

# Robert T Batey

## List of Publications by Year in descending order

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96  
papers

8,062  
citations

41344

49  
h-index

49909

87  
g-index

178  
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178  
docs citations

178  
times ranked

5127  
citing authors

#	ARTICLE	IF	CITATIONS
1	Regulation of Gene Expression Through Effector-dependent Conformational Switching by Cobalamin Riboswitches. <i>Journal of Molecular Biology</i> , 2022, 434, 167585.	4.2	8
2	The DNA-Binding High-Mobility Group Box Domain of Sox Family Proteins Directly Interacts with RNA <i>In Vitro</i> . <i>Biochemistry</i> , 2022, 61, 943-951.	2.5	9
3	SPRINT: a Cas13a-based platform for detection of small molecules. <i>Nucleic Acids Research</i> , 2020, 48, e101-e101.	14.5	56
4	hnRNPK recognition of the B motif of Xist and other biological RNAs. <i>Nucleic Acids Research</i> , 2020, 48, 9320-9335.	14.5	25
5	High Affinity Binding of N2-Modified Guanine Derivatives Significantly Disrupts the Ligand Binding Pocket of the Guanine Riboswitch. <i>Molecules</i> , 2020, 25, 2295.	3.8	9
6	Small molecule regulated sgRNAs enable control of genome editing in <i>E. coli</i> by Cas9. <i>Nature Communications</i> , 2020, 11, 1394.	12.8	28
7	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. <i>Rna</i> , 2020, 26, 982-995.	3.5	100
8	The Sox2 transcription factor binds RNA. <i>Nature Communications</i> , 2020, 11, 1805.	12.8	77
9	Spen links RNA-mediated endogenous retrovirus silencing and X chromosome inactivation. <i>ELife</i> , 2020, 9, .	6.0	33
10	Requirements for efficient ligand-gated co-transcriptional switching in designed variants of the <i>B. subtilis</i> pbuE adenine-responsive riboswitch in <i>E. coli</i> . <i>PLoS ONE</i> , 2020, 15, e0243155.	2.5	12
11	Structural basis for 2'-deoxyguanosine recognition by the 2'-dG-II class of riboswitches. <i>Nucleic Acids Research</i> , 2019, 47, 10931-10941.	14.5	11
12	The glucocorticoid receptor DNA-binding domain recognizes RNA hairpin structures with high affinity. <i>Nucleic Acids Research</i> , 2019, 47, 8180-8192.	14.5	24
13	A functional genetic screen reveals sequence preferences within a key tertiary interaction in cobalamin riboswitches required for ligand selectivity. <i>Nucleic Acids Research</i> , 2018, 46, 9094-9105.	14.5	11
14	A multicolor riboswitch-based platform for imaging of RNA in live mammalian cells. <i>Nature Chemical Biology</i> , 2018, 14, 964-971.	8.0	114
15	Structure-Activity Relationship of Flavin Analogues That Target the Flavin Mononucleotide Riboswitch. <i>ACS Chemical Biology</i> , 2018, 13, 2908-2919.	3.4	49
16	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. <i>Rna</i> , 2017, 23, 655-672.	3.5	158
17	Recurrent RNA motifs as scaffolds for genetically encodable small-molecule biosensors. <i>Nature Chemical Biology</i> , 2017, 13, 295-301.	8.0	104
18	Cobalamin riboswitches exhibit a broad range of ability to discriminate between methylcobalamin and adenosylcobalamin. <i>Journal of Biological Chemistry</i> , 2017, 292, 11650-11658.	3.4	38

