolysaccharide from strain <i>Paenibacillus polymyxa</i> 2020. <i>PLoS ONE</i> , 2021, 16, e0253482.	1.1	17
8	Beyond Restriction Modification: Epigenomic Roles of DNA Methylation in Prokaryotes. <i>Annual Review of Microbiology</i> , 2021, 75, 129-149.	2.9	37
9	Complete Genome Sequence of an Extremely Halophilic Archaeon from Great Salt Lake, <i>Halobacterium</i> sp. GSL-19. <i>Microbiology Resource Announcements</i> , 2021, 10, e0052021.	0.3	2
10	Characterization of Bisl Homologs. <i>Frontiers in Microbiology</i> , 2021, 12, 689929.	1.5	0
11	Complete Genome and Methylome Analysis of the Box-Shaped Halophilic Archaeon <i>Haloarcula sinaiensis</i> ATCC 33800. <i>Microbiology Resource Announcements</i> , 2021, 10, e0061921.	0.3	2
12	Rapid identification of methylase specificity (RIMS-seq) jointly identifies methylated motifs and generates shotgun sequencing of bacterial genomes. <i>Nucleic Acids Research</i> , 2021, 49, e113-e113.	6.5	9
13	Genomic Stability and Genetic Defense Systems in <i>Dolosigranulum pigrum</i> , a Candidate Beneficial Bacterium from the Human Microbiome. <i>MSystems</i> , 2021, 6, e0042521.	1.7	11
14	Genome Sequence of <i>Halobacterium</i> sp. Strain BOL4-2, Isolated and Cultured from Salar de Uyuni, Bolivia. <i>Microbiology Resource Announcements</i> , 2021, 10, e0104521.	0.3	2
15	Structure of Hhal endonuclease with cognate DNA at an atomic resolution of 1.0 Å... <i>Nucleic Acids Research</i> , 2020, 48, 1466-1478.	6.5	5
16	Biochemical and molecular characterization of a restriction endonuclease <i>Tvu2HI</i> from <i>Thermoactinomyces vulgaris</i> 2H and study of its R-M system. <i>International Journal of Biological Macromolecules</i> , 2020, 164, 3105-3113.	3.6	1
17	Prevalence of phase variable epigenetic invertons among host-associated bacteria. <i>Nucleic Acids Research</i> , 2020, 48, 11468-11485.	6.5	20
18	Genome Sequence of <i>Salarchaeum</i> sp. Strain JOR-1, an Extremely Halophilic Archaeon from the Dead Sea. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	7

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19	Complete Genome Sequences and Methylome Analyses of <i>Cutibacterium acnes</i> subsp. <i>acnes</i> Strains DSM 16379 and DSM 1897 <sup>T</sup> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	5
20	Analysis of a phase-variable restriction modification system of the human gut symbiont <i>Bacteroides fragilis</i> . <i>Nucleic Acids Research</i> , 2020, 48, 11040-11053.	6.5	10
21	Complete genome and methylome analysis of <i>Neisseria meningitidis</i> associated with increased serogroup Y disease. <i>Scientific Reports</i> , 2020, 10, 3644.	1.6	2
22	Complete Genome Sequences and Methylome Analysis of Two Environmental <i>Spirochaetes</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
23	We need to keep a reproducible trace of facts, predictions, and hypotheses from gene to function in the era of big data. <i>PLoS Biology</i> , 2020, 18, e3000999.	2.6	8
24	Methylomes of Two Extremely Halophilic Archaea Species, <i>Haloarcula marismortui</i> and <i>Haloferax mediterranei</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	8
25	Genome Sequences and Methylation Patterns of <i>Natrinema versiforme</i> BOL5-4 and <i>Natrinema pallidum</i> BOL6-1, Two Extremely Halophilic Archaea from a Bolivian Salt Mine. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	7
26	Red-Brown Pigmentation of <i>Acidipropionibacterium jensenii</i> Is Tied to Haemolytic Activity and <i>cyl</i> -Like Gene Cluster. <i>Microorganisms</i> , 2019, 7, 512.	1.6	10
