Richard G Brennan

List of Publications by Year
in descending order

64	7,395	136950	114465
papers	citations	32 h-index	63 g-index

65	65	65	6932
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The nucleotide messenger (p)ppGpp is an anti-inducer of the purine synthesis transcription regulator PurR inBacillus. Nucleic Acids Research, 2022, 50, 847-866.	14.5	19
2	Molecular dissection of the glutamine synthetase-GlnR nitrogen regulatory circuitry in Gram-positive bacteria. Nature Communications, 2022, 13, .	12.8	12
3	Structural Basis for Virulence Activation of Francisella tularensis. Molecular Cell, 2021, 81, 139-152.e10.	9.7	21
4	Structures of Neisseria gonorrhoeae MtrR-operator complexes reveal molecular mechanisms of DNA recognition and antibiotic resistance-conferring clinical mutations. Nucleic Acids Research, 2021, 49, 4155-4170.	14.5	13
5	Evolution of a Ïƒâ€“(c-di-GMP)â€“anti-Ïƒ switch. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	11
6	MarR family proteins are important regulators of clinically relevant antibiotic resistance. Protein Science, 2020, 29, 647-653.	7.6	27
7	The Salmonella Secreted Effector SarA/SteE Mimics Cytokine Receptor Signaling to Activate STAT3. Cell Host and Microbe, 2020, 27, 129-139.e4.	11.0	42
8	c-di-GMP Arms an Anti-Ïƒ to Control Progression of Multicellular Differentiation in Streptomyces. Molecular Cell, 2020, 77, 586-599.e6.	9.7	58
9	Optimization of a Noncanonical Anti-infective: Interrogation of the Target Binding Pocket for a Small-Molecule Inhibitor of Escherichia coli Polysaccharide Capsule Expression. Antimicrobial Agents and Chemotherapy, 2020, 65, .	3.2	2
10	Crystal structure of an Escherichia coli Hfq Core (residues 2â€“69)â€“DNA complex reveals multifunctional nucleic acid binding sites. Nucleic Acids Research, 2020, 48, 3987-3997.	14.5	27
11	When is a transcription factor a NAP?. Current Opinion in Microbiology, 2020, 55, 26-33.	5.1	48
12	Structural, Biochemical, and In Vivo Characterization of MtrR-Mediated Resistance to Innate Antimicrobials by the Human Pathogen Neisseria gonorrhoeae. Journal of Bacteriology, 2019, 201, .	2.2	13
13	Control of meristem determinacy by trehalose 6-phosphate phosphatases is uncoupled from enzymatic activity. Nature Plants, 2019, 5, 352-357.	9.3	70
14	The MerR-like protein BldC binds DNA direct repeats as cooperative multimers to regulate Streptomyces development. Nature Communications, 2018, 9, 1139.	12.8	26
15	Trehalose pathway as an antifungal target. Virulence, 2017, 8, 143-149.	4.4	53
16	The Streptomyces master regulator BldD binds c-di-GMP sequentially to create a functional BldD2-(c-di-GMP)4 complex. Nucleic Acids Research, 2017, 45, 6923-6933.	14.5	37
17	Central Role of the Trehalose Biosynthesis Pathway in the Pathogenesis of Human Fungal Infections: Opportunities and Challenges for Therapeutic Development. Microbiology and Molecular Biology Reviews, 2017, 81, .	6.6	93
18	Dissection of the molecular circuitry controlling virulence in Francisella tularensis. Genes and Development, 2017, 31, 1549-1560.	5.9	39

