Julian Lee

List of Publications by Year
in descending order

55	1,098	516710	414414
papers	citations	16	32
		h-index	g-index

55	55	55	1027
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Steady state of an auto-regulatory gene network with partial binding and transcription leakage. Journal of the Korean Physical Society, 2021, 78, 351-356.	0.7	0
2	Derivation of a nonequilibrium Markov six-state model in the presence of a time-reversal antisymmetric variable. Journal of the Korean Physical Society, 2021, 79, 666.	0.7	0
3	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
4	Analytic Form of the Quasi-stationary Distribution of a Simple Birth-Death Process. Journal of the Korean Physical Society, 2020, 77, 457-462.	0.7	0
5	Bifurcations of a Positive Feedback Loop with Partial Binding. Journal of the Korean Physical Society, 2020, 76, 762-768.	0.7	1
6	Hydrodynamic interaction facilitates the unsteady transport of two neighboring vesicles. Journal of Chemical Physics, 2019, 151, 094108.	3.0	4
7	Analytic Form of the Phase Boundary for a Self-Regulatory Gene Circuit with Baseline Production. Journal of the Korean Physical Society, 2019, 74, 989-993.	0.7	0
8	Gillespie Simulation of Rare Events in a Genetic Regulatory Network. Journal of the Korean Physical Society, 2019, 74, 907-911.	0.7	0
9	Transfer matrix algorithm for computing the exact partition function of a square lattice polymer. Computer Physics Communications, 2018, 228, 11-21.	7.5	5
10	Derivation of Markov processes that violate detailed balance. Physical Review E, 2018, 97, 032110.	2.1	10
11	Transfer Matrix Algorithm for Computing the Geometric Quantities of a Square Lattice Polymer. Journal of the Korean Physical Society, 2018, 73, 1808-1813.	0.7	0
12	Quantitative analysis of a transient dynamics of a gene regulatory network. Physical Review E, 2018, 98, .	2.1	15
13	Geometrical properties of interior segments of two-dimensional lattice polymer confined in a square box. Physica A: Statistical Mechanics and Its Applications, 2018, 506, 868-872.	2.6	0
14	Protein contact prediction by using information theory. Journal of the Korean Physical Society, 2017, 70, 876-879.	0.7	3
15	<i>In Silico</i> Development of Quorum‑Sensing Inhibitors. Bulletin of the Korean Chemical Society, 2017, 38, 728-734.	1.9	7
16	Analysis of precision and accuracy in a simple model of machine learning. Journal of the Korean Physical Society, 2017, 71, 866-870.	0.7	1
17	Study on the ground states of a square-lattice polymer by using exhaustive enumeration. Journal of the Korean Physical Society, 2016, 69, 1518-1522.	0.7	3
18	Microcanonical analysis of a finite-size nonequilibrium system. Physical Review E, 2016, 93, 052148.	2.1	3

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19	Stability analysis of an autocatalytic protein model. AIP Advances, 2016, 6, 055013.	1.3	5
20	Schottky anomaly in a repulsive lattice polymer. Journal of the Korean Physical Society, 2016, 68, 288-295.	0.7	4
21	Analytic model of the Schottky anomaly and phase transition. Journal of the Korean Physical Society, 2015, 67, 1133-1136.	0.7	6
22	Study on collapse and folding transitions of a lattice protein using exact enumeration. AIP Advances, 2015, 5, 127211.	1.3	5
23	Low-temperature conformational transition of a square-lattice polymer. Journal of the Korean Physical Society, 2015, 66, 1797-1801.	0.7	3
24	Finite-size phase diagram of the Wako-Saitô-Muñoz-Eaton α-helix model. Journal of the Korean Physical Society, 2015, 67, 1187-1191.	0.7	1
25	Method for identification of rigid domains and hinge residues in proteins based on exhaustive enumeration. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1054-1067.	2.6	5
26	Low-temperature behavior of the finite-size one-dimensional Ising model and the partition function zeros. Journal of the Korean Physical Society, 2014, 65, 676-683.	0.7	8
27	Phase diagram of the Wako-Saitô-Muñoz-Eaton β hairpin model obtained from the partition-function zeros. Journal of the Korean Physical Society, 2014, 65, 671-675.	0.7	2
28	Single Molecule Conformational Memory Extraction: P5ab RNA Hairpin. Journal of Physical Chemistry B, 2014, 118, 6597-6603.	2.6	35
29	Principles of maximum entropy and maximum caliber in statistical physics. Reviews of Modern Physics, 2013, 85, 1115-1141.	45.6	298
30	Partition function zeros of a square-lattice homopolymer with nearest- and next-nearest-neighbor interactions. Physical Review E, 2013, 87, 052601.	2.1	18
31	Exact Partition Function Zeros of The Wako-Saitô-Muñoz-Eaton Protein Model. Physical Review Letters, 2013, 110, 248101.	7.8	30
32	Exact partition function zeros of the Wako-Saitô-Muñoz-Eaton β hairpin model. Physical Review E, 2013, 88, 022710.	2.1	11
33	Exact Enumeration of Protein Conformations from Fragment Assembly. Journal of Physics: Conference Series, 2013, 410, 012071.	0.4	0
34	Exact partition functions of a polymer on a square lattice up to chain length 38. Journal of Physics: Conference Series, 2013, 454, 012083.	0.4	3
35	A derivation of the master equation from path entropy maximization. Journal of Chemical Physics, 2012, 137, 074103.	3.0	20
36	Exact partition function zeros of a polymer on a simple cubic lattice. Physical Review E, 2012, 86, 011802.	2.1	34