27	Complete Genome Sequence and Methylome Analysis of <i>Thermoactinomyces vulgaris</i> 2H. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
28	Complete Genome Sequence and Methylome Analysis of <i>Deinococcus wulumuqiensis</i> 479. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
29	Methylome Characterization of <i>Burkholderia pseudomallei</i> Strain 982 at Single-Base Resolution. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
30	Complete Genome Sequence and Methylome Analysis of <i>Sphaerotilus natans</i> subsp. <i>sulfidivorans</i> D-507. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
31	The non-specific adenine DNA methyltransferase M.EcoGII. <i>Nucleic Acids Research</i> , 2018, 46, 840-848.	6.5	41
32	Complete Genome Sequences of Two <i>Rhodobacter</i> Strains. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	1
33	Complete Genome Sequence of the Freshwater Bacterium <i>Beggiatoa leptomitiformis</i> Strain D-401. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
34	Complete Genome Sequence and Methylome Analysis of <i>Bacillus caldolyticus</i> NEB414. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
35	<i>Acidipropionibacterium virtanenii</i> sp. nov., isolated from malted barley. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3175-3183.	0.8	9
36	DNA target recognition domains in the Type I restriction and modification systems of <i>Staphylococcus aureus</i> . <i>Nucleic Acids Research</i> , 2017, 45, 3395-3406.	6.5	27

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37	Complete Genome and Methylome Analysis of Psychrotrophic Bacterial Isolates from Lake Untersee in Antarctica. <i>Genome Announcements</i> , 2017, 5, .	0.8	14
38	Complete Genome Sequence and Methylome Analysis of <i>Acinetobacter calcoaceticus</i> 65. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
39	Complete Genome and Methylome Sequences of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovars Typhimurium, Saintpaul, and Stanleyville from the SARA/SARB Collection. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
40	Whole-Genome Sequence and Methylome Analysis of the Freshwater Colorless Sulfur Bacterium <i>Thioflexothrix psekupsi</i> D3. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
41	The third restriction-modification system from <i>Thermus aquaticus</i> YT-1: solving the riddle of two TaqI specificities. <i>Nucleic Acids Research</i> , 2017, 45, 9005-9018.	6.5	3
42	Restriction-modification mediated barriers to exogenous DNA uptake and incorporation employed by <i>Prevotella intermedia</i> . <i>PLoS ONE</i> , 2017, 12, e0185234.	1.1	18
43	De novo assembly of genomes from long sequence reads reveals uncharted territories of <i>Propionibacterium freudenreichii</i> . <i>BMC Genomics</i> , 2017, 18, 790.	1.2	16
44	Complete Genome Sequence of <i>Brevibacterium linens</i> SMQ-1335. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
45	Novel Methyltransferase Recognition Motif Identified in <i>Chania multitudinisentens</i> RB-25T gen. nov., sp. nov.. <i>Frontiers in Microbiology</i> , 2016, 7, 1362.	1.5	9
46	Complete Genome Sequence of a Strain of <i>Azospirillum thiophilum</i> Isolated from a Sulfide Spring. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
47	Complete Genome and Methylome Sequences of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Panama (ATCC 7378) and <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Sloterdijk (ATCC 15791). <i>Genome Announcements</i> , 2016, 4, .	0.8	15
