

Fareed Aboul-ela

List of Publications by Citations

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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.

17
papers

1,444
citations

12
h-index

18
g-index

18
ext. papers

1,520
ext. citations

7.5
avg, IF

3.77
L-index

#	Paper	IF	Citations
17	Base-base mismatches. Thermodynamics of double helix formation for dCA3XA3G + dCT3YT3G (X, Y = A,C,G,T). <i>Nucleic Acids Research</i> , 1985 , 13, 4811-24	20.1	411
16	The structure of the human immunodeficiency virus type-1 TAR RNA reveals principles of RNA recognition by Tat protein. <i>Journal of Molecular Biology</i> , 1995 , 253, 313-32	6.5	355
15	Structure of HIV-1 TAR RNA in the absence of ligands reveals a novel conformation of the trinucleotide bulge. <i>Nucleic Acids Research</i> , 1996 , 24, 3974-81	20.1	207
14	Rational design of inhibitors of HIV-1 TAR RNA through the stabilisation of electrostatic "hot spots". <i>Journal of Molecular Biology</i> , 2004 , 336, 343-56	6.5	115
13	Structure-based drug design targeting an inactive RNA conformation: exploiting the flexibility of HIV-1 TAR RNA. <i>Journal of Molecular Biology</i> , 2004 , 336, 625-38	6.5	110
12	Structural basis for contrasting activities of ribosome binding thiazole antibiotics. <i>Chemistry and Biology</i> , 2003 , 10, 769-78		79
11	A mechanism for S-adenosyl methionine assisted formation of a riboswitch conformation: a small molecule with a strong arm. <i>Nucleic Acids Research</i> , 2009 , 37, 6528-39	20.1	43
10	Novel three-dimensional 1H-13C-31P triple resonance experiments for sequential backbone correlations in nucleic acids. <i>Journal of Biomolecular NMR</i> , 1995 , 5, 315-20	3	30
9	Linking aptamer-ligand binding and expression platform folding in riboswitches: prospects for mechanistic modeling and design. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015 , 6, 631-50	9.3	24
8	The impact of a ligand binding on strand migration in the SAM-I riboswitch. <i>PLoS Computational Biology</i> , 2013 , 9, e1003069	5	20
7	Conformational heterogeneity of the SAM-I riboswitch transcriptional ON state: a chaperone-like role for S-adenosyl methionine. <i>Journal of Molecular Biology</i> , 2012 , 418, 331-49	6.5	14
6	Basis for ligand discrimination between ON and OFF state riboswitch conformations: the case of the SAM-I riboswitch. <i>Rna</i> , 2012 , 18, 1230-43	5.8	14
5	Targeting the A site RNA of the Escherichia coli ribosomal 30 S subunit by 2XO-methyl oligoribonucleotides: a quantitative equilibrium dialysis binding assay and differential effects of aminoglycoside antibiotics. <i>Biochemical Journal</i> , 2004 , 383, 201-8	3.8	12
4	Energy landscape analysis for regulatory RNA finding using scalable distributed cyberinfrastructure. <i>Concurrency Computation Practice and Experience</i> , 2011 , 23, 2292-2304	1.4	6
3	The Perturbed Free-Energy Landscape: Linking Ligand Binding to Biomolecular Folding. <i>ChemBioChem</i> , 2021 , 22, 1499-1516	3.8	2
2	Protocol for efficient fluorescence 3Xend-labeling of native noncoding RNA domains. <i>MethodsX</i> , 2020 , 7, 101148	1.9	1
1	Statistical mechanical prediction of ligand perturbation to RNA secondary structure and application to riboswitches. <i>Journal of Computational Chemistry</i> , 2020 , 41, 1521-1537	3.5	1

