

Adrian R FerrÃ©-D'amarÃ©

List of Publications by Year in descending order

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120
papers

10,698
citations

29994

54
h-index

32761

100
g-index

120
all docs

120
docs citations

120
times ranked

7434
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of a hepatitis delta virus ribozyme. <i>Nature</i> , 1998, 395, 567-574.	13.7	747
2	Recognition by Max of its cognate DNA through a dimeric b/HLH/Z domain. <i>Nature</i> , 1993, 363, 38-45.	13.7	727
3	Molecular basis of mouse microphthalmia (mi) mutations helps explain their developmental and phenotypic consequences. <i>Nature Genetics</i> , 1994, 8, 256-263.	9.4	505
4	Crystal structure of a hairpin ribozyme-inhibitor complex with implications for catalysis. <i>Nature</i> , 2001, 410, 780-786.	13.7	441
5	Structural Basis of glmS Ribozyme Activation by Glucosamine-6-Phosphate. <i>Science</i> , 2006, 313, 1752-1756.	6.0	357
6	The structure and function of small nucleolar ribonucleoproteins. <i>Nucleic Acids Research</i> , 2007, 35, 1452-1464.	6.5	337
7	Structural basis for activity of highly efficient RNA mimics of green fluorescent protein. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 658-663.	3.6	299
8	Transition State Stabilization by a Catalytic RNA. <i>Science</i> , 2002, 298, 1421-1424.	6.0	271
9	Cocrystal Structure of a tRNA ⁵⁵ Pseudouridine Synthase. <i>Cell</i> , 2001, 107, 929-939.	13.5	259
10	Pseudouridine Synthases. <i>Chemistry and Biology</i> , 2006, 13, 1125-1135.	6.2	236
11	Crystal Structures of the Thi-Box Riboswitch Bound to Thiamine Pyrophosphate Analogs Reveal Adaptive RNA-Small Molecule Recognition. <i>Structure</i> , 2006, 14, 1459-1468.	1.6	236
12	Structural basis of G-quadruplex unfolding by the DEAH/RHA helicase DHX36. <i>Nature</i> , 2018, 558, 465-469.	13.7	224
13	Recognition of the bacterial second messenger cyclic diguanylate by its cognate riboswitch. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1212-1217.	3.6	176
14	Riboswitches: Discovery of Drugs That Target Bacterial Gene-Regulatory RNAs. <i>Accounts of Chemical Research</i> , 2011, 44, 1329-1338.	7.6	175
15	Use of Cis- and Trans-Ribozymes to Remove 5' and 3' Heterogeneities From Milligrams of In Vitro Transcribed RNA. <i>Nucleic Acids Research</i> , 1996, 24, 977-978.	6.5	173
16	Small Self-cleaving Ribozymes. <i>Cold Spring Harbor Perspectives in Biology</i> , 2010, 2, a003574-a003574.	2.3	164
17	RNA-Puzzles Round II: assessment of RNA structure prediction programs applied to three large RNA structures. <i>Rna</i> , 2015, 21, 1066-1084.	1.6	161
18	Cocrystal structure of a class I preQ1 riboswitch reveals a pseudoknot recognizing an essential hypermodified nucleobase. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 343-344.	3.6	160

