Benny Chor

List of Publications by Year
in descending order

55 papers	2,104 citations	279798 23 h-index	243625 44 g-index
58 all docs	58 docs citations	58 times ranked	1606 citing authors

#	ARTICLE	IF	CITATIONS
1	Inter-chromosomal k-mer distances. BMC Genomics, 2021, 22, 644.	2.8	1
2	The Functional 3D Organization of Unicellular Genomes. Scientific Reports, 2019, 9, 12734.	3.3	0
3	A High Quartet Distance Construction. Annals of Combinatorics, 2019, 23, 51-65.	0.6	1
4	A deep neural network approach for learning intrinsic protein-RNA binding preferences. Bioinformatics, 2018, 34, i638-i646.	4.1	68
5	Cases in which ancestral maximum likelihood will be confusingly misleading. Journal of Theoretical Biology, 2017, 420, 318-323.	1.7	1
6	Inversion symmetry of DNA k-mer counts: validity and deviations. BMC Genomics, 2016, 17, 696.	2.8	32
7	BioNSi: A Discrete Biological Network Simulator Tool. Journal of Proteome Research, 2016, 15, 2871-2880.	3.7	16
8	CRISPR Detection From Short Reads Using Partial Overlap Graphs. Journal of Computational Biology, 2016, 23, 461-471.	1.6	5
9	Extending partial haplotypes to full genome haplotypes using chromosome conformation capture data. Bioinformatics, 2016, 32, i559-i566.	4.1	17
10	Do tree split probabilities determine the branch lengths?. Journal of Theoretical Biology, 2015, 374, 54-59.	1.7	1
11	Representative Selection in Nonmetric Datasets. Applied Artificial Intelligence, 2015, 29, 807-838.	3.2	3
12	Hierarchical Partitioning of Metazoan Protein Conservation Profiles Provides New Functional Insights. PLoS ONE, 2014, 9, e90282.	2.5	1
13	Computational Thinking in Life Science Education. PLoS Computational Biology, 2014, 10, e1003897.	3.2	64
14	String graph construction using incremental hashing. Bioinformatics, 2014, 30, 3515-3523.	4.1	16
15	The effective application of a discrete transition model to explore cell-cycle regulation in yeast. BMC Research Notes, 2013, 6, 311.	1.4	8
16	Detecting Phylogenetic Signals in Eukaryotic Whole Genome Sequences. Journal of Computational Biology, 2012, 19, 945-956.	1.6	11
17	A Phylogenetic Approach to Music Performance Analysis. Journal of New Music Research, 2012, 41, 195-222.	0.8	14
18	Approximate Maximum Parsimony and Ancestral Maximum Likelihood. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 183-187.	3.0	15

