Jun S Liu

List of Publications by Year
in descending order

83 papers	25,563 citations	61857 43 h-index	69108 77 g-index
85 all docs	85 docs citations	85 times ranked	33213 citing authors

#	Article	IF	Citations
1	Topological domains in mammalian genomes identified by analysis of chromatin interactions. Nature, 2012, 485, 376-380.	13.7	5,786
2	TIMER: A Web Server for Comprehensive Analysis of Tumor-Infiltrating Immune Cells. Cancer Research, 2017, 77, e108-e110.	0.4	4,049
3	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	13.7	1,974
4	Comprehensive analyses of tumor immunity: implications for cancer immunotherapy. Genome Biology, 2016, 17, 174.	3.8	1,768
5	MAGeCK enables robust identification of essential genes from genome-scale CRISPR/Cas9 knockout screens. Genome Biology, 2014, 15, 554.	3.8	1,614
6	Sequential Monte Carlo Methods for Dynamic Systems. Journal of the American Statistical Association, 1998, 93, 1032-1044.	1.8	1,140
7	Sequential Imputations and Bayesian Missing Data Problems. Journal of the American Statistical Association, 1994, 89, 278-288.	1.8	665
8	An algorithm for finding protein–DNA binding sites with applications to chromatin-immunoprecipitation microarray experiments. Nature Biotechnology, 2002, 20, 835-839.	9.4	617
9	Bayesian Haplotype Inference for Multiple Linked Single-Nucleotide Polymorphisms. American Journal of Human Genetics, 2002, 70, 157-169.	2.6	591
10	Monte Carlo Strategies in Scientific Computing. Springer Series in Statistics, 2004, , .	0.9	531
11	The Collapsed Gibbs Sampler in Bayesian Computations with Applications to a Gene Regulation Problem. Journal of the American Statistical Association, 1994, 89, 958-966.	1.8	504
12	The Spo0A regulon of Bacillus subtilis. Molecular Microbiology, 2003, 50, 1683-1701.	1.2	466
13	Partition-Ligation–Expectation-Maximization Algorithm for Haplotype Inference with Single-Nucleotide Polymorphisms. American Journal of Human Genetics, 2002, 71, 1242-1247.	2.6	458
14	Metropolized independent sampling with comparisons to rejection sampling and importance sampling. Statistics and Computing, 1996, 6, 113-119.	0.8	381
15	Quality control, modeling, and visualization of CRISPR screens with MAGeCK-VISPR. Genome Biology, 2015, 16, 281.	3.8	330
16	Integrating regulatory motif discovery and genome-wide expression analysis. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3339-3344.	3.3	319
17	The Program of Gene Transcription for a Single Differentiating Cell Type during Sporulation in Bacillus subtilis. PLoS Biology, 2004, 2, e328.	2.6	308
18	Landscape of tumor-infiltrating T cell repertoire of human cancers. Nature Genetics, 2016, 48, 725-732.	9.4	288

