

# Ehud Shapiro

## List of Publications by Year in descending order

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Version: 2024-02-01

77  
papers

7,705  
citations

147801

31  
h-index

106344

65  
g-index

81  
all docs

81  
docs citations

81  
times ranked

9227  
citing authors

#	ARTICLE	IF	CITATIONS
1	Retrospective cell lineage reconstruction in humans by using short tandem repeats. <i>Cell Reports Methods</i> , 2021, 1, 100054.	2.9	9
2	Comparison of seven single cell whole genome amplification commercial kits using targeted sequencing. <i>Scientific Reports</i> , 2021, 11, 17171.	3.3	19
3	Benchmarked approaches for reconstruction of in vitro cell lineages and in silico models of <i>C. elegans</i> and <i>M. musculus</i> developmental trees. <i>Cell Systems</i> , 2021, 12, 810-826.e4.	6.2	36
4	Efficient acquisition of tens of thousands of short tandem repeats in single-cell whole-genome-amplified DNA. <i>STAR Protocols</i> , 2021, 2, 100828.	1.2	0
5	Short tandem repeat stutter model inferred from direct measurement of in vitro stutter noise. <i>Nucleic Acids Research</i> , 2019, 47, 2436-2445.	14.5	15
6	On the journey from nematode to human, scientists dive by the zebrafish cell lineage tree. <i>Genome Biology</i> , 2018, 19, 63.	8.8	2
7	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	6.0	1,547
8	A generic, cost-effective, and scalable cell lineage analysis platform. <i>Genome Research</i> , 2016, 26, 1588-1599.	5.5	34
9	eSTGt: a programming and simulation environment for population dynamics. <i>BMC Bioinformatics</i> , 2016, 17, 187.	2.6	4
10	Synthesis and cell-free cloning of DNA libraries using programmable microfluidics. <i>Nucleic Acids Research</i> , 2016, 44, e35-e35.	14.5	23
11	Accuracy of Answers to Cell Lineage Questions Depends on Single-Cell Genomics Data Quality and Quantity. <i>PLoS Computational Biology</i> , 2016, 12, e1004983.	3.2	5
12	Rationally designed, heterologous <i>S. cerevisiae</i> transcripts expose novel expression determinants. <i>RNA Biology</i> , 2015, 12, 972-984.	3.1	39
13	Accurate, Model-Based Tuning of Synthetic Gene Expression Using Introns in <i>S. cerevisiae</i> . <i>PLoS Genetics</i> , 2014, 10, e1004407.	3.5	31
14	Lineage grammars: describing, simulating and analyzing population dynamics. <i>BMC Bioinformatics</i> , 2014, 15, 249.	2.6	5
15	Single cell analysis exposes intratumor heterogeneity and suggests that FLT3-ITD is a late event in leukemogenesis. <i>Experimental Hematology</i> , 2014, 42, 457-463.	0.4	22
16	Heuristic for Maximizing DNA Reuse in Synthetic DNA Library Assembly. <i>ACS Synthetic Biology</i> , 2014, 3, 529-542.	3.8	16
17	Correcting the bias against interdisciplinary research. <i>ELife</i> , 2014, 3, e02576.	6.0	2
18	Single-cell sequencing-based technologies will revolutionize whole-organism science. <i>Nature Reviews Genetics</i> , 2013, 14, 618-630.	16.3	1,012

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19	Molecules reach consensus. <i>Nature Nanotechnology</i> , 2013, 8, 703-705.	31.5	14
20	A synthetic biology approach for evaluating the functional contribution of designer cellulosome components to deconstruction of cellulosic substrates. <i>Biotechnology for Biofuels</i> , 2013, 6, 182.	6.2	76
21	Mapping the translation initiation landscape of an <i>S. cerevisiae</i> gene using fluorescent proteins. <i>Genomics</i> , 2013, 102, 419-429.	2.9	9
22	A library of programmable DNAzymes that operate in a cellular environment. <i>Scientific Reports</i> , 2013, 3, 1535.	3.3	51
23	Comparing Algorithms That Reconstruct Cell Lineage Trees Utilizing Information on Microsatellite Mutations. <i>PLoS Computational Biology</i> , 2013, 9, e1003297.	3.2	16
24	Cell Lineage Analysis of the Mammalian Female Germline. <i>PLoS Genetics</i> , 2012, 8, e1002477.	3.5	60
25	A mechanical Turing machine: blueprint for a biomolecular computer. <i>Interface Focus</i> , 2012, 2, 497-503.	3.0	22
26	Programmable In Vivo Selection of Arbitrary DNA Sequences. <i>PLoS ONE</i> , 2012, 7, e47795.	2.5	1
27	Cell lineage analysis of acute leukemia relapse uncovers the role of replication-rate heterogeneity and microsatellite instability. <i>Blood</i> , 2012, 120, 603-612.	1.4	67
28	De Novo DNA Synthesis Using Single-Molecule PCR. <i>Methods in Molecular Biology</i> , 2012, 852, 35-47.	0.9	1
29	Detection of Multiple Disease Indicators by an Autonomous Biomolecular Computer. <i>Nano Letters</i> , 2011, 11, 2989-2996.	9.1	42
30	Muscle-Bound Primordial Stem Cells Give Rise to Myofiber-Associated Myogenic and Non-Myogenic Progenitors. <i>PLoS ONE</i> , 2011, 6, e25605.	2.5	9
31	Colon Stem Cell and Crypt Dynamics Exposed by Cell Lineage Reconstruction. <i>PLoS Genetics</i> , 2011, 7, e1002192.	3.5	52
32	Processing DNA molecules as text. <i>Systems and Synthetic Biology</i> , 2010, 4, 227-236.	1.0	15
33	Single-Cell Phylogenetic analysis provides Novel Insight Into Resistance Mechanisms In AML. <i>Blood</i> , 2010, 116, 178-178.	1.4	0
34	Molecular implementation of simple logic programs. <i>Nature Nanotechnology</i> , 2009, 4, 642-648.	31.5	121
35	Amplification of multiple genomic loci from single cells isolated by laser micro-dissection of tissues. <i>BMC Biotechnology</i> , 2008, 8, 17.	3.3	69
36	Towards molecular computers that operate in a biological environment. <i>Physica D: Nonlinear Phenomena</i> , 2008, 237, 1165-1172.	2.8	70