#	ARTICLE	IF	CITATIONS
19	Genomic DNA k-mer spectra: models and modalities. Genome Biology, 2009, 10, R108.	9.6	165
20	Biological Networks: Comparison, Conservation, and Evolution via Relative Description Length. Journal of Computational Biology, 2007, 14, 817-838.	1.6	12
21	Genomic analysis of COP9 signalosome function in Drosophila melanogaster reveals a role in temporal regulation of gene expression. Molecular Systems Biology, 2007, 3, 108.	7.2	41
22	Analytic solutions of maximum likelihood on forks of four taxa. Mathematical Biosciences, 2007, 208, 347-358.	1.9	4
23	Forbidden pentaâ€peptides. Protein Science, 2007, 16, 2251-2259.	7.6	26
24	Analytic solutions for three taxon ML trees with variable rates across sites. Discrete Applied Mathematics, 2007, 155, 750-758.	0.9	21
25	Maximum Likelihood Molecular Clock Comb: Analytic Solutions. Journal of Computational Biology, 2006, 13, 819-837.	1.6	7
26	The Average Common Substring Approach to Phylogenomic Reconstruction. Journal of Computational Biology, 2006, 13, 336-350.	1.6	184
27	Finding a maximum likelihood tree is hard. Journal of the ACM, 2006, 53, 722-744.	2.2	44
28	Maximum Likelihood Jukes-Cantor Triplets: Analytic Solutions. Molecular Biology and Evolution, 2006, 23, 626-632.	8.9	39
29	Information Theoretic Approaches to Whole Genome Phylogenies. Lecture Notes in Computer Science, 2005, , 283-295.	1.3	6
30	Maximum likelihood of evolutionary trees: hardness and approximation. Bioinformatics, 2005, 21, i97-i106.	4.1	72
31	Maximum Likelihood of Evolutionary Trees Is Hard. Lecture Notes in Computer Science, 2005, , 296-310.	1.3	35
32	Molecular Clock Fork Phylogenies: Closed Form Analytic Maximum Likelihood Solutions. Systematic Biology, 2004, 53, 963-967.	5.6	44
33	ANCESTRAL MAXIMUM LIKELIHOOD OF EVOLUTIONARY TREES IS HARD. Journal of Bioinformatics and Computational Biology, 2004, 02, 257-271.	0.8	17
34	Maximum likelihood on four taxa phylogenetic trees. , 2003, , .		12
35	On Privacy and Partition Arguments. Information and Computation, 2001, 167, 2-9.	0.7	7
36	Multiple Maxima of Likelihood in Phylogenetic Trees: An Analytic Approach. Molecular Biology and Evolution, 2000, 17, 1529-1541.	8.9	115

#	Article	IF	Citations
37	RHOâ€"Radiation Hybrid Ordering. Genome Research, 2000, 10, 365-378.	5.5	25
38	Solvability in Asynchronous Environments II: Finite Interactive Tasks. SIAM Journal on Computing, 1999, 29, 351-377.	1.0	8
39	From Quartets to Phylogenetic Trees. Lecture Notes in Computer Science, 1998, , 36-53.	1.3	5
40	Constructing Phylogenies from Quartets: Elucidation of Eutherian Superordinal Relationships. Journal of Computational Biology, 1998, 5, 377-390.	1.6	34
41	A Geometric Approach to Betweenness. SIAM Journal on Discrete Mathematics, 1998, 11, 511-523.	0.8	75
42	On Constructing Radiation Hybrid Maps. Journal of Computational Biology, 1997, 4, 517-533.	1.6	34
43	The privacy of dense symmetric functions. Computational Complexity, 1995, 5, 43-59.	0.3	5
44	Private Computations over the Integers. SIAM Journal on Computing, 1995, 24, 376-386.	1.0	23
45	On the structure of the privacy hierarchy. Journal of Cryptology, 1994, 7, 53-60.	2.8	24
46	Wait-Free Consensus Using Asynchronous Hardware. SIAM Journal on Computing, 1994, 23, 701-712.	1.0	40
47	Secret sharing over infinite domains. Journal of Cryptology, 1993, 6, 87-95.	2.8	32
48	A communication-privacy tradeoff for modular addition. Information Processing Letters, 1993, 45, 205-210.	0.6	49
49	A Zero-One Law for Boolean Privacy. SIAM Journal on Discrete Mathematics, 1991, 4, 36-47.	0.8	117
50	Simple constant-time consensus protocols in realistic failure models. Journal of the ACM, 1989, 36, 591-614.	2.2	50
51	On the power of two-point based sampling. Journal of Complexity, 1989, 5, 96-106.	1.3	146
52	Secret Sharing Over Infinite Domains. , 1989, , 299-306.		11
53	RSA and Rabin Functions: Certain Parts are as Hard as the Whole. SIAM Journal on Computing, 1988, 17, 194-209.	1.0	275
54	The Bit Security of Modular Squaring given Partial Factorization of the Modulos. , 1985, , 448-457.		7

#	ARTICLE	IF	CITATIONS
55	RSA/Rabin least significant bits are $$ frac{1} {2} + frac{1} {{poly left({log N} ight)}} $$ secure (Extended Abstract). , 1984, , 303-313.		6