

## List of Publications by Year in descending order

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86  
papers

15,216  
citations

218592

26  
h-index

64755

79  
g-index

91  
all docs

91  
docs citations

91  
times ranked

16206  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	6.0	12,623
2	The evolution of tumour phylogenetics: principles and practice. <i>Nature Reviews Genetics</i> , 2017, 18, 213-229.	7.7	240
3	Molecular crowding shapes gene expression in synthetic cellular nanosystems. <i>Nature Nanotechnology</i> , 2013, 8, 602-608.	15.6	215
4	Local Rules Simulation of the Kinetics of Virus Capsid Self-Assembly. <i>Biophysical Journal</i> , 1998, 75, 2626-2636.	0.2	148
5	Optimal Haplotype Block-Free Selection of Tagging SNPs for Genome-Wide Association Studies. <i>Genome Research</i> , 2004, 14, 1633-1640.	2.4	113
6	Single-Cell Genetic Analysis of Ductal Carcinoma in Situ and Invasive Breast Cancer Reveals Enormous Tumor Heterogeneity yet Conserved Genomic Imbalances and Gain of MYC during Progression. <i>American Journal of Pathology</i> , 2012, 181, 1807-1822.	1.9	104
7	Bioinformatics Curriculum Guidelines: Toward a Definition of Core Competencies. <i>PLoS Computational Biology</i> , 2014, 10, e1003496.	1.5	102
8	The development and application of bioinformatics core competencies to improve bioinformatics training and education. <i>PLoS Computational Biology</i> , 2018, 14, e1005772.	1.5	84
9	Frequencies of amino acid strings in globular protein sequences indicate suppression of blocks of consecutive hydrophobic residues. <i>Protein Science</i> , 2001, 10, 1023-1031.	3.1	83
10	Simulation Study of the Contribution of Oligomer/Oligomer Binding to Capsid Assembly Kinetics. <i>Biophysical Journal</i> , 2006, 90, 57-64.	0.2	67
11	Exploring the Parameter Space of Complex Self-Assembly through Virus Capsid Models. <i>Biophysical Journal</i> , 2008, 94, 772-783.	0.2	59
12	Robustness of Inference of Haplotype Block Structure. <i>Journal of Computational Biology</i> , 2003, 10, 13-19.	0.8	54
13	Applying unmixing to gene expression data for tumor phylogeny inference. <i>BMC Bioinformatics</i> , 2010, 11, 42.	1.2	54
14	Machine Learning and Radiogenomics: Lessons Learned and Future Directions. <i>Frontiers in Oncology</i> , 2018, 8, 228.	1.3	54
15	Haplotypes and informative SNP selection algorithms. , 2003, , .		52
16	Mixed Integer Linear Programming for Maximum-Parsimony Phylogeny Inference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 323-331.	1.9	50
17	Algorithms to Model Single Gene, Single Chromosome, and Whole Genome Copy Number Changes Jointly in Tumor Phylogenetics. <i>PLoS Computational Biology</i> , 2014, 10, e1003740.	1.5	46
18	Local Rules Theory Applied to Polyomavirus Polymorphic Capsid Assemblies. <i>Virology</i> , 2000, 268, 461-470.	1.1	44

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19	Frequencies of hydrophobic and hydrophilic runs and alternations in proteins of known structure. <i>Protein Science</i> , 2006, 15, 102-112.	3.1	42
20	Phylogenetic analysis of multiprobe fluorescence in situ hybridization data from tumor cell populations. <i>Bioinformatics</i> , 2013, 29, i189-i198.	1.8	40
21	Deconvolution and phylogeny inference of structural variations in tumor genomic samples. <i>Bioinformatics</i> , 2018, 34, i357-i365.	1.8	40
22	RECONSTRUCTING TUMOR PHYLOGENIES FROM HETEROGENEOUS SINGLE-CELL DATA. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 407-427.	0.3	35
23	Classifying the Progression of Ductal Carcinoma from Single-Cell Sampled Data via Integer Linear Programming: A Case Study. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 643-655.	1.9	33
24	Surveying Capsid Assembly Pathways through Simulation-Based Data Fitting. <i>Biophysical Journal</i> , 2012, 103, 1545-1554.	0.2	31
25	Applying Molecular Crowding Models to Simulations of Virus Capsid Assembly In Vitro. <i>Biophysical Journal</i> , 2014, 106, 310-320.	0.2	31
26	Single-Cell Genetic Analysis Reveals Insights into Clonal Development of Prostate Cancers and Indicates Loss of PTEN as a Marker of Poor Prognosis. <i>American Journal of Pathology</i> , 2014, 184, 2671-2686.	1.9	29
27	Queue-based method for efficient simulation of biological self-assembly systems. <i>Journal of Computational Physics</i> , 2005, 204, 100-120.	1.9	28
28	Robust unmixing of tumor states in array comparative genomic hybridization data. <i>Bioinformatics</i> , 2010, 26, i106-i114.	1.8	28
29	Inferring models of multiscale copy number evolution for single-tumor phylogenetics. <i>Bioinformatics</i> , 2015, 31, i258-i267.	1.8	28
30	Aneuploidy, TP53 mutation, and amplification of MYC correlate with increased intratumor heterogeneity and poor prognosis of breast cancer patients. <i>Genes Chromosomes and Cancer</i> , 2018, 57, 165-175.	1.5	27
31	A comparative genomics approach to identifying the plasticity transcriptome. <i>BMC Neuroscience</i> , 2007, 8, 20.	0.8	24
32	Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.5	24
33	Simulated De Novo Assembly of Golgi Compartments by Selective Cargo Capture during Vesicle Budding and Targeted Vesicle Fusion. <i>Biophysical Journal</i> , 2008, 95, 1674-1688.	0.2	23
34	Network-Based Inference of Cancer Progression from Microarray Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 200-212.	1.9	22
35	The evolution of single cell-derived colorectal cancer cell lines is dominated by the continued selection of tumor-specific genomic imbalances, despite random chromosomal instability. <i>Carcinogenesis</i> , 2018, 39, 993-1005.	1.3	20
36	Pathway Complexity of Model Virus Capsid Assembly Systems. <i>Computational and Mathematical Methods in Medicine</i> , 2008, 9, 277-293.	0.7	18

