

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
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120
all docs

120
docs citations

120
times ranked

7434
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	The fluorescent aptamer Squash extensively repurposes the adenine riboswitch fold. <i>Nature Chemical Biology</i> , 2022, 18, 191-198.	3.9	12
3	The bacterial yjdF riboswitch regulates translation through its tRNA-like fold. <i>Journal of Biological Chemistry</i> , 2022, 298, 101934.	1.6	1
4	Improving RNA Crystal Diffraction Quality by Postcrystallization Treatment. <i>Methods in Molecular Biology</i> , 2021, 2323, 25-37.	0.4	1
5	The emerging structural complexity of G-quadruplex RNAs. <i>Rna</i> , 2021, 27, 390-402.	1.6	56
6	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
7	An uncommon $[K^{2+}(Mg^{2+})_2]$ metal ion triad imparts stability and selectivity to the Guanidine-I riboswitch. <i>Rna</i> , 2021, 27, 1257-1264.	1.6	4
8	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
9	Fluorogenic aptamers resolve the flexibility of RNA junctions using orientation-dependent FRET. <i>Rna</i> , 2021, 27, 433-444.	1.6	22
10	Parallel Discovery Strategies Provide a Basis for Riboswitch Ligand Design. <i>Cell Chemical Biology</i> , 2020, 27, 1241-1249.e4.	2.5	13
11	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
12	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
13	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
14	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
15	Monitoring co-transcriptional folding of riboswitches through helicase unwinding. <i>Methods in Enzymology</i> , 2019, 623, 209-227.	0.4	2
16	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
17	From fluorescent proteins to fluorogenic RNAs: Tools for imaging cellular macromolecules. <i>Protein Science</i> , 2019, 28, 1374-1386.	3.1	31
18	Structure and functional reselection of the Mango-III fluorogenic RNA aptamer. <i>Nature Chemical Biology</i> , 2019, 15, 472-479.	3.9	83

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19	RNA G-quadruplex is resolved by repetitive and ATP-dependent mechanism of DHX36. Nature Communications, 2019, 10, 1855.	5.8	56
20	Protein and RNA dynamical fingerprinting. Nature Communications, 2019, 10, 1026.	5.8	72
21	Synthetic ligands for PreQ1 riboswitches provide structural and mechanistic insights into targeting RNA tertiary structure. Nature Communications, 2019, 10, 1501.	5.8	66
22	Isothermal Titration Calorimetry Measurements of Riboswitch-Ligand Interactions. Methods in Molecular Biology, 2019, 1964, 75-87.	0.4	9
23	Convergent Use of Heptacoordination for Cation Selectivity by RNA and Protein Metalloregulators. Cell Chemical Biology, 2018, 25, 962-973.e5.	2.5	23
24	Crystal Structures of the Mango-II RNA Aptamer Reveal Heterogeneous Fluorophore Binding and Guide Engineering of Variants with Improved Selectivity and Brightness. Biochemistry, 2018, 57, 3544-3548.	1.2	49
25	Structural basis of G-quadruplex unfolding by the DEAH/RHA helicase DHX36. Nature, 2018, 558, 465-469.	13.7	224
26	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	1.6	158
27	Structural basis for high-affinity fluorophore binding and activation by RNA Mango. Nature Chemical Biology, 2017, 13, 807-813.	3.9	105
28	Long-Range Interactions in Riboswitch Control of Gene Expression. Annual Review of Biophysics, 2017, 46, 455-481.	4.5	65
29	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. Rna, 2017, 23, 355-364.	1.6	13
30	A homodimer interface without base pairs in an RNA mimic of red fluorescent protein. Nature Chemical Biology, 2017, 13, 1195-1201.	3.9	111
31	Structural Principles of Fluorescent RNA Aptamers. Trends in Pharmacological Sciences, 2017, 38, 928-939.	4.0	40
32	Many Activities, One Structure: Functional Plasticity of Ribozyme Folds. Molecules, 2016, 21, 1570.	1.7	19
33	The tRNA Elbow in Structure, Recognition and Evolution. Life, 2016, 6, 3.	1.1	63
34	RNA Binding: Getting Specific about Specificity. Cell Chemical Biology, 2016, 23, 1177-1178.	2.5	4
35	In vitro evolution of coenzyme-independent variants from the <i>glmS</i> ribozyme structural scaffold. Methods, 2016, 106, 76-81.	1.9	8
36	Use of the U1A Protein to Facilitate Crystallization and Structure Determination of Large RNAs. Methods in Molecular Biology, 2016, 1320, 67-76.	0.4	7

