Qing Zhou

List of Publications by Year
in descending order

30 papers	1,713 citations	623734 14 h-index	526287 27 g-index
30 all docs	30 docs citations	30 times ranked	2646 citing authors

#	Article	IF	Citations
1	ChIP-Seq of transcription factors predicts absolute and differential gene expression in embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21521-21526.	7.1	312
2	Smaller desert dust cooling effect estimated from analysis of dust size and abundance. Nature Geoscience, 2017, 10, 274-278.	12.9	306
3	A gene regulatory network in mouse embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 16438-16443.	7.1	246
4	CisModule: De novo discovery of cis-regulatory modules by hierarchical mixture modeling. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 12114-12119.	7.1	189
5	Modeling within-motif dependence for transcription factor binding site predictions. Bioinformatics, 2004, 20, 909-916.	4.1	129
6	Equi-energy sampler with applications in statistical inference and statistical mechanics. Annals of Statistics, 2006, 34, 1581.	2.6	129
7	Computational Discovery of Gene Regulatory Binding Motifs: A Bayesian Perspective. Statistical Science, 2004, 19, 188.	2.8	62
8	A boosting approach for motif modeling using ChIP-chip data. Bioinformatics, 2005, 21, 2636-2643.	4.1	54
9	Learning Sparse Causal Gaussian Networks With Experimental Intervention: Regularization and Coordinate Descent. Journal of the American Statistical Association, 2013, 108, 288-300.	3.1	49
10	Extracting sequence features to predict protein–DNA interactions: a comparative study. Nucleic Acids Research, 2008, 36, 4137-4148.	14.5	40
11	Identification of Context-Dependent Motifs by Contrasting ChIP Binding Data. Bioinformatics, 2010, 26, 2826-2832.	4.1	36
12	Learning Large-Scale Bayesian Networks with the sparsebn Package. Journal of Statistical Software, 2019, 91, .	3.7	21
13	Multi-Domain Sampling With Applications to Structural Inference of Bayesian Networks. Journal of the American Statistical Association, 2011, 106, 1317-1330.	3.1	20
14	Penalized estimation of directed acyclic graphs from discrete data. Statistics and Computing, 2019, 29, 161-176.	1.5	18
15	Coupling hidden Markov models for the discovery of Cis-regulatory modules in multiple species. Annals of Applied Statistics, 2007, 1, .	1.1	15
16	Random Walk over Basins of Attraction to Construct Ising Energy Landscapes. Physical Review Letters, 2011, 106, 180602.	7.8	14
17	Finding multiple minimum-energy conformations of the hydrophobic-polar protein model via multidomain sampling. Physical Review E, 2012, 86, 031909.	2.1	13
18	Optimizing Regularized Cholesky Score for Order-Based Learning of Bayesian Networks. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2021, 43, 3555-3572.	13.9	13

#	ARTICLE	IF	CITATIONS
19	Energy landscape of a spin-glass model: Exploration and characterization. Physical Review E, 2009, 79, 051117.	2.1	11
20	Detecting clustering and ordering binding patterns among transcription factors via point process models. Bioinformatics, 2014, 30, 2263-2271.	4.1	9
21	Reconstructing the energy landscape of a distribution from Monte Carlo samples. Annals of Applied Statistics, 2008, 2, .	1.1	9
22	Searching ChIP-seq genomic islands for combinatorial regulatory codes in mouse embryonic stem cells. BMC Genomics, 2011, 12, 515.	2.8	6
23	A penalized Bayesian approach to predicting sparse proteinâ€"DNA binding landscapes. Bioinformatics, 2014, 30, 636-643.	4.1	4
24	Heterogeneity in DNA Multiple Alignments: Modeling, Inference, and Applications in Motif Finding. Biometrics, 2010, 66, 694-704.	1.4	3
25	On Weight Matrix and Free Energy Models for Sequence Motif Detection. Journal of Computational Biology, 2010, 17, 1621-1638.	1.6	3
26	Causal network learning with non-invertible functional relationships. Computational Statistics and Data Analysis, 2021, 156, 107141.	1.2	1
27	Partitioned hybrid learning of Bayesian network structures. Machine Learning, 2022, 111, 1695-1738.	5.4	1
28	In silico prediction of transcription factors that interact with the E2F family of transcription factors. , 0, , .		0
29	Honest Confidence Sets for High-Dimensional Regression by Projection and Shrinkage. Journal of the American Statistical Association, 2023, 118, 469-488.	3.1	0
30	Defining the Mechanism of Transcription Factor-Induced Epigenetic Reprogramming.. Blood, 2009, 114, SCI-41-SCI-41.	1.4	0