

# Niles A Pierce

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

10,424  
citations

159585

30  
h-index

315739

38  
g-index

46  
all docs

46  
docs citations

46  
times ranked

8033  
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Performance Allosteric Conditional Guide RNAs for Mammalian Cell-Selective Regulation of CRISPR/Cas. <i>ACS Synthetic Biology</i> , 2021, 10, 964-971.	3.8	21
2	Hybridization chain reaction enables a unified approach to multiplexed, quantitative, high-resolution immunohistochemistry and <i>in situ</i> hybridization. <i>Development (Cambridge)</i> , 2021, 148, .	2.5	35
3	A Unified Dynamic Programming Framework for the Analysis of Interacting Nucleic Acid Strands: Enhanced Models, Scalability, and Speed. <i>ACS Synthetic Biology</i> , 2020, 9, 2665-2678.	3.8	48
4	Multiplexed Quantitative In Situ Hybridization for Mammalian Cells on a Slide: qHCR and dHCR Imaging (v3.0). <i>Methods in Molecular Biology</i> , 2020, 2148, 143-156.	0.9	4
5	Multiplexed Quantitative In Situ Hybridization for Mammalian or Bacterial Cells in Suspension: qHCR Flow Cytometry (v3.0). <i>Methods in Molecular Biology</i> , 2020, 2148, 127-141.	0.9	0
6	Multiplexed Quantitative In Situ Hybridization with Subcellular or Single-Molecule Resolution Within Whole-Mount Vertebrate Embryos: qHCR and dHCR Imaging (v3.0). <i>Methods in Molecular Biology</i> , 2020, 2148, 159-178.	0.9	12
7	Conditional Guide RNAs: Programmable Conditional Regulation of CRISPR/Cas Function in Bacterial and Mammalian Cells via Dynamic RNA Nanotechnology. <i>ACS Central Science</i> , 2019, 5, 1241-1249.	11.3	83
8	Multidimensional quantitative analysis of mRNA expression within intact vertebrate embryos. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	56
9	Signal Transduction in Human Cell Lysate <i>via</i> Dynamic RNA Nanotechnology. <i>ACS Synthetic Biology</i> , 2018, 7, 2796-2802.	3.8	12
10	Third-generation <i>in situ</i> hybridization chain reaction: multiplexed, quantitative, sensitive, versatile, robust. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	776
11	Constrained Multistate Sequence Design for Nucleic Acid Reaction Pathway Engineering. <i>Journal of the American Chemical Society</i> , 2017, 139, 3134-3144.	13.7	102
12	Single-molecule RNA detection at depth via hybridization chain reaction and tissue hydrogel embedding and clearing. <i>Development (Cambridge)</i> , 2016, 143, 2862-7.	2.5	174
13	Mapping a multiplexed zoo of mRNA expression. <i>Development (Cambridge)</i> , 2016, 143, 3632-3637.	2.5	198
14	Multiplexed miRNA northern blots via hybridization chain reaction. <i>Nucleic Acids Research</i> , 2016, 44, gkw503.	14.5	70
15	Combinatorial Analysis of mRNA Expression Patterns in Mouse Embryos Using Hybridization Chain Reaction. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.prot083832.	0.3	33
16	Sequence Design for a Test Tube of Interacting Nucleic Acid Strands. <i>ACS Synthetic Biology</i> , 2015, 4, 1086-1100.	3.8	52
17	Next-Generation <i>in Situ</i> Hybridization Chain Reaction: Higher Gain, Lower Cost, Greater Durability. <i>ACS Nano</i> , 2014, 8, 4284-4294.	14.6	504
18	Developmental Self-Assembly of a DNA Tetrahedron. <i>ACS Nano</i> , 2014, 8, 3251-3259.	14.6	97

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19	Conditional Dicer Substrate Formation via Shape and Sequence Transduction with Small Conditional RNAs. <i>Journal of the American Chemical Society</i> , 2013, 135, 17322-17330.	13.7	36
20	Selective Nucleic Acid Capture with Shielded Covalent Probes. <i>Journal of the American Chemical Society</i> , 2013, 135, 9691-9699.	13.7	31
21	Localizing transcripts to single cells suggests an important role of uncultured deltaproteobacteria in the termite gut hydrogen economy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16163-16168.	7.1	29
22	NUPACK: Analysis and design of nucleic acid systems. <i>Journal of Computational Chemistry</i> , 2011, 32, 170-173.	3.3	1,289
23	Nucleic acid sequence design via efficient ensemble defect optimization. <i>Journal of Computational Chemistry</i> , 2011, 32, 439-452.	3.3	161
24	Programmable in situ amplification for multiplexed imaging of mRNA expression. <i>Nature Biotechnology</i> , 2010, 28, 1208-1212.	17.5	567
25	Programming biomolecular self-assembly pathways. <i>Nature</i> , 2008, 451, 318-322.	27.8	1,339
26	Thermodynamic Analysis of Interacting Nucleic Acid Strands. <i>SIAM Review</i> , 2007, 49, 65-88.	9.5	297
27	An autonomous polymerization motor powered by DNA hybridization. <i>Nature Nanotechnology</i> , 2007, 2, 490-494.	31.5	303
28	Topological constraints in nucleic acid hybridization kinetics. <i>Nucleic Acids Research</i> , 2005, 33, 4090-4095.	14.5	88
29	Paradigms for computational nucleic acid design. <i>Nucleic Acids Research</i> , 2004, 32, 1392-1403.	14.5	181
30	Adjoint and defect error bounding and correction for functional estimates. <i>Journal of Computational Physics</i> , 2004, 200, 769-794.	3.8	98
31	An algorithm for computing nucleic acid base-pairing probabilities including pseudoknots. <i>Journal of Computational Chemistry</i> , 2004, 25, 1295-1304.	3.3	173
32	A Synthetic DNA Walker for Molecular Transport. <i>Journal of the American Chemical Society</i> , 2004, 126, 10834-10835.	13.7	720
33	From The Cover: Triggered amplification by hybridization chain reaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15275-15278.	7.1	1,643
34	Progress in adjoint error correction for integral functionals. <i>Computing and Visualization in Science</i> , 2004, 6, 113-121.	1.2	38
35	Exact rotamer optimization for protein design. <i>Journal of Computational Chemistry</i> , 2003, 24, 232-243.	3.3	115
36	A partition function algorithm for nucleic acid secondary structure including pseudoknots. <i>Journal of Computational Chemistry</i> , 2003, 24, 1664-1677.	3.3	342

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37	Adjoint and Defect Error Bounding and Correction for Functional Estimates. , 2003, , .		12
38	Protein Design is NP-hard. Protein Engineering, Design and Selection, 2002, 15, 779-782.	2.1	205
39	Analytic adjoint solutions for the quasi-one-dimensional Euler equations. Journal of Fluid Mechanics, 2001, 426, 327-345.	3.4	109
40	Adjoint Recovery of Superconvergent Functionals from PDE Approximations. SIAM Review, 2000, 42, 247-264.	9.5	280
41	Improved lift and drag estimates using adjoint Euler equations. , 1999, , .		47