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19	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. <i>Rna</i> , 2017, 23, 655-672.	1.6	158
20	Rapid Construction of Empirical RNA Fitness Landscapes. <i>Science</i> , 2010, 330, 376-379.	6.0	157
21	Probing the solution structure of the DNA-binding protein Max by a combination of proteolysis and mass spectrometry. <i>Protein Science</i> , 1995, 4, 1088-1099.	3.1	149
22	Riboswitches: small-molecule recognition by gene regulatory RNAs. <i>Current Opinion in Structural Biology</i> , 2007, 17, 273-279.	2.6	140
23	Ribozymes and Riboswitches: Modulation of RNA Function by Small Molecules. <i>Biochemistry</i> , 2010, 49, 9123-9131.	1.2	140
24	Co-crystal structure of a T-box riboswitch stem I domain in complex with its cognate tRNA. <i>Nature</i> , 2013, 500, 363-366.	13.7	136
25	Structural basis of specific tRNA aminoacylation by a small in vitro selected ribozyme. <i>Nature</i> , 2008, 454, 358-361.	13.7	133
26	Use of dynamic light scattering to assess crystallizability of macromolecules and macromolecular assemblies. <i>Structure</i> , 1994, 2, 357-359.	1.6	131
27	Structure of Protein L7Ae Bound to a K-Turn Derived from an Archaeal Box H/ACA sRNA at 1.8 Å... Resolution. <i>Structure</i> , 2004, 12, 893-903.	1.6	131
28	A general module for RNA crystallization. <i>Journal of Molecular Biology</i> , 1998, 279, 621-631.	2.0	117
29	A homodimer interface without base pairs in an RNA mimic of red fluorescent protein. <i>Nature Chemical Biology</i> , 2017, 13, 1195-1201.	3.9	111
30	Structural Basis for Specific, High-Affinity Tetracycline Binding by an In Vitro Evolved Aptamer and Artificial Riboswitch. <i>Chemistry and Biology</i> , 2008, 15, 1125-1137.	6.2	108
31	Structural basis for high-affinity fluorophore binding and activation by RNA Mango. <i>Nature Chemical Biology</i> , 2017, 13, 807-813.	3.9	105
32	The Cbf5-Nop10 complex is a molecular bracket that organizes box H/ACA RNPs. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 1101-1107.	3.6	104
33	Direct pKa Measurement of the Active-Site Cytosine in a Genomic Hepatitis Delta Virus Ribozyme. <i>Journal of the American Chemical Society</i> , 2001, 123, 8447-8452.	6.6	100
34	RNA FOLDS: Insights from Recent Crystal Structures. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1999, 28, 57-73.	18.3	97
35	Idiosyncratically tuned switching behavior of riboswitch aptamer domains revealed by comparative small-angle X-ray scattering analysis. <i>Rna</i> , 2010, 16, 598-609.	1.6	97
36	Synthesis and applications of RNAs with position-selective labelling and mosaic composition. <i>Nature</i> , 2015, 522, 368-372.	13.7	95

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37	Essential Role of an Active-Site Guanine in <i>glmS</i> Ribozyme Catalysis. <i>Journal of the American Chemical Society</i> , 2007, 129, 14858-14859.	6.6	87
38	A nested double pseudoknot is required for self-cleavage activity of both the genomic and antigenomic hepatitis delta virus ribozymes. <i>Rna</i> , 1999, 5, 720-727.	1.6	85
39	Insights into the mechanism of a G-quadruplex-unwinding DEAH-box helicase. <i>Nucleic Acids Research</i> , 2015, 43, 2223-2231.	6.5	84
40	Crystal Structure of Pseudouridine Synthase RluA: Indirect Sequence Readout through Protein-Induced RNA Structure. <i>Molecular Cell</i> , 2006, 24, 535-545.	4.5	83
41	Structure and functional reselection of the Mango-III fluorogenic RNA aptamer. <i>Nature Chemical Biology</i> , 2019, 15, 472-479.	3.9	83
42	Requirement of Helix P2.2 and Nucleotide G1 for Positioning the Cleavage Site and Cofactor of the <i>glmS</i> Ribozyme. <i>Journal of Molecular Biology</i> , 2007, 373, 178-189.	2.0	82
43	[10] Dynamic light scattering in evaluating crystallizability of macromolecules. <i>Methods in Enzymology</i> , 1997, 276, 157-166.	0.4	80
44	Validating Fragment-Based Drug Discovery for Biological RNAs: Lead Fragments Bind and Remodel the TPP Riboswitch Specifically. <i>Chemistry and Biology</i> , 2014, 21, 591-595.	6.2	79
45	Thermodynamic analysis of ligand binding and ligand binding-induced tertiary structure formation by the thiamine pyrophosphate riboswitch. <i>Rna</i> , 2010, 16, 186-196.	1.6	73
46	The Box H/ACA Ribonucleoprotein Complex: Interplay of RNA and Protein Structures in Post-transcriptional RNA Modification. <i>Journal of Biological Chemistry</i> , 2010, 285, 805-809.	1.6	72
47	Protein and RNA dynamical fingerprinting. <i>Nature Communications</i> , 2019, 10, 1026.	5.8	72
48	Riboswitch function: Flipping the switch or tuning the dimmer?. <i>RNA Biology</i> , 2010, 7, 328-332.	1.5	69
49	RNA-modifying enzymes. <i>Current Opinion in Structural Biology</i> , 2003, 13, 49-55.	2.6	66
50	Synthetic ligands for PreQ1 riboswitches provide structural and mechanistic insights into targeting RNA tertiary structure. <i>Nature Communications</i> , 2019, 10, 1501.	5.8	66
51	Long-Range Interactions in Riboswitch Control of Gene Expression. <i>Annual Review of Biophysics</i> , 2017, 46, 455-481.	4.5	65
52	Allosteric Tertiary Interactions Preorganize the c-di-GMP Riboswitch and Accelerate Ligand Binding. <i>ACS Chemical Biology</i> , 2012, 7, 920-927.	1.6	64
53	The tRNA Elbow in Structure, Recognition and Evolution. <i>Life</i> , 2016, 6, 3.	1.1	63
54	The <i>glmS</i> ribozyme: use of a small molecule coenzyme by a gene-regulatory RNA. <i>Quarterly Reviews of Biophysics</i> , 2010, 43, 423-447.	2.4	59

