List of Publications by Year
in descending order

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	Reconstructing tumor clonal lineage trees incorporating single-nucleotide variants, copy number alterations and structural variations. Bioinformatics, 2022, 38, i125-i133.	1.8	2
2	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
3	Assessing the contribution of tumor mutational phenotypes to cancer progression risk. PLoS Computational Biology, 2021, 17, e1008777.	1.5	2
4	Tumor heterogeneity assessed by sequencing and fluorescence *in situ* hybridization (FISH) data. Bioinformatics, 2021, 37, 4704-4711.	1.8	5
5	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
6	ConTreeDP: A consensus method of tumor trees based on maximum directed partition support problem. , 2021, , .		2
7	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
8	Robust and accurate deconvolution of tumor populations uncovers evolutionary mechanisms of breast cancer metastasis. Bioinformatics, 2020, 36, i407-i416.	1.8	7
9	Tumor Copy Number Deconvolution Integrating Bulk and Single-Cell Sequencing Data. Journal of Computational Biology, 2020, 27, 565-598.	0.8	10
10	Tumor Copy Number Deconvolution Integrating Bulk and Single-Cell Sequencing Data. Lecture Notes in Computer Science, 2019, , 174-189.	1.0	3
11	Computational Models for Cancer Phylogenetics. Computational Biology, 2019, , 243-275.	0.1	3
12	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
13	Aneuploidy, *TP53* mutation, and amplification of *MYC* correlate with increased intratumor heterogeneity and poor prognosis of breast cancer patients. Genes Chromosomes and Cancer, 2018, 57, 165-175.	1.5	27
14	Deconvolution and phylogeny inference of structural variations in tumor genomic samples. Bioinformatics, 2018, 34, i357-i365.	1.8	40
15	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. Carcinogenesis, 2018, 39, 993-1005.	1.3	20
16	A method for efficient Bayesian optimization of self-assembly systems from scattering data. BMC Systems Biology, 2018, 12, 65.	3.0	5
17	Machine Learning and Radiogenomics: Lessons Learned and Future Directions. Frontiers in Oncology, 2018, 8, 228.	1.3	54
18	The development and application of bioinformatics core competencies to improve bioinformatics training and education. PLoS Computational Biology, 2018, 14, e1005772.	1.5	84

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19	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
20	The evolution of tumour phylogenetics: principles and practice. Nature Reviews Genetics, 2017, 18, 213-229.	7.7	240
21	Quantitative computational models of molecular self-assembly in systems biology. Physical Biology, 2017, 14, 035003.	0.8	13
22	Automated deconvolution of structured mixtures from heterogeneous tumor genomic data. PLoS Computational Biology, 2017, 13, e1005815.	1.5	8
23	Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum) Tj ETQq1 1 0.784314 rgBT /Over	1.5	24
24	Modeling Effects of RNA on Capsid Assembly Pathways via Coarse-Grained Stochastic Simulation. PLoS ONE, 2016, 11, e0156547.	1.1	7
25	Medoidshift clustering applied to genomic bulk tumor data. BMC Genomics, 2016, 17, 6.	1.2	4
26	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. International Journal of Cancer, 2016, 138, 98-109.	2.3	16
27	Classifying the Progression of Ductal Carcinoma from Single-Cell Sampled Data via Integer Linear Programming: A Case Study. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 643-655.	1.9	33
28	FISHtrees 3.0: Tumor Phylogenetics Using a Ploidy Probe. PLoS ONE, 2016, 11, e0158569.	1.1	13
29	Reference-free inference of tumor phylogenies from single-cell sequencing data. BMC Genomics, 2015, 16, S7.	1.2	10
30	A simplicial complex-based approach to unmixing tumor progression data. BMC Bioinformatics, 2015, 16, 254.	1.2	11
31	Inferring models of multiscale copy number evolution for single-tumor phylogenetics. Bioinformatics, 2015, 31, i258-i267.	1.8	28
32	Bioinformatics Curriculum Guidelines: Toward a Definition of Core Competencies. PLoS Computational Biology, 2014, 10, e1003496.	1.5	102
33	Algorithms to Model Single Gene, Single Chromosome, and Whole Genome Copy Number Changes Jointly in Tumor Phylogenetics. PLoS Computational Biology, 2014, 10, e1003740.	1.5	46
34	Single-Cell Genetic Analysis Reveals Insights into Clonal Development of Prostate Cancers and Indicates Loss of PTEN as a Marker of Poor Prognosis. American Journal of Pathology, 2014, 184, 2671-2686.	1.9	29
35	A Novel Subset of Human tumors that Simultaneously Overexpress Multiple E2F-responsive Genes Found in Breast, Ovarian, and Prostate Cancers. Cancer Informatics, 2014, 13s5, CIN.S14062.	0.9	17
36	Applying Molecular Crowding Models to Simulations of Virus Capsid Assembly InÂVitro. Biophysical Journal, 2014, 106, 310-320.	0.2	31

