Chengfei Yan

List of Publications by Year
in descending order

16 papers	661 citations	759233 12 h-index	940533 16 g-index
17 all docs	17 docs citations	17 times ranked	1228 citing authors

#	Article	IF	Citations
1	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	2.6	148
2	HiC-spector: a matrix library for spectral and reproducibility analysis of Hi-C contact maps. Bioinformatics, 2017, 33, 2199-2201.	4.1	92
3	Fully Blind Docking at the Atomic Level for Protein-Peptide Complex Structure Prediction. Structure, 2016, 24, 1842-1853.	3.3	86
4	Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. Nature Methods, 2020, 17, 807-814.	19.0	71
5	MDockPeP: An abâ€initio proteinâ€“peptide docking server. Journal of Computational Chemistry, 2018, 39, 2409-2413.	3.3	59
6	Genomics and data science: an application within an umbrella. Genome Biology, 2019, 20, 109.	8.8	46
7	Predicting peptide binding sites on protein surfaces by clustering chemical interactions. Journal of Computational Chemistry, 2015, 36, 49-61.	3.3	41
8	Iterative Knowledge-Based Scoring Functions Derived from Rigid and Flexible Decoy Structures: Evaluation with the 2013 and 2014 CSAR Benchmarks. Journal of Chemical Information and Modeling, 2016, 56, 1013-1021.	5.4	21
9	Inclusion of the orientational entropic effect and lowâ€resolution experimental information for proteinâ€“protein docking in Critical Assessment of PRedicted Interactions (CAPRI). Proteins: Structure, Function and Bioinformatics, 2013, 81, 2183-2191.	2.6	18
10	Automated Large-Scale File Preparation, Docking, and Scoring: Evaluation of ITScore and STScore Using the 2012 Community Structureâ€“Activity Resource Benchmark. Journal of Chemical Information and Modeling, 2013, 53, 1905-1914.	5.4	18
11	Improving binding mode and binding affinity predictions of docking by ligand-based search of protein conformations: evaluation in D3R grand challenge 2015. Journal of Computer-Aided Molecular Design, 2017, 31, 689-699.	2.9	15
12	Computation and Simulation of the Structural Characteristics of the Kidney Urea Transporter and Behaviors of Urea Transport. Journal of Physical Chemistry B, 2015, 119, 5124-5131.	2.6	13
13	Performance of MDockPP in CAPRI rounds 28â€29 and 31â€35 including the prediction of waterâ€mediated interactions. Proteins: Structure, Function and Bioinformatics, 2017, 85, 424-434.	2.6	11
14	MDock: An Ensemble Docking Suite for Molecular Docking, Scoring and In Silico Screening. Methods in Pharmacology and Toxicology, 2015, , 153-166.	0.2	8
15	Building a Hybrid Physical-Statistical Classifier for Predicting the Effect of Variants Related to Protein-Drug Interactions. Structure, 2019, 27, 1469-1481.e3.	3.3	6
16	The Usage of ACCLUSTER for Peptide Binding Site Prediction. Methods in Molecular Biology, 2017, 1561, 3-9.	0.9	2