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55	The hairpin ribozyme. <i>Biopolymers</i> , 2004, 73, 71-78.	1.2	56
56	RNA G-quadruplex is resolved by repetitive and ATP-dependent mechanism of DHX36. <i>Nature Communications</i> , 2019, 10, 1855.	5.8	56
57	The emerging structural complexity of G-quadruplex RNAs. <i>Rna</i> , 2021, 27, 390-402.	1.6	56
58	Crystal structure of a cAMP riboswitch reveals an internally pseudo-dimeric RNA. <i>EMBO Journal</i> , 2014, 33, 2692-2703.	3.5	53
59	Dramatic Improvement of Crystals of Large RNAs by Cation Replacement and Dehydration. <i>Structure</i> , 2014, 22, 1363-1371.	1.6	52
60	Tracking RNA with light: selection, structure, and design of fluorescence turn-on RNA aptamers. <i>Quarterly Reviews of Biophysics</i> , 2019, 52, e8.	2.4	50
61	YbxF and YlxQ are bacterial homologs of L7Ae and bind K-turns but not K-loops. <i>Rna</i> , 2012, 18, 759-770.	1.6	49
62	Direct Evaluation of tRNA Aminoacylation Status by the T-Box Riboswitch Using tRNA-mRNA Stacking and Steric Readout. <i>Molecular Cell</i> , 2014, 55, 148-155.	4.5	49
63	Crystal Structures of the Mango-II RNA Aptamer Reveal Heterogeneous Fluorophore Binding and Guide Engineering of Variants with Improved Selectivity and Brightness. <i>Biochemistry</i> , 2018, 57, 3544-3548.	1.2	49
64	Use of the spliceosomal protein U1A to facilitate crystallization and structure determination of complex RNAs. <i>Methods</i> , 2010, 52, 159-167.	1.9	46
65	New molecular engineering approaches for crystallographic studies of large RNAs. <i>Current Opinion in Structural Biology</i> , 2014, 26, 9-15.	2.6	46
66	A Helicase Unwinds Hexanucleotide Repeat RNA G-Quadruplexes and Facilitates Repeat-Associated Non-AUG Translation. <i>Journal of the American Chemical Society</i> , 2021, 143, 7368-7379.	6.6	43
67	RNA quaternary structure and global symmetry. <i>Trends in Biochemical Sciences</i> , 2015, 40, 211-220.	3.7	40
68	Structural Principles of Fluorescent RNA Aptamers. <i>Trends in Pharmacological Sciences</i> , 2017, 38, 928-939.	4.0	40
69	The Roles of Metal Ions in Regulation by Riboswitches. <i>Metal Ions in Life Sciences</i> , 2011, 9, 141-173.	1.0	40
70	Recognition of the bacterial alarmone ZMP through long-distance association of two RNA subdomains. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 679-685.	3.6	39
71	Modulation of quaternary structure and enhancement of ligand binding by the K-turn of tandem glycine riboswitches. <i>Rna</i> , 2013, 19, 167-176.	1.6	38
72	Structure and mechanism of the T-box riboswitches. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015, 6, 419-433.	3.2	38