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19	Intrinsically disordered RGG/RC domains mediate degenerate specificity in RNA binding. <i>Nucleic Acids Research</i> , 2017, 45, 7984-7996.	14.5	165
20	Mechanistic Insights into Cofactor-Dependent Coupling of RNA Folding and mRNA Transcription/Translation by a Cobalamin Riboswitch. <i>Cell Reports</i> , 2016, 15, 1100-1110.	6.4	36
21	Soaking Hexamine Cations into RNA Crystals to Obtain Derivatives for Phasing Diffraction Data. <i>Methods in Molecular Biology</i> , 2016, 1320, 219-232.	0.9	10
22	Structure-guided Mutational Analysis of Gene Regulation by the <i>Bacillus subtilis</i> pbuE Adenine-responsive Riboswitch in a Cellular Context. <i>Journal of Biological Chemistry</i> , 2015, 290, 4464-4475.	3.4	28
23	Design of Modular "Plug-and-Play" Expression Platforms Derived from Natural Riboswitches for Engineering Novel Genetically Encodable RNA Regulatory Devices. <i>Methods in Enzymology</i> , 2015, 550, 41-71.	1.0	11
24	Metal Ion-Mediated Nucleobase Recognition by the ZTP Riboswitch. <i>Chemistry and Biology</i> , 2015, 22, 829-837.	6.0	44
25	A Highly Coupled Network of Tertiary Interactions in the SAM-I Riboswitch and Their Role in Regulatory Tuning. <i>Journal of Molecular Biology</i> , 2015, 427, 3473-3490.	4.2	10
26	Riboswitches: still a lot of undiscovered country. <i>Rna</i> , 2015, 21, 560-563.	3.5	23
27	Structural basis for diversity in the SAM clan of riboswitches. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6624-6629.	7.1	57
28	A Disconnect between High-Affinity Binding and Efficient Regulation by Antifolates and Purines in the Tetrahydrofolate Riboswitch. <i>Chemistry and Biology</i> , 2014, 21, 205-216.	6.0	45
29	The purine riboswitch as a model system for exploring RNA biology and chemistry. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 919-930.	1.9	29
30	Single-Molecule Conformational Dynamics of a Biologically Functional Hydroxocobalamin Riboswitch. <i>Journal of the American Chemical Society</i> , 2014, 136, 16832-16843.	13.7	40
31	Lariat lessons. <i>Nature</i> , 2014, 514, 173-174.	27.8	0
32	Advances in methods for native expression and purification of RNA for structural studies. <i>Current Opinion in Structural Biology</i> , 2014, 26, 1-8.	5.7	23
33	Nucleotides Adjacent to the Ligand-Binding Pocket are Linked to Activity Tuning in the Purine Riboswitch. <i>Journal of Molecular Biology</i> , 2013, 425, 1596-1611.	4.2	50
34	Modularity of Select Riboswitch Expression Platforms Enables Facile Engineering of Novel Genetic Regulatory Devices. <i>ACS Synthetic Biology</i> , 2013, 2, 463-472.	3.8	105
35	Engineering modular "ON"™ RNA switches using biological components. <i>Nucleic Acids Research</i> , 2013, 41, 10449-10461.	14.5	83
36	Structure and mechanism of purine-binding riboswitches. <i>Quarterly Reviews of Biophysics</i> , 2012, 45, 345-381.	5.7	70

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37	B12 cofactors directly stabilize an mRNA regulatory switch. <i>Nature</i> , 2012, 492, 133-137.	27.8	171
38	Single-Molecule Studies of the Lysine Riboswitch Reveal Effector-Dependent Conformational Dynamics of the Aptamer Domain. <i>Biochemistry</i> , 2012, 51, 9223-9233.	2.5	45
39	Insights into the Regulatory Landscape of the Lysine Riboswitch. <i>Journal of Molecular Biology</i> , 2012, 423, 17-33.	4.2	38
40	Riboswitches: Structures and Mechanisms. <i>Cold Spring Harbor Perspectives in Biology</i> , 2011, 3, a003533-a003533.	5.5	295
41	The Structure of a Tetrahydrofolate-Sensing Riboswitch Reveals Two Ligand Binding Sites in a Single Aptamer. <i>Structure</i> , 2011, 19, 1413-1423.	3.3	117
42	Recognition of <i>S</i> -adenosylmethionine by riboswitches. <i>Wiley Interdisciplinary Reviews RNA</i> , 2011, 2, 299-311.	6.4	54
43	Novel Ligands for a Purine Riboswitch Discovered by RNA-Ligand Docking. <i>Chemistry and Biology</i> , 2011, 18, 324-335.	6.0	93
44	Molecular sensing by the aptamer domain of the FMN riboswitch: a general model for ligand binding by conformational selection. <i>Nucleic Acids Research</i> , 2011, 39, 8586-8598.	14.5	95
45	Free State Conformational Sampling of the SAM-I Riboswitch Aptamer Domain. <i>Structure</i> , 2010, 18, 787-797.	3.3	167
46	Structural basis for recognition of <i>S</i> -adenosylhomocysteine by riboswitches. <i>Rna</i> , 2010, 16, 2144-2155.	3.5	72
47	Discrimination between Closely Related Cellular Metabolites by the SAM-I Riboswitch. <i>Journal of Molecular Biology</i> , 2010, 396, 761-772.	4.2	65
48	Preparation of Group I Introns for Biochemical Studies and Crystallization Assays by Native Affinity Purification. <i>PLoS ONE</i> , 2009, 4, e6740.	2.5	8
49	Analysis of a Critical Interaction within the Archaeal Box C/D Small Ribonucleoprotein Complex. <i>Journal of Biological Chemistry</i> , 2009, 284, 15317-15324.	3.4	4
50	Telomere capping proteins are structurally related to RPA with an additional telomere-specific domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19298-19303.	7.1	62
51	Adaptive Ligand Binding by the Purine Riboswitch in the Recognition of Guanine and Adenine Analogs. <i>Structure</i> , 2009, 17, 857-868.	3.3	112
52	A switch in time: Detailing the life of a riboswitch. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2009, 1789, 584-591.	1.9	83
53	A Structural Basis for the Recognition of 2-Deoxyguanosine by the Purine Riboswitch. <i>Journal of Molecular Biology</i> , 2009, 385, 938-948.	4.2	58
54	Monitoring RNA-Ligand Interactions Using Isothermal Titration Calorimetry. <i>Methods in Molecular Biology</i> , 2009, 540, 97-114.	0.9	39

