Erik Winfree

List of Publications by Year
in descending order

106 papers	20,400 citations	41258 49 h-index	31759 101 g-index
117 all docs	117 docs citations	117 times ranked	8250 citing authors

#	Article	IF	Citations
1	Stochastic chemical reaction networks for robustly approximating arbitrary probability distributions. Theoretical Computer Science, 2020, 801, 64-95.	0.5	7
2	A domain-level DNA strand displacement reaction enumerator allowing arbitrary non-pseudoknotted secondary structures. Journal of the Royal Society Interface, 2020, 17, 20190866.	1.5	18
3	Programming and simulating chemical reaction networks on a surface. Journal of the Royal Society Interface, 2020, 17, 20190790.	1.5	21
4	Verifying polymer reaction networks using bisimulation. Theoretical Computer Science, 2020, 843, 84-114.	0.5	0
5	Chemical Reaction Networks and Stochastic Local Search. Lecture Notes in Computer Science, 2019, , 1-20.	1.0	4
6	Reversible Computation Using Swap Reactions on a Surface. Lecture Notes in Computer Science, 2019, , 174-196.	1.0	0
7	Verifying chemical reaction network implementations: A bisimulation approach. Theoretical Computer Science, 2019, 765, 3-46.	0.5	14
8	Diverse and robust molecular algorithms using reprogrammable DNA self-assembly. Nature, 2019, 567, 366-372.	13.7	198
9	Verifying chemical reaction network implementations: A pathway decomposition approach. Theoretical Computer Science, 2019, 765, 67-96.	0.5	11
10	Efficient Parameter Estimation for DNA Kinetics Modeled as Continuous-Time Markov Chains. Lecture Notes in Computer Science, 2019, , 80-99.	1.0	2
11	Automated sequence-level analysis of kinetics and thermodynamics for domain-level DNA strand-displacement systems. Journal of the Royal Society Interface, 2018, 15, 20180107.	1.5	13
12	Effective design principles for leakless strand displacement systems. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E12182-E12191.	3.3	94
13	Optimizing Tile Set Size While Preserving Proofreading with a DNA Self-assembly Compiler. Lecture Notes in Computer Science, 2018, , 37-54.	1.0	1
14	Physical principles for DNA tile self-assembly. Chemical Society Reviews, 2017, 46, 3808-3829.	18.7	71
15	Inferring Parameters for an Elementary Step Model of DNA Structure Kinetics with Locally Context-Dependent Arrhenius Rates. Lecture Notes in Computer Science, 2017, , 172-187.	1.0	7
16	A cargo-sorting DNA robot. Science, 2017, 357, .	6.0	426
17	A General-Purpose CRN-to-DSD Compiler with Formal Verification, Optimization, and Simulation Capabilities. Lecture Notes in Computer Science, 2017, , 232-248.	1.0	22
18	Enzyme-free nucleic acid dynamical systems. Science, 2017, 358, .	6.0	274

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19	Chemical Boltzmann Machines. Lecture Notes in Computer Science, 2017, , 210-231.	1.0	21
20	Time Complexity of Computation and Construction in the Chemical Reaction Network-Controlled Tile Assembly Model. Lecture Notes in Computer Science, 2016, , 165-182.	1.0	6
21	Verifying Chemical Reaction Network Implementations: A Bisimulation Approach. Lecture Notes in Computer Science, 2016, , 114-134.	1.0	3
22	Thermodynamics and kinetics of DNA nanotube polymerization from single-filament measurements. Chemical Science, 2015, 6, 2252-2267.	3.7	39
23	Increasing Redundancy Exponentially Reduces Error Rates during Algorithmic Self-Assembly. ACS Nano, 2015, 9, 5760-5771.	7.3	10
24	Determining hydrodynamic forces in bursting bubbles using DNA nanotube mechanics. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6086-E6095.	3.3	20
25	Stochastic Simulation of the Kinetics of Multiple Interacting Nucleic Acid Strands. Lecture Notes in Computer Science, 2015, , 194-211.	1.0	31
26	Universal Computation and Optimal Construction in the Chemical Reaction Network-Controlled Tile Assembly Model. Lecture Notes in Computer Science, 2015, , 34-54.	1.0	12
27	Leakless DNA Strand Displacement Systems. Lecture Notes in Computer Science, 2015, , 133-153.	1.0	50
28	Diversity in the dynamical behaviour of a compartmentalized programmable biochemical oscillator. Nature Chemistry, 2014, 6, 295-302.	6.6	201
29	Parallel and Scalable Computation and Spatial Dynamics with DNA-Based Chemical Reaction Networks on a Surface. Lecture Notes in Computer Science, 2014, , 114-131.	1.0	37
30	Active self-assembly of algorithmic shapes and patterns in polylogarithmic time. , 2013, , .		70
31	On the biophysics and kinetics of toehold-mediated DNA strand displacement. Nucleic Acids Research, 2013, 41, 10641-10658.	6.5	423
32	Integrating DNA strand-displacement circuitry with DNA tile self-assembly. Nature Communications, 2013, 4, 1965.	5.8	183
33	DNA Sticky End Design and Assignment for Robust Algorithmic Self-assembly. Lecture Notes in Computer Science, 2013, , 61-75.	1.0	15
34	Robust self-replication of combinatorial information via crystal growth and scission. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6405-6410.	3.3	107
35	Direct Atomic Force Microscopy Observation of DNA Tile Crystal Growth at the Single-Molecule Level. Journal of the American Chemical Society, 2012, 134, 10485-10492.	6.6	28
36	Ensemble Bayesian Analysis of Bistability in a Synthetic Transcriptional Switch. ACS Synthetic Biology, 2012, 1, 299-316.	1.9	53