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73	The <i>glmS</i> Ribozyme Tunes the Catalytically Critical pK_a of Its Coenzyme Glucosamine-6-phosphate. <i>Journal of the American Chemical Society</i> , 2011, 133, 14188-14191.	6.6	36
74	Real-time monitoring of single ZTP riboswitches reveals a complex and kinetically controlled decision landscape. <i>Nature Communications</i> , 2020, 11, 4531.	5.8	36
75	Crystal structure of the highly divergent pseudouridine synthase TruD reveals a circular permutation of a conserved fold. <i>Rna</i> , 2004, 10, 1026-1033.	1.6	34
76	Global analysis of riboswitches by small-angle X-ray scattering and calorimetry. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 1020-1029.	0.9	34
77	From fluorescent proteins to fluorogenic RNAs: Tools for imaging cellular macromolecules. <i>Protein Science</i> , 2019, 28, 1374-1386.	3.1	31
78	An in vitro evolved <i>glmS</i> ribozyme has the wild-type fold but loses coenzyme dependence. <i>Nature Chemical Biology</i> , 2013, 9, 805-810.	3.9	28
79	Rapid RNA-ligand interaction analysis through high-information content conformational and stability landscapes. <i>Nature Communications</i> , 2015, 6, 8898.	5.8	28
80	Precursor complex structure of pseudouridine synthase TruB suggests coupling of active site perturbations to an RNA-sequestering peripheral protein domain. <i>Protein Science</i> , 2005, 14, 2201-2206.	3.1	26
81	Crystal structure of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) frameshifting pseudoknot. <i>Rna</i> , 2022, 28, 239-249.	1.6	25
82	Binding between G Quadruplexes at the Homodimer Interface of the Corn RNA Aptamer Strongly Activates Thioflavin T Fluorescence. <i>Cell Chemical Biology</i> , 2019, 26, 1159-1168.e4.	2.5	24
83	Convergent Use of Heptacoordination for Cation Selectivity by RNA and Protein Metalloregulators. <i>Cell Chemical Biology</i> , 2018, 25, 962-973.e5.	2.5	23
84	Fluorogenic aptamers resolve the flexibility of RNA junctions using orientation-dependent FRET. <i>Rna</i> , 2021, 27, 433-444.	1.6	22
85	Anti-cooperative Biphasic Equilibrium Binding of Transcription Factor Upstream Stimulatory Factor to Its Cognate DNA Monitored by Protein Fluorescence Changes. <i>Journal of Biological Chemistry</i> , 1995, 270, 19325-19329.	1.6	21
86	Crystallization of the Hairpin Ribozyme: Illustrative Protocols. , 2004, 252, 303-312.		21
87	Glucosamine and Glucosamine-6-phosphate Derivatives: Catalytic Cofactor Analogues for the <i>glmS</i> Ribozyme. <i>Journal of Organic Chemistry</i> , 2013, 78, 4730-4743.	1.7	21
88	Structure-Guided Engineering of the Homodimeric Mango-IV Fluorescence Turn-on Aptamer Yields an RNA FRET Pair. <i>Structure</i> , 2020, 28, 776-785.e3.	1.6	20
89	SEWAL: an open-source platform for next-generation sequence analysis and visualization. <i>Nucleic Acids Research</i> , 2010, 38, 7908-7915.	6.5	19
90	Use of a coenzyme by the <i>glmS</i> ribozyme-riboswitch suggests primordial expansion of RNA chemistry by small molecules. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2011, 366, 2942-2948.	1.8	19

