Shiyong Liu

List of Publications by Year
in descending order

31	1,081	430874 18	434195 31
papers	citations	h-index	g-index

35	35	35	1516
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Two novel RNA-binding proteins identification through computational prediction and experimental validation. Genomics, 2022, 114, 149-160.	2.9	0
2	Molecular insight into coordination sites for substrates and their coupling kinetics in Na⁺/HCO₃^{â^'} cotransporter NBCe1. Journal of Physiology, 2022, 600, 3083-3111.	2.9	5
3	Protein-DNA complex structure modeling based on structural template. Biochemical and Biophysical Research Communications, 2021, 577, 152-157.	2.1	1
4	RR3DD: an RNA global structure-based RNA three-dimensional structural classification database. RNA Biology, 2021, , 1-9.	3.1	2
5	P3DOCK: a proteinâ€“RNA docking webserver based on template-based and template-free docking. Bioinformatics, 2020, 36, 96-103.	4.1	15
6	PRIME-3D2D is a 3D2D model to predict binding sites of proteinâ€“RNA interaction. Communications Biology, 2020, 3, 384.	4.4	11
7	A novel antiviral lncRNA, EDAL, shields a T309 O-GlcNAcylation site to promote EZH2 lysosomal degradation. Genome Biology, 2020, 21, 228.	8.8	38
8	RMalign: an RNA structural alignment tool based on a novel scoring function RMscore. BMC Genomics, 2019, 20, 276.	2.8	20
9	CPPred: coding potential prediction based on the global description of RNA sequence. Nucleic Acids Research, 2019, 47, e43-e43.	14.5	84
10	Structural modeling of human cardiac sodium channel pore domain. Journal of Biomolecular Structure and Dynamics, 2018, 36, 2268-2278.	3.5	4
11	Deep-RBPPred: Predicting RNA binding proteins in the proteome scale based on deep learning. Scientific Reports, 2018, 8, 15264.	3.3	42
12	Small GTPases SAR1A and SAR1B regulate the trafficking of the cardiac sodium channel Nav1.5. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 3672-3684.	3.8	20
13	RBPPred: predicting RNA-binding proteins from sequence using SVM. Bioinformatics, 2017, 33, 854-862.	4.1	75
14	Rabies viruses leader RNA interacts with host Hsc70 and inhibits virus replication. Oncotarget, 2017, 8, 43822-43837.	1.8	13
15	Template-Based Modeling of Protein-RNA Interactions. PLoS Computational Biology, 2016, 12, e1005120.	3.2	29
16	Break CDK2/Cyclin E1 Interface Allosterically with Small Peptides. PLoS ONE, 2014, 9, e109154.	2.5	19
17	Preorientation of protein and RNA just before contacting. Journal of Biomolecular Structure and Dynamics, 2013, 31, 716-728.	3.5	10
18	A novel protocol for three-dimensional structure prediction of RNA-protein complexes. Scientific Reports, 2013, 3, 1887.	3.3	57

#	Article	IF	Citations
19	Novel EDA p.Ile260Ser Mutation Linked to Non-syndromic Hypodontia. Journal of Dental Research, 2013, 92, 500-506.	5.2	21
20	The dataset for proteinâ€“RNA binding affinity. Protein Science, 2013, 22, 1808-1811.	7.6	32
21	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987.	2.6	87
22	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
23	ASPDock: protein-protein docking algorithm using atomic solvation parameters model. BMC Bioinformatics, 2011, 12, 36.	2.6	31
24	DECK: Distance and environment-dependent, coarse-grained, knowledge-based potentials for protein-protein docking. BMC Bioinformatics, 2011, 12, 280.	2.6	47
25	Dynamic property is a key determinant for proteinâ€“protein interactions. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1323-1331.	2.6	11
26	Chemically Induced Dimerization of Human Nonpancreatic Secretory Phospholipase A2 by Bis-indole Derivatives. Journal of Medicinal Chemistry, 2008, 51, 3360-3366.	6.4	9
27	D<scp>ockground</scp> proteinâ€“protein docking decoy set. Bioinformatics, 2008, 24, 2634-2635.	4.1	66
28	Nonnatural protein-protein interaction-pair design by key residues grafting. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5330-5335.	7.1	75
29	A combinatorial score to distinguish biological and nonbiological proteinâ€“protein interfaces. Proteins: Structure, Function and Bioinformatics, 2006, 64, 68-78.	2.6	25
30	Quaternary Structure, Substrate Selectivity and Inhibitor Design for SARS 3C-Like Proteinase. Current Pharmaceutical Design, 2006, 12, 4555-4564.	1.9	28
31	Virtual Screening of Novel Noncovalent Inhibitors for SARS-CoV 3C-like Proteinase. Journal of Chemical Information and Modeling, 2005, 45, 10-17.	5.4	65