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19	Structural and In Vivo Studies on Trehalose-6-Phosphate Synthase from Pathogenic Fungi Provide Insights into Its Catalytic Mechanism, Biological Necessity, and Potential for Novel Antifungal Drug Design. MBio, 2017, 8, .	4.1	26
20	Structures of trehalose-6-phosphate phosphatase from pathogenic fungi reveal the mechanisms of substrate recognition and catalysis. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7148-7153.	7.1	44
21	Structural and Biochemical Characterization of the Francisella tularensis Pathogenicity Regulator, Macrophage Locus Protein A (MglA). PLoS ONE, 2015, 10, e0128225.	2.5	9
22	Glutathione activates virulence gene expression of an intracellular pathogen. Nature, 2015, 517, 170-173.	27.8	217
23	HipBAâ€“promoter structures reveal the basis of heritable multidrug tolerance. Nature, 2015, 524, 59-64.	27.8	206
24	Mutations within the mepA Operator Affect Binding of the MepR Regulatory Protein and Its Induction by MepA Substrates in Staphylococcus aureus. Journal of Bacteriology, 2015, 197, 1104-1114.	2.2	8
25	Mapping Hfq-RNA interaction surfaces using tryptophan fluorescence quenching. Nucleic Acids Research, 2014, 42, 2736-2749.	14.5	75
26	Recognition of U-rich RNA by Hfq from the Gram-positive pathogenListeria monocytogenes. Rna, 2014, 20, 1548-1559.	3.5	31
27	Tetrameric c-di-GMP Mediates Effective Transcription Factor Dimerization to Control Streptomyces Development. Cell, 2014, 158, 1136-1147.	28.9	219
28	Crystal Structure of a MepR-DNA Complex Reveals the Mechanism of Transcription Repression of S. Aureus Multidrug Efflux Pump mepA. Biophysical Journal, 2013, 104, 256a.	0.5	1
29	A Single Acidic Residue Can Guide Binding Site Selection but Does Not Govern QacR Cationic-Drug Affinity. PLoS ONE, 2011, 6, e15974.	2.5	15
30	The crystal structure of the TetR family transcriptional repressor SimR bound to DNA and the role of a flexible N-terminal extension in minor groove binding. Nucleic Acids Research, 2011, 39, 9433-9447.	14.5	61
31	Structure of Escherichia coli Hfq bound to polyriboadenylate RNA. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19292-19297.	7.1	332
32	QacRâ^'Cation Recognition Is Mediated by a Redundancy of Residues Capable of Charge Neutralization. Biochemistry, 2008, 47, 8122-8129.	2.5	32
33	Hfq structure, function and ligand binding. Current Opinion in Microbiology, 2007, 10, 125-133.	5.1	354
34	Multidrug-Binding Transcription Factor QacR Binds the Bivalent Aromatic Diamidines DB75 and DB359 in Multiple Positions. Journal of the American Chemical Society, 2007, 129, 8389-8395.	13.7	31
35	Characterization of the Multiple Transferable Resistance Repressor, MtrR, from Neisseria gonorrhoeae. Journal of Bacteriology, 2005, 187, 5008-5012.	2.2	43
36	The TetR Family of Transcriptional Repressors. Microbiology and Molecular Biology Reviews, 2005, 69, 326-356.	6.6	989

