

# Richard J Roberts

## List of Publications by Year in descending order

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119  
papers

11,529  
citations

71102

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h-index

29157

104  
g-index

127  
all docs

127  
docs citations

127  
times ranked

8671  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | HhaI methyltransferase flips its target base out of the DNA helix. <i>Cell</i> , 1994, 76, 357-369.   | 28.9 | 988       |
| 2  | REBASE—a database for DNA restriction and modification: enzymes, genes and genomes. <i>Nucleic Acids Research</i> , 2015, 43, D298-D299.  | 14.5 | 748       |
| 3  | REBASE—a database for DNA restriction and modification: enzymes, genes and genomes. <i>Nucleic Acids Research</i> , 2010, 38, D234-D236.  | 14.5 | 736       |
| 4  | A nomenclature for restriction enzymes, DNA methyltransferases, homing endonucleases and their genes. <i>Nucleic Acids Research</i> , 2003, 31, 1805-1812.                              | 14.5 | 634       |
| 5  | Predictive motifs derived from cytosine methyltransferases. <i>Nucleic Acids Research</i> , 1989, 17, 2421-2435.  | 14.5 | 513       |
| 6  | NEBcutter: a program to cleave DNA with restriction enzymes. <i>Nucleic Acids Research</i> , 2003, 31, 3688-3691.   | 14.5 | 510       |
| 7  | The advantages of SMRT sequencing. <i>Genome Biology</i> , 2013, 14, .  | 8.8  | 487       |
| 8  | The DNA (cytosine-5) methyltransferases. <i>Nucleic Acids Research</i> , 1994, 22, 1-10.  | 14.5 | 444       |
| 9  | Restriction Endonuclease. <i>CRC Critical Reviews in Biochemistry</i> , 1976, 4, 123-164.   | 2.0  | 443       |
| 10 | Crystal structure of the HhaI DNA methyltransferase complexed with S-adenosyl-l-methionine. <i>Cell</i> , 1993, 74, 299-307.  | 28.9 | 391       |
| 11 | 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. | 17.5 | 365       |
| 12 | The Epigenomic Landscape of Prokaryotes. <i>PLoS Genetics</i> , 2016, 12, e1005854.   | 3.5  | 348       |
| 13 | BASE FLIPPING. <i>Annual Review of Biochemistry</i> , 1998, 67, 181-198.  | 11.1 | 327       |
| 14 | The advantages of SMRT sequencing. <i>Genome Biology</i> , 2013, 14, 405.   | 8.8  | 324       |
| 15 | Characterization of DNA methyltransferase specificities using single-molecule, real-time DNA sequencing. <i>Nucleic Acids Research</i> , 2012, 40, e29-e29.                             | 14.5 | 306       |
| 16 | The methylomes of six bacteria. <i>Nucleic Acids Research</i> , 2012, 40, 11450-11462.  | 14.5 | 269       |
| 17 | REBASE—enzymes and genes for DNA restriction and modification. <i>Nucleic Acids Research</i> , 2007, 35, D269-D270.   | 14.5 | 229       |
| 18 | REBASE: restriction enzymes and methyltransferases. <i>Nucleic Acids Research</i> , 2003, 31, 418-420.  | 14.5 | 205       |