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37	Reply to 'Complexity of molecular crowding in cell-free enzymatic reaction networks'. Nature Nanotechnology, 2014, 9, 407-408.	15.6	0
38	A mixed integer linear programming model to reconstruct phylogenies from single nucleotide polymorphism haplotypes under the maximum parsimony criterion. Algorithms for Molecular Biology, 2013, 8, 3.	0.3	9
39	Molecular crowding shapes gene expression in synthetic cellular nanosystems. Nature Nanotechnology, 2013, 8, 602-608.	15.6	215
40	Tumor Phylogenetics in the NGS Era: Strategies, Challenges, and Future Prospects. , 2013, , 335-357.		0
41	Phylogenetic analysis of multiprobe fluorescence in situ hybridization data from tumor cell populations. Bioinformatics, 2013, 29, i189-i198.	1.8	40
42	A Report of the Curriculum Task Force of the ISCB Education Committee. PLoS Computational Biology, 2012, 8, e1002570.	1.5	10
43	Inference of Tumor Phylogenies from Genomic Assays on Heterogeneous Samples. Journal of Biomedicine and Biotechnology, 2012, 2012, 1-16.	3.0	12
44	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. American Journal of Pathology, 2012, 181, 1807-1822.	1.9	104
45	Surveying Capsid Assembly Pathways through Simulation-Based Data Fitting. Biophysical Journal, 2012, 103, 1545-1554.	0.2	31
46	Three-Dimensional Stochastic Off-Lattice Model of Binding Chemistry in Crowded Environments. PLoS ONE, 2012, 7, e30131.	1.1	3
47	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
48	Unified regression model of binding equilibria in crowded environments. Scientific Reports, 2011, 1, 97.	1.6	7
49	An Optimization-Based Sampling Scheme for Phylogenetic Trees. Journal of Computational Biology, 2011, 18, 1599-1609.	0.8	0
50	Generalized Buneman Pruning for Inferring the Most Parsimonious Multi-State Phylogeny. Journal of Computational Biology, 2011, 18, 445-457.	0.8	7
51	An Optimization-Based Sampling Scheme for Phylogenetic Trees. Lecture Notes in Computer Science, 2011, , 252-266.	1.0	1
52	Applying unmixing to gene expression data for tumor phylogeny inference. BMC Bioinformatics, 2010, 11, 42.	1.2	54
53	A parameter estimation technique for stochastic self-assembly systems and its application to human papillomavirus self-assembly. Physical Biology, 2010, 7, 045005.	0.8	16
54	Discrete, continuous, and stochastic models of protein sorting in the Golgi apparatus. Physical Review E, 2010, 81, 011914.	0.8	18