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55	Strategies in RNA Crystallography. <i>Methods in Enzymology</i> , 2009, 469, 119-139.	1.0	50
56	Determining Structures of RNA Aptamers and Riboswitches by X-Ray Crystallography. <i>Methods in Molecular Biology</i> , 2009, 535, 135-163.	0.9	42
57	Beyond Crystallography: Investigating the Conformational Dynamics of the Purine Riboswitch. <i>Springer Series in Biophysics</i> , 2009, , 215-228.	0.4	2
58	Riboswitches: Emerging Themes in RNA Structure and Function. <i>Annual Review of Biophysics</i> , 2008, 37, 117-133.	10.0	346
59	Structure of the SAM-II riboswitch bound to S-adenosylmethionine. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 177-182.	8.2	229
60	Ligand-dependent folding of the three-way junction in the purine riboswitch. <i>Rna</i> , 2008, 14, 675-684.	3.5	91
61	Crystal Structure of the Lysine Riboswitch Regulatory mRNA Element. <i>Journal of Biological Chemistry</i> , 2008, 283, 22347-22351.	3.4	168
62	Structural insights into metabolite-sensing mRNAs. <i>FASEB Journal</i> , 2008, 22, 259.1.	0.5	0
63	Improved native affinity purification of RNA. <i>Rna</i> , 2007, 13, 1384-1389.	3.5	106
64	Mutational Analysis of the Purine Riboswitch Aptamer Domain. <i>Biochemistry</i> , 2007, 46, 13297-13309.	2.5	83
65	A General Strategy to Solve the Phase Problem in RNA Crystallography. <i>Structure</i> , 2007, 15, 761-772.	3.3	111
66	Structural studies of ligand binding by mRNA riboswitches. <i>FASEB Journal</i> , 2007, 21, A41.	0.5	0
67	Modified Pyrimidines Specifically Bind the Purine Riboswitch. <i>Journal of the American Chemical Society</i> , 2006, 128, 14214-14215.	13.7	80
68	Mix-and-Match Riboswitches. <i>ACS Chemical Biology</i> , 2006, 1, 751-754.	3.4	40
69	Thermodynamic and Kinetic Characterization of Ligand Binding to the Purine Riboswitch Aptamer Domain. <i>Journal of Molecular Biology</i> , 2006, 359, 754-768.	4.2	246
70	Erratum to "Thermodynamic and Kinetic Characterization of Ligand Binding to the Purine Riboswitch Aptamer Domain" [J. Mol. Biol. 359 (2006) 754-768]. <i>Journal of Molecular Biology</i> , 2006, 363, 624.	4.2	1
71	Structural Studies of the Purine and SAM Binding Riboswitches. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2006, 71, 259-268.	1.1	30
72	Structure of the S-adenosylmethionine riboswitch regulatory mRNA element. <i>Nature</i> , 2006, 441, 1172-1175.	27.8	375