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|----|--|------|-----------|
| 19 | On base flipping. <i>Cell</i> , 1995, 82, 9-12.  | 28.9 | 170       |
| 20 | MHhal binds tightly to substrates containing mismatches at the target base. <i>Nucleic Acids Research</i> , 1995, 23, 1388-1395.   | 14.5 | 162       |
| 21 | 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.  | 4.2  | 162       |
| 22 | A specific endonuclease from <i>Haemophilus haemolyticus</i> . <i>Journal of Molecular Biology</i> , 1976, 103, 199-208.   | 4.2  | 161       |
| 23 | 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.   | 7.1  | 153       |
| 24 | REBASE—restriction enzymes and DNA methyltransferases. <i>Nucleic Acids Research</i> , 2004, 33, D230-D232.  | 14.5 | 150       |
| 25 | The complex methylome of the human gastric pathogen <i>Helicobacter pylori</i> . <i>Nucleic Acids Research</i> , 2014, 42, 2415-2432.  | 14.5 | 132       |
| 26 | REBASE—restriction enzymes and methylases. <i>Nucleic Acids Research</i> , 2001, 29, 268-269.  | 14.5 | 121       |
| 27 | Identifying Protein Function—A Call for Community Action. <i>PLoS Biology</i> , 2004, 2, e42.  | 5.6  | 116       |
| 28 | 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.  | 7.1  | 115       |
| 29 | 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       |
| 30 | 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. | 7.1  | 97        |
| 31 | A Structural Basis for the Preferential Binding of Hemimethylated DNA by HhaI DNA Methyltransferase. <i>Journal of Molecular Biology</i> , 1996, 263, 597-606.   | 4.2  | 90        |
| 32 | A unique family of Mrr-like modification-dependent restriction endonucleases. <i>Nucleic Acids Research</i> , 2010, 38, 5527-5534.   | 14.5 | 77        |
| 33 | A specific endonuclease from <i>Bacillus caldolyticus</i> . <i>Nucleic Acids Research</i> , 1978, 5, 3457-3468.  | 14.5 | 72        |
| 34 | 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.                 | 4.2  | 68        |
| 35 | Comparative characterization of the PvuRts11 family of restriction enzymes and their application in mapping genomic 5-hydroxymethylcytosine. <i>Nucleic Acids Research</i> , 2011, 39, 9294-9305.  | 14.5 | 67        |
| 36 | Specificity of the ModA11, ModA12 and ModD1 epigenetic regulator N6-adenine DNA methyltransferases of <i>Neisseria meningitidis</i> . <i>Nucleic Acids Research</i> , 2015, 43, 4150-4162.   | 14.5 | 58        |

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|----|---|------|-----------|
| 37 | The complete methylome of <i>Helicobacter pylori</i> UM032. <i>BMC Genomics</i> , 2015, 16, 424.  | 2.8  | 57        |
| 38 | The COMBREX Project: Design, Methodology, and Initial Results. <i>PLoS Biology</i> , 2013, 11, e1001638.  | 5.6  | 54        |
| 39 | Genome-Wide Methylation Patterns in <i>Salmonella enterica</i> Subsp. <i>enterica</i> Serovars. <i>PLoS ONE</i> , 2015, 10, e0123639.   | 2.5  | 51        |
| 40 | COMBREX: a project to accelerate the functional annotation of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2011, 39, D11-D14.   | 14.5 | 47        |
| 41 | COMBREX-DB: an experiment centered database of protein function: knowledge, predictions and knowledge gaps. <i>Nucleic Acids Research</i> , 2016, 44, D330-D335.  | 14.5 | 47        |
| 42 | DNA nicking by <i>HinP1I</i> endonuclease: bending, base flipping and minor groove expansion. <i>Nucleic Acids Research</i> , 2006, 34, 939-948.  | 14.5 | 44        |
| 43 | Recognition sequence of restriction endonuclease <i>KpnI</i> from <i>Klebsiella pneumoniae</i> . <i>Nucleic Acids Research</i> , 1978, 5, 4055-4064.  | 14.5 | 42        |
| 44 | An Asymmetric Complex of Restriction Endonuclease <i>MspI</i> on Its Palindromic DNA Recognition Site. <i>Structure</i> , 2004, 12, 1741-1747.  | 3.3  | 41        |
| 45 | The non-specific adenine DNA methyltransferase <i>M.EcoGII</i> . <i>Nucleic Acids Research</i> , 2018, 46, 840-848.   | 14.5 | 41        |
| 46 | Beyond Restriction Modification: Epigenomic Roles of DNA Methylation in Prokaryotes. <i>Annual Review of Microbiology</i> , 2021, 75, 129-149.  | 7.3  | 37        |
| 47 | Structure of <i>HinP1I</i> endonuclease reveals a striking similarity to the monomeric restriction enzyme <i>MspI</i> . <i>Nucleic Acids Research</i> , 2005, 33, 1892-1901.                                    | 14.5 | 31        |
| 48 | Complete Genome Sequence of ER2796, a DNA Methyltransferase-Deficient Strain of <i>Escherichia coli</i> K-12. <i>PLoS ONE</i> , 2015, 10, e0127446.   | 2.5  | 31        |
| 49 | Identification of genes with fast-evolving regions in microbial genomes. <i>Nucleic Acids Research</i> , 2004, 32, 6347-6357.   | 14.5 | 30        |
| 50 | Complete Genome Sequence of Enteroinvasive <i>Escherichia coli</i> O96:H19 Associated with a Severe Foodborne Outbreak. <i>Genome Announcements</i> , 2015, 3, .  | 0.8  | 29        |
| 51 | Sequence-specific cleavage of RNA by Type II restriction enzymes. <i>Nucleic Acids Research</i> , 2010, 38, 8257-8268.  | 14.5 | 28        |
| 52 | 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.  | 14.5 | 27        |
| 53 | Identification of Restriction-Modification Systems of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> CNCM I-2494 by SMRT Sequencing and Associated Methylome Analysis. <i>PLoS ONE</i> , 2014, 9, e94875. | 2.5  | 25        |
| 54 | Selection of restriction endonucleases using artificial cells. <i>Nucleic Acids Research</i> , 2007, 35, e83.   | 14.5 | 24        |

