Pirooz Vakili

List of Publications by Year in descending order

33 papers	691 citations	687363 13 h-index	839539 18 g-index
34 all docs	34 docs citations	34 times ranked	909 citing authors

#	Article	IF	Citations
1	Achieving reliability and high accuracy in automated protein docking: Cluspro, PIPER, SDU, and stability analysis in CAPRI rounds 13â€“19. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3124-3130.	2.6	211
2	Using a standard clock technique for efficient simulation. Operations Research Letters, 1991, 10, 445-452.	0.7	86
3	Encounter complexes and dimensionality reduction in proteinâ€“protein association. ELife, 2014, 3, e01370.	6.0	61
4	Massively parallel and distributed simulation of a class of discrete event systems. ACM Transactions on Modeling and Computer Simulation, 1992, 2, 214-238.	0.8	42
5	Protein Docking by the Underestimation of Free Energy Funnels in the Space of Encounter Complexes. PLoS Computational Biology, 2008, 4, e1000191.	3.2	41
6	On the efficient generation of discrete event sample paths under different system parameter values. Mathematics and Computers in Simulation, 1988, 30, 347-370.	4.4	27
7	A Non-myopic Utility Function for Statistical Global Optimization Algorithms. Journal of Global Optimization, 1999, 14, 283-298.	1.8	26
8	Energy Minimization on Manifolds for Docking Flexible Molecules. Journal of Chemical Theory and Computation, 2015, 11, 1063-1076.	5.3	24
9	Comparing Markov Chains Simulated in Parallel. Probability in the Engineering and Informational Sciences, 1994, 8, 309-326.	0.8	22
10	Rigid Body Energy Minimization on Manifolds for Molecular Docking. Journal of Chemical Theory and Computation, 2012, 8, 4374-4380.	5.3	22
11	SDU: A Semidefinite Programming-Based Underestimation Method for Stochastic Global Optimization in Protein Docking. IEEE Transactions on Automatic Control, 2007, 52, 664-676.	5.7	20
12	Variance reduction algorithms for parallel replicated simulation of uniformized Markov chains. Discrete Event Dynamic Systems: Theory and Applications, 1996, 6, 159-180.	1.5	15
13	The Impact of Side-Chain Packing on Protein Docking Refinement. Journal of Chemical Information and Modeling, 2015, 55, 872-881.	5.4	15
14	Control variate technique: A constructive approach. , 2008, , .		12
15	A New Efficient Simulation Strategy for Pricing Path-Dependent Options. , 2006, , .		10
16	Designing heterogeneous hierarchical material systems: a holistic approach to structural and materials design. MRS Communications, 2019, 9, 628-636.	1.8	10
17	Focused gridâ€based resampling for protein docking and mapping. Journal of Computational Chemistry, 2016, 37, 961-970.	3.3	6
18	Improved cluster ranking in proteinâ€“protein docking using a regression approach. Computational and Structural Biotechnology Journal, 2021, 19, 2269-2278.	4.1	6

#	Article	IF	Citations
19	Correlation of Markov chains simulated in parallel. , 1992, , .		4
20	Protein-protein docking with reduced potentials by exploiting multi-dimensional energy funnels. , 2006, 2006, 5330-3.		4
21	A new approach to rigid body minimization with application to molecular docking. , 2012, , 2983-2988.		4
22	Using Uniformization for Derivative Estimation in Simulation. , 1990, , .		4
23	Uniformization based sensitivity estimation for a class of discrete-event systems. Discrete Event Dynamic Systems: Theory and Applications, 1994, 4, 171-195.	1.5	3
24	A message passing approach to Side Chain Positioning with applications in protein docking refinement. , 2012, , 2310-2315.		3
25	A new distributed algorithm for side-chain positioning in the process of protein docking. , 2013, , 739-744.		3
26	Parallel replicated simulation of Markov chains. , 1993, , .		2
27	Optimizing noisy funnel-like functions on the euclidean group with applications to protein docking. , 2007, , .		2
28	Flexible refinement of protein-ligand docking on manifolds. , 2013, , 1392-1397.		2
29	Efficient Maintenance and Update of Nonbonded Lists in Macromolecular Simulations. Journal of Chemical Theory and Computation, 2014, 10, 4449-4454.	5.3	2
30	Optimization on the space of rigid and flexible motions: An alternative manifold optimization approach. , 2014, 2014, 5825-5830.		1
31	A Subspace Semi-Definite programming-based Underestimation (SSDU) method for stochastic global optimization in protein docking. , 2014, 2014, 4623-4628.		1
32	Importance sampling for parametric estimation. , 2010, , .		0
33	Control variates for sensitivity estimation. , 2010, , .		0