Niles A Pierce

List of Publications by Year in descending order

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159585 315739 10,424 41 30 38 citations h-index g-index papers 46 46 46 8033 all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	From The Cover: Triggered amplification by hybridization chain reaction. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15275-15278.	7.1	1,643
2	Programming biomolecular self-assembly pathways. Nature, 2008, 451, 318-322.	27.8	1,339
3	NUPACK: Analysis and design of nucleic acid systems. Journal of Computational Chemistry, 2011, 32, 170-173.	3.3	1,289
4	Third-generation $\langle i \rangle$ in situ $\langle i \rangle$ hybridization chain reaction: multiplexed, quantitative, sensitive, versatile, robust. Development (Cambridge), 2018, 145, .	2.5	776
5	A Synthetic DNA Walker for Molecular Transport. Journal of the American Chemical Society, 2004, 126, 10834-10835.	13.7	720
6	Programmable in situ amplification for multiplexed imaging of mRNA expression. Nature Biotechnology, 2010, 28, 1208-1212.	17.5	567
7	Next-Generation <i>in Situ</i> Hybridization Chain Reaction: Higher Gain, Lower Cost, Greater Durability. ACS Nano, 2014, 8, 4284-4294.	14.6	504
8	A partition function algorithm for nucleic acid secondary structure including pseudoknots. Journal of Computational Chemistry, 2003, 24, 1664-1677.	3.3	342
9	An autonomous polymerization motor powered by DNA hybridization. Nature Nanotechnology, 2007, 2, 490-494.	31.5	303
10	Thermodynamic Analysis of Interacting Nucleic Acid Strands. SIAM Review, 2007, 49, 65-88.	9.5	297
11	Adjoint Recovery of Superconvergent Functionals from PDE Approximations. SIAM Review, 2000, 42, 247-264.	9.5	280
12	Protein Design is NP-hard. Protein Engineering, Design and Selection, 2002, 15, 779-782.	2.1	205
13	Mapping a multiplexed zoo of mRNA expression. Development (Cambridge), 2016, 143, 3632-3637.	2.5	198
14	Paradigms for computational nucleic acid design. Nucleic Acids Research, 2004, 32, 1392-1403.	14.5	181
15	Single-molecule RNA detection at depth via hybridization chain reaction and tissue hydrogel embedding and clearing. Development (Cambridge), 2016, 143, 2862-7.	2.5	174
16	An algorithm for computing nucleic acid base-pairing probabilities including pseudoknots. Journal of Computational Chemistry, 2004, 25, 1295-1304.	3.3	173
17	Nucleic acid sequence design via efficient ensemble defect optimization. Journal of Computational Chemistry, 2011, 32, 439-452.	3.3	161
18	Exact rotamer optimization for protein design. Journal of Computational Chemistry, 2003, 24, 232-243.	3.3	115

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19	Analytic adjoint solutions for the quasi-one-dimensional Euler equations. Journal of Fluid Mechanics, 2001, 426, 327-345.	3.4	109
20	Constrained Multistate Sequence Design for Nucleic Acid Reaction Pathway Engineering. Journal of the American Chemical Society, 2017, 139, 3134-3144.	13.7	102
21	Adjoint and defect error bounding and correction for functional estimates. Journal of Computational Physics, 2004, 200, 769-794.	3.8	98
22	Developmental Self-Assembly of a DNA Tetrahedron. ACS Nano, 2014, 8, 3251-3259.	14.6	97
23	Topological constraints in nucleic acid hybridization kinetics. Nucleic Acids Research, 2005, 33, 4090-4095.	14.5	88
24	Conditional Guide RNAs: Programmable Conditional Regulation of CRISPR/Cas Function in Bacterial and Mammalian Cells via Dynamic RNA Nanotechnology. ACS Central Science, 2019, 5, 1241-1249.	11.3	83
25	Multiplexed miRNA northern blots via hybridization chain reaction. Nucleic Acids Research, 2016, 44, gkw503.	14.5	70
26	Multidimensional quantitative analysis of mRNA expression within intact vertebrate embryos. Development (Cambridge), 2018, 145, .	2.5	56
27	Sequence Design for a Test Tube of Interacting Nucleic Acid Strands. ACS Synthetic Biology, 2015, 4, 1086-1100.	3.8	52
28	A Unified Dynamic Programming Framework for the Analysis of Interacting Nucleic Acid Strands: Enhanced Models, Scalability, and Speed. ACS Synthetic Biology, 2020, 9, 2665-2678.	3.8	48
29	Improved lift and drag estimates using adjoint Euler equations. , 1999, , .		47
30	Progress in adjoint error correction for integral functionals. Computing and Visualization in Science, 2004, 6, 113-121.	1.2	38
31	Conditional Dicer Substrate Formation via Shape and Sequence Transduction with Small Conditional RNAs. Journal of the American Chemical Society, 2013, 135, 17322-17330.	13.7	36
32	Hybridization chain reaction enables a unified approach to multiplexed, quantitative, high-resolution immunohistochemistry and <i>in situ</i> hybridization. Development (Cambridge), 2021, 148, .	2.5	35
33	Combinatorial Analysis of mRNA Expression Patterns in Mouse Embryos Using Hybridization Chain Reaction. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot083832.	0.3	33
34	Selective Nucleic Acid Capture with Shielded Covalent Probes. Journal of the American Chemical Society, 2013, 135, 9691-9699.	13.7	31
35	Localizing transcripts to single cells suggests an important role of uncultured deltaproteobacteria in the termite gut hydrogen economy. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16163-16168.	7.1	29
36	High-Performance Allosteric Conditional Guide RNAs for Mammalian Cell-Selective Regulation of CRISPR/Cas. ACS Synthetic Biology, 2021, 10, 964-971.	3.8	21

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37	Adjoint and Defect Error Bounding and Correction for Functional Estimates. , 2003, , .		12
38	Signal Transduction in Human Cell Lysate <i>via</i> Dynamic RNA Nanotechnology. ACS Synthetic Biology, 2018, 7, 2796-2802.	3.8	12
39	Multiplexed Quantitative In Situ Hybridization with Subcellular or Single-Molecule Resolution Within Whole-Mount Vertebrate Embryos: qHCR and dHCR Imaging (v3.0). Methods in Molecular Biology, 2020, 2148, 159-178.	0.9	12
40	Multiplexed Quantitative In Situ Hybridization for Mammalian Cells on a Slide: qHCR and dHCR Imaging (v3.0). Methods in Molecular Biology, 2020, 2148, 143-156.	0.9	4
41	Multiplexed Quantitative In Situ Hybridization for Mammalian or Bacterial Cells in Suspension: qHCR Flow Cytometry (v3.0). Methods in Molecular Biology, 2020, 2148, 127-141.	0.9	0