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37	Structure and mechanism of the DEAH-box riboswitches. Wiley Interdisciplinary Reviews RNA, 2015, 6, 419-433.	3.2	38
38	On the shoulders of giants. Rna, 2015, 21, 504-505.	1.6	1
39	Rapid RNA-ligand interaction analysis through high-information content conformational and stability landscapes. Nature Communications, 2015, 6, 8898.	5.8	28
40	Insights into the mechanism of a G-quadruplex-unwinding DEAH-box helicase. Nucleic Acids Research, 2015, 43, 2223-2231.	6.5	84
41	RNA quaternary structure and global symmetry. Trends in Biochemical Sciences, 2015, 40, 211-220.	3.7	40
42	Synthesis and applications of RNAs with position-selective labelling and mosaic composition. Nature, 2015, 522, 368-372.	13.7	95
43	Recognition of the bacterial alarmone ZMP through long-distance association of two RNA subdomains. Nature Structural and Molecular Biology, 2015, 22, 679-685.	3.6	39
44	<i>RNA-Puzzles</i> Round II: assessment of RNA structure prediction programs applied to three large RNA structures. Rna, 2015, 21, 1066-1084.	1.6	161
45	Post-crystallization Improvement of RNA Crystal Diffraction Quality. Methods in Molecular Biology, 2015, 1316, 13-24.	0.4	2
46	Post-crystallization Improvement of RNA Crystals by Synergistic Ion Exchange and Dehydration. Bio-protocol, 2015, 5, .	0.2	1
47	Crystallographic Analysis of TPP Riboswitch Binding by Small-Molecule Ligands Discovered Through Fragment-Based Drug Discovery Approaches. Methods in Enzymology, 2014, 549, 221-233.	0.4	3
48	A Flexible, Scalable Method for Preparation of Homogeneous Aminoacylated tRNAs. Methods in Enzymology, 2014, 549, 105-113.	0.4	9
49	Crystal structure of a γ -AMP riboswitch reveals an internally pseudo-dimeric RNA. EMBO Journal, 2014, 33, 2692-2703.	3.5	53
50	Global analysis of riboswitches by small-angle X-ray scattering and calorimetry. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 1020-1029.	0.9	34
51	Structural basis for activity of highly efficient RNA mimics of green fluorescent protein. Nature Structural and Molecular Biology, 2014, 21, 658-663.	3.6	299
52	Dramatic Improvement of Crystals of Large RNAs by Cation Replacement and Dehydration. Structure, 2014, 22, 1363-1371.	1.6	52
53	New molecular engineering approaches for crystallographic studies of large RNAs. Current Opinion in Structural Biology, 2014, 26, 9-15.	2.6	46
54	Validating Fragment-Based Drug Discovery for Biological RNAs: Lead Fragments Bind and Remodel the TPP Riboswitch Specifically. Chemistry and Biology, 2014, 21, 591-595.	6.2	79

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55	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
56	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
57	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
58	Glucosamine and Glucosamine-6-phosphate Derivatives: Catalytic Cofactor Analogues for the glmS Ribozyme. <i>Journal of Organic Chemistry</i> , 2013, 78, 4730-4743.	1.7	21
59	An in vitro evolved glmS ribozyme has the wild-type fold but loses coenzyme dependence. <i>Nature Chemical Biology</i> , 2013, 9, 805-810.	3.9	28
60	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
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	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
63	The <i>glmS</i> Ribozyme Tunes the Catalytically Critical pKa of Its Coenzyme Glucosamine-6-phosphate. <i>Journal of the American Chemical Society</i> , 2011, 133, 14188-14191.	6.6	36
64	Stop the nonsense. <i>Nature</i> , 2011, 474, 289-290.	13.7	1
65	Riboswitches: Discovery of Drugs That Target Bacterial Gene-Regulatory RNAs. <i>Accounts of Chemical Research</i> , 2011, 44, 1329-1338.	7.6	175
66	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
67	The Roles of Metal Ions in Regulation by Riboswitches. <i>Metal Ions in Life Sciences</i> , 2011, 9, 141-173.	1.0	40
68	An RNP switch raises a roadblock. <i>Nature Chemical Biology</i> , 2010, 6, 5-6.	3.9	1
69	SEWAL: an open-source platform for next-generation sequence analysis and visualization. <i>Nucleic Acids Research</i> , 2010, 38, 7908-7915.	6.5	19
70	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
71	Riboswitch function: Flipping the switch or tuning the dimmer?. <i>RNA Biology</i> , 2010, 7, 328-332.	1.5	69
72	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