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|----|---|------|-----------|
| 55 | Novel m4C modification in type I restriction-modification systems. <i>Nucleic Acids Research</i> , 2016, 44, gkw743.  | 14.5 | 23        |
| 56 | Structure of Type III Restriction-Modification Enzyme MmI in Complex with DNA Has Implications for Engineering New Specificities. <i>PLoS Biology</i> , 2016, 14, e1002442.   | 5.6  | 23        |
| 57 | A genetic dissection of the LlaI restriction cassette reveals insights on a novel bacteriophage resistance system. <i>BMC Microbiology</i> , 2006, 6, 40.   | 3.3  | 20        |
| 58 | Prevalence of phase variable epigenetic invertons among host-associated bacteria. <i>Nucleic Acids Research</i> , 2020, 48, 11468-11485.  | 14.5 | 20        |
| 59 | Two crystal forms of the restriction enzyme MspI-DNA complex show the same novel structure. <i>Protein Science</i> , 2005, 14, 2590-2600.   | 7.6  | 18        |
| 60 | Restriction-modification mediated barriers to exogenous DNA uptake and incorporation employed by <i>Prevotella intermedia</i> . <i>PLoS ONE</i> , 2017, 12, e0185234.   | 2.5  | 18        |
| 61 | Production and Characterization of the exopolysaccharide from strain <i>Paenibacillus polymyxa</i> 2020. <i>PLoS ONE</i> , 2021, 16, e0253482.  | 2.5  | 17        |
| 62 | De novo assembly of genomes from long sequence reads reveals uncharted territories of <i>Propionibacterium freudenreichii</i> . <i>BMC Genomics</i> , 2017, 18, 790.  | 2.8  | 16        |
| 63 | Using shotgun sequence data to find active restriction enzyme genes. <i>Nucleic Acids Research</i> , 2009, 37, e1-e1.   | 14.5 | 15        |
| 64 | 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        |
| 65 | Complete Genome and Methylome Analysis of Psychrotrophic Bacterial Isolates from Lake Untersee in Antarctica. <i>Genome Announcements</i> , 2017, 5, .  | 0.8  | 14        |
| 66 | BspRI restriction endonuclease: cloning, expression in <i>Escherichia coli</i> and sequential cleavage mechanism. <i>Nucleic Acids Research</i> , 2010, 38, 7155-7166.  | 14.5 | 11        |
| 67 | COMBEX: COMputational BRidge to EXperiments. <i>Biochemical Society Transactions</i> , 2011, 39, 581-583.   | 3.4  | 11        |
| 68 | Complete Genome Sequence of the Freshwater Colorless Sulfur Bacterium <i>Beggiatoa leptomitiformis</i> Neotype Strain D-402 <sup>T</sup> . <i>Genome Announcements</i> , 2015, 3, .   | 0.8  | 11        |
| 69 | 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.  | 3.8  | 11        |
| 70 | Metagenomic methylation patterns resolve bacterial genomes of unusual size and structural complexity. <i>ISME Journal</i> , 2022, 16, 1921-1931.  | 9.8  | 11        |
| 71 | Structure of the Q237W mutant of HhaI DNA methyltransferase: an insight into protein-protein interactions. <i>Biological Chemistry</i> , 2004, 385, 373-379.  | 2.5  | 10        |
| 72 | 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.  | 3.6  | 10        |

