

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 | The Human Cell Atlas. ELife, 2017, 6, . | 6.0 | 1,547 |
| 2 | Single-cell sequencing-based technologies will revolutionize whole-organism science. Nature Reviews Genetics, 2013, 14, 618-630. | 16.3 | 1,012 |
| 3 | An autonomous molecular computer for logical control of gene expression. Nature, 2004, 429, 423-429. | 27.8 | 857 |
| 4 | Programmable and autonomous computing machine made of biomolecules. Nature, 2001, 414, 430-434. | 27.8 | 648 |
| 5 | Application of a stochastic name-passing calculus to representation and simulation of molecular processes. Information Processing Letters, 2001, 80, 25-31. | 0.6 | 361 |
| 6 | BioAmbients: an abstraction for biological compartments. Theoretical Computer Science, 2004, 325, 141-167. | 0.9 | 354 |
| 7 | The family of concurrent logic programming languages. ACM Computing Surveys, 1989, 21, 413-510. | 23.0 | 344 |
| 8 | Cellular abstractions: Cells as computation. Nature, 2002, 419, 343-343. | 27.8 | 234 |
| 9 | DNA molecule provides a computing machine with both data and fuel. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2191-2196. | 7.1 | 221 |
| 10 | Object oriented programming in Concurrent Prolog. New Generation Computing, 1983, 1, 25-48. | 3.3 | 143 |
| 11 | Representation and simulation of biochemical processes using the π -calculus process algebra. , 2000, , 459-70. | | 141 |
| 12 | Genomic Variability within an Organism Exposes Its Cell Lineage Tree. PLoS Computational Biology, 2005, 1, e50. | 3.2 | 124 |
| 13 | Molecular implementation of simple logic programs. Nature Nanotechnology, 2009, 4, 642-648. | 31.5 | 121 |
| 14 | Stochastic computing with biomolecular automata. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9960-9965. | 7.1 | 93 |
| 15 | A synthetic biology approach for evaluating the functional contribution of designer cellulosome components to deconstruction of cellulosic substrates. Biotechnology for Biofuels, 2013, 6, 182. | 6.2 | 76 |
| 16 | Towards molecular computers that operate in a biological environment. Physica D: Nonlinear Phenomena, 2008, 237, 1165-1172. | 2.8 | 70 |
| 17 | Amplification of multiple genomic loci from single cells isolated by laser micro-dissection of tissues. BMC Biotechnology, 2008, 8, 17. | 3.3 | 69 |
| 18 | Cell lineage analysis of acute leukemia relapse uncovers the role of replication-rate heterogeneity and microsatellite instability. Blood, 2012, 120, 603-612. | 1.4 | 67 |

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|----|---|------|-----------|
| 19 | Cell Lineage Analysis of a Mouse Tumor. <i>Cancer Research</i> , 2008, 68, 5924-5931. | 0.9 | 63 |
| 20 | Cell Lineage Analysis of the Mammalian Female Germline. <i>PLoS Genetics</i> , 2012, 8, e1002477. | 3.5 | 60 |
| 21 | Colon Stem Cell and Crypt Dynamics Exposed by Cell Lineage Reconstruction. <i>PLoS Genetics</i> , 2011, 7, e1002192. | 3.5 | 52 |
| 22 | A library of programmable DNAzymes that operate in a cellular environment. <i>Scientific Reports</i> , 2013, 3, 1535. | 3.3 | 51 |
| 23 | Bringing DNA Computers To Life. <i>Scientific American</i> , 2006, 294, 44-51. | 1.0 | 50 |
| 24 | Recursive construction of perfect DNA molecules from imperfect oligonucleotides. <i>Molecular Systems Biology</i> , 2008, 4, 191. | 7.2 | 50 |
| 25 | The λ -calculus as an Abstraction for Biomolecular Systems. <i>Natural Computing Series</i> , 2004, , 219-266. | 2.2 | 45 |
| 26 | Specialisation of Prolog and FCP programs using abstract interpretation. <i>New Generation Computing</i> , 1988, 6, 159-186. | 3.3 | 44 |
| 27 | Logic goes in vitro. <i>Nature Nanotechnology</i> , 2007, 2, 84-85. | 31.5 | 44 |
| 28 | Reconstruction of Cell Lineage Trees in Mice. <i>PLoS ONE</i> , 2008, 3, e1939. | 2.5 | 43 |
| 29 | Detection of Multiple Disease Indicators by an Autonomous Biomolecular Computer. <i>Nano Letters</i> , 2011, 11, 2989-2996. | 9.1 | 42 |
| 30 | Rationally designed, heterologous <i>S. cerevisiae</i> transcripts expose novel expression determinants. <i>RNA Biology</i> , 2015, 12, 972-984. | 3.1 | 39 |
| 31 | 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 |
| 32 | A parallel implementation of Flat Concurrent Prolog. <i>International Journal of Parallel Programming</i> , 1986, 15, 245-275. | 1.5 | 35 |
| 33 | Estimating Cell Depth from Somatic Mutations. <i>PLoS Computational Biology</i> , 2008, 4, e1000058. | 3.2 | 35 |
| 34 | A generic, cost-effective, and scalable cell lineage analysis platform. <i>Genome Research</i> , 2016, 26, 1588-1599. | 5.5 | 34 |
| 35 | 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 |
| 36 | Systems programming in concurrent prolog. , 1984, , . | | 29 |

