

Adrian R Ferr'-D amar'

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

115
papers

8,855
citations

50
h-index

93
g-index

120
ext. papers

9,834
ext. citations

12.4
avg, IF

6.48
L-index

#	Paper	IF	Citations
115	The bacterial yjdF riboswitch regulates translation through its tRNA-like fold.. <i>Journal of Biological Chemistry</i> , 2022 , 101934	5.4	
114	Fluorogenic aptamers resolve the flexibility of RNA junctions using orientation-dependent FRET. <i>Rna</i> , 2021 , 27, 433-444	5.8	6
113	Crystal structure of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) frameshifting pseudoknot. <i>Rna</i> , 2021 ,	5.8	2
112	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	16.4	9
111	Improving RNA Crystal Diffraction Quality by Postcrystallization Treatment. <i>Methods in Molecular Biology</i> , 2021 , 2323, 25-37	1.4	1
110	The emerging structural complexity of G-quadruplex RNAs. <i>Rna</i> , 2021 , 27, 390-402	5.8	11
109	An uncommon [K(Mg)] metal ion triad imparts stability and selectivity to the Guanidine-I riboswitch. <i>Rna</i> , 2021 , 27, 1257-1264	5.8	2
108	Engineering Crystal Packing in RNA Structures I: Past and Future Strategies for Engineering RNA Packing in Crystals. <i>Crystals</i> , 2021 , 11,	2.3	3
107	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	5.2	8
106	Parallel Discovery Strategies Provide a Basis for Riboswitch Ligand Design. <i>Cell Chemical Biology</i> , 2020 , 27, 1241-1249.e4	8.2	4
105	Real-time monitoring of single ZTP riboswitches reveals a complex and kinetically controlled decision landscape. <i>Nature Communications</i> , 2020 , 11, 4531	17.4	12
104	Monitoring co-transcriptional folding of riboswitches through helicase unwinding. <i>Methods in Enzymology</i> , 2019 , 623, 209-227	1.7	1
103	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	8.2	12
102	From fluorescent proteins to fluorogenic RNAs: Tools for imaging cellular macromolecules. <i>Protein Science</i> , 2019 , 28, 1374-1386	6.3	21
101	Structure and functional reselection of the Mango-III fluorogenic RNA aptamer. <i>Nature Chemical Biology</i> , 2019 , 15, 472-479	11.7	48
100	RNA G-quadruplex is resolved by repetitive and ATP-dependent mechanism of DHX36. <i>Nature Communications</i> , 2019 , 10, 1855	17.4	35
99	Protein and RNA dynamical fingerprinting. <i>Nature Communications</i> , 2019 , 10, 1026	17.4	35

98	Synthetic ligands for PreQ riboswitches provide structural and mechanistic insights into targeting RNA tertiary structure. <i>Nature Communications</i> , 2019 , 10, 1501	17.4	23
97	Isothermal Titration Calorimetry Measurements of Riboswitch-Ligand Interactions. <i>Methods in Molecular Biology</i> , 2019 , 1964, 75-87	1.4	4
96	Co-crystal structure of the iMango-III fluorescent RNA aptamer using an X-ray free-electron laser. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019 , 75, 547-551	1.1	5
95	Tracking RNA with light: selection, structure, and design of fluorescence turn-on RNA aptamers. <i>Quarterly Reviews of Biophysics</i> , 2019 , 52, e8	7	27
94	Structural basis of G-quadruplex unfolding by the DEAH/RHA helicase DHX36. <i>Nature</i> , 2018 , 558, 465-469	90.4	138
93	Convergent Use of Heptacoordination for Cation Selectivity by RNA and Protein Metalloregulators. <i>Cell Chemical Biology</i> , 2018 , 25, 962-973.e5	8.2	12
92	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	3.2	31
91	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. <i>Rna</i> , 2017 , 23, 655-672	5.8	118
90	Structural basis for high-affinity fluorophore binding and activation by RNA Mango. <i>Nature Chemical Biology</i> , 2017 , 13, 807-813	11.7	77
89	Long-Range Interactions in Riboswitch Control of Gene Expression. <i>Annual Review of Biophysics</i> , 2017 , 46, 455-481	21.1	41
88	A divalent cation-dependent variant of the ribozyme with stringent Ca selectivity co-opts a preexisting nonspecific metal ion-binding site. <i>Rna</i> , 2017 , 23, 355-364	5.8	10
87	A homodimer interface without base pairs in an RNA mimic of red fluorescent protein. <i>Nature Chemical Biology</i> , 2017 , 13, 1195-1201	11.7	67
86	Structural Principles of Fluorescent RNA Aptamers. <i>Trends in Pharmacological Sciences</i> , 2017 , 38, 928-939	13.2	31
85	RNA Binding: Getting Specific about Specificity. <i>Cell Chemical Biology</i> , 2016 , 23, 1177-1178	8.2	2
84	In vitro evolution of coenzyme-independent variants from the glmS ribozyme structural scaffold. <i>Methods</i> , 2016 , 106, 76-81	4.6	3
83	Use of the U1A Protein to Facilitate Crystallization and Structure Determination of Large RNAs. <i>Methods in Molecular Biology</i> , 2016 , 1320, 67-76	1.4	6
82	Many Activities, One Structure: Functional Plasticity of Ribozyme Folds. <i>Molecules</i> , 2016 , 21,	4.8	16
81	The tRNA Elbow in Structure, Recognition and Evolution. <i>Life</i> , 2016 , 6,	3	35

