Yi Xiao

List of Publications by Year
in descending order

58 papers	1,769 citations	394421 19 h-index	302126 39 g-index
58 all docs	58 docs citations	58 times ranked	1699 citing authors

#	Article	IF	Citations
1	Automated and fast building of three-dimensional RNA structures. Scientific Reports, 2012, 2, 734.	3.3	176
2	RNA-Puzzles Round II: assessment of RNA structure prediction programs applied to three large RNA structures. Rna, 2015, 21, 1066-1084.	3.5	161
3	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	3.5	158
4	Molecular Mechanism of Evolution and Human Infection with SARS-CoV-2. Viruses, 2020, 12, 428.	3.3	140
5	Optimization of RNA 3D structure prediction using evolutionary restraints of nucleotideâ€“nucleotide interactions from direct coupling analysis. Nucleic Acids Research, 2017, 45, 6299-6309.	14.5	103
6	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. Rna, 2020, 26, 982-995.	3.5	100
7	3dRNA v2.0: An Updated Web Server for RNA 3D Structure Prediction. International Journal of Molecular Sciences, 2019, 20, 4116.	4.1	92
8	Analytical Method for Yrast Line States in Interacting Bose-Einstein Condensates. Physical Review Letters, 2001, 86, 2200-2203.	7.8	91
9	3dRNAscore: a distance and torsion angle dependent evaluation function of 3D RNA structures. Nucleic Acids Research, 2015, 43, e63-e63.	14.5	82
10	A novel protocol for three-dimensional structure prediction of RNA-protein complexes. Scientific Reports, 2013, 3, 1887.	3.3	57
11	Role of Ligand Binding in Structural Organization ofAddA-riboswitch Aptamer: A Molecular Dynamics Simulation. Journal of Biomolecular Structure and Dynamics, 2011, 29, 403-416.	3.5	41
12	Folding kinetics of WW domains with the united residue force field for bridging microscopic motions and experimental measurements. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18243-18248.	7.1	36
13	Folding Mechanism of Beta-Hairpin Trpzip2: Heterogeneity, Transition State and Folding Pathways. International Journal of Molecular Sciences, 2009, 10, 2838-2848.	4.1	31
14	3dRNA: Building RNA 3D structure with improved template library. Computational and Structural Biotechnology Journal, 2020, 18, 2416-2423.	4.1	31
15	Evaluation of RNA secondary structure prediction for both base-pairing and topology. Biophysics Reports, 2018, 4, 123-132.	0.8	28
16	Insights into Ligand Binding to PreQ1 Riboswitch Aptamer from Molecular Dynamics Simulations. PLoS ONE, 2014, 9, e92247.	2.5	26
17	Dynamics of metal ions around an RNA molecule. Physical Review E, 2019, 99, 012420.	2.1	24
18	HNADOCK: a nucleic acid docking server for modeling RNA/DNAâ€“RNA/DNA 3D complex structures. Nucleic Acids Research, 2019, 47, W35-W42.	14.5	24

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19	Genomic Variants in NEURL, GJA1 and CUX2 Significantly Increase Genetic Susceptibility to Atrial Fibrillation. Scientific Reports, 2018, 8, 3297.	3.3	21
20	Angiotensin II increases angiogenesis by NFâ€ºBâ€“mediated transcriptional activation of angiogenic factor AGGF1. FASEB Journal, 2018, 32, 5051-5062.	0.5	21
21	Using 3dRNA for RNA 3â€D Structure Prediction and Evaluation. Current Protocols in Bioinformatics, 2017, 57, 5.9.1-5.9.12.	25.8	20
22	3dRPC: a web server for 3D RNAâ€“protein structure prediction. Bioinformatics, 2018, 34, 1238-1240.	4.1	20
23	Prediction of RNA secondary structure with pseudoknots using coupled deep neural networks. Biophysics Reports, 2020, 6, 146-154.	0.8	19
24	Electrostatics of Prokaryotic Ribosome and Its Biological Implication. Biophysical Journal, 2020, 118, 1205-1212.	0.5	19
25	Computational Study of Unfolding and Regulation Mechanism of preQ1 Riboswitches. PLoS ONE, 2012, 7, e45239.	2.5	17
26	Types and concentrations of metal ions affect local structure and dynamics of RNA. Physical Review E, 2016, 94, 040401.	2.1	16
27	Computational evidence that fast translation speed can increase the probability of cotranslational protein folding. Scientific Reports, 2015, 5, 15316.	3.3	14
28	The protein folding network indicates that the ultrafast folding mutant of villin headpiece subdomain has a deeper folding funnel. Journal of Chemical Physics, 2011, 134, 205104.	3.0	13
29	Using 3dRPC for RNAâ€“protein complex structure prediction. Biophysics Reports, 2016, 2, 95-99.	0.8	13
30	A pair-conformation-dependent scoring function for evaluating 3D RNA-protein complex structures. PLoS ONE, 2017, 12, e0174662.	2.5	13
31	A novel folding pathway of the villin headpiece subdomain HP35. Physical Chemistry Chemical Physics, 2019, 21, 18219-18226.	2.8	13
32	A fast tomographic method for searching the minimum free energy path. Journal of Chemical Physics, 2014, 141, 154109.	3.0	12
33	Nonlinear analysis of correlations in Alu repeat sequences in DNA. Physical Review E, 2003, 68, 061913.	2.1	11
34	Preorientation of protein and RNA just before contacting. Journal of Biomolecular Structure and Dynamics, 2013, 31, 716-728.	3.5	10
35	Simulation study of the role of the ribosomal exit tunnel on protein folding. Physical Review E, 2013, 87, 022701.	2.1	10
36	Length-Dependent Deep Learning Model for RNA Secondary Structure Prediction. Molecules, 2022, 27, 1030.	3.8	10