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|----|---|------|-----------|
| 37 | RNA Computing in a Living Cell. <i>Science</i> , 2008, 322, 387-388. | 12.6 | 28 |
| 38 | De novo DNA synthesis using single molecule PCR. <i>Nucleic Acids Research</i> , 2008, 36, e107-e107. | 14.5 | 25 |
| 39 | Synthesis and cell-free cloning of DNA libraries using programmable microfluidics. <i>Nucleic Acids Research</i> , 2016, 44, e35-e35. | 14.5 | 23 |
| 40 | A mechanical Turing machine: blueprint for a biomolecular computer. <i>Interface Focus</i> , 2012, 2, 497-503. | 3.0 | 22 |
| 41 | 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 |
| 42 | Comparison of seven single cell whole genome amplification commercial kits using targeted sequencing. <i>Scientific Reports</i> , 2021, 11, 17171. | 3.3 | 19 |
| 43 | Concurrent Prolog: A Progress Report. , 1987, , 277-313. | | 19 |
| 44 | 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 |
| 45 | Fair, biased, and self-balancing merge operators: Their specification and implementation in Concurrent Prolog. <i>New Generation Computing</i> , 1984, 2, 221-240. | 3.3 | 16 |
| 46 | Comparing Algorithms That Reconstruct Cell Lineage Trees Utilizing Information on Microsatellite Mutations. <i>PLoS Computational Biology</i> , 2013, 9, e1003297. | 3.2 | 16 |
| 47 | Heuristic for Maximizing DNA Reuse in Synthetic DNA Library Assembly. <i>ACS Synthetic Biology</i> , 2014, 3, 529-542. | 3.8 | 16 |
| 48 | Processing DNA molecules as text. <i>Systems and Synthetic Biology</i> , 2010, 4, 227-236. | 1.0 | 15 |
| 49 | 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 |
| 50 | Molecules reach consensus. <i>Nature Nanotechnology</i> , 2013, 8, 703-705. | 31.5 | 14 |
| 51 | A layered method for process and code mapping. <i>New Generation Computing</i> , 1987, 5, 185-205. | 3.3 | 12 |
| 52 | Multiway merge with constant delay in Concurrent Prolog. <i>New Generation Computing</i> , 1986, 4, 211-216. | 3.3 | 11 |
| 53 | Compiling OR-parallelism into AND-parallelism. <i>New Generation Computing</i> , 1987, 5, 45-61. | 3.3 | 11 |
| 54 | 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 |

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|----|--|-----|-----------|
| 55 | 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 |
| 56 | Retrospective cell lineage reconstruction in humans by using short tandem repeats. <i>Cell Reports Methods</i> , 2021, 1, 100054. | 2.9 | 9 |
| 57 | Concurrent Prolog: A progress report. , 1986, , 277-313. | | 8 |
| 58 | The languages FCP(:) and FCP(;?). <i>New Generation Computing</i> , 1990, 7, 89-107. | 3.3 | 8 |
| 59 | Concurrent algorithmic debugging. <i>ACM SIGPLAN Notices</i> , 1989, 24, 248-260. | 0.2 | 6 |
| 60 | Notes on the complexity of systolic programs. <i>Journal of Parallel and Distributed Computing</i> , 1987, 4, 250-265. | 4.1 | 5 |
| 61 | Lineage grammars: describing, simulating and analyzing population dynamics. <i>BMC Bioinformatics</i> , 2014, 15, 249. | 2.6 | 5 |
| 62 | 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 |
| 63 | eSTGt: a programming and simulation environment for population dynamics. <i>BMC Bioinformatics</i> , 2016, 17, 187. | 2.6 | 4 |
| 64 | A sequential abstract machine for flat concurrent prolog. <i>The Journal of Logic Programming</i> , 1989, 7, 85-123. | 1.7 | 3 |
| 65 | OR-parallel PROLOG in flat concurrent PROLOG. <i>The Journal of Logic Programming</i> , 1989, 6, 243-267. | 1.7 | 3 |
| 66 | 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 |
| 67 | Correcting the bias against interdisciplinary research. <i>ELife</i> , 2014, 3, e02576. | 6.0 | 2 |
| 68 | Programmable In Vivo Selection of Arbitrary DNA Sequences. <i>PLoS ONE</i> , 2012, 7, e47795. | 2.5 | 1 |
| 69 | De Novo DNA Synthesis Using Single-Molecule PCR. <i>Methods in Molecular Biology</i> , 2012, 852, 35-47. | 0.9 | 1 |
| 70 | The Family of Concurrent Logic Programming Languages. , 1991, , 359-485. | | 1 |
| 71 | Guest editor's™ preface. <i>New Generation Computing</i> , 1984, 2, 305-308. | 3.3 | 0 |
| 72 | Guest editors's™ preface. <i>New Generation Computing</i> , 1990, 7, 85-87. | 3.3 | 0 |

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|----|--|-----|-----------|
| 73 | Efficient acquisition of tens of thousands of short tandem repeats in single-cell whole-genome-amplified DNA. STAR Protocols, 2021, 2, 100828. | 1.2 | 0 |
| 74 | Injecting Life with Computers. Lecture Notes in Computer Science, 2004, , 1-1. | 1.3 | 0 |
| 75 | A universal mechanism ties genotype to phenotype in trinucleotide diseases. PLoS Computational Biology, 2005, preprint, e235. | 3.2 | 0 |
| 76 | Single-Cell Phylogenetic analysis provides Novel Insight Into Resistance Mechanisms In AML. Blood, 2010, 116, 178-178. | 1.4 | 0 |
| 77 | A distributed locking algorithm for a transactions system in flat concurrent prolog. Lecture Notes in Computer Science, 1989, , 304-320. | 1.3 | 0 |