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37	Microcanonical origin of the maximum entropy principle for open systems. Physical Review E, 2012, 86, 041126.	2.1	8
38	Refinement of protein termini in template–based modeling using conformational space annealing. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2725-2734.	2.6	25
39	Parallel algorithm for calculation of the exact partition function of a lattice polymer. Computer Physics Communications, 2011, 182, 1027-1033.	7.5	19
40	Collapse transition of a square-lattice polymer with next nearest-neighbor interaction. Journal of Chemical Physics, 2011, 135, 204102.	3.0	25
41	The FALC-Loop web server for protein loop modeling. Nucleic Acids Research, 2011, 39, W210-W214.	14.5	101
42	Protein loop modeling by using fragment assembly and analytical loop closure. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3428-3436.	2.6	90
43	Exact partition function zeros and the collapse transition of a two-dimensional lattice polymer. Journal of Chemical Physics, 2010, 133, 114106.	3.0	42
44	A new method for prediction of RNA secondary structure with pseudoknots, based on helix removal and refinement. Optimization, 2009, 58, 861-869.	1.7	0
45	Protein Loop Modeling Using Fragment Assembly. Journal of the Korean Physical Society, 2008, 52, 1137-1142.	0.7	7
46	Exhaustive Enumeration of Fragment-Assembled Protein Conformations. Journal of the Korean Physical Society, 2008, 52, 137-142.	0.7	2
47	Protein Structure Prediction Using the Hybrid Energy Function, Fragment Assembly and Double Optimization. Journal of the Korean Physical Society, 2008, 52, 143-151.	0.7	1
48	Protein Structure Prediction Using a Hybrid Energy Function and an Exact Enumeration. Journal of the Korean Physical Society, 2008, 53, 873-879.	0.7	1
49	Measures for the assessment of fuzzy predictions of protein secondary structure. Proteins: Structure, Function and Bioinformatics, 2006, 65, 453-462.	2.6	11
50	Protein folding using fragment assembly and physical energy function. Journal of Chemical Physics, 2006, 125, 194908.	3.0	9
51	Protein structure prediction based on fragment assembly and parameter optimization. Biophysical Chemistry, 2005, 115, 209-214.	2.8	38
52	Prediction of protein solvent accessibility using fuzzy k-nearest neighbor method. Bioinformatics, 2005, 21, 2844-2849.	4.1	81
53	Prediction of protein tertiary structure using PROFESY, a novel method based on fragment assembly and conformational space annealing. Proteins: Structure, Function and Bioinformatics, 2004, 56, 704-714.	2.6	74
54	Exact Partition Function Zeros of Two-Dimensional Lattice Polymers. Journal of the Korean Physical Society, 2004, 44, 617.	0.7	18

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55	Exact zeros of the partition function for a continuum system with double Gaussian peaks. Physical Review E, 2000, 62, 4558-4563.	2.1	6