

# Jun S Liu

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

81  
papers

17,059  
citations

41  
h-index

85  
g-index

85  
ext. papers

22,089  
ext. citations

10  
avg, IF

6.58  
L-index

#	Paper	IF	Citations
81	A RIPK1-regulated inflammatory microglial state in amyotrophic lateral sclerosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	10
80	Reduction of mNAT1/hNAT2 Contributes to Cerebral Endothelial Necroptosis and A $\beta$ Accumulation in Alzheimer's Disease. <i>Cell Reports</i> , <b>2020</b> , 33, 108447	10.6	7
79	Determinants of transcription factor regulatory range. <i>Nature Communications</i> , <b>2020</b> , 11, 2472	17.4	13
78	Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2020</b> , 17, 647-656	3	1
77	SIMPLEs: a single-cell RNA sequencing imputation strategy preserving gene modules and cell clusters variation. <i>NAR Genomics and Bioinformatics</i> , <b>2020</b> , 2, lqaa077	3.7	3
76	Monte Carlo Approximation of Bayes Factors via Mixing With Surrogate Distributions. <i>Journal of the American Statistical Association</i> , <b>2020</b> , 1-16	2.8	2
75	Computational Deconvolution of Tumor-Infiltrating Immune Components with Bulk Tumor Gene Expression Data. <i>Methods in Molecular Biology</i> , <b>2020</b> , 2120, 249-262	1.4	6
74	Bayesian Detection of Convergent Rate Changes of Conserved Noncoding Elements on Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , <b>2019</b> , 36, 1086-1100	8.3	17
73	Bayesian hidden Markov tree models for clustering genes with shared evolutionary history. <i>Annals of Applied Statistics</i> , <b>2019</b> , 13,	2.1	3
72	Convergent regulatory evolution and loss of flight in paleognathous birds. <i>Science</i> , <b>2019</b> , 364, 74-78	33.3	103
71	Landscape of B cell immunity and related immune evasion in human cancers. <i>Nature Genetics</i> , <b>2019</b> , 51, 560-567	36.3	56
70	cepip: context-dependent epigenomic weighting for prioritization of regulatory variants and disease-associated genes. <i>Genome Biology</i> , <b>2017</b> , 18, 52	18.3	27
69	Revisit linear regression-based deconvolution methods for tumor gene expression data. <i>Genome Biology</i> , <b>2017</b> , 18, 127	18.3	30
68	TIMER: A Web Server for Comprehensive Analysis of Tumor-Infiltrating Immune Cells. <i>Cancer Research</i> , <b>2017</b> , 77, e108-e110	10.1	1919
67	Comprehensive analyses of tumor immunity: implications for cancer immunotherapy. <i>Genome Biology</i> , <b>2016</b> , 17, 174	18.3	942
66	Landscape of tumor-infiltrating T cell repertoire of human cancers. <i>Nature Genetics</i> , <b>2016</b> , 48, 725-32	36.3	193
65	Network analysis of gene essentiality in functional genomics experiments. <i>Genome Biology</i> , <b>2015</b> , 16, 239	18.3	41

64	Quality control, modeling, and visualization of CRISPR screens with MAGeCK-VISPR. <i>Genome Biology</i> , <b>2015</b> , 16, 281	18.3	171
63	Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , <b>2014</b> , 506, 376-81	50.4	1426
62	Association pattern discovery via theme dictionary models. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , <b>2014</b> , 76, 319-347	3.9	5
61	Expansion of biological pathways based on evolutionary inference. <i>Cell</i> , <b>2014</b> , 158, 213-25	56.2	75
60	The distribution of genomic variations in human iPSCs is related to replication-timing reorganization during reprogramming. <i>Cell Reports</i> , <b>2014</b> , 7, 70-8	10.6	21
59	MAGeCK enables robust identification of essential genes from genome-scale CRISPR/Cas9 knockout screens. <i>Genome Biology</i> , <b>2014</b> , 15, 554	18.3	821
58	Understanding spatial organizations of chromosomes via statistical analysis of Hi-C data. <i>Quantitative Biology</i> , <b>2013</b> , 1, 156-174	3.9	22
57	Bayesian hierarchical model of protein-binding microarray k-mer data reduces noise and identifies transcription factor subclasses and preferred k-mers. <i>Bioinformatics</i> , <b>2013</b> , 29, 1390-8	7.2	13
56	Lookahead Strategies for Sequential Monte Carlo. <i>Statistical Science</i> , <b>2013</b> , 28,	2.4	28
55	Bayesian inference of spatial organizations of chromosomes. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1002893	14.0	140
54	Statistical Methods in Bioinformatics <b>2013</b> , 101-149		
53	Topological domains in mammalian genomes identified by analysis of chromatin interactions. <i>Nature</i> , <b>2012</b> , 485, 376-80	50.4	4098
52	Nonparametric hierarchical Bayes analysis of binomial data via Bernstein polynomial priors. <i>Canadian Journal of Statistics</i> , <b>2012</b> , 40, 328-344	0.4	3
51	Cooperation between Polycomb and androgen receptor during oncogenic transformation. <i>Genome Research</i> , <b>2012</b> , 22, 322-31	9.7	97
50	Statistical Learning and Modeling of TF-DNA Binding <b>2011</b> , 55-72		
49	Tmod: toolbox of motif discovery. <i>Bioinformatics</i> , <b>2010</b> , 26, 405-7	7.2	16
48	The EM Algorithm and the Rise of Computational Biology. <i>Statistical Science</i> , <b>2010</b> , 25,	2.4	2
47	Extracting sequence features to predict protein-DNA interactions: a comparative study. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, 4137-48	20.1	39