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19	Blind Deconvolution via Sequential Imputations. Journal of the American Statistical Association, 1995, 90, 567-576.	1.8	252
20	Parameter Expansion for Data Augmentation. Journal of the American Statistical Association, 1999, 94, 1264-1274.	1.8	236
21	Bayesian Models for Multiple Local Sequence Alignment and Gibbs Sampling Strategies. Journal of the American Statistical Association, 1995, 90, 1156-1170.	1.8	235
22	Sequential Monte Carlo Methods for Statistical Analysis of Tables. Journal of the American Statistical Association, 2005, 100, 109-120.	1.8	231
23	Convergent regulatory evolution and loss of flight in paleognathous birds. Science, 2019, 364, 74-78.	6.0	189
24	Bayesian Inference of Spatial Organizations of Chromosomes. PLoS Computational Biology, 2013, 9, e1002893.	1.5	188
25	Genomic Sequence Is Highly Predictive of Local Nucleosome Depletion. PLoS Computational Biology, 2008, 4, e13.	1.5	156
26	Haplotype Block Partitioning and Tag SNP Selection Using Genotype Data and Their Applications to Association Studies. Genome Research, 2004, 14, 908-916.	2.4	143
27	Modeling within-motif dependence for transcription factor binding site predictions. Bioinformatics, 2004, 20, 909-916.	1.8	129
28	Sequential importance sampling for nonparametric Bayes models: The next generation. Canadian Journal of Statistics, 1999, 27, 251-267.	0.6	128
29	Nonparametric hierarchical Bayes via sequential imputations. Annals of Statistics, 1996, 24, 911.	1.4	125
30	Cooperation between Polycomb and androgen receptor during oncogenic transformation. Genome Research, 2012, 22, 322-331.	2.4	122
31	Landscape of B cell immunity and related immune evasion in human cancers. Nature Genetics, 2019, 51, 560-567.	9.4	115
32	Expansion of Biological Pathways Based on Evolutionary Inference. Cell, 2014, 158, 213-225.	13.5	107
33	Rejection Control and Sequential Importance Sampling. Journal of the American Statistical Association, 1998, 93, 1022-1031.	1.8	99
34	Defining a Centromere-like Element in Bacillus subtilis by Identifying the Binding Sites for the Chromosome-Anchoring Protein RacA. Molecular Cell, 2005, 17, 773-782.	4.5	93
35	BioOptimizer: a Bayesian scoring function approach to motif discovery. Bioinformatics, 2004, 20, 1557-1564.	1.8	88
36	Computational Discovery of Gene Regulatory Binding Motifs: A Bayesian Perspective. Statistical Science, 2004, 19, 188.	1.6	62

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37	Markovian Structures in Biological Sequence Alignments. Journal of the American Statistical Association, 1999, 94, 1-15.	1.8	60
38	A new sequential importance sampling method and its application to the two-dimensional hydrophobicâ€"hydrophilic model. Journal of Chemical Physics, 2002, 117, 3492-3498.	1.2	58
39	A boosting approach for motif modeling using ChIP-chip data. Bioinformatics, 2005, 21, 2636-2643.	1.8	54
40	On Side-Chain Conformational Entropy of Proteins. PLoS Computational Biology, 2006, 2, e168.	1.5	51
41	Network analysis of gene essentiality in functional genomics experiments. Genome Biology, 2015, 16, 239.	3.8	50
42	Monte Carlo Bayesian Signal Processing for Wireless Communications. Journal of Signal Processing Systems, 2002, 30, 89-105.	1.0	46
43	BEST: Binding-site Estimation Suite of Tools. Bioinformatics, 2005, 21, 2909-2911.	1.8	46
44	Incorporating Genotyping Uncertainty in Haplotype Inference for Single-Nucleotide Polymorphisms. American Journal of Human Genetics, 2004, 74, 495-510.	2.6	45
45	Revisit linear regression-based deconvolution methods for tumor gene expression data. Genome Biology, 2017, 18, 127.	3.8	45
46	Extracting sequence features to predict proteinâ€"DNA interactions: a comparative study. Nucleic Acids Research, 2008, 36, 4137-4148.	6.5	40
47	Bayesian Detection of Convergent Rate Changes of Conserved Noncoding Elements on Phylogenetic Trees. Molecular Biology and Evolution, 2019, 36, 1086-1100.	3.5	39
48	A RIPK1-regulated inflammatory microglial state in amyotrophic lateral sclerosis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	36
49	Lookahead Strategies for Sequential Monte Carlo. Statistical Science, 2013, 28, .	1.6	35
50	Haplotype Information and Linkage Disequilibrium Mapping for Single Nucleotide Polymorphisms. Genome Research, 2003, 13, 2112-2117.	2.4	34
51	cepip: context-dependent epigenomic weighting for prioritization of regulatory variants and disease-associated genes. Genome Biology, 2017, 18, 52.	3.8	33
52	A suite of web-based programs to search for transcriptional regulatory motifs. Nucleic Acids Research, 2004, 32, W204-W207.	6.5	30
53	Statistical inference and Monte Carlo algorithms. Test, 1996, 5, 249-344.	0.7	29
54	Understanding spatial organizations of chromosomes via statistical analysis of Hiâ€C data. Quantitative Biology, 2013, 1, 156-174.	0.3	29

