

Tanggis Bohnuud

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11526450/publications.pdf>

Version: 2024-02-01

13
papers

2,194
citations

840776

11
h-index

1125743

13
g-index

13
all docs

13
docs citations

13
times ranked

3584
citing authors

#	ARTICLE	IF	CITATIONS
1	A benchmark testing ground for integrating homology modeling and protein docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 10-16.	2.6	29
2	ClusPro PeptiDock: efficient global docking of peptide recognition motifs using FFT. <i>Bioinformatics</i> , 2017, 33, 3299-3301.	4.1	102
3	New additions to the <scp>C</scp>lus<scp>P</scp>ro server motivated by <scp>CAPRI</scp>. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 435-444.	2.6	395
4	Detection of Peptide-Binding Sites on Protein Surfaces Using the Peptimap Server. <i>Methods in Molecular Biology</i> , 2017, 1561, 11-20.	0.9	8
5	Focused grid-based resampling for protein docking and mapping. <i>Journal of Computational Chemistry</i> , 2016, 37, 961-970.	3.3	6
6	Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CASP-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 323-348.	2.6	148
7	The FTMap family of web servers for determining and characterizing ligand-binding hot spots of proteins. <i>Nature Protocols</i> , 2015, 10, 733-755.	12.0	496
8	Evidence of Conformational Selection Driving the Formation of Ligand Binding Sites in Protein-Protein Interfaces. <i>PLoS Computational Biology</i> , 2014, 10, e1003872.	3.2	22
9	How good is automated protein docking?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 2159-2166.	2.6	570
10	Detection of peptide-binding sites on protein surfaces: The first step toward the modeling and targeting of peptide-mediated interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 2096-2105.	2.6	95
11	Application of asymmetric statistical potentials to antibody-protein docking. <i>Bioinformatics</i> , 2012, 28, 2608-2614.	4.1	156
12	Computational mapping reveals dramatic effect of Hoogsteen breathing on duplex DNA reactivity with formaldehyde. <i>Nucleic Acids Research</i> , 2012, 40, 7644-7652.	14.5	37
13	FTMAP: extended protein mapping with user-selected probe molecules. <i>Nucleic Acids Research</i> , 2012, 40, W271-W275.	14.5	130