46	Genomic sequence is highly predictive of local nucleosome depletion. <i>PLoS Computational Biology</i> , <b>2008</b> , 4, e13	5	145
45	Bayesian Methods in Biological Sequence Analysis <b>2008</b> , 67-96		
44	On learning strategies for evolutionary Monte Carlo. <i>Statistics and Computing</i> , <b>2007</b> , 17, 23-38	1.8	21
43	Monte Carlo sampling of near-native structures of proteins with applications. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 66, 61-8	4.2	18
42	On side-chain conformational entropy of proteins. <i>PLoS Computational Biology</i> , <b>2006</b> , 2, e168	5	44
41	Statistical assessment of the global regulatory role of histone acetylation in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , <b>2006</b> , 7, R70	18.3	21
40	A coalescence-guided hierarchical Bayesian method for haplotype inference. <i>American Journal of Human Genetics</i> , <b>2006</b> , 79, 313-22	11	25
39	Sequential Monte Carlo Methods for Statistical Analysis of Tables. <i>Journal of the American Statistical Association</i> , <b>2005</b> , 100, 109-120	2.8	152
38	Defining a centromere-like element in <i>Bacillus subtilis</i> by Identifying the binding sites for the chromosome-anchoring protein RacA. <i>Molecular Cell</i> , <b>2005</b> , 17, 773-82	17.6	80
37	Stopping-time resampling for sequential Monte Carlo methods. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , <b>2005</b> , 67, 199-217	3.9	21
36	BEST: binding-site estimation suite of tools. <i>Bioinformatics</i> , <b>2005</b> , 21, 2909-11	7.2	36
35	A boosting approach for motif modeling using ChIP-chip data. <i>Bioinformatics</i> , <b>2005</b> , 21, 2636-43	7.2	46
34	Computational Discovery of Gene Regulatory Binding Motifs: A Bayesian Perspective. <i>Statistical Science</i> , <b>2004</b> , 19, 188	2.4	54
33	BioOptimizer: a Bayesian scoring function approach to motif discovery. <i>Bioinformatics</i> , <b>2004</b> , 20, 1557-64	7.2	79
32	Modeling within-motif dependence for transcription factor binding site predictions. <i>Bioinformatics</i> , <b>2004</b> , 20, 909-16	7.2	111
31	A suite of web-based programs to search for transcriptional regulatory motifs. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, W204-7	20.1	27
30	Haplotype block partitioning and tag SNP selection using genotype data and their applications to association studies. <i>Genome Research</i> , <b>2004</b> , 14, 908-16	9.7	119
29	Monte Carlo Strategies in Scientific Computing. <i>Springer Series in Statistics</i> , <b>2004</b> ,	0.3	120