80	RNA quaternary structure and global symmetry. <i>Trends in Biochemical Sciences</i> , 2015 , 40, 211-20	10.3	32
79	Synthesis and applications of RNAs with position-selective labelling and mosaic composition. <i>Nature</i> , 2015 , 522, 368-72	50.4	75
78	Recognition of the bacterial alarmone ZMP through long-distance association of two RNA subdomains. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 679-85	17.6	28
77	RNA-Puzzles Round II: assessment of RNA structure prediction programs applied to three large RNA structures. <i>Rna</i> , 2015 , 21, 1066-84	5.8	122
76	Structure and mechanism of the T-box riboswitches. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015 , 6, 419-33	9.3	29
75	On the shoulders of giants. <i>Rna</i> , 2015 , 21, 504-5	5.8	1
74	Rapid RNA-ligand interaction analysis through high-information content conformational and stability landscapes. <i>Nature Communications</i> , 2015 , 6, 8898	17.4	23
73	Insights into the mechanism of a G-quadruplex-unwinding DEAH-box helicase. <i>Nucleic Acids Research</i> , 2015 , 43, 2223-31	20.1	66
72	Post-crystallization Improvement of RNA Crystals by Synergistic Ion Exchange and Dehydration. <i>Bio-protocol</i> , 2015 , 5,	0.9	1
71	Post-crystallization Improvement of RNA Crystal Diffraction Quality. <i>Methods in Molecular Biology</i> , 2015 , 1316, 13-24	1.4	2
70	Structural basis for activity of highly efficient RNA mimics of green fluorescent protein. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 658-63	17.6	235
69	Dramatic improvement of crystals of large RNAs by cation replacement and dehydration. <i>Structure</i> , 2014 , 22, 1363-1371	5.2	40
68	New molecular engineering approaches for crystallographic studies of large RNAs. <i>Current Opinion in Structural Biology</i> , 2014 , 26, 9-15	8.1	34
67	Validating fragment-based drug discovery for biological RNAs: lead fragments bind and remodel the TPP riboswitch specifically. <i>Chemistry and Biology</i> , 2014 , 21, 591-5		55
66	Direct evaluation of tRNA aminoacylation status by the T-box riboswitch using tRNA-mRNA stacking and steric readout. <i>Molecular Cell</i> , 2014 , 55, 148-55	17.6	37
65	Crystallographic analysis of TPP riboswitch binding by small-molecule ligands discovered through fragment-based drug discovery approaches. <i>Methods in Enzymology</i> , 2014 , 549, 221-33	1.7	3
64	A flexible, scalable method for preparation of homogeneous aminoacylated tRNAs. <i>Methods in Enzymology</i> , 2014 , 549, 105-13	1.7	7
63	Crystal structure of a c-di-AMP riboswitch reveals an internally pseudo-dimeric RNA. <i>EMBO Journal</i> , 2014 , 33, 2692-703	13	46

