

Sorin Istrail

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

16,093
citations

186265

28
h-index

149698

56
g-index

65
all docs

65
docs citations

65
times ranked

16689
citing authors

#	ARTICLE	IF	CITATIONS
1	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	12.6	12,623
2	The Genome of the Sea Urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 2006, 314, 941-952.	12.6	1,018
3	Algorithmic strategies for the single nucleotide polymorphism haplotype assembly problem. <i>Briefings in Bioinformatics</i> , 2002, 3, 23-31.	6.5	187
4	Whole-genome shotgun assembly and comparison of human genome assemblies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1916-1921.	7.1	164
5	Logic functions of the genomic cis-regulatory code. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4954-4959.	7.1	159
6	Robust Proofs of NP-Hardness for Protein Folding: General Lattices and Energy Potentials. <i>Journal of Computational Biology</i> , 1997, 4, 1-22.	1.6	113
7	Optimal Haplotype Block-Free Selection of Tagging SNPs for Genome-Wide Association Studies. <i>Genome Research</i> , 2004, 14, 1633-1640.	5.5	113
8	The linkage disequilibrium maps of three human chromosomes across four populations reflect their demographic history and a common underlying recombination pattern. <i>Genome Research</i> , 2005, 15, 454-462.	5.5	107
9	HapCompass: A Fast Cycle Basis Algorithm for Accurate Haplotype Assembly of Sequence Data. <i>Journal of Computational Biology</i> , 2012, 19, 577-590.	1.6	101
10	The Transcriptome of the Sea Urchin Embryo. <i>Science</i> , 2006, 314, 960-962.	12.6	85
11	Haplotype assembly in polyploid genomes and identical by descent shared tracts. <i>Bioinformatics</i> , 2013, 29, i352-i360.	4.1	85
12	The regulatory genome and the computer. <i>Developmental Biology</i> , 2007, 310, 187-195.	2.0	76
13	Transcriptome of American Oysters, <i>Crassostrea virginica</i> , in Response to Bacterial Challenge: Insights into Potential Mechanisms of Disease Resistance. <i>PLoS ONE</i> , 2014, 9, e105097.	2.5	74
14	A Survey of Computational Methods for Determining Haplotypes. <i>Lecture Notes in Computer Science</i> , 2004, , 26-47.	1.3	72
15	Gene and alternative splicing annotation with AIR. <i>Genome Research</i> , 2005, 15, 54-66.	5.5	70
16	Optimal Selection of SNP Markers for Disease Association Studies. <i>Human Heredity</i> , 2004, 58, 190-202.	0.8	63
17	Intellectual Disability Is Associated with Increased Runs of Homozygosity in Simplex Autism. <i>American Journal of Human Genetics</i> , 2013, 93, 103-109.	6.2	63
18	A quantitative reference transcriptome for <i>Nematostella vectensis</i> early embryonic development: a pipeline for de novo assembly in emerging model systems. <i>EvoDevo</i> , 2013, 4, 16.	3.2	57

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19	Practical Algorithms and Fixed-Parameter Tractability for the Single Individual SNP Haplotyping Problem. <i>Lecture Notes in Computer Science</i> , 2002, , 29-43.	1.3	56
20	Robustness of Inference of Haplotype Block Structure. <i>Journal of Computational Biology</i> , 2003, 10, 13-19.	1.6	54
21	Haplotypes and informative SNP selection algorithms. , 2003, , .		52
22	Pathway-based genetic analysis of preterm birth. <i>Genomics</i> , 2013, 101, 163-170.	2.9	51
23	Polynomial and APX-hard cases of the individual haplotyping problem. <i>Theoretical Computer Science</i> , 2005, 335, 109-125.	0.9	50
24	Functional cis-regulatory genomics for systems biology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3930-3935.	7.1	50
25	Physical Mapping by STS Hybridization: Algorithmic Strategies and the Challenge of Software Evaluation. <i>Journal of Computational Biology</i> , 1995, 2, 219-273.	1.6	47
26	Lattice and Off-Lattice Side Chain Models of Protein Folding: Linear Time Structure Prediction Better than 86% of Optimal. <i>Journal of Computational Biology</i> , 1997, 4, 241-259.	1.6	42
27	dbPTB: a database for preterm birth. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bar069.	3.0	39
28	Comparative immunopeptidomics of humans and their pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13268-13272.	7.1	38
29	Islands of Tractability for Parsimony Haplotyping. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006, 3, 303-311.	3.0	24
30	QColors: an algorithm for conservative viral quasispecies reconstruction from short and non-contiguous next generation sequencing reads. <i>In Silico Biology</i> , 2011, 11, 193-201.	0.9	22
31	Combinatorial Problems Arising in SNP and Haplotype Analysis. <i>Lecture Notes in Computer Science</i> , 2003, , 26-47.	1.3	17
32	The Clark Phaseable Sample Size Problem: Long-Range Phasing and Loss of Heterozygosity in GWAS. <i>Journal of Computational Biology</i> , 2011, 18, 323-333.	1.6	16
33	Pathway-based analysis of genomic variation data. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 622-626.	3.3	16
34	Epitope prediction algorithms for peptide-based vaccine design. <i>Proceedings</i> , 2003, 2, 17-26.	0.1	16
35	Global analysis of sequence diversity within HIV-1 subtypes across geographic regions. <i>Future Virology</i> , 2012, 7, 505-517.	1.8	13
36	Global Comparison of Drug Resistance Mutations After First-Line Antiretroviral Therapy Across Human Immunodeficiency Virus-1 Subtypes. <i>Open Forum Infectious Diseases</i> , 2016, 3, ofv158.	0.9	12