48	COMBEX-DB: an experiment centered database of protein function: knowledge, predictions and knowledge gaps. <i>Nucleic Acids Research</i> , 2016, 44, D330-D335.	6.5	47
49	Novel m4C modification in type I restriction-modification systems. <i>Nucleic Acids Research</i> , 2016, 44, gkw743.	6.5	23
50	Expression and purification of the modification-dependent restriction enzyme Bisl and its homologous enzymes. <i>Scientific Reports</i> , 2016, 6, 28579.	1.6	8
51	Complete Genome Sequence and Methylome Analysis of <i>Aeromonas hydrophila</i> Strain YL17, Isolated from a Compost Pile. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
52	Complete Genome and Methylome Sequences of Two <i>Salmonella enterica</i> spp. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
53	Structure of Type III Restriction-Modification Enzyme Mmel in Complex with DNA Has Implications for Engineering New Specificities. <i>PLoS Biology</i> , 2016, 14, e1002442.	2.6	23
54	The Epigenomic Landscape of Prokaryotes. <i>PLoS Genetics</i> , 2016, 12, e1005854.	1.5	348

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55	Comparative Methylome Analysis of the Occasional Ruminant Respiratory Pathogen <i>Bibersteinia trehalosi</i> . PLoS ONE, 2016, 11, e0161499.	1.1	6
56	Complete Genome Sequence of <i>Curtobacterium</i> sp. Strain MR_MD2014, Isolated from Topsoil in Woods Hole, Massachusetts. Genome Announcements, 2015, 3, .	0.8	3
57	Complete Genome Sequence of <i>Streptomyces</i> sp. Strain CCM_MD2014, Isolated from Topsoil in Woods Hole, Massachusetts. Genome Announcements, 2015, 3, .	0.8	1
58	Complete Genome Sequence of the Freshwater Colorless Sulfur Bacterium <i>Beggiatoa leptomitiformis</i> Neotype Strain D-402 <sup>T</sup> . Genome Announcements, 2015, 3, .	0.8	11
59	Genome-Wide Methylation Patterns in <i>Salmonella enterica</i> Subsp. <i>enterica</i> Serovars. PLoS ONE, 2015, 10, e0123639.	1.1	51
60	Complete Genome Sequence of Enteroinvasive <i>Escherichia coli</i> O96:H19 Associated with a Severe Foodborne Outbreak. Genome Announcements, 2015, 3, .	0.8	29
61	Complete Genome Sequence and Methylome Analysis of <i>Bacillus</i> Strain X1. Genome Announcements, 2015, 3, .	0.8	5
62	REBASE—a database for DNA restriction and modification: enzymes, genes and genomes. Nucleic Acids Research, 2015, 43, D298-D299.	6.5	748
63	Ten Simple Rules to Win a Nobel Prize. PLoS Computational Biology, 2015, 11, e1004084.	1.5	9
64	Specificity of the ModA11, ModA12 and ModD1 epigenetic regulator N6-adenine DNA methyltransferases of <i>Neisseria meningitidis</i> . Nucleic Acids Research, 2015, 43, 4150-4162.	6.5	58
65	Complete Genome Sequence Analysis of <i>Bacillus subtilis</i> T30. Genome Announcements, 2015, 3, .	0.8	5
66	The complete methylome of <i>Helicobacter pylori</i> UM032. BMC Genomics, 2015, 16, 424.	1.2	57
67	Complete Genome Sequence of ER2796, a DNA Methyltransferase-Deficient Strain of <i>Escherichia coli</i> K-12. PLoS ONE, 2015, 10, e0127446.	1.1	31
68	Identification of Restriction-Modification Systems of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> CNCM I-2494 by SMRT Sequencing and Associated Methylome Analysis. PLoS ONE, 2014, 9, e94875.	1.1	25
69	The complex methylome of the human gastric pathogen <i>Helicobacter pylori</i> . Nucleic Acids Research, 2014, 42, 2415-2432.	6.5	132
70	The advantages of SMRT sequencing. Genome Biology, 2013, 14, .	3.8	487
71	The COMBREX Project: Design, Methodology, and Initial Results. PLoS Biology, 2013, 11, e1001638.	2.6	54