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|----|---|------|-----------|
| 73 | 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.   | 14.5 | 10        |
| 74 | Ten Simple Rules to Win a Nobel Prize. <i>PLoS Computational Biology</i> , 2015, 11, e1004084.  | 3.2  | 9         |
| 75 | Novel Methyltransferase Recognition Motif Identified in <i>Chania multitudinisentens</i> RB-25T gen. nov., sp. nov.. <i>Frontiers in Microbiology</i> , 2016, 7, 1362.  | 3.5  | 9         |
| 76 | 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.                                 | 14.5 | 9         |
| 77 | <i>Acidipropionibacterium virtanenii</i> sp. nov., isolated from malted barley. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3175-3183.   | 1.7  | 9         |
| 78 | The <i>Bsa</i> HI restriction-modification system: Cloning, sequencing and analysis of conserved motifs. <i>BMC Molecular Biology</i> , 2008, 9, 48.  | 3.0  | 8         |
| 79 | 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         |
| 80 | Expression and purification of the modification-dependent restriction enzyme <i>Bis</i> I and its homologous enzymes. <i>Scientific Reports</i> , 2016, 6, 28579.   | 3.3  | 8         |
| 81 | 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         |
| 82 | Methylomes of Two Extremely Halophilic Archaea Species, <i>Haloarcula marismortui</i> and <i>Haloferax mediterranei</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .   | 0.6  | 8         |
| 83 | Genome-wide identification of 5-methylcytosine sites in bacterial genomes by high-throughput sequencing of <i>Msp</i> JI restriction fragments. <i>PLoS ONE</i> , 2021, 16, e0247541.   | 2.5  | 8         |
| 84 | 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.  | 5.6  | 8         |
| 85 | The early days of bioinformatics publishing. <i>Bioinformatics</i> , 2000, 16, 2-4.   | 4.1  | 7         |
| 86 | 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, . | 0.6  | 7         |
| 87 | 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, .   | 0.6  | 7         |
| 88 | 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.                                     | 2.5  | 6         |
| 89 | Comparative Methylome Analysis of the Occasional Ruminant Respiratory Pathogen <i>Bibersteinia trehalosi</i> . <i>PLoS ONE</i> , 2016, 11, e0161499.  | 2.5  | 6         |
| 90 | Complete Genome Sequence and Methylome Analysis of <i>Bacillus</i> Strain X1. <i>Genome Announcements</i> , 2015, 3, .  | 0.8  | 5         |