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37	Role of Residue 147 in the Gene Regulatory Function of the Escherichia coli Purine Repressor. Biochemistry, 2002, 41, 511-520.	2.5	16
38	Hfq. Molecular Cell, 2002, 9, 23-30.	9.7	503
39	Structural basis for cooperative DNA binding by two dimers of the multidrug-binding protein QacR. EMBO Journal, 2002, 21, 1210-1218.	7.8	215
40	Structures of the pleiotropic translational regulator Hfq and an Hfq-RNA complex: a bacterial Sm-like protein. EMBO Journal, 2002, 21, 3546-3556.	7.8	382
41	Introduction: multidrug resistance. Seminars in Cell and Developmental Biology, 2001, 12, 201-204.	5.0	2
42	Structural Mechanisms of QacR Induction and Multidrug Recognition. Science, 2001, 294, 2158-2163.	12.6	365
43	Crystal structure of the transcription activator BmrR bound to DNA and a drug. Nature, 2001, 409, 378-382.	27.8	249
44	Characterization of the SarA virulence gene regulator of Staphylococcus aureus. Molecular Microbiology, 1999, 33, 307-316.	2.5	108
45	Structural Basis of Multidrug Recognition by BmrR, a Transcription Activator of a Multidrug Transporter. Cell, 1999, 96, 353-362.	28.9	175
46	The Role of Lysine 55 in Determining the Specificity of the Purine Repressor for its Operators through Minor Groove Interactions. Journal of Molecular Biology, 1999, 291, 347-361.	4.2	48
47	The structure of PurR mutant L54M shows an alternative route to DNA kinking. Nature Structural Biology, 1998, 5, 436-441.	9.7	22
48	Structure-Based Redesign of Corepressor Specificity of the Escherichia coli Purine Repressor by Substitution of Residue 190,. Biochemistry, 1998, 37, 971-982.	2.5	15
49	The X-ray Structure of the PurR-Guanine-purF Operator Complex Reveals the Contributions of Complementary Electrostatic Surfaces and a Water-mediated Hydrogen Bond to Corepressor Specificity and Binding Affinity. Journal of Biological Chemistry, 1997, 272, 22648-22653.	3.4	49
50	Preliminary structural studies on the multiâ€ligandâ€binding domain of the transcription activator, BmrR, from bacillus subtilis. Protein Science, 1997, 6, 2465-2468.	7.6	10
51	A Positively Charged Residue Bound in the Minor Groove Does Not Alter the Bending of a DNA Duplex. Journal of the American Chemical Society, 1996, 118, 13073-13074.	13.7	12
52	Allosteric transition intermediates modelled by crosslinked haemoglobins. Nature, 1995, 375, 84-87.	27.8	90
53	Nuclear protein CBP is a coactivator for the transcription factor CREB. Nature, 1994, 370, 223-226.	27.8	1,429
54	The winged-helix DNA-binding motif: Another helix-turn-helix takeoff. Cell, 1993, 74, 773-776.	28.9	241

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55	DNA recognition by the helix-turn-helix motif. Current Opinion in Structural Biology, 1992, 2, 100-108.	5.7	35
56	Interactions of the helix-turn-helix binding domain. Current Opinion in Structural Biology, 1991, 1, 80-88.	5.7	36
57	Crystallization of mutant lysozymes from bacteriophage T4. Journal of Crystal Growth, 1988, 90, 160-167.	1.5	13
58	Crystallization of a complex of cro repressor with a 17 base-pair operator. Journal of Molecular Biology, 1986, 188, 115-118.	4.2	36
59	Studies on the crystallization of the cro protein-pseudo OR3 complex. Journal of Crystal Growth, 1986, 76, 715-718.	1.5	0
60	X-ray structure of cytidine-5â€²-O-dimethylphosphate. Novel stacking between the ribosyl O(2â€²) hydroxyl oxygen atom and the base. Nucleic Acids Research, 1984, 12, 6813-6825.	14.5	4
61	Crystal structure and conformation of the phosphotriester adenosine 5'-O-(diethyl phosphate). Possible steric and conformational mechanisms for the biochemical and biological effects arising from phosphate alkylation. Journal of the American Chemical Society, 1984, 106, 5671-5676.	13.7	9
62	Molecular and crystal structure of O4-methyluridine. Reaction coordinates for an incipient nucleophilic attack seen by short intermolecular sugar-base interactions. Journal of the American Chemical Society, 1983, 105, 7737-7742.	13.7	16
63	The X-Ray Structure Of 3,4,5,7-Tetra-O-Acetyl 2,6-Anhydro-D-Glycero-D-Talo-Heptonamide. Journal of Carbohydrate Chemistry, 1983, 2, 115-128.	1.1	0
64	Occurrence of the Unusual2C5(1C4) Chair Conformation in Two Carbohydrates and the Reverse Anomeric Effect. X-Ray Structures of 3,4,5,7-Tetra-O-Acetyl-2,6-Anhydro-D-Glycero-D-Ido-Heptonamide (1) and 3,4,5,7-Tetra-O-Acetyl-2,6-Anhydro-D-Glycero-L-Gluco-Heptonamide (2). Journal of Carbohydrate Chemistry, 1982, 1, 85-103.	1.1	7