28	The program of gene transcription for a single differentiating cell type during sporulation in <i>Bacillus subtilis</i> . <i>PLoS Biology</i> , <b>2004</b> , 2, e328	9.7	276
27	Incorporating genotyping uncertainty in haplotype inference for single-nucleotide polymorphisms. <i>American Journal of Human Genetics</i> , <b>2004</b> , 74, 495-510	11	34
26	Dynamic Programming Algorithms for Haplotype Block Partitioning and Tag SNP Selection Using Haplotype Data or Genotype Data. <i>Lecture Notes in Computer Science</i> , <b>2004</b> , 96-112	0.9	
25	Haplotype Inference and Its Application in Linkage Disequilibrium Mapping. <i>Lecture Notes in Computer Science</i> , <b>2004</b> , 48-61	0.9	2
24	Haplotype information and linkage disequilibrium mapping for single nucleotide polymorphisms. <i>Genome Research</i> , <b>2003</b> , 13, 2112-7	9.7	25
23	Integrating regulatory motif discovery and genome-wide expression analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 3339-44	11.5	274
22	The Spo0A regulon of <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , <b>2003</b> , 50, 1683-701	4.1	392
21	An algorithm for finding protein-DNA binding sites with applications to chromatin-immunoprecipitation microarray experiments. <i>Nature Biotechnology</i> , <b>2002</b> , 20, 835-9	44.5	542
20	Monte Carlo Bayesian Signal Processing for Wireless Communications. <i>Journal of Signal Processing Systems</i> , <b>2002</b> , 30, 89-105		28
19	A new sequential importance sampling method and its application to the two-dimensional hydrophobic/hydrophilic model. <i>Journal of Chemical Physics</i> , <b>2002</b> , 117, 3492-3498	3.9	53
18	Monte Carlo Bayesian Signal Processing for Wireless Communications <b>2002</b> , 89-105		3
17	Bayesian haplotype inference for multiple linked single-nucleotide polymorphisms. <i>American Journal of Human Genetics</i> , <b>2002</b> , 70, 157-69	11	531
16	Partition-ligation-expectation-maximization algorithm for haplotype inference with single-nucleotide polymorphisms. <i>American Journal of Human Genetics</i> , <b>2002</b> , 71, 1242-7	11	425
15	Sequential importance sampling for nonparametric Bayes models: The next generation. <i>Canadian Journal of Statistics</i> , <b>1999</b> , 27, 251-267	0.4	98
14	Parameter Expansion for Data Augmentation. <i>Journal of the American Statistical Association</i> , <b>1999</b> , 94, 1264-1274	2.8	182
13	Markovian Structures in Biological Sequence Alignments. <i>Journal of the American Statistical Association</i> , <b>1999</b> , 94, 1-15	2.8	50
12	Sequential Monte Carlo Methods for Dynamic Systems. <i>Journal of the American Statistical Association</i> , <b>1998</b> , 93, 1032-1044	2.8	927
11	Rejection Control and Sequential Importance Sampling. <i>Journal of the American Statistical Association</i> , <b>1998</b> , 93, 1022-1031	2.8	75

10	Predictive Updating Methods with Application to Bayesian Classification. <i>Journal of the Royal Statistical Society Series B: Methodological</i> , <b>1996</b> , 58, 397-415		5
9	Nonparametric hierarchical Bayes via sequential imputations. <i>Annals of Statistics</i> , <b>1996</b> , 24, 911	3.2	99
8	Statistical inference and Monte Carlo algorithms. <i>Test</i> , <b>1996</b> , 5, 249-344	1.1	20
7	Metropolized independent sampling with comparisons to rejection sampling and importance sampling. <i>Statistics and Computing</i> , <b>1996</b> , 6, 113-119	1.8	297
6	Bayesian Models for Multiple Local Sequence Alignment and Gibbs Sampling Strategies. <i>Journal of the American Statistical Association</i> , <b>1995</b> , 90, 1156-1170	2.8	193
5	Blind Deconvolution via Sequential Imputations. <i>Journal of the American Statistical Association</i> , <b>1995</b> , 90, 567-576	2.8	182
4	Sequential Imputations and Bayesian Missing Data Problems. <i>Journal of the American Statistical Association</i> , <b>1994</b> , 89, 278-288	2.8	502
3	The Collapsed Gibbs Sampler in Bayesian Computations with Applications to a Gene Regulation Problem. <i>Journal of the American Statistical Association</i> , <b>1994</b> , 89, 958-966	2.8	372
2	Stratification and optimal resampling for sequential Monte Carlo. <i>Biometrika</i> ,	2	1
1	Neuronized Priors for Bayesian Sparse Linear Regression. <i>Journal of the American Statistical Association</i> , 1-16	2.8	2