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37	Proteinarium: Multi-sample protein-protein interaction analysis and visualization tool. <i>Genomics</i> , 2020, 112, 4288-4296.	2.9	10
38	Elementary bounded languages. <i>Information and Control</i> , 1978, 39, 177-191.	1.1	8
39	Finding Anchors for Genomic Sequence Comparison. <i>Journal of Computational Biology</i> , 2005, 12, 762-776.	1.6	8
40	HAPLOTYPE PHASING BY MULTI-ASSEMBLY OF SHARED HAPLOTYPES: PHASE-DEPENDENT INTERACTIONS BETWEEN RARE VARIANTS. , 2010, , 88-99.		8
41	On complements of some bounded context-sensitive languages. <i>Information and Control</i> , 1979, 42, 283-289.	1.1	6
42	The chimeric mapping problem: Algorithmic strategies and performance evaluation on synthetic genomic data. <i>Computers & Chemistry</i> , 1994, 18, 207-220.	1.2	6
43	QColors: An algorithm for conservative viral quasispecies reconstruction from short and non-contiguous next generation sequencing reads. , 2011, , .		6
44	Invariant patterns in crystal lattices: Implications for protein folding algorithms (extended abstract). <i>Lecture Notes in Computer Science</i> , 1996, , 288-303.	1.3	6
45	Eric Davidson's Regulatory Genome for Computer Science: Causality, Logic, and Proof Principles of the Genomic cis-Regulatory Code. <i>Journal of Computational Biology</i> , 2019, 26, 653-684.	1.6	5
46	Physical Mapping with Repeated Probes: The Hypergraph Superstring Problem. <i>Lecture Notes in Computer Science</i> , 1999, , 66-77.	1.3	5
47	Finding anchors for genomic sequence comparison. , 2004, , .		4
48	Islands of tractability for parsimony haplotyping. , 2005, , 65-72.		4
49	Practical Computational Methods for Regulatory Genomics: A cisGRN-Lexicon and cisGRN-Browser for Gene Regulatory Networks. <i>Methods in Molecular Biology</i> , 2010, 674, 369-399.	0.9	4
50	DELISHUS: an efficient and exact algorithm for genome-wide detection of deletion polymorphism in autism. <i>Bioinformatics</i> , 2012, 28, i154-i162.	4.1	3
51	How Does the Regulatory Genome Work?. <i>Journal of Computational Biology</i> , 2019, 26, 685-695.	1.6	3
52	Inferring Piecewise Ancestral History from Haploid Sequences. <i>Lecture Notes in Computer Science</i> , 2004, , 62-73.	1.3	3
53	TUMOR HAPLOTYPE ASSEMBLY ALGORITHMS FOR CANCER GENOMICS. , 2013, , .		3
54	Combinatorial and statistical prediction of gene expression from haplotype sequence. <i>Bioinformatics</i> , 2020, 36, i194-i202.	4.1	2

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55	Conservative Extensions of Linkage Disequilibrium Measures from Pairwise to Multi-loci and Algorithms for Optimal Tagging SNP Selection. Lecture Notes in Computer Science, 2011, , 468-482.	1.3	2
56	Tumor haplotype assembly algorithms for cancer genomics. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 3-14.	0.7	2
57	On the Concept of Cis-regulatory Information: From Sequence Motifs to Logic Functions. Natural Computing Series, 2009, , 731-742.	2.2	1
58	The Clark Phase-able Sample Size Problem: Long-Range Phasing and Loss of Heterozygosity in GWAS. Lecture Notes in Computer Science, 2010, , 158-173.	1.3	1
59	Chomsky-Schutzenberger representations for families of languages and grammatical types. Lecture Notes in Computer Science, 1981, , 333-347.	1.3	1
60	Workshop: Robust algorithms for inferring haplotype phase and deletion polymorphism from high-throughput whole genome sequence data. , 2012, , .		0
61	Tractatus: An Exact and Subquadratic Algorithm for Inferring Identical-by-Descent Multi-shared Haplotype Tracts. Lecture Notes in Computer Science, 2014, , 1-17.	1.3	0
62	Michael Waterman's Contributions to Computational Biology and Bioinformatics. Journal of Computational Biology, 0, , .	1.6	0