62	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	6	30
61	Analysis of riboswitch structure and ligand binding using small-angle X-ray scattering (SAXS). <i>Methods in Molecular Biology</i> , 2014 , 1103, 211-25	1.4	7
60	Co-crystal structure of a T-box riboswitch stem I domain in complex with its cognate tRNA. <i>Nature</i> , 2013 , 500, 363-6	50.4	105
59	Glucosamine and glucosamine-6-phosphate derivatives: catalytic cofactor analogues for the glmS ribozyme. <i>Journal of Organic Chemistry</i> , 2013 , 78, 4730-43	4.2	20
58	An in vitro evolved glmS ribozyme has the wild-type fold but loses coenzyme dependence. <i>Nature Chemical Biology</i> , 2013 , 9, 805-10	11.7	26
57	Modulation of quaternary structure and enhancement of ligand binding by the K-turn of tandem glycine riboswitches. <i>Rna</i> , 2013 , 19, 167-76	5.8	35
56	Allosteric tertiary interactions preorganize the c-di-GMP riboswitch and accelerate ligand binding. <i>ACS Chemical Biology</i> , 2012 , 7, 920-7	4.9	57
55	YbxF and YlxQ are bacterial homologs of L7Ae and bind K-turns but not K-loops. <i>Rna</i> , 2012 , 18, 759-70	5.8	38
54	Riboswitches: discovery of drugs that target bacterial gene-regulatory RNAs. <i>Accounts of Chemical Research</i> , 2011 , 44, 1329-38	24.3	150
53	The glmS ribozyme tunes the catalytically critical pK(a) of its coenzyme glucosamine-6-phosphate. <i>Journal of the American Chemical Society</i> , 2011 , 133, 14188-91	16.4	35
52	Use of a coenzyme by the glmS ribozyme-riboswitch suggests primordial expansion of RNA chemistry by small molecules. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2011 , 366, 2942-8	5.8	19
51	The roles of metal ions in regulation by riboswitches. <i>Metal Ions in Life Sciences</i> , 2011 , 9, 141-73		32
50	SEWAL: an open-source platform for next-generation sequence analysis and visualization. <i>Nucleic Acids Research</i> , 2010 , 38, 7908-15	20.1	18
49	The glmS ribozyme: use of a small molecule coenzyme by a gene-regulatory RNA. <i>Quarterly Reviews of Biophysics</i> , 2010 , 43, 423-47	7	53
48	Riboswitch function: flipping the switch or tuning the dimmer?. <i>RNA Biology</i> , 2010 , 7, 328-32	4.8	58
47	Idiosyncratically tuned switching behavior of riboswitch aptamer domains revealed by comparative small-angle X-ray scattering analysis. <i>Rna</i> , 2010 , 16, 598-609	5.8	88
46	Thermodynamic analysis of ligand binding and ligand binding-induced tertiary structure formation by the thiamine pyrophosphate riboswitch. <i>Rna</i> , 2010 , 16, 186-96	5.8	61
45	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, 805-9	5.4	60

44	Rapid construction of empirical RNA fitness landscapes. <i>Science</i> , 2010 , 330, 376-9	33.3	119
43	Use of the spliceosomal protein U1A to facilitate crystallization and structure determination of complex RNAs. <i>Methods</i> , 2010 , 52, 159-67	4.6	41
42	Ribozymes and riboswitches: modulation of RNA function by small molecules. <i>Biochemistry</i> , 2010 , 49, 9123-31	3.2	125
41	Small self-cleaving ribozymes. <i>Cold Spring Harbor Perspectives in Biology</i> , 2010 , 2, a003574	10.2	134
40	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, 343-4	17.6	136
39	Recognition of the bacterial second messenger cyclic diguanylate by its cognate riboswitch. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 1212-7	17.6	163
38	Structure-guided engineering of the regioselectivity of RNA ligase ribozymes. <i>Journal of the American Chemical Society</i> , 2009 , 131, 3532-40	16.4	16
37	Crystallization of the glmS ribozyme-riboswitch. <i>Methods in Molecular Biology</i> , 2009 , 540, 129-39	1.4	16
36	Ribozymes and riboswitches: modulation of RNA function by small molecules. <i>FASEB Journal</i> , 2009 , 23, 326.1	0.9	
35	Structural basis of specific tRNA aminoacylation by a small in vitro selected ribozyme. <i>Nature</i> , 2008 , 454, 358-61	50.4	112
34	Structural basis for specific, high-affinity tetracycline binding by an in vitro evolved aptamer and artificial riboswitch. <i>Chemistry and Biology</i> , 2008 , 15, 1125-37		87
33	Riboswitches: small-molecule recognition by gene regulatory RNAs. <i>Current Opinion in Structural Biology</i> , 2007 , 17, 273-9	8.1	130
32	The structure and function of small nucleolar ribonucleoproteins. <i>Nucleic Acids Research</i> , 2007 , 35, 1452-64	64.1	285
31	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, 178-89	6.5	75
30	Essential role of an active-site guanine in glmS ribozyme catalysis. <i>Journal of the American Chemical Society</i> , 2007 , 129, 14858-9	16.4	80
29	Crystal structures of the thi-box riboswitch bound to thiamine pyrophosphate analogs reveal adaptive RNA-small molecule recognition. <i>Structure</i> , 2006 , 14, 1459-68	5.2	211
28	Structural basis of glmS ribozyme activation by glucosamine-6-phosphate. <i>Science</i> , 2006 , 313, 1752-6	33.3	334
27	Crystal structure of pseudouridine synthase RluA: indirect sequence readout through protein-induced RNA structure. <i>Molecular Cell</i> , 2006 , 24, 535-45	17.6	69