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91	Many Activities, One Structure: Functional Plasticity of Ribozyme Folds. <i>Molecules</i> , 2016, 21, 1570.	1.7	19
92	Structure-Guided Engineering of the Regioselectivity of RNA Ligase Ribozymes. <i>Journal of the American Chemical Society</i> , 2009, 131, 3532-3540.	6.6	18
93	Methods to Crystallize RNA. <i>Current Protocols in Nucleic Acid Chemistry</i> , 2000, 1, Unit 7.6.	0.5	16
94	Crystallization of the glmS Ribozyme-Riboswitch. <i>Methods in Molecular Biology</i> , 2009, 540, 129-139.	0.4	16
95	U1A RNA-binding domain at 1.8 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1521-1524.	2.5	14
96	A divalent cation-dependent variant of the <i>glmS</i> ribozyme with stringent Ca ²⁺ selectivity co-opts a preexisting nonspecific metal ion-binding site. <i>Rna</i> , 2017, 23, 355-364.	1.6	13
97	Parallel Discovery Strategies Provide a Basis for Riboswitch Ligand Design. <i>Cell Chemical Biology</i> , 2020, 27, 1241-1249.e4.	2.5	13
98	The fluorescent aptamer Squash extensively repurposes the adenine riboswitch fold. <i>Nature Chemical Biology</i> , 2022, 18, 191-198.	3.9	12
99	A Flexible, Scalable Method for Preparation of Homogeneous Aminoacylated tRNAs. <i>Methods in Enzymology</i> , 2014, 549, 105-113.	0.4	9
100	Isothermal Titration Calorimetry Measurements of Riboswitch-Ligand Interactions. <i>Methods in Molecular Biology</i> , 2019, 1964, 75-87.	0.4	9
101	In vitro evolution of coenzyme-independent variants from the glmS ribozyme structural scaffold. <i>Methods</i> , 2016, 106, 76-81.	1.9	8
102	Analysis of Riboswitch Structure and Ligand Binding Using Small-Angle X-ray Scattering (SAXS). <i>Methods in Molecular Biology</i> , 2014, 1103, 211-225.	0.4	8
103	Engineering Crystal Packing in RNA Structures I: Past and Future Strategies for Engineering RNA Packing in Crystals. <i>Crystals</i> , 2021, 11, 952.	1.0	7
104	Use of the U1A Protein to Facilitate Crystallization and Structure Determination of Large RNAs. <i>Methods in Molecular Biology</i> , 2016, 1320, 67-76.	0.4	7
105	Co-crystal structure of the Mango-III fluorescent RNA aptamer using an X-ray free-electron laser. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 547-551.	0.4	6
106	How RNA closes a Diel. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 206-208.	3.6	5
107	RNA Binding: Getting Specific about Specificity. <i>Cell Chemical Biology</i> , 2016, 23, 1177-1178.	2.5	4
108	An uncommon [K ⁺ (Mg ²⁺) ₂] metal ion triad imparts stability and selectivity to the Guanidine-I riboswitch. <i>Rna</i> , 2021, 27, 1257-1264.	1.6	4

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109	Crystallographic Analysis of TPP Riboswitch Binding by Small-Molecule Ligands Discovered Through Fragment-Based Drug Discovery Approaches. <i>Methods in Enzymology</i> , 2014, 549, 221-233.	0.4	3
110	Monitoring co-transcriptional folding of riboswitches through helicase unwinding. <i>Methods in Enzymology</i> , 2019, 623, 209-227.	0.4	2
111	Post-crystallization Improvement of RNA Crystal Diffraction Quality. <i>Methods in Molecular Biology</i> , 2015, 1316, 13-24.	0.4	2
112	An RNP switch raises a roadblock. <i>Nature Chemical Biology</i> , 2010, 6, 5-6.	3.9	1
113	Stop the nonsense. <i>Nature</i> , 2011, 474, 289-290.	13.7	1
114	On the shoulders of giants. <i>Rna</i> , 2015, 21, 504-505.	1.6	1
115	Improving RNA Crystal Diffraction Quality by Postcrystallization Treatment. <i>Methods in Molecular Biology</i> , 2021, 2323, 25-37.	0.4	1
116	Post-crystallization Improvement of RNA Crystals by Synergistic Ion Exchange and Dehydration. <i>Bio-protocol</i> , 2015, 5, .	0.2	1
117	The bacterial yjdF riboswitch regulates translation through its tRNA-like fold. <i>Journal of Biological Chemistry</i> , 2022, 298, 101934.	1.6	1
118	RNA methods: From sequence to structure and dynamics. <i>Methods</i> , 2010, 52, 123-124.	1.9	0
119	Ribozyme Structural Elements: Hairpin Ribozyme. , 2004, , 743-746.		0
120	Ribozymes and riboswitches: modulation of RNA function by small molecules. <i>FASEB Journal</i> , 2009, 23, 326.1.	0.2	0