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37	Simple evolution of complex crystal species. Natural Computing, 2012, 11, 187-197.	1.8	0
38	Scaling Up Digital Circuit Computation with DNA Strand Displacement Cascades. Science, 2011, 332, 1196-1201.	6.0	1,294
39	Neural network computation with DNA strand displacement cascades. Nature, 2011, 475, 368-372.	13.7	931
40	A simple DNA gate motif for synthesizing large-scale circuits. Journal of the Royal Society Interface, 2011, 8, 1281-1297.	1.5	210
41	Synthetic in vitro transcriptional oscillators. Molecular Systems Biology, 2011, 7, 465.	3.2	271
42	Timing molecular motion and production with a synthetic transcriptional clock. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E784-93.	3.3	208
43	Efficient Turing-Universal Computation with DNA Polymers. Lecture Notes in Computer Science, 2011, , 123-140.	1.0	80
44	Molecular robots guided by prescriptive landscapes. Nature, 2010, 465, 206-210.	13.7	843
45	Self-assembly of carbon nanotubes into two-dimensional geometries using DNA origami templates. Nature Nanotechnology, 2010, 5, 61-66.	15.6	567
46	DNA as a universal substrate for chemical kinetics. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5393-5398.	3.3	649
47	Robustness and modularity properties of a non-covalent DNA catalytic reaction. Nucleic Acids Research, 2010, 38, 4182-4197.	6.5	95
48	Toward De Novo Recapitulation of Cytoskeleton Dynamics with DNA Nanotubes. Biophysical Journal, 2010, 98, 556a-557a.	0.2	2
49	Programmable Control of Nucleation for Algorithmic Self-Assembly. SIAM Journal on Computing, 2010, 39, 1581-1616.	0.8	52
50	An information-bearing seed for nucleating algorithmic self-assembly. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6054-6059.	3.3	235
51	Error suppression mechanisms for DNA tile self-assembly and their simulation. Natural Computing, 2009, 8, 589-612.	1.8	35
52	Control of DNA Strand Displacement Kinetics Using Toehold Exchange. Journal of the American Chemical Society, 2009, 131, 17303-17314.	6.6	1,239
53	Programmability ofÂChemical Reaction Networks. Natural Computing Series, 2009, , 543-584.	2.2	83
54	DNA as a Universal Substrate for Chemical Kinetics. Lecture Notes in Computer Science, 2009, , 57-69.	1.0	34

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55	A Simple DNA Gate Motif for Synthesizing Large-Scale Circuits. Lecture Notes in Computer Science, 2009, , 70-89.	1.0	58
56	Combining self-healing and proofreading in self-assembly. Natural Computing, 2008, 7, 203-218.	1.8	21
57	How crystals that sense and respond to their environments could evolve. Natural Computing, 2008, 7, 219-237.	1.8	12
58	Computation with finite stochastic chemical reaction networks. Natural Computing, 2008, 7, 615-633.	1.8	201
59	Toward Reliable Algorithmic Self-Assembly of DNA Tiles: A Fixed-Width Cellular Automaton Pattern. Nano Letters, 2008, 8, 1791-1797.	4.5	180
60	Dynamic Allosteric Control of Noncovalent DNA Catalysis Reactions. Journal of the American Chemical Society, 2008, 130, 13921-13926.	6.6	67
61	Toward molecular programming with DNA. ACM SIGPLAN Notices, 2008, 43, 1-1.	0.2	0
62	Toward molecular programming with DNA. Operating Systems Review (ACM), 2008, 42, 1-1.	1.5	5
63	Toward molecular programming with DNA. , 2008, , .		1
64	Toward molecular programming with DNA. Computer Architecture News, 2008, 36, 1-1.	2.5	1
65	Engineering Entropy-Driven Reactions and Networks Catalyzed by DNA. Science, 2007, 318, 1121-1125.	6.0	1,022
66	Thermodynamic Analysis of Interacting Nucleic Acid Strands. SIAM Review, 2007, 49, 65-88.	4.2	297
67	Synthesis of crystals with a programmable kinetic barrier to nucleation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15236-15241.	3.3	168
68	Complexity of Selfâ€Assembled Shapes. SIAM Journal on Computing, 2007, 36, 1544-1569.	0.8	189
69	Reducing Facet Nucleation during Algorithmic Self-Assembly. Nano Letters, 2007, 7, 2913-2919.	4.5	61
70	An autonomous polymerization motor powered by DNA hybridization. Nature Nanotechnology, 2007, 2, 490-494.	15.6	303
71	Algorithmic Self-Assembly of DNA. , 2006, , .		70
72	Catalyzed Relaxation of a Metastable DNA Fuel. Journal of the American Chemical Society, 2006, 128, 12211-12220.	6.6	164