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37	Discrete, continuous, and stochastic models of protein sorting in the Golgi apparatus. <i>Physical Review E</i> , 2010, 81, 011914.	0.8	18
38	Stochastic off-lattice modeling of molecular self-assembly in crowded environments by Greenâ€™s function reaction dynamics. <i>Physical Review E</i> , 2008, 78, 031911.	0.8	17
39	A Novel Subset of Human tumors that Simultaneously Overexpress Multiple E2F-responsive Genes Found in Breast, Ovarian, and Prostate Cancers. <i>Cancer Informatics</i> , 2014, 13s5, CIN.S14062.	0.9	17
40	A parameter estimation technique for stochastic self-assembly systems and its application to human papillomavirus self-assembly. <i>Physical Biology</i> , 2010, 7, 045005.	0.8	16
41	Phylogenetic analysis of multiple FISH markers in oral tongue squamous cell carcinoma suggests that a diverse distribution of copy number changes is associated with poor prognosis. <i>International Journal of Cancer</i> , 2016, 138, 98-109.	2.3	16
42	Efficiently Finding the Most Parsimonious Phylogenetic Tree Via Linear Programming. , 2007, , 37-48.		15
43	Fixed Parameter Tractability of Binary Near-Perfect Phylogenetic Tree Reconstruction. <i>Lecture Notes in Computer Science</i> , 2006, , 667-678.	1.0	14
44	Quantitative computational models of molecular self-assembly in systems biology. <i>Physical Biology</i> , 2017, 14, 035003.	0.8	13
45	FISHtrees 3.0: Tumor Phylogenetics Using a Ploidy Probe. <i>PLoS ONE</i> , 2016, 11, e0158569.	1.1	13
46	Computational models of molecular self-organization in cellular environments. <i>Cell Biochemistry and Biophysics</i> , 2007, 48, 16-31.	0.9	12
47	Inference of Tumor Phylogenies from Genomic Assays on Heterogeneous Samples. <i>Journal of Biomedicine and Biotechnology</i> , 2012, 2012, 1-16.	3.0	12
48	A simplicial complex-based approach to unmixing tumor progression data. <i>BMC Bioinformatics</i> , 2015, 16, 254.	1.2	11
49	A Report of the Curriculum Task Force of the ISCB Education Committee. <i>PLoS Computational Biology</i> , 2012, 8, e1002570.	1.5	10
50	Reference-free inference of tumor phylogenies from single-cell sequencing data. <i>BMC Genomics</i> , 2015, 16, S7.	1.2	10
51	Tumor Copy Number Deconvolution Integrating Bulk and Single-Cell Sequencing Data. <i>Journal of Computational Biology</i> , 2020, 27, 565-598.	0.8	10
52	A mixed integer linear programming model to reconstruct phylogenies from single nucleotide polymorphism haplotypes under the maximum parsimony criterion. <i>Algorithms for Molecular Biology</i> , 2013, 8, 3.	0.3	9
53	Simple Reconstruction of Binary Near-Perfect Phylogenetic Trees. <i>Lecture Notes in Computer Science</i> , 2006, , 799-806.	1.0	9
54	OPTIMAL IMPERFECT PHYLOGENY RECONSTRUCTION AND HAPLOTYPING (IPPH). , 2006, , .		9