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55	Determinants of transcription factor regulatory range. Nature Communications, 2020, 11, 2472.	5.8	28
56	A Coalescence-Guided Hierarchical Bayesian Method for Haplotype Inference. American Journal of Human Genetics, 2006, 79, 313-322.	2.6	26
57	Reduction of mNAT1/hNAT2 Contributes to Cerebral Endothelial Necroptosis and AÎ² Accumulation in Alzheimerâ€™s Disease. Cell Reports, 2020, 33, 108447.	2.9	26
58	Statistical assessment of the global regulatory role of histone acetylation in Saccharomyces cerevisiae. Genome Biology, 2006, 7, R70.	13.9	24
59	On learning strategies for evolutionary Monte Carlo. Statistics and Computing, 2007, 17, 23-38.	0.8	24
60	The Distribution of Genomic Variations in Human iPSCs Is Related to Replication-Timing Reorganization during Reprogramming. Cell Reports, 2014, 7, 70-78.	2.9	24
61	Stopping-time resampling for sequential Monte Carlo methods. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2005, 67, 199-217.	1.1	23
62	Monte Carlo sampling of near-native structures of proteins with applications. Proteins: Structure, Function and Bioinformatics, 2006, 66, 61-68.	1.5	20
63	Tmod: toolbox of motif discovery. Bioinformatics, 2010, 26, 405-407.	1.8	18
64	Computational Deconvolution of Tumor-Infiltrating Immune Components with Bulk Tumor Gene Expression Data. Methods in Molecular Biology, 2020, 2120, 249-262.	0.4	18
65	Bayesian hierarchical model of protein-binding microarray k-mer data reduces noise and identifies transcription factor subclasses and preferred k-mers. Bioinformatics, 2013, 29, 1390-1398.	1.8	16
66	Predictive Updating Methods with Application to Bayesian Classification. Journal of the Royal Statistical Society Series B: Methodological, 1996, 58, 397-415.	0.8	12
67	The EM Algorithm and the Rise of Computational Biology. Statistical Science, 2010, 25, .	1.6	7
68	Association Pattern Discovery Via Theme Dictionary Models. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2014, 76, 319-347.	1.1	7
69	Neuronized Priors for Bayesian Sparse Linear Regression. Journal of the American Statistical Association, 2022, 117, 1695-1710.	1.8	7
70	Bayesian hidden Markov tree models for clustering genes with shared evolutionary history. Annals of Applied Statistics, 2019, 13, .	0.5	6
71	SIMPLEs: a single-cell RNA sequencing imputation strategy preserving gene modules and cell clusters variation. NAR Genomics and Bioinformatics, 2020, 2, lqaa077.	1.5	6
72	Monte Carlo Approximation of Bayes Factors via Mixing With Surrogate Distributions. Journal of the American Statistical Association, 2020, , 1-16.	1.8	5

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73	Monte Carlo Bayesian Signal Processing for Wireless Communications. , 2002, , 89-105.		4
74	Nonparametric hierarchical Bayes analysis of binomial data via Bernstein polynomial priors. Canadian Journal of Statistics, 2012, 40, 328-344.	0.6	3
75	Exploring the conformational space for protein folding with sequential Monte Carlo. Annals of Applied Statistics, 2018, 12, .	0.5	3
76	Stratification and optimal resampling for sequential Monte Carlo. Biometrika, 2022, 109, 181-194.	1.3	3
77	Haplotype Inference and Its Application in Linkage Disequilibrium Mapping. Lecture Notes in Computer Science, 2004, , 48-61.	1.0	2
78	Bayesian Analysis of Rank Data with Covariates and Heterogeneous Rankers. Statistical Science, 2022, 37, .	1.6	2
79	Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	1.9	1
80	Bayesian Methods in Biological Sequence Analysis. , 2008, , 67-96.		0
81	Dynamic Programming Algorithms for Haplotype Block Partitioning and Tag SNP Selection Using Haplotype Data or GenotypeÂData. Lecture Notes in Computer Science, 2004, , 96-112.	1.0	0
82	Statistical Learning and Modeling of TF-DNA Binding. , 2011, , 55-72.		0
83	Statistical Methods in Bioinformatics. , 2013, , 101-149.		0