

CITATION REPORT

List of articles citing

A systematic analysis of scoring functions in rigid-body protein docking: The delicate balance between the predictive rate improvement and the risk of overtraining

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Proteins: Structure, Function and Bioinformatics, 2017, 85, 1287-1297.

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#	Paper	IF	Citations
12	Flexible Protein-Protein Docking with SwarmDock. <i>Methods in Molecular Biology</i> , 2018 , 1764, 413-428	1.4	10
11	SKEMPI 2.0: an updated benchmark of changes in protein-protein binding energy, kinetics and thermodynamics upon mutation. <i>Bioinformatics</i> , 2019 , 35, 462-469	7.2	92
10	Computational Modeling of Designed Ankyrin Repeat Protein Complexes with Their Targets. <i>Journal of Molecular Biology</i> , 2019 , 431, 2852-2868	6.5	2
9	Modeling of Protein Complexes and Molecular Assemblies with pyDock. <i>Methods in Molecular Biology</i> , 2020 , 2165, 175-198	1.4	2
8	Template-Based Modeling of Protein Complexes Using the PPI3D Web Server. <i>Methods in Molecular Biology</i> , 2020 , 2165, 139-155	1.4	2
7	SKEMPI 2.0: An updated benchmark of changes in protein-protein binding energy, kinetics and thermodynamics upon mutation.		1
6	A Guide for Protein-Protein Docking Using SwarmDock. <i>Methods in Molecular Biology</i> , 2020 , 2165, 199-2164		1
5	PPI-Hotspot: Database of Protein-Protein Interaction Hot Spots.. <i>Journal of Chemical Information and Modeling</i> , 2022 ,	6.1	0
4	Prediction of Protein-Protein Binding Affinities from Unbound Protein Structures. <i>Methods in Molecular Biology</i> , 2022 , 2385, 335-351	1.4	0
3	Improving classification of correct and incorrect protein-protein docking models by augmenting the training set.		0
2	Multi-state modeling of antibody-antigen complexes with SAXS profiles and deep-learning models. 2022 ,		0
1	Improving classification of correct and incorrect protein-protein docking models by augmenting the training set. 2023 , 3,		0