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73	Enzyme-Free Nucleic Acid Logic Circuits. Science, 2006, 314, 1585-1588.	6.0	1,440
74	Construction of an in vitro bistable circuit from synthetic transcriptional switches. Molecular Systems Biology, 2006, 2, 68.	3.2	287
75	Complexity of Compact Proofreading for Self-assembled Patterns. Lecture Notes in Computer Science, 2006, , 305-324.	1.0	33
76	Self-healing Tile Sets. , 2006, , 55-78.		55
77	DNA Hybridization Catalysts and Catalyst Circuits. Lecture Notes in Computer Science, 2005, , 329-343.	1.0	11
78	Programmable Control of Nucleation for Algorithmic Self-assembly. Lecture Notes in Computer Science, 2005, , 319-328.	1.0	35
79	Complexity of Self-assembled Shapes. Lecture Notes in Computer Science, 2005, , 344-354.	1.0	26
80	Self-replication and Evolution of DNA Crystals. Lecture Notes in Computer Science, 2005, , 734-743.	1.0	19
81	The computational power of Benenson automata. Theoretical Computer Science, 2005, 344, 279-297.	0.5	23
82	Two Computational Primitives for Algorithmic Self-Assembly:Â Copying and Counting. Nano Letters, 2005, 5, 2586-2592.	4.5	197
83	Proofreading Tile Sets: Error Correction for Algorithmic Self-Assembly. Lecture Notes in Computer Science, 2004, , 126-144.	1.0	129
84	Paradigms for computational nucleic acid design. Nucleic Acids Research, 2004, 32, 1392-1403.	6.5	181
85	Self-Assembled Circuit Patterns. Lecture Notes in Computer Science, 2004, , 91-107.	1.0	67
86	Design and Characterization of Programmable DNA Nanotubes. Journal of the American Chemical Society, 2004, 126, 16344-16352.	6.6	454
87	One Dimensional Boundaries for DNA Tile Self-Assembly. Lecture Notes in Computer Science, 2004, , 108-125.	1.0	17
88	Algorithmic Self-Assembly of DNA Sierpinski Triangles. PLoS Biology, 2004, 2, e424.	2.6	696
89	Protein Design is NP-hard. Protein Engineering, Design and Selection, 2002, 15, 779-782.	1.0	205
90	String tile models for DNA computing by self-assembly. Lecture Notes in Computer Science, 2001, , 63-88.	1.0	23

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91	Algorithmic Self-Assembly of DNA: Theoretical Motivations and 2D Assembly Experiments. Journal of Biomolecular Structure and Dynamics, 2000, 17, 263-270.	2.0	92
92	Two Dimensions and Two States in DNA Nanotechnology. Journal of Biomolecular Structure and Dynamics, 2000, 17, 253-262.	2.0	13
93	The program-size complexity of self-assembled squares (extended abstract). , 2000, , .		259
94	Construction, Analysis, Ligation, and Self-Assembly of DNA Triple Crossover Complexes. Journal of the American Chemical Society, 2000, 122, 1848-1860.	6.6	644
95	Error correction in DNA computing: Misclassification and strand loss. DIMACS Series in Discrete Mathematics and Theoretical Computer Science, 2000, , 49-63.	0.0	6
96	Experimental progress in computation by self-assembly of DNA tilings. DIMACS Series in Discrete Mathematics and Theoretical Computer Science, 2000, , 123-140.	0.0	38
97	On Applying Molecular Computation to the Data Encryption Standard. Journal of Computational Biology, 1999, 6, 53-63.	0.8	102
98	On the Reduction of Errors in DNA Computation. Journal of Computational Biology, 1999, 6, 65-75.	0.8	17
99	Design and self-assembly of two-dimensional DNA crystals. Nature, 1998, 394, 539-544.	13.7	2,663
100	A Sticker-Based Model for DNA Computation. Journal of Computational Biology, 1998, 5, 615-629.	0.8	170
101	A sticker based model for DNA computation. DIMACS Series in Discrete Mathematics and Theoretical Computer Science, 1998, , 1-29.	0.0	26
102	On applying molecular computation to the data encryption standard. DIMACS Series in Discrete Mathematics and Theoretical Computer Science, 1998, , 31-44.	0.0	11
103	Universal computation via self-assembly of DNA: Some theory and experiments. DIMACS Series in Discrete Mathematics and Theoretical Computer Science, 1998, , 191-213.	0.0	122
104	Complexity of restricted and unrestricted models of molecular computation. DIMACS Series in Discrete Mathematics and Theoretical Computer Science, 1996, , 187-198.	0.0	15
105	On the computational power of DNA annealing and ligation. DIMACS Series in Discrete Mathematics and Theoretical Computer Science, 1996, , 199-221.	0.0	126
106	Organizing centers in a cellular excitable medium. Physica D: Nonlinear Phenomena, 1985, 17, 109-115.	1.3	36