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37	Computational study of stability of an H-H-type pseudoknot motif. Physical Review E, 2015, 92, 062705.	2.1	9
38	Periodic synchronization in a system of coupled phase oscillators with attractive and repulsive interactions. Frontiers of Physics, 2018, 13, 1.	5.0	9
39	Molecular dynamics simulation of the binding process of ligands to the add adenine riboswitch aptamer. Physical Review E, 2019, 100, 022412.	2.1	9
40	Antitumor Activities of tRNA-Derived Fragments and tRNA Halves from Non-pathogenic Escherichia coli Strains on Colorectal Cancer and Their Structure-Activity Relationship. MSystems, 2022, 7, e0016422.	3.8	9
41	Design of Tat-Activated Cdk9 Inhibitor. International Journal of Peptide Research and Therapeutics, 2019, 25, 807-817.	1.9	7
42	Improving the replica-exchange molecular-dynamics method for efficient sampling in the temperature space. Physical Review E, 2015, 91, 052708.	2.1	6
43	Multistable states in a system of coupled phase oscillators with inertia. Scientific Reports, 2017, 7, 42178.	3.3	6
44	Pathway regulation mechanism revealed by cotranslational folding of villin headpiece subdomain HP35. Physical Review E, 2020, 101, 052403.	2.1	5
45	Using the generalized Born surface area model to fold proteins yields more effective sampling while qualitatively preserving the folding landscape. Physical Review E, 2020, 101, 062417.	2.1	5
46	Modeling of the Long-Term Epidemic Dynamics of COVID-19 in the United States. International Journal of Environmental Research and Public Health, 2021, 18, 7594.	2.6	5
47	Structural modeling of human cardiac sodium channel pore domain. Journal of Biomolecular Structure and Dynamics, 2018, 36, 2268-2278.	3.5	4
48	Molecular dynamics study of ways of RNA base-pair formation. Physical Review E, 2020, 102, 032403.	2.1	4
49	Inference of RNA structural contacts by direct coupling analysis. Communications in Information and Systems, 2019, 19, 279-297.	0.5	4
50	LOCAL COMPLEXITY OF PROTEIN SEQUENCES. International Journal of Modern Physics C, 2003, 14, 1191-1199.	1.7	3
51	A symmetry-related sequence-structure relation of proteins. Science Bulletin, 2005, 50, 536-538.	1.7	3
52	Learning the Fastest RNA Folding Path Based on Reinforcement Learning and Monte Carlo Tree Search. Molecules, 2021, 26, 4420.	3.8	3
53	Role of cotranslational folding for Î²-sheet-enriched proteins: A perspective from molecular dynamics simulations. Physical Review E, 2022, 105, 024402.	2.1	3
54	CHAOTIC DYNAMICS OF A FIVE-DIMENSIONAL NONLINEAR NETWORK. International Journal of Modern Physics C, 2007, 18, 335-342.	1.7	1

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55	Hierarchical Conformational Dynamics Confers Thermal Adaptability to preQ1 RNA Riboswitches. Journal of Molecular Biology, 2020, 432, 4523-4543.	4.2	1
56	DYNAMIC MOVES IN LATTICE SIMULATION OF PROTEIN FOLDING. International Journal of Modern Physics C, 2004, 15, 885-892.	1.7	0
57	Design of a Genetically Programmed Biomimetic Lipase Nanoreactor. ACS Applied Bio Materials, 2021, 4, 3518-3523.	4.6	0
58	Comparison of two algorithms of direct coupling analysis of protein. Communications in Information and Systems, 2019, 19, 1-15.	0.5	0