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	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
2	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
3	CPPred: coding potential prediction based on the global description of RNA sequence. Nucleic Acids Research, 2019, 47, e43-e43.	14.5	84
4	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
5	RBPPred: predicting RNA-binding proteins from sequence using SVM. Bioinformatics, 2017, 33, 854-862.	4.1	75
6	D<scp>ockground</scp> proteinâ€“protein docking decoy set. Bioinformatics, 2008, 24, 2634-2635.	4.1	66
7	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
8	A novel protocol for three-dimensional structure prediction of RNA-protein complexes. Scientific Reports, 2013, 3, 1887.	3.3	57
9	DECK: Distance and environment-dependent, coarse-grained, knowledge-based potentials for protein-protein docking. BMC Bioinformatics, 2011, 12, 280.	2.6	47
10	Deep-RBPPred: Predicting RNA binding proteins in the proteome scale based on deep learning. Scientific Reports, 2018, 8, 15264.	3.3	42
11	A novel antiviral lncRNA, EDAL, shields a T309 O-GlcNAcylation site to promote EZH2 lysosomal degradation. Genome Biology, 2020, 21, 228.	8.8	38
12	The dataset for proteinâ€“RNA binding affinity. Protein Science, 2013, 22, 1808-1811.	7.6	32
13	ASPDock: protein-protein docking algorithm using atomic solvation parameters model. BMC Bioinformatics, 2011, 12, 36.	2.6	31
14	Template-Based Modeling of Protein-RNA Interactions. PLoS Computational Biology, 2016, 12, e1005120.	3.2	29
15	Quaternary Structure, Substrate Selectivity and Inhibitor Design for SARS 3C-Like Proteinase. Current Pharmaceutical Design, 2006, 12, 4555-4564.	1.9	28
16	A combinatorial score to distinguish biological and nonbiological proteinâ€“protein interfaces. Proteins: Structure, Function and Bioinformatics, 2006, 64, 68-78.	2.6	25
17	Novel EDA p.Ile260Ser Mutation Linked to Non-syndromic Hypodontia. Journal of Dental Research, 2013, 92, 500-506.	5.2	21
18	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

#	Article	IF	Citations
19	RMalign: an RNA structural alignment tool based on a novel scoring function RMscore. BMC Genomics, 2019, 20, 276.	2.8	20
20	Break CDK2/Cyclin E1 Interface Allosterically with Small Peptides. PLoS ONE, 2014, 9, e109154.	2.5	19
21	P3DOCK: a proteinâ€“RNA docking webserver based on template-based and template-free docking. Bioinformatics, 2020, 36, 96-103.	4.1	15
22	Rabies viruses leader RNA interacts with host Hsc70 and inhibits virus replication. Oncotarget, 2017, 8, 43822-43837.	1.8	13
23	Dynamic property is a key determinant for proteinâ€“protein interactions. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1323-1331.	2.6	11
24	PRIME-3D2D is a 3D2D model to predict binding sites of proteinâ€“RNA interaction. Communications Biology, 2020, 3, 384.	4.4	11
25	Preorientation of protein and RNA just before contacting. Journal of Biomolecular Structure and Dynamics, 2013, 31, 716-728.	3.5	10
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	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
28	Structural modeling of human cardiac sodium channel pore domain. Journal of Biomolecular Structure and Dynamics, 2018, 36, 2268-2278.	3.5	4
29	RR3DD: an RNA global structure-based RNA three-dimensional structural classification database. RNA Biology, 2021, , 1-9.	3.1	2
30	Protein-DNA complex structure modeling based on structural template. Biochemical and Biophysical Research Communications, 2021, 577, 152-157.	2.1	1
31	Two novel RNA-binding proteins identification through computational prediction and experimental validation. Genomics, 2022, 114, 149-160.	2.9	0