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55	Evaluating Spatial Constraints in Cellular Assembly Processes Using a Monte Carlo Approach. Cell Biochemistry and Biophysics, 2006, 45, 195-202.	0.9	8
56	Automated deconvolution of structured mixtures from heterogeneous tumor genomic data. PLoS Computational Biology, 2017, 13, e1005815.	1.5	8
57	Efficient stochastic sampling of first-passage times with applications to self-assembly simulations. Journal of Chemical Physics, 2008, 129, 204109.	1.2	7
58	Unified regression model of binding equilibria in crowded environments. Scientific Reports, 2011, 1, 97.	1.6	7
59	Generalized Buneman Pruning for Inferring the Most Parsimonious Multi-State Phylogeny. Journal of Computational Biology, 2011, 18, 445-457.	0.8	7
60	Modeling Effects of RNA on Capsid Assembly Pathways via Coarse-Grained Stochastic Simulation. PLoS ONE, 2016, 11, e0156547.	1.1	7
61	Robust and accurate deconvolution of tumor populations uncovers evolutionary mechanisms of breast cancer metastasis. Bioinformatics, 2020, 36, i407-i416.	1.8	7
62	Investigating Scaling Effects on Virus Capsid-Like Self-Assembly Using Discrete Event Simulations. IEEE Transactions on Nanobioscience, 2007, 6, 235-241.	2.2	6
63	A Consensus Tree Approach for Reconstructing Human Evolutionary History and Detecting Population Substructure. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 918-928.	1.9	5
64	A method for efficient Bayesian optimization of self-assembly systems from scattering data. BMC Systems Biology, 2018, 12, 65.	3.0	5
65	Tumor heterogeneity assessed by sequencing and fluorescence <i>in situ</i> hybridization (FISH) data. Bioinformatics, 2021, 37, 4704-4711.	1.8	5
66	Understanding actin organization in cell structure through lattice based Monte Carlo simulations. Mcb Mechanics and Chemistry of Biosystems, 2004, 1, 123-31.	0.3	5
67	Parameter effects on binding chemistry in crowded media using a two-dimensional stochastic off-lattice model. Physical Review E, 2009, 80, 041918.	0.8	4
68	Medoidshift clustering applied to genomic bulk tumor data. BMC Genomics, 2016, 17, 6.	1.2	4
69	Tumor Copy Number Deconvolution Integrating Bulk and Single-Cell Sequencing Data. Lecture Notes in Computer Science, 2019, , 174-189.	1.0	3
70	Computational Models for Cancer Phylogenetics. Computational Biology, 2019, , 243-275.	0.1	3
71	Neural Network Deconvolution Method for Resolving Pathway-Level Progression of Tumor Clonal Expression Programs With Application to Breast Cancer Brain Metastases. Frontiers in Physiology, 2020, 11, 1055.	1.3	3
72	Inferring Piecewise Ancestral History from Haploid Sequences. Lecture Notes in Computer Science, 2004, , 62-73.	1.0	3

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73	Three-Dimensional Stochastic Off-Lattice Model of Binding Chemistry in Crowded Environments. PLoS ONE, 2012, 7, e30131.	1.1	3
74	Phylogenies Derived from Matched Transcriptome Reveal the Evolution of Cell Populations and Temporal Order of Perturbed Pathways in Breast Cancer Brain Metastases. Lecture Notes in Computer Science, 2019, , 3-28.	1.0	3
75	Assessing the contribution of tumor mutational phenotypes to cancer progression risk. PLoS Computational Biology, 2021, 17, e1008777.	1.5	2
76	Joint Clustering of Single-Cell Sequencing and Fluorescence In Situ Hybridization Data for Reconstructing Clonal Heterogeneity in Cancers. Journal of Computational Biology, 2021, 28, 1035-1051.	0.8	2
77	ConTreeDP: A consensus method of tumor trees based on maximum directed partition support problem. , 2021, , .		2
78	Reconstructing tumor clonal lineage trees incorporating single-nucleotide variants, copy number alterations and structural variations. Bioinformatics, 2022, 38, i125-i133.	1.8	2
79	Haplotype Parsing. Applied Bioinformatics, 2004, 3, 181-191.	1.7	1
80	Derivative-Free Optimization of Rate Parameters of Capsid Assembly Models from Bulk in Vitro Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 844-855.	1.9	1
81	An Optimization-Based Sampling Scheme for Phylogenetic Trees. Lecture Notes in Computer Science, 2011, , 252-266.	1.0	1
82	Network-Based Inference of Cancer Progression from Microarray Data. , 2008, , 268-279.		1
83	An Optimization-Based Sampling Scheme for Phylogenetic Trees. Journal of Computational Biology, 2011, 18, 1599-1609.	0.8	0
84	Tumor Phylogenetics in the NGS Era: Strategies, Challenges, and Future Prospects. , 2013, , 335-357.		0
85	Reply to 'Complexity of molecular crowding in cell-free enzymatic reaction networks'. Nature Nanotechnology, 2014, 9, 407-408.	15.6	0
86	Semi-deconvolution of bulk and single-cell RNA-seq data with application to metastatic progression in breast cancer. Bioinformatics, 2022, 38, i386-i394.	1.8	0