72	The advantages of SMRT sequencing. Genome Biology, 2013, 14, 405.	3.8	324

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73	The methylomes of six bacteria. <i>Nucleic Acids Research</i> , 2012, 40, 11450-11462.	6.5	269
74	Characterization of DNA methyltransferase specificities using single-molecule, real-time DNA sequencing. <i>Nucleic Acids Research</i> , 2012, 40, e29-e29.	6.5	306
75	Genome-wide mapping of methylated adenine residues in pathogenic <i>Escherichia coli</i> using single-molecule real-time sequencing. <i>Nature Biotechnology</i> , 2012, 30, 1232-1239.	9.4	365
76	COMBREX: a project to accelerate the functional annotation of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2011, 39, D11-D14.	6.5	47
77	The MspJI family of modification-dependent restriction endonucleases for epigenetic studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11040-11045.	3.3	115
78	Comparative characterization of the PvuRtsII family of restriction enzymes and their application in mapping genomic 5-hydroxymethylcytosine. <i>Nucleic Acids Research</i> , 2011, 39, 9294-9305.	6.5	67
79	COMBREX: COMputational BRidge to EXperiments. <i>Biochemical Society Transactions</i> , 2011, 39, 581-583.	1.6	11
80	Sequence-specific cleavage of RNA by Type II restriction enzymes. <i>Nucleic Acids Research</i> , 2010, 38, 8257-8268.	6.5	28
81	BspRI restriction endonuclease: cloning, expression in <i>Escherichia coli</i> and sequential cleavage mechanism. <i>Nucleic Acids Research</i> , 2010, 38, 7155-7166.	6.5	11
82	REBASE—a database for DNA restriction and modification: enzymes, genes and genomes. <i>Nucleic Acids Research</i> , 2010, 38, D234-D236.	6.5	736
83	A unique family of Mrr-like modification-dependent restriction endonucleases. <i>Nucleic Acids Research</i> , 2010, 38, 5527-5534.	6.5	77
84	Using shotgun sequence data to find active restriction enzyme genes. <i>Nucleic Acids Research</i> , 2009, 37, e1-e1.	6.5	15
85	The BsaHI restriction-modification system: Cloning, sequencing and analysis of conserved motifs. <i>BMC Molecular Biology</i> , 2008, 9, 48.	3.0	8
86	Identification of GATC- and CCGG-recognizing Type II REases and their putative specificity-determining positions using Scan2S—a novel motif scan algorithm with optional secondary structure constraints. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 631-640.	1.5	3
87	RimO, a MiaB-like enzyme, methylthiolates the universally conserved Asp88 residue of ribosomal protein S12 in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1826-1831.	3.3	97
88	REBASE—enzymes and genes for DNA restriction and modification. <i>Nucleic Acids Research</i> , 2007, 35, D269-D270.	6.5	229
89	Selection of restriction endonucleases using artificial cells. <i>Nucleic Acids Research</i> , 2007, 35, e83.	6.5	24
90	A genetic dissection of the LlaII restriction cassette reveals insights on a novel bacteriophage resistance system. <i>BMC Microbiology</i> , 2006, 6, 40.	1.3	20

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91	DNA nicking by HinP1I endonuclease: bending, base flipping and minor groove expansion. <i>Nucleic Acids Research</i> , 2006, 34, 939-948.	6.5	44
92	Two crystal forms of the restriction enzyme MspI-DNA complex show the same novel structure. <i>Protein Science</i> , 2005, 14, 2590-2600.	3.1	18
93	How restriction enzymes became the workhorses of molecular biology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5905-5908.	3.3	153