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73	Riboswitches: Fold and Function. <i>Chemistry and Biology</i> , 2006, 13, 805-807.	6.0	37
74	Structures of regulatory elements in mRNAs. <i>Current Opinion in Structural Biology</i> , 2006, 16, 299-306.	5.7	57
75	The bipartite architecture of the sRNA in an archaeal box C/D complex is a primary determinant of specificity. <i>Nucleic Acids Research</i> , 2006, 34, 5039-5051.	14.5	18
76	Riboswitches: natural SELEXion. <i>Cellular and Molecular Life Sciences</i> , 2005, 62, 2401-2404.	5.4	12
77	Structure of a class II TrmH tRNA-modifying enzyme from <i>Aquifex aeolicus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 722-728.	0.7	23
78	A general method for rapid and nondenaturing purification of RNAs. <i>Rna</i> , 2004, 10, 988-995.	3.5	72
79	Structure of a natural guanine-responsive riboswitch complexed with the metabolite hypoxanthine. <i>Nature</i> , 2004, 432, 411-415.	27.8	471
80	Curse of the Hairpin Loop. <i>Structure</i> , 2004, 12, 731-732.	3.3	2
81	Structural Insights Into the Signal Recognition Particle. <i>Annual Review of Biochemistry</i> , 2004, 73, 539-557.	11.1	123
82	Quantitation of free energy profiles in RNA-ligand interactions by nucleotide analog interference mapping. <i>Rna</i> , 2003, 9, 1282-1289.	3.5	11
83	Structural and Energetic Analysis of Metal Ions Essential to SRP Signal Recognition Domain Assembly. <i>Biochemistry</i> , 2002, 41, 11703-11710.	2.5	42
84	Structural and energetic analysis of RNA recognition by a universally conserved protein from the signal recognition particle. <i>Journal of Molecular Biology</i> , 2001, 307, 229-246.	4.2	89
85	Large-Scale Purification of a Stable Form of Recombinant Tobacco Etch Virus Protease. <i>BioTechniques</i> , 2001, 30, 544-554.	1.8	113
86	A universal mode of helix packing in RNA. <i>Nature Structural Biology</i> , 2001, 8, 339-343.	9.7	228
87	Crystal Structure of the Ribonucleoprotein Core of the Signal Recognition Particle. <i>Science</i> , 2000, 287, 1232-1239.	12.6	369
88	Tertiary Motifs in RNA Structure and Folding. <i>Angewandte Chemie - International Edition</i> , 1999, 38, 2326-2343.	13.8	393
89	The parallel universe of RNA folding. <i>Nature Structural Biology</i> , 1998, 5, 337-340.	9.7	20
90	Effects of polyvalent cations on the folding of an rRNA three-way junction and binding of ribosomal protein S15. <i>Rna</i> , 1998, 4, 984-997.	3.5	63

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91	Interaction of the <i>Bacillus stearothermophilus</i> Ribosomal Protein S15 with 16 S rRNA: I. Defining the Minimal RNA Site. <i>Journal of Molecular Biology</i> , 1996, 261, 536-549.	4.2	70
92	Interaction of the <i>Bacillus stearothermophilus</i> Ribosomal Protein S15 with 16 S rRNA: II. Specificity Determinants of RNA-Protein Recognition. <i>Journal of Molecular Biology</i> , 1996, 261, 550-567.	4.2	54
93	Improved large scale culture of <i>Methylophilus methylotrophus</i> for <sup>13</sup> C/ <sup>15</sup> N labeling and random fractional deuteration of ribonucleotides. <i>Nucleic Acids Research</i> , 1996, 24, 4836-4837.	14.5	25
94	[ <sup>13</sup> C] Preparation of isotopically enriched RNAs for heteronuclear NMR. <i>Methods in Enzymology</i> , 1995, 261, 300-322.	1.0	137
95	Preparation of isotopically labeled ribonucleotides for multidimensional NMR spectroscopy of RNA. <i>Nucleic Acids Research</i> , 1992, 20, 4515-4523.	14.5	288
96	Comparison of operator-specific and nonspecific DNA binding of the $\lambda$ .cl repressor: [KCl] and pH effects. <i>Biochemistry</i> , 1991, 30, 6677-6688.	2.5	56