

Cunliang Geng

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

820
citations

687363

13
h-index

940533

16
g-index

23
all docs

23
docs citations

23
times ranked

1073
citing authors

#	ARTICLE	IF	CITATIONS
1	Large-scale prediction of binding affinity in protein–small ligand complexes: the PRODIGY-LIG web server. <i>Bioinformatics</i> , 2019, 35, 1585-1587.	4.1	130
2	Blind prediction of homo– and hetero–protein complexes: The CASP13–CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1200-1221.	2.6	99
3	Performance of HADDOCK and a simple contact-based protein–ligand binding affinity predictor in the D3R Grand Challenge 2. <i>Journal of Computer-Aided Molecular Design</i> , 2018, 32, 175-185.	2.9	97
4	Finding the “hot spot”: Are predictors of binding affinity changes upon mutations in protein–protein interactions ready for it?. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2019, 9, e1410.	14.6	86
5	iScore: a novel graph kernel-based function for scoring protein–protein docking models. <i>Bioinformatics</i> , 2020, 36, 112-121.	4.1	62
6	iSEE: Interface structure, evolution, and energy-based machine learning predictor of binding affinity changes upon mutations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 110-119.	2.6	58
7	DeepRank: a deep learning framework for data mining 3D protein-protein interfaces. <i>Nature Communications</i> , 2021, 12, 7068.	12.8	56
8	N-Glycoform Diversity of Cellobiohydrolase I from <i>Penicillium decumbens</i> and Synergism of Nonhydrolytic Glycoform in Cellulose Degradation. <i>Journal of Biological Chemistry</i> , 2012, 287, 15906-15915.	3.4	55
9	matchms - processing and similarity evaluation of mass spectrometry data.. <i>Journal of Open Source Software</i> , 2020, 5, 2411.	4.6	48
10	Information-Driven, Ensemble Flexible Peptide Docking Using HADDOCK. <i>Methods in Molecular Biology</i> , 2017, 1561, 109-138.	0.9	35
11	Exploring the interplay between experimental methods and the performance of predictors of binding affinity change upon mutations in protein complexes. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 291-299.	2.1	26
12	Purification, Cloning, Characterization and Essential Amino Acid Residues Analysis of a New β -Carrageenase from <i>Cellulophaga</i> sp. QY3. <i>PLoS ONE</i> , 2013, 8, e64666.	2.5	22
13	An overview of data-driven HADDOCK strategies in CAPRI rounds 38–45. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1029-1036.	2.6	11
14	The pdb2sql Python Package: Parsing, Manipulation and Analysis of PDB Files Using SQL Queries. <i>Journal of Open Source Software</i> , 2020, 5, 2077.	4.6	7
15	iScore: An MPI supported software for ranking protein–protein docking models based on a random walk graph kernel and support vector machines. <i>SoftwareX</i> , 2020, 11, 100462.	2.6	5
16	How Processive Enzymes Work: the Application of Molecular Dynamics Simulation to Study the Catalytic Mechanism. <i>Scientia Sinica Vitae</i> , 2012, 42, 603-612.	0.3	0