

Reza Behrouzi

List of Publications by Year in descending order

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14
papers

431
citations

1039880

9
h-index

1199470

12
g-index

16
all docs

16
docs citations

16
times ranked

590
citing authors

#	ARTICLE	IF	CITATIONS
1	Effects of Preferential Counterion Interactions on the Specificity of RNA Folding. <i>Journal of Physical Chemistry Letters</i> , 2018, 9, 5726-5732.	2.1	1
2	Evolving Models of Heterochromatin: From Foci to Liquid Droplets. <i>Molecular Cell</i> , 2017, 67, 725-727.	4.5	23
3	Recruitment dynamics of ESCRT-III and Vps4 to endosomes and implications for reverse membrane budding. <i>ELife</i> , 2017, 6, .	2.8	138
4	Entropic stabilization of folded RNA in crowded solutions measured by SAXS. <i>Nucleic Acids Research</i> , 2016, 44, gkw597.	6.5	18
5	Heterochromatin assembly by interrupted Sir3 bridges across neighboring nucleosomes. <i>ELife</i> , 2016, 5, .	2.8	30
6	Molecular crowding overcomes the destabilizing effects of mutations in a bacterial ribozyme. <i>Nucleic Acids Research</i> , 2015, 43, 1170-1176.	6.5	23
7	Crowders Perturb the Entropy of RNA Energy Landscapes to Favor Folding. <i>Journal of the American Chemical Society</i> , 2013, 135, 10055-10063.	6.6	49
8	Native Architecture Encodes Cooperativity and Specificity in RNA Folding Intermediates. <i>Biophysical Journal</i> , 2012, 102, 645a-646a.	0.2	0
9	Cooperative Tertiary Interaction Network Guides RNA Folding. <i>Cell</i> , 2012, 149, 348-357.	13.5	88
10	Rendering RNA in 3D. <i>Nature Methods</i> , 2012, 9, 552-553.	9.0	0
11	Structural Rearrangements Linked to Global Folding Pathways of the Azoarcus Group I Ribozyme. <i>Journal of Molecular Biology</i> , 2009, 386, 1167-1178.	2.0	37
12	Kinetics and Mechanism of RNA Folding studied by SAXS. <i>Biophysical Journal</i> , 2009, 96, 575a.	0.2	3
13	Adaptation of proteins to different environments: A comparison of proteome structural properties in <i>Bacillus subtilis</i> and <i>Escherichia coli</i> . <i>Journal of Theoretical Biology</i> , 2007, 244, 127-132.	0.8	9
14	Modeling directed ligand passage toward enzyme active site by a $\tilde{\text{double}}$ cellular automata TM model. <i>Biochemical and Biophysical Research Communications</i> , 2005, 333, 1-4.	1.0	8