

Julian Lee

List of Publications by Year in descending order

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55
papers

1,098
citations

516710

16
h-index

414414

32
g-index

55
all docs

55
docs citations

55
times ranked

1027
citing authors

#	ARTICLE	IF	CITATIONS
1	Principles of maximum entropy and maximum caliber in statistical physics. <i>Reviews of Modern Physics</i> , 2013, 85, 1115-1141.	45.6	298
2	The FALC-Loop web server for protein loop modeling. <i>Nucleic Acids Research</i> , 2011, 39, W210-W214.	14.5	101
3	Protein loop modeling by using fragment assembly and analytical loop closure. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3428-3436.	2.6	90
4	Prediction of protein solvent accessibility using fuzzy k-nearest neighbor method. <i>Bioinformatics</i> , 2005, 21, 2844-2849.	4.1	81
5	Prediction of protein tertiary structure using PROFESY, a novel method based on fragment assembly and conformational space annealing. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 704-714.	2.6	74
6	Exact partition function zeros and the collapse transition of a two-dimensional lattice polymer. <i>Journal of Chemical Physics</i> , 2010, 133, 114106.	3.0	42
7	Protein structure prediction based on fragment assembly and parameter optimization. <i>Biophysical Chemistry</i> , 2005, 115, 209-214.	2.8	38
8	Single Molecule Conformational Memory Extraction: P5ab RNA Hairpin. <i>Journal of Physical Chemistry B</i> , 2014, 118, 6597-6603.	2.6	35
9	Exact partition function zeros of a polymer on a simple cubic lattice. <i>Physical Review E</i> , 2012, 86, 011802.	2.1	34
10	Exact Partition Function Zeros of The Wako-Saito-Muoz-Eaton Protein Model. <i>Physical Review Letters</i> , 2013, 110, 248101.	7.8	30
11	Refinement of protein termini in template-based modeling using conformational space annealing. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2725-2734.	2.6	25
12	Collapse transition of a square-lattice polymer with next nearest-neighbor interaction. <i>Journal of Chemical Physics</i> , 2011, 135, 204102.	3.0	25
13	A derivation of the master equation from path entropy maximization. <i>Journal of Chemical Physics</i> , 2012, 137, 074103.	3.0	20
14	Parallel algorithm for calculation of the exact partition function of a lattice polymer. <i>Computer Physics Communications</i> , 2011, 182, 1027-1033.	7.5	19
15	Partition function zeros of a square-lattice homopolymer with nearest- and next-nearest-neighbor interactions. <i>Physical Review E</i> , 2013, 87, 052601.	2.1	18
16	Exact Partition Function Zeros of Two-Dimensional Lattice Polymers. <i>Journal of the Korean Physical Society</i> , 2004, 44, 617.	0.7	18
17	Quantitative analysis of a transient dynamics of a gene regulatory network. <i>Physical Review E</i> , 2018, 98, .	2.1	15
18	Measures for the assessment of fuzzy predictions of protein secondary structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 453-462.	2.6	11

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19	Exact partition function zeros of the Wako-Saito-Muoz-Eaton hairpin model. <i>Physical Review E</i> , 2013, 88, 022710.	2.1	11
20	Derivation of Markov processes that violate detailed balance. <i>Physical Review E</i> , 2018, 97, 032110.	2.1	10
21	Protein folding using fragment assembly and physical energy function. <i>Journal of Chemical Physics</i> , 2006, 125, 194908.	3.0	9
22	Microcanonical origin of the maximum entropy principle for open systems. <i>Physical Review E</i> , 2012, 86, 041126.	2.1	8
23	Low-temperature behavior of the finite-size one-dimensional Ising model and the partition function zeros. <i>Journal of the Korean Physical Society</i> , 2014, 65, 676-683.	0.7	8
24	<i>In Silico</i> Development of Quorum Sensing Inhibitors. <i>Bulletin of the Korean Chemical Society</i> , 2017, 38, 728-734.	1.9	7
25	Protein Loop Modeling Using Fragment Assembly. <i>Journal of the Korean Physical Society</i> , 2008, 52, 1137-1142.	0.7	7
26	Exact zeros of the partition function for a continuum system with double Gaussian peaks. <i>Physical Review E</i> , 2000, 62, 4558-4563.	2.1	6
27	Analytic model of the Schottky anomaly and phase transition. <i>Journal of the Korean Physical Society</i> , 2015, 67, 1133-1136.	0.7	6
28	Study on collapse and folding transitions of a lattice protein using exact enumeration. <i>AIP Advances</i> , 2015, 5, 127211.	1.3	5
29	Method for identification of rigid domains and hinge residues in proteins based on exhaustive enumeration. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1054-1067.	2.6	5
30	Stability analysis of an autocatalytic protein model. <i>AIP Advances</i> , 2016, 6, 055013.	1.3	5
31	Transfer matrix algorithm for computing the exact partition function of a square lattice polymer. <i>Computer Physics Communications</i> , 2018, 228, 11-21.	7.5	5
32	Schottky anomaly in a repulsive lattice polymer. <i>Journal of the Korean Physical Society</i> , 2016, 68, 288-295.	0.7	4
33	Hydrodynamic interaction facilitates the unsteady transport of two neighboring vesicles. <i>Journal of Chemical Physics</i> , 2019, 151, 094108.	3.0	4
34	Exact partition functions of a polymer on a square lattice up to chain length 38. <i>Journal of Physics: Conference Series</i> , 2013, 454, 012083.	0.4	3
35	Low-temperature conformational transition of a square-lattice polymer. <i>Journal of the Korean Physical Society</i> , 2015, 66, 1797-1801.	0.7	3
36	Study on the ground states of a square-lattice polymer by using exhaustive enumeration. <i>Journal of the Korean Physical Society</i> , 2016, 69, 1518-1522.	0.7	3