94	Structure of HinP1I endonuclease reveals a striking similarity to the monomeric restriction enzyme MspI. <i>Nucleic Acids Research</i> , 2005, 33, 1892-1901.	6.5	31
95	Identifying Protein Function—A Call for Community Action. <i>PLoS Biology</i> , 2004, 2, e42.	2.6	116
96	Identification of genes with fast-evolving regions in microbial genomes. <i>Nucleic Acids Research</i> , 2004, 32, 6347-6357.	6.5	30
97	REBASE—restriction enzymes and DNA methyltransferases. <i>Nucleic Acids Research</i> , 2004, 33, D230-D232.	6.5	150
98	An Asymmetric Complex of Restriction Endonuclease MspI on Its Palindromic DNA Recognition Site. <i>Structure</i> , 2004, 12, 1741-1747.	1.6	41
99	Structure of the Q237W mutant of HhaI DNA methyltransferase: an insight into protein-protein interactions. <i>Biological Chemistry</i> , 2004, 385, 373-379.	1.2	10
100	A nomenclature for restriction enzymes, DNA methyltransferases, homing endonucleases and their genes. <i>Nucleic Acids Research</i> , 2003, 31, 1805-1812.	6.5	634
101	REBASE: restriction enzymes and methyltransferases. <i>Nucleic Acids Research</i> , 2003, 31, 418-420.	6.5	205
102	NEBcutter: a program to cleave DNA with restriction enzymes. <i>Nucleic Acids Research</i> , 2003, 31, 3688-3691.	6.5	510
103	REBASE—restriction enzymes and methylases. <i>Nucleic Acids Research</i> , 2001, 29, 268-269.	6.5	121
104	The early days of bioinformatics publishing. <i>Bioinformatics</i> , 2000, 16, 2-4.	1.8	7
105	Structure of a binary complex of Hha I methyltransferase with S-adenosyl-L-methionine formed in the presence of a short non-specific DNA oligonucleotide. Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1999, 287, 201-209.	2.0	68
106	Structures of HhaI methyltransferase complexed with substrates containing mismatches at the target base. <i>Nature Structural Biology</i> , 1998, 5, 872-877.	9.7	102
107	BASE FLIPPING. <i>Annual Review of Biochemistry</i> , 1998, 67, 181-198.	5.0	327
108	Enzymatic C5-Cytosine Methylation of DNA: Mechanistic Implications of New Crystal Structures for HhaI Methyltransferase-DNA-AdoHcy Complexes. <i>Journal of Molecular Biology</i> , 1996, 261, 634-645.	2.0	162

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109	A Structural Basis for the Preferential Binding of Hemimethylated DNA by HhaI DNA Methyltransferase. <i>Journal of Molecular Biology</i> , 1996, 263, 597-606.	2.0	90
110	MHhaI binds tightly to substrates containing mismatches at the target base. <i>Nucleic Acids Research</i> , 1995, 23, 1388-1395.	6.5	162
111	On base flipping. <i>Cell</i> , 1995, 82, 9-12.	13.5	170
112	HhaI methyltransferase flips its target base out of the DNA helix. <i>Cell</i> , 1994, 76, 357-369.	13.5	988
113	The DNA (cytosine-5) methyltransferases. <i>Nucleic Acids Research</i> , 1994, 22, 1-10.	6.5	444
114	Crystal structure of the HhaI DNA methyltransferase complexed with S-adenosyl-L-methionine. <i>Cell</i> , 1993, 74, 299-307.	13.5	391
115	Predictive motifs derived from cytosine methyltransferases. <i>Nucleic Acids Research</i> , 1989, 17, 2421-2435.	6.5	513
116	Recognition sequence of restriction endonuclease KpnI from <i>Klebsiella pneumoniae</i> . <i>Nucleic Acids Research</i> , 1978, 5, 4055-4064.	6.5	42
117	A specific endonuclease from <i>Bacillus caldolyticus</i> . <i>Nucleic Acids Research</i> , 1978, 5, 3457-3468.	6.5	72
118	A specific endonuclease from <i>Haemophilus haemolyticus</i> . <i>Journal of Molecular Biology</i> , 1976, 103, 199-208.	2.0	161
119	Restriction Endonuclease. <i>CRC Critical Reviews in Biochemistry</i> , 1976, 4, 123-164.	2.0	443