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73	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
74	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
75	Rapid Construction of Empirical RNA Fitness Landscapes. <i>Science</i> , 2010, 330, 376-379.	6.0	157
76	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
77	RNA methods: From sequence to structure and dynamics. <i>Methods</i> , 2010, 52, 123-124.	1.9	0
78	Ribozymes and Riboswitches: Modulation of RNA Function by Small Molecules. <i>Biochemistry</i> , 2010, 49, 9123-9131.	1.2	140
79	Small Self-cleaving Ribozymes. <i>Cold Spring Harbor Perspectives in Biology</i> , 2010, 2, a003574-a003574.	2.3	164
80	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
81	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
82	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
83	Crystallization of the glmS Ribozyme-Riboswitch. <i>Methods in Molecular Biology</i> , 2009, 540, 129-139.	0.4	16
84	Ribozymes and riboswitches: modulation of RNA function by small molecules. <i>FASEB Journal</i> , 2009, 23, 326.1.	0.2	0
85	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
86	Structural basis of specific tRNA aminoacylation by a small in vitro selected ribozyme. <i>Nature</i> , 2008, 454, 358-361.	13.7	133
87	The structure and function of small nucleolar ribonucleoproteins. <i>Nucleic Acids Research</i> , 2007, 35, 1452-1464.	6.5	337
88	Requirement of Helix P2.2 and Nucleotide G1 for Positioning the Cleavage Site and Cofactor of the glmS Ribozyme. <i>Journal of Molecular Biology</i> , 2007, 373, 178-189.	2.0	82
89	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
90	Riboswitches: small-molecule recognition by gene regulatory RNAs. <i>Current Opinion in Structural Biology</i> , 2007, 17, 273-279.	2.6	140

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91	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
92	Pseudouridine Synthases. <i>Chemistry and Biology</i> , 2006, 13, 1125-1135.	6.2	236
93	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
94	Structural Basis of glmS Ribozyme Activation by Glucosamine-6-Phosphate. <i>Science</i> , 2006, 313, 1752-1756.	6.0	357
95	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
96	How RNA closes a Diel. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 206-208.	3.6	5
97	The Cbf5â€“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
98	Crystallization of the Hairpin Ribozyme: Illustrative Protocols. , 2004, 252, 303-312.		21
99	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
100	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
101	The hairpin ribozyme. <i>Biopolymers</i> , 2004, 73, 71-78.	1.2	56
102	Ribozyme Structural Elements: Hairpin Ribozyme. , 2004, , 743-746.		0
103	RNA-modifying enzymes. <i>Current Opinion in Structural Biology</i> , 2003, 13, 49-55.	2.6	66
104	U1A RNA-binding domain at 1.8 Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1521-1524.	2.5	14
105	Transition State Stabilization by a Catalytic RNA. <i>Science</i> , 2002, 298, 1421-1424.	6.0	271
106	Cocrystal Structure of a tRNA Î·55 Pseudouridine Synthase. <i>Cell</i> , 2001, 107, 929-939.	13.5	259
107	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
108	Crystal structure of a hairpin ribozymeâ€“inhibitor complex with implications for catalysis. <i>Nature</i> , 2001, 410, 780-786.	13.7	441

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109	Methods to Crystallize RNA. <i>Current Protocols in Nucleic Acid Chemistry</i> , 2000, 1, Unit 7.6.	0.5	16
110	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
111	RNA FOLDS: Insights from Recent Crystal Structures. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1999, 28, 57-73.	18.3	97
112	Crystal structure of a hepatitis delta virus ribozyme. <i>Nature</i> , 1998, 395, 567-574.	13.7	747
113	A general module for RNA crystallization. <i>Journal of Molecular Biology</i> , 1998, 279, 621-631.	2.0	117
114	[10] Dynamic light scattering in evaluating crystallizability of macromolecules. <i>Methods in Enzymology</i> , 1997, 276, 157-166.	0.4	80
115	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
116	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
117	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
118	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
119	Use of dynamic light scattering to assess crystallizability of macromolecules and macromolecular assemblies. <i>Structure</i> , 1994, 2, 357-359.	1.6	131
120	Recognition by Max of its cognate DNA through a dimeric b/HLH/Z domain. <i>Nature</i> , 1993, 363, 38-45.	13.7	727