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List of Publications by Citations

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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	Topological domains in mammalian genomes identified by analysis of chromatin interactions. *Nature*, **2012**, 485, 376-80	50.4	4098
80	TIMER: A Web Server for Comprehensive Analysis of Tumor-Infiltrating Immune Cells. *Cancer Research*, **2017**, 77, e108-e110	10.1	1919
79	Genetics of rheumatoid arthritis contributes to biology and drug discovery. *Nature*, **2014**, 506, 376-81	50.4	1426
78	Comprehensive analyses of tumor immunity: implications for cancer immunotherapy. *Genome Biology*, **2016**, 17, 174	18.3	942
77	Sequential Monte Carlo Methods for Dynamic Systems. *Journal of the American Statistical Association*, **1998**, 93, 1032-1044	2.8	927
76	MAGeCK enables robust identification of essential genes from genome-scale CRISPR/Cas9 knockout screens. *Genome Biology*, **2014**, 15, 554	18.3	821
75	An algorithm for finding protein-DNA binding sites with applications to chromatin-immunoprecipitation microarray experiments. *Nature Biotechnology*, **2002**, 20, 835-9	44.5	542
74	Bayesian haplotype inference for multiple linked single-nucleotide polymorphisms. *American Journal of Human Genetics*, **2002**, 70, 157-69	11	531
73	Sequential Imputations and Bayesian Missing Data Problems. *Journal of the American Statistical Association*, **1994**, 89, 278-288	2.8	502
72	Partition-ligation-expectation-maximization algorithm for haplotype inference with single-nucleotide polymorphisms. *American Journal of Human Genetics*, **2002**, 71, 1242-7	11	425
71	The Spo0A regulon of Bacillus subtilis. *Molecular Microbiology*, **2003**, 50, 1683-701	4.1	392
70	The Collapsed Gibbs Sampler in Bayesian Computations with Applications to a Gene Regulation Problem. *Journal of the American Statistical Association*, **1994**, 89, 958-966	2.8	372
69	Metropolized independent sampling with comparisons to rejection sampling and importance sampling. *Statistics and Computing*, **1996**, 6, 113-119	1.8	297
68	The program of gene transcription for a single differentiating cell type during sporulation in Bacillus subtilis. *PLoS Biology*, **2004**, 2, e328	9.7	276
67	Integrating regulatory motif discovery and genome-wide expression analysis. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 3339-44	11.5	274
66	Landscape of tumor-infiltrating T cell repertoire of human cancers. *Nature Genetics*, **2016**, 48, 725-32	36.3	193
65	Bayesian Models for Multiple Local Sequence Alignment and Gibbs Sampling Strategies. *Journal of the American Statistical Association*, **1995**, 90, 1156-1170	2.8	193