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37	Microcanonical analysis of a finite-size nonequilibrium system. <i>Physical Review E</i> , 2016, 93, 052148.	2.1	3
38	Protein contact prediction by using information theory. <i>Journal of the Korean Physical Society</i> , 2017, 70, 876-879.	0.7	3
39	Phase diagram of the Wako-Saito-Muñoz-Eaton \hat{I}^2 hairpin model obtained from the partition-function zeros. <i>Journal of the Korean Physical Society</i> , 2014, 65, 671-675.	0.7	2
40	Exhaustive Enumeration of Fragment-Assembled Protein Conformations. <i>Journal of the Korean Physical Society</i> , 2008, 52, 137-142.	0.7	2
41	Finite-size phase diagram of the Wako-Saito-Muñoz-Eaton \hat{I}^{\pm} -helix model. <i>Journal of the Korean Physical Society</i> , 2015, 67, 1187-1191.	0.7	1
42	Analysis of precision and accuracy in a simple model of machine learning. <i>Journal of the Korean Physical Society</i> , 2017, 71, 866-870.	0.7	1
43	Protein Structure Prediction Using the Hybrid Energy Function, Fragment Assembly and Double Optimization. <i>Journal of the Korean Physical Society</i> , 2008, 52, 143-151.	0.7	1
44	Protein Structure Prediction Using a Hybrid Energy Function and an Exact Enumeration. <i>Journal of the Korean Physical Society</i> , 2008, 53, 873-879.	0.7	1
45	Bifurcations of a Positive Feedback Loop with Partial Binding. <i>Journal of the Korean Physical Society</i> , 2020, 76, 762-768.	0.7	1
46	A new method for prediction of RNA secondary structure with pseudoknots, based on helix removal and refinement. <i>Optimization</i> , 2009, 58, 861-869.	1.7	0
47	Exact Enumeration of Protein Conformations from Fragment Assembly. <i>Journal of Physics: Conference Series</i> , 2013, 410, 012071.	0.4	0
48	Transfer Matrix Algorithm for Computing the Geometric Quantities of a Square Lattice Polymer. <i>Journal of the Korean Physical Society</i> , 2018, 73, 1808-1813.	0.7	0
49	Geometrical properties of interior segments of two-dimensional lattice polymer confined in a square box. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2018, 506, 868-872.	2.6	0
50	Analytic Form of the Phase Boundary for a Self-Regulatory Gene Circuit with Baseline Production. <i>Journal of the Korean Physical Society</i> , 2019, 74, 989-993.	0.7	0
51	Gillespie Simulation of Rare Events in a Genetic Regulatory Network. <i>Journal of the Korean Physical Society</i> , 2019, 74, 907-911.	0.7	0
52	Analytic Form of the Quasi-stationary Distribution of a Simple Birth-Death Process. <i>Journal of the Korean Physical Society</i> , 2020, 77, 457-462.	0.7	0
53	Steady state of an auto-regulatory gene network with partial binding and transcription leakage. <i>Journal of the Korean Physical Society</i> , 2021, 78, 351-356.	0.7	0
54	Derivation of a nonequilibrium Markov six-state model in the presence of a time-reversal antisymmetric variable. <i>Journal of the Korean Physical Society</i> , 2021, 79, 666.	0.7	0

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55	Conversion of a stable fixed point into a transient peak by stochastic fluctuation in a gene regulatory network. Journal of the Korean Physical Society, 2021, 79, 660-665.	0.7	0