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55	Robust unmixing of tumor states in array comparative genomic hybridization data. Bioinformatics, 2010, 26, i106-i114.	1.8	28
56	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
57	Network-Based Inference of Cancer Progression from Microarray Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 200-212.	1.9	22
58	Exploring the Parameter Space of Complex Self-Assembly through Virus Capsid Models. Biophysical Journal, 2008, 94, 772-783.	0.2	59
59	Simulated De Novo Assembly of Golgi Compartments by Selective Cargo Capture during Vesicle Budding and Targeted Vesicle Fusion. Biophysical Journal, 2008, 95, 1674-1688.	0.2	23
60	Mixed Integer Linear Programming for Maximum-Parsimony Phylogeny Inference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 323-331.	1.9	50
61	Pathway Complexity of Model Virus Capsid Assembly Systems. Computational and Mathematical Methods in Medicine, 2008, 9, 277-293.	0.7	18
62	Efficient stochastic sampling of first-passage times with applications to self-assembly simulations. Journal of Chemical Physics, 2008, 129, 204109.	1.2	7
63	Stochastic off-lattice modeling of molecular self-assembly in crowded environments by Green's function reaction dynamics. Physical Review E, 2008, 78, 031911.	0.8	17
64	Network-Based Inference of Cancer Progression from Microarray Data. , 2008, , 268-279.		1
65	RECONSTRUCTING TUMOR PHYLOGENIES FROM HETEROGENEOUS SINGLE-CELL DATA. Journal of Bioinformatics and Computational Biology, 2007, 05, 407-427.	0.3	35
66	Investigating Scaling Effects on Virus Capsid-Like Self-Assembly Using Discrete Event Simulations. IEEE Transactions on Nanobioscience, 2007, 6, 235-241.	2.2	6
67	A comparative genomics approach to identifying the plasticity transcriptome. BMC Neuroscience, 2007, 8, 20.	0.8	24
68	Computational models of molecular self-organization in cellular environments. Cell Biochemistry and Biophysics, 2007, 48, 16-31.	0.9	12
69	Efficiently Finding the Most Parsimonious Phylogenetic Tree Via Linear Programming. , 2007, , 37-48.		15
70	Simulation Study of the Contribution of Oligomer/Oligomer Binding to Capsid Assembly Kinetics. Biophysical Journal, 2006, 90, 57-64.	0.2	67
71	Frequencies of hydrophobic and hydrophilic runs and alternations in proteins of known structure. Protein Science, 2006, 15, 102-112.	3.1	42
72	Evaluating Spatial Constraints in Cellular Assembly Processes Using a Monte Carlo Approach. Cell Biochemistry and Biophysics, 2006, 45, 195-202.	0.9	8

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73	Simple Reconstruction of Binary Near-Perfect Phylogenetic Trees. Lecture Notes in Computer Science, 2006, , 799-806.	1.0	9
74	Fixed Parameter Tractability of Binary Near-Perfect Phylogenetic Tree Reconstruction. Lecture Notes in Computer Science, 2006, , 667-678.	1.0	14
75	OPTIMAL IMPERFECT PHYLOGENY RECONSTRUCTION AND HAPLOTYPING (IPPH). , 2006, , .		9
76	Queue-based method for efficient simulation of biological self-assembly systems. Journal of Computational Physics, 2005, 204, 100-120.	1.9	28
77	Optimal Haplotype Block-Free Selection of Tagging SNPs for Genome-Wide Association Studies. Genome Research, 2004, 14, 1633-1640.	2.4	113
78	Haplotype Parsing. Applied Bioinformatics, 2004, 3, 181-191.	1.7	1
79	Inferring Piecewise Ancestral History from Haploid Sequences. Lecture Notes in Computer Science, 2004, , 62-73.	1.0	3
80	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
81	Robustness of Inference of Haplotype Block Structure. Journal of Computational Biology, 2003, 10, 13-19.	0.8	54
82	Haplotypes and informative SNP selection algorithms. , 2003, , .		52
83	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	6.0	12,623
84	Frequencies of amino acid strings in globular protein sequences indicate suppression of blocks of consecutive hydrophobic residues. Protein Science, 2001, 10, 1023-1031.	3.1	83
85	â€œLocal Rulesâ€•Theory Applied to Polyomavirus Polymorphic Capsid Assemblies. Virology, 2000, 268, 461-470.	1.1	44
86	Local Rules Simulation of the Kinetics of Virus Capsid Self-Assembly. Biophysical Journal, 1998, 75, 2626-2636.	0.2	148