64	Parameter Expansion for Data Augmentation. *Journal of the American Statistical Association*, **1999**, 94, 1264-1274	2.8	182
63	Blind Deconvolution via Sequential Imputations. *Journal of the American Statistical Association*, **1995**, 90, 567-576	2.8	182
62	Quality control, modeling, and visualization of CRISPR screens with MAGeCK-VISPR. *Genome Biology*, **2015**, 16, 281	18.3	171
61	Sequential Monte Carlo Methods for Statistical Analysis of Tables. *Journal of the American Statistical Association*, **2005**, 100, 109-120	2.8	152
60	Genomic sequence is highly predictive of local nucleosome depletion. *PLoS Computational Biology*, **2008**, 4, e13	5	145
59	Bayesian inference of spatial organizations of chromosomes. *PLoS Computational Biology*, **2013**, 9, e1002893	5	140
58	Monte Carlo Strategies in Scientific Computing. *Springer Series in Statistics*, **2004**,	0.3	120
57	Haplotype block partitioning and tag SNP selection using genotype data and their applications to association studies. *Genome Research*, **2004**, 14, 908-16	9.7	119
56	Modeling within-motif dependence for transcription factor binding site predictions. *Bioinformatics*, **2004**, 20, 909-16	7.2	111
55	Convergent regulatory evolution and loss of flight in paleognathous birds. *Science*, **2019**, 364, 74-78	33.3	103
54	Nonparametric hierarchical Bayes via sequential imputations. *Annals of Statistics*, **1996**, 24, 911	3.2	99
53	Sequential importance sampling for nonparametric Bayes models: The next generation. *Canadian Journal of Statistics*, **1999**, 27, 251-267	0.4	98
52	Cooperation between Polycomb and androgen receptor during oncogenic transformation. *Genome Research*, **2012**, 22, 322-31	9.7	97
51	Defining a centromere-like element in Bacillus subtilis by Identifying the binding sites for the chromosome-anchoring protein RacA. *Molecular Cell*, **2005**, 17, 773-82	17.6	80
50	BioOptimizer: a Bayesian scoring function approach to motif discovery. *Bioinformatics*, **2004**, 20, 1557-64	7.2	79
49	Expansion of biological pathways based on evolutionary inference. *Cell*, **2014**, 158, 213-25	56.2	75
48	Rejection Control and Sequential Importance Sampling. *Journal of the American Statistical Association*, **1998**, 93, 1022-1031	2.8	75
47	Landscape of B cell immunity and related immune evasion in human cancers. *Nature Genetics*, **2019**, 51, 560-567	36.3	56

46	Computational Discovery of Gene Regulatory Binding Motifs: A Bayesian Perspective. *Statistical Science*, **2004**, 19, 188	2.4	54
45	A new sequential importance sampling method and its application to the two-dimensional hydrophobic–hydrophilic model. *Journal of Chemical Physics*, **2002**, 117, 3492-3498	3.9	53
44	Markovian Structures in Biological Sequence Alignments. *Journal of the American Statistical Association*, **1999**, 94, 1-15	2.8	50
43	A boosting approach for motif modeling using ChIP-chip data. *Bioinformatics*, **2005**, 21, 2636-43	7.2	46
42	On side-chain conformational entropy of proteins. *PLoS Computational Biology*, **2006**, 2, e168	5	44
41	Network analysis of gene essentiality in functional genomics experiments. *Genome Biology*, **2015**, 16, 239	18.3	41
40	Extracting sequence features to predict protein-DNA interactions: a comparative study. *Nucleic Acids Research*, **2008**, 36, 4137-48	20.1	39
39	BEST: binding-site estimation suite of tools. *Bioinformatics*, **2005**, 21, 2909-11	7.2	36
38	Incorporating genotyping uncertainty in haplotype inference for single-nucleotide polymorphisms. *American Journal of Human Genetics*, **2004**, 74, 495-510	11	34
37	Revisit linear regression-based deconvolution methods for tumor gene expression data. *Genome Biology*, **2017**, 18, 127	18.3	30
36	Lookahead Strategies for Sequential Monte Carlo. *Statistical Science*, **2013**, 28,	2.4	28
35	Monte Carlo Bayesian Signal Processing for Wireless Communications. *Journal of Signal Processing Systems*, **2002**, 30, 89-105		28
34	cepip: context-dependent epigenomic weighting for prioritization of regulatory variants and disease-associated genes. *Genome Biology*, **2017**, 18, 52	18.3	27
33	A suite of web-based programs to search for transcriptional regulatory motifs. *Nucleic Acids Research*, **2004**, 32, W204-7	20.1	27
32	A coalescence-guided hierarchical Bayesian method for haplotype inference. *American Journal of Human Genetics*, **2006**, 79, 313-22	11	25
31	Haplotype information and linkage disequilibrium mapping for single nucleotide polymorphisms. *Genome Research*, **2003**, 13, 2112-7	9.7	25
30	Understanding spatial organizations of chromosomes via statistical analysis of Hi-C data. *Quantitative Biology*, **2013**, 1, 156-174	3.9	22
29	The distribution of genomic variations in human iPSCs is related to replication-timing reorganization during reprogramming. *Cell Reports*, **2014**, 7, 70-8	10.6	21