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37	RNA Computing in a Living Cell. <i>Science</i> , 2008, 322, 387-388.	12.6	28
38	Estimating Cell Depth from Somatic Mutations. <i>PLoS Computational Biology</i> , 2008, 4, e1000058.	3.2	35
39	De novo DNA synthesis using single molecule PCR. <i>Nucleic Acids Research</i> , 2008, 36, e107-e107.	14.5	25
40	Cell Lineage Analysis of a Mouse Tumor. <i>Cancer Research</i> , 2008, 68, 5924-5931.	0.9	63
41	Recursive construction of perfect DNA molecules from imperfect oligonucleotides. <i>Molecular Systems Biology</i> , 2008, 4, 191.	7.2	50
42	Reconstruction of Cell Lineage Trees in Mice. <i>PLoS ONE</i> , 2008, 3, e1939.	2.5	43
43	Logic goes in vitro. <i>Nature Nanotechnology</i> , 2007, 2, 84-85.	31.5	44
44	Bringing DNA Computers To Life. <i>Scientific American</i> , 2006, 294, 44-51.	1.0	50
45	Tapping the computing power of biological molecules gives rise to tiny machines that can speak directly to living cells. <i>Scientific American</i> , 2006, 294, 44-51.	1.0	19
46	Genomic Variability within an Organism Exposes Its Cell Lineage Tree. <i>PLoS Computational Biology</i> , 2005, 1, e50.	3.2	124
47	A universal mechanism ties genotype to phenotype in trinucleotide diseases. <i>PLoS Computational Biology</i> , 2005, preprint, e235.	3.2	0
48	Stochastic computing with biomolecular automata. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9960-9965.	7.1	93
49	An autonomous molecular computer for logical control of gene expression. <i>Nature</i> , 2004, 429, 423-429.	27.8	857
50	BioAmbients: an abstraction for biological compartments. <i>Theoretical Computer Science</i> , 2004, 325, 141-167.	0.9	354
51	The $\pi$ -calculus as an Abstraction for Biomolecular Systems. <i>Natural Computing Series</i> , 2004, , 219-266.	2.2	45
52	Injecting Life with Computers. <i>Lecture Notes in Computer Science</i> , 2004, , 1-1.	1.3	0
53	DNA molecule provides a computing machine with both data and fuel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2191-2196.	7.1	221
54	Cellular abstractions: Cells as computation. <i>Nature</i> , 2002, 419, 343-343.	27.8	234

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55	Application of a stochastic name-passing calculus to representation and simulation of molecular processes. Information Processing Letters, 2001, 80, 25-31.	0.6	361
56	Programmable and autonomous computing machine made of biomolecules. Nature, 2001, 414, 430-434.	27.8	648
57	Representation and simulation of biochemical processes using the $\lambda$ -calculus process algebra. , 2000, , 459-70.		141
58	The Family of Concurrent Logic Programming Languages. , 1991, , 359-485.		1
59	Guest editorsâ€™ preface. New Generation Computing, 1990, 7, 85-87.	3.3	0
60	The languages FCP(:) and FCP(,;?). New Generation Computing, 1990, 7, 89-107.	3.3	8
61	A sequential abstract machine for flat concurrent prolog. The Journal of Logic Programming, 1989, 7, 85-123.	1.7	3
62	OR-parallel PROLOG in flat concurrent PROLOG. The Journal of Logic Programming, 1989, 6, 243-267.	1.7	3
63	The family of concurrent logic programming languages. ACM Computing Surveys, 1989, 21, 413-510.	23.0	344
64	Concurrent algorithmic debugging. ACM SIGPLAN Notices, 1989, 24, 248-260.	0.2	6
65	A distributed locking algorithm for a transactions system in flat concurrent prolog. Lecture Notes in Computer Science, 1989, , 304-320.	1.3	0
66	Specialisation of Prolog and FCP programs using abstract interpretation. New Generation Computing, 1988, 6, 159-186.	3.3	44
67	Notes on the complexity of systolic programs. Journal of Parallel and Distributed Computing, 1987, 4, 250-265.	4.1	5
68	A layered method for process and code mapping. New Generation Computing, 1987, 5, 185-205.	3.3	12
69	Compiling OR-parallelism into AND-parallelism. New Generation Computing, 1987, 5, 45-61.	3.3	11
70	Concurrent Prolog: A Progress Report. , 1987, , 277-313.		19
71	Concurrent Prolog: A progress report. , 1986, , 277-313.		8
72	Multiway merge with constant delay in Concurrent Prolog. New Generation Computing, 1986, 4, 211-216.	3.3	11

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73	A parallel implementation of Flat Concurrent Prolog. International Journal of Parallel Programming, 1986, 15, 245-275.	1.5	35
74	Systems programming in concurrent prolog. , 1984, , .		29
75	Fair, biased, and self-balancing merge operators: Their specification and implementation in Concurrent Prolog. New Generation Computing, 1984, 2, 221-240.	3.3	16
76	Guest editor's preface. New Generation Computing, 1984, 2, 305-308.	3.3	0
77	Object oriented programming in Concurrent Prolog. New Generation Computing, 1983, 1, 25-48.	3.3	143