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|-----|--|------|-----------|
| 91  | Complete Genome Sequence Analysis of <i>Bacillus subtilis</i> T30. <i>Genome Announcements</i> , 2015, 3, .  | 0.8  | 5         |
| 92  | Complete Genome and Methylome Sequences of Two <i>Salmonella enterica</i> spp. <i>Genome Announcements</i> , 2016, 4, .  | 0.8  | 5         |
| 93  | Structure of HhaI endonuclease with cognate DNA at an atomic resolution of 1.0 Å... <i>Nucleic Acids Research</i> , 2020, 48, 1466-1478.   | 14.5 | 5         |
| 94  | Complete Genome Sequences and Methylome Analyses of <i>Cutibacterium acnes</i> subsp. <i>acnes</i> Strains DSM 16379 and DSM 1897. <i>Microbiology Resource Announcements</i> , 2020, 9, .   | 0.6  | 5         |
| 95  | Complete Genome Sequence and Methylome Analysis of <i>Acinetobacter calcoaceticus</i> 65. <i>Genome Announcements</i> , 2017, 5, .   | 0.8  | 4         |
| 96  | Whole-Genome Sequence and Methylome Analysis of the Freshwater Colorless Sulfur Bacterium <i>Thioflexothrix pseukupsi</i> D3. <i>Genome Announcements</i> , 2017, 5, .   | 0.8  | 4         |
| 97  | 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, .   | 0.6  | 4         |
| 98  | 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. | 2.6  | 3         |
| 99  | Complete Genome Sequence of <i>Curtobacterium</i> sp. Strain MR_MD2014, Isolated from Topsoil in Woods Hole, Massachusetts. <i>Genome Announcements</i> , 2015, 3, .   | 0.8  | 3         |
| 100 | Complete Genome Sequence of <i>Brevibacterium linens</i> SMQ-1335. <i>Genome Announcements</i> , 2016, 4, .  | 0.8  | 3         |
| 101 | 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.   | 14.5 | 3         |
| 102 | Complete Genome Sequence and Methylome Analysis of <i>Deinococcus wulumuqiensis</i> 479. <i>Microbiology Resource Announcements</i> , 2019, 8, .   | 0.6  | 3         |
| 103 | Methylome Characterization of <i>Burkholderia pseudomallei</i> Strain 982 at Single-Base Resolution. <i>Microbiology Resource Announcements</i> , 2019, 8, .   | 0.6  | 3         |
| 104 | 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         |
| 105 | Complete Genome Sequence of the Freshwater Bacterium <i>Beggiatoa leptomitiformis</i> Strain D-401. <i>Genome Announcements</i> , 2018, 6, .   | 0.8  | 2         |
| 106 | Complete Genome Sequence and Methylome Analysis of <i>Thermoactinomyces vulgaris</i> 2H. <i>Microbiology Resource Announcements</i> , 2019, 8, .   | 0.6  | 2         |
| 107 | Complete genome and methylome analysis of <i>Neisseria meningitidis</i> associated with increased serogroup Y disease. <i>Scientific Reports</i> , 2020, 10, 3644.   | 3.3  | 2         |
| 108 | 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.   | 0.6  | 2         |

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|-----|---|-----|-----------|
| 109 | 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.  | 0.6 | 2         |
| 110 | Complete Genome Sequences and Methylome Analysis of Two Environmental <i>Spirochaetes</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .   | 0.6 | 2         |
| 111 | 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.   | 0.6 | 2         |
| 112 | Complete Genome Sequence of <i>Streptomyces</i> sp. Strain CCM_MD2014, Isolated from Topsoil in Woods Hole, Massachusetts. <i>Genome Announcements</i> , 2015, 3, .   | 0.8 | 1         |
| 113 | Complete Genome Sequences of Two <i>Rhodobacter</i> Strains. <i>Microbiology Resource Announcements</i> , 2018, 7, .  | 0.6 | 1         |
| 114 | Complete Genome Sequence and Methylome Analysis of <i>Bacillus caldolyticus</i> NEB414. <i>Genome Announcements</i> , 2018, 6, .  | 0.8 | 1         |
| 115 | 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. | 7.5 | 1         |
| 116 | Complete Genome Sequence and Methylome Analysis of <i>Sphaerotilus natans</i> subsp. <i>sulfidivorans</i> D-507. <i>Microbiology Resource Announcements</i> , 2019, 8, .  | 0.6 | 1         |
| 117 | Genome Sequence of the Early 20th-Century Extreme Halophile <i>Halobacterium</i> sp. Strain NRC-34001. <i>Microbiology Resource Announcements</i> , 2022, 11, e0118121.   | 0.6 | 1         |
| 118 | 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.  | 3.3 | 0         |
| 119 | Characterization of <i>BisI</i> Homologs. <i>Frontiers in Microbiology</i> , 2021, 12, 689929.  | 3.5 | 0         |