Shide Liang

List of Publications by Year
in descending order

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32	1,678	471371 17	414303 32
papers	citations	h-index	g-index

33	33	33	2162
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	De novo protein design by an energy function based on series expansion in distance and orientation dependence. Bioinformatics, 2021, 38, 86-93.	1.8	8
2	Prediction of immunogenicity for humanized and full human therapeutic antibodies. PLoS ONE, 2020, 15, e0238150.	1.1	10
3	SVMTriP: A Method to Predict B-Cell Linear Antigenic Epitopes. Methods in Molecular Biology, 2020, 2131, 299-307.	0.4	18
4	EPCES and EPSVR: Prediction of B-Cell Antigenic Epitopes on Protein Surfaces with Conformational Information. Methods in Molecular Biology, 2020, 2131, 289-297.	0.4	2
5	LEAP: Highly accurate prediction of protein loop conformations by integrating coarseâ€grained sampling and optimized energy scores with allâ€atom refinement of backbone and side chains. Journal of Computational Chemistry, 2014, 35, 335-341.	1.5	34
6	Kotai Antibody Builder: automated high-resolution structural modeling of antibodies. Bioinformatics, 2014, 30, 3279-3280.	1.8	50
7	Highâ€resolution modeling of antibody structures by a combination of bioinformatics, expert knowledge, and molecular simulations. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1624-1635.	1.5	46
8	A novel function prediction approach using protein overlap networks. BMC Systems Biology, 2013, 7, 61.	3.0	13
9	Conformational B-Cell Epitope Prediction on Antigen Protein Structures: A Review of Current Algorithms and Comparison with Common Binding Site Prediction Methods. PLoS ONE, 2013, 8, e62249.	1.1	101
10	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987.	1.5	87
11	Protein Loop Modeling with Optimized Backbone Potential Functions. Journal of Chemical Theory and Computation, 2012, 8, 1820-1827.	2.3	17
12	SVMTriP: A Method to Predict Antigenic Epitopes Using Support Vector Machine to Integrate Tri-Peptide Similarity and Propensity. PLoS ONE, 2012, 7, e45152.	1.1	269
13	Protein loop selection using orientationâ€dependent force fields derived by parameter optimization. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2260-2267.	1.5	8
14	Protein side chain modeling with orientationâ€dependent atomic force fields derived by series expansions. Journal of Computational Chemistry, 2011, 32, 1680-1686.	1.5	35
15	Fast and accurate prediction of protein side-chain conformations. Bioinformatics, 2011, 27, 2913-2914.	1.8	53
16	EPSVR and EPMeta: prediction of antigenic epitopes using support vector regression and multiple server results. BMC Bioinformatics, 2010, 11, 381.	1.2	140
17	Incorporating receptor flexibility in the molecular design of protein interfaces. Protein Engineering, Design and Selection, 2009, 22, 575-586.	1.0	13
18	Prediction of antigenic epitopes on protein surfaces by consensus scoring. BMC Bioinformatics, 2009, 10, 302.	1.2	99

#	Article	IF	Citations
19	Consensus scoring for enriching nearâ€native structures from proteinâ€“protein docking decoys. Proteins: Structure, Function and Bioinformatics, 2009, 75, 397-403.	1.5	36
20	Refining nearâ€native proteinâ€“protein docking decoys by local resampling and energy minimization. Proteins: Structure, Function and Bioinformatics, 2009, 76, 309-316.	1.5	10
21	Side-chain modeling with an optimized scoring function. Protein Science, 2009, 11, 322-331.	3.1	114
22	Exploring the Molecular Design of Protein Interaction Sites with Molecular Dynamics Simulations and Free Energy Calculations. Biochemistry, 2009, 48, 399-414.	1.2	47
23	Fold recognition by concurrent use of solvent accessibility and residue depth. Proteins: Structure, Function and Bioinformatics, 2007, 68, 636-645.	1.5	87
24	A simple reference state makes a significant improvement in nearâ€native selections from structurally refined docking decoys. Proteins: Structure, Function and Bioinformatics, 2007, 69, 244-253.	1.5	59
25	Protein binding site prediction using an empirical scoring function. Nucleic Acids Research, 2006, 34, 3698-3707.	6.5	223
26	Prediction of the interaction site on the surface of an isolated protein structure by analysis of side chain energy scores. Proteins: Structure, Function and Bioinformatics, 2004, 57, 548-557.	1.5	17
27	Effective scoring function for protein sequence design. Proteins: Structure, Function and Bioinformatics, 2003, 54, 271-281.	1.5	43
28	Beyond the rotamer library: Genetic algorithm combined with the disturbing mutation process for upbuilding protein side-chains. Proteins: Structure, Function and Bioinformatics, 2002, 50, 49-62.	1.5	14
29	Construction of protein binding sites in scaffold structures. Biopolymers, 2000, 54, 515-523.	1.2	15
30	Grafting of protein-protein binding sites. Science Bulletin, 2000, 45, 1707-1712.	1.7	1
31	Grafting of Protein-Protein Interaction Epitope. Journal of Biomolecular Structure and Dynamics, 2000, 17, 821-828.	2.0	7
32	Rational screenning in combinatorial peptide libraries of protein functional loop. Science Bulletin, 1999, 44, 2150-2154.	1.7	0