26	Pseudouridine synthases. <i>Chemistry and Biology</i> , 2006 , 13, 1125-35		186
25	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, 2201-6	6.3	26
24	The Cbf5-Nop10 complex is a molecular bracket that organizes box H/ACA RNPs. <i>Nature Structural and Molecular Biology</i> , 2005 , 12, 1101-7	17.6	96
23	Crystallization of the hairpin ribozyme: illustrative protocols. <i>Methods in Molecular Biology</i> , 2004 , 252, 303-11	1.4	19
22	Crystal structure of the highly divergent pseudouridine synthase TruD reveals a circular permutation of a conserved fold. <i>Rna</i> , 2004 , 10, 1026-33	5.8	30
21	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	5.2	120
20	The hairpin ribozyme. <i>Biopolymers</i> , 2004 , 73, 71-8	2.2	54
19	Ribozyme Structural Elements: Hairpin Ribozyme 2004 , 743-746		
18	RNA-modifying enzymes. <i>Current Opinion in Structural Biology</i> , 2003 , 13, 49-55	8.1	63
17	U1A RNA-binding domain at 1.8 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 1521-4		14
16	Transition state stabilization by a catalytic RNA. <i>Science</i> , 2002 , 298, 1421-4	33.3	252
15	Crystal structure of a hairpin ribozyme-inhibitor complex with implications for catalysis. <i>Nature</i> , 2001 , 410, 780-6	50.4	402
14	Methods to crystallize RNA. <i>Current Protocols in Nucleic Acid Chemistry</i> , 2001 , Chapter 7, Unit 7.6	0.5	11
13	Cocrystal structure of a tRNA ^{Psi55} pseudouridine synthase: nucleotide flipping by an RNA-modifying enzyme. <i>Cell</i> , 2001 , 107, 929-39	56.2	234
12	Direct pK(a) measurement of the active-site cytosine in a genomic hepatitis delta virus ribozyme. <i>Journal of the American Chemical Society</i> , 2001 , 123, 8447-52	16.4	94
11	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, 720-7	5.8	75
10	RNA folds: insights from recent crystal structures. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1999 , 28, 57-73		86
9	Crystal structure of a hepatitis delta virus ribozyme. <i>Nature</i> , 1998 , 395, 567-74	50.4	660

8	A general module for RNA crystallization. <i>Journal of Molecular Biology</i> , 1998 , 279, 621-31	6.5	105
7	[10] Dynamic light scattering in evaluating crystallizability of macromolecules. <i>Methods in Enzymology</i> , 1997 , 276, 157-166	1.7	62
6	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, 977-8	20.1	156
5	Probing the solution structure of the DNA-binding protein Max by a combination of proteolysis and mass spectrometry. <i>Protein Science</i> , 1995 , 4, 1088-99	6.3	139
4	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, 19325-9	5.4	17
3	Molecular basis of mouse microphthalmia (mi) mutations helps explain their developmental and phenotypic consequences. <i>Nature Genetics</i> , 1994 , 8, 256-63	36.3	451
2	Use of dynamic light scattering to assess crystallizability of macromolecules and macromolecular assemblies. <i>Structure</i> , 1994 , 2, 357-9	5.2	120
1	Recognition by Max of its cognate DNA through a dimeric b/HLH/Z domain. <i>Nature</i> , 1993 , 363, 38-45	50.4	658