28	On learning strategies for evolutionary Monte Carlo. *Statistics and Computing*, **2007**, 17, 23-38	1.8	21
27	Statistical assessment of the global regulatory role of histone acetylation in Saccharomyces cerevisiae. *Genome Biology*, **2006**, 7, R70	18.3	21
26	Stopping-time resampling for sequential Monte Carlo methods. *Journal of the Royal Statistical Society Series B: Statistical Methodology*, **2005**, 67, 199-217	3.9	21
25	Statistical inference and Monte Carlo algorithms. *Test*, **1996**, 5, 249-344	1.1	20
24	Monte Carlo sampling of near-native structures of proteins with applications. *Proteins: Structure, Function and Bioinformatics*, **2007**, 66, 61-8	4.2	18
23	Bayesian Detection of Convergent Rate Changes of Conserved Noncoding Elements on Phylogenetic Trees. *Molecular Biology and Evolution*, **2019**, 36, 1086-1100	8.3	17
22	Tmod: toolbox of motif discovery. *Bioinformatics*, **2010**, 26, 405-7	7.2	16
21	Determinants of transcription factor regulatory range. *Nature Communications*, **2020**, 11, 2472	17.4	13
20	Bayesian hierarchical model of protein-binding microarray k-mer data reduces noise and identifies transcription factor subclasses and preferred k-mers. *Bioinformatics*, **2013**, 29, 1390-8	7.2	13
19	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,	11.5	10
18	Reduction of mNAT1/hNAT2 Contributes to Cerebral Endothelial Necroptosis and A□Accumulation in AlzheimerWsDisease. *Cell Reports*, **2020**, 33, 108447	10.6	7
17	Computational Deconvolution of Tumor-Infiltrating Immune Components with Bulk Tumor Gene Expression Data. *Methods in Molecular Biology*, **2020**, 2120, 249-262	1.4	6
16	Association pattern discovery via theme dictionary models. *Journal of the Royal Statistical Society Series B: Statistical Methodology*, **2014**, 76, 319-347	3.9	5
15	Predictive Updating Methods with Application to Bayesian Classification. *Journal of the Royal Statistical Society Series B: Methodological*, **1996**, 58, 397-415		5
14	Bayesian hidden Markov tree models for clustering genes with shared evolutionary history. *Annals of Applied Statistics*, **2019**, 13,	2.1	3
13	Nonparametric hierarchical Bayes analysis of binomial data via Bernstein polynomial priors. *Canadian Journal of Statistics*, **2012**, 40, 328-344	0.4	3
12	Monte Carlo Bayesian Signal Processing for Wireless Communications **2002**, 89-105		3
11	SIMPLEs: a single-cell RNA sequencing imputation strategy preserving gene modules and cell clusters variation. *NAR Genomics and Bioinformatics*, **2020**, 2, lqaa077	3.7	3

10	The EM Algorithm and the Rise of Computational Biology. *Statistical Science*, **2010**, 25,	2.4	2
9	Haplotype Inference and Its Application in Linkage Disequilibrium Mapping. *Lecture Notes in Computer Science*, **2004**, 48-61	0.9	2
8	Monte Carlo Approximation of Bayes Factors via Mixing With Surrogate Distributions. *Journal of the American Statistical Association*, **2020**, 1-16	2.8	2
7	Neuronized Priors for Bayesian Sparse Linear Regression. *Journal of the American Statistical Association*,1-16	2.8	2
6	Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2020**, 17, 647-656	3	1
5	Stratification and optimal resampling for sequential Monte Carlo. *Biometrika*,	2	1
4	Bayesian Methods in Biological Sequence Analysis **2008**, 67-96		
3	Dynamic Programming Algorithms for Haplotype Block Partitioning and Tag SNP Selection Using Haplotype Data or Genotype Data. *Lecture Notes in Computer Science*, **2004**, 96-112	0.9	
2	Statistical Learning and Modeling of TF-DNA Binding **2011**, 55-72		
1	Statistical Methods in Bioinformatics **2013**, 101-149		