

Wing Hung Wong

List of Publications by Year in descending order

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172
papers

23,063
citations

16451

64
h-index

8630

146
g-index

176
all docs

176
docs citations

176
times ranked

31713
citing authors

#	ARTICLE	IF	CITATIONS
1	Collaborative Multilabel Classification. Journal of the American Statistical Association, 2023, 118, 913-924.	3.1	1
2	Mini-Batch Metropolisâ€Hastings With Reversible SGLD Proposal. Journal of the American Statistical Association, 2022, 117, 386-394.	3.1	1
3	Coupled Generation. Journal of the American Statistical Association, 2022, 117, 1243-1253.	3.1	0
4	scJoint integrates atlas-scale single-cell RNA-seq and ATAC-seq data with transfer learning. Nature Biotechnology, 2022, 40, 703-710.	17.5	70
5	On the identifiability of the isoform deconvolution problem: application to select the proper fragment length in an RNA-seq library. Bioinformatics, 2022, , .	4.1	0
6	DeepCAGE: Incorporating Transcription Factors in Genome-Wide Prediction of Chromatin Accessibility. Genomics, Proteomics and Bioinformatics, 2022, 20, 496-507.	6.9	7
7	Leveraging cell-type-specific regulatory networks to interpret genetic variants in abdominal aortic aneurysm. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	8
8	Regulatory analysis of single cell multiome gene expression and chromatin accessibility data with scREG. Genome Biology, 2022, 23, 114.	8.8	22
9	Network Effects of the 15q13.3 Microdeletion on the Transcriptome and Epigenome in Human-Induced Neurons. Biological Psychiatry, 2021, 89, 497-509.	1.3	17
10	hReg-CNCC reconstructs a regulatory network in human cranial neural crest cells and annotates variants in a developmental context. Communications Biology, 2021, 4, 442.	4.4	10
11	Density estimation using deep generative neural networks. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	47
12	Modeling regulatory network topology improves genome-wide analyses of complex human traits. Nature Communications, 2021, 12, 2851.	12.8	17
13	Simultaneous deep generative modelling and clustering of single-cell genomic data. Nature Machine Intelligence, 2021, 3, 536-544.	16.0	59
14	MIMIC: an optimization method to identify cell type-specific marker panel for cell sorting. Briefings in Bioinformatics, 2021, 22, .	6.5	1
15	Dynamic chromatin regulatory landscape of human CAR T cell exhaustion. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	36
16	Sensitive detection of tumor mutations from blood and its application to immunotherapy prognosis. Nature Communications, 2021, 12, 4172.	12.8	16
17	Abstract 24: Multi-feature ensemble learning on cell-free dna for accurately detecting and locating cancer. Cancer Research, 2021, 81, 24-24.	0.9	3
18	Sc-compReg enables the comparison of gene regulatory networks between conditions using single-cell data. Nature Communications, 2021, 12, 4763.	12.8	12

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19	Detecting Strong Signals in Gene Perturbation Experiments: An Adaptive Approach With Power Guarantee and FDR Control. <i>Journal of the American Statistical Association</i> , 2020, 115, 1747-1755.	3.1	1
20	Chromatin accessibility landscape and regulatory network of high-altitude hypoxia adaptation. <i>Nature Communications</i> , 2020, 11, 4928.	12.8	43
21	A method for scoring the cell type-specific impacts of noncoding variants in personal genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21364-21372.	7.1	16
22	Time course regulatory analysis based on paired expression and chromatin accessibility data. <i>Genome Research</i> , 2020, 30, 622-634.	5.5	35
23	Integrated functional genomic analyses of Klinefelter and Turner syndromes reveal global network effects of altered X chromosome dosage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4864-4873.	7.1	66
24	Feature Consistency Training With JPEG Compressed Images. <i>IEEE Transactions on Circuits and Systems for Video Technology</i> , 2020, 30, 4769-4780.	8.3	11
25	Meta-analysis of peptides to detect protein significance. <i>Statistics and Its Interface</i> , 2020, 13, 465-474.	0.3	0
26	QuatNet: Quaternion-Based Head Pose Estimation With Multiregression Loss. <i>IEEE Transactions on Multimedia</i> , 2019, 21, 1035-1046.	7.2	100
27	DC3 is a method for deconvolution and coupled clustering from bulk and single-cell genomics data. <i>Nature Communications</i> , 2019, 10, 4613.	12.8	57
28	Xrare: a machine learning method jointly modeling phenotypes and genetic evidence for rare disease diagnosis. <i>Genetics in Medicine</i> , 2019, 21, 2126-2134.	2.4	56
29	TFAP2C- and p63-Dependent Networks Sequentially Rearrange Chromatin Landscapes to Drive Human Epidermal Lineage Commitment. <i>Cell Stem Cell</i> , 2019, 24, 271-284.e8.	11.1	76
30	Haplotype-resolved and integrated genome analysis of the cancer cell line HepG2. <i>Nucleic Acids Research</i> , 2019, 47, 3846-3861.	14.5	45
31	DeepTACT: predicting 3D chromatin contacts via bootstrapping deep learning. <i>Nucleic Acids Research</i> , 2019, 47, e60-e60.	14.5	101
32	Comprehensive, integrated, and phased whole-genome analysis of the primary ENCODE cell line K562. <i>Genome Research</i> , 2019, 29, 472-484.	5.5	78
33	81 INTEGRATED ANALYSIS OF GENE EXPRESSION, DNA METHYLATION AND CHROMATIN ACCESSIBILITY IN A HUMAN IPSC-TO-INDUCED-NEURON MODEL OF THE 15Q13.3 MICRODELETION. <i>European Neuropsychopharmacology</i> , 2019, 29, S105.	0.7	0
34	CRISPhieRmix: a hierarchical mixture model for CRISPR pooled screens. <i>Genome Biology</i> , 2018, 19, 159.	8.8	36
35	CRISPR Activation Screens Systematically Identify Factors that Drive Neuronal Fate and Reprogramming. <i>Cell Stem Cell</i> , 2018, 23, 758-771.e8.	11.1	161
36	Confnet: Predict with Confidence. , 2018, , .		8

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37	Correlation-Based Face Detection for Recognizing Faces in Videos. , 2018, , .		3
38	Unsupervised clustering and epigenetic classification of single cells. Nature Communications, 2018, 9, 2410.	12.8	100
39	Integrative analysis of single-cell genomics data by coupled nonnegative matrix factorizations. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7723-7728.	7.1	156
40	Towards high performance data analytic on heterogeneous many-core systems: A study on Bayesian Sequential Partitioning. Journal of Parallel and Distributed Computing, 2018, 122, 36-50.	4.1	1
41	CancerDetector: ultrasensitive and non-invasive cancer detection at the resolution of individual reads using cell-free DNA methylation sequencing data. Nucleic Acids Research, 2018, 46, e89-e89.	14.5	131
42	A 1.86mJ/Gb/query bit-plane payload machine learning processor in 90nm CMOS. , 2018, , .		0
43	Extensive and deep sequencing of the Venter/HuRef genome for developing and benchmarking genome analysis tools. Scientific Data, 2018, 5, 180261.	5.3	6
44	Phased Genome Sequencing Through Chromosome Sorting. Methods in Molecular Biology, 2017, 1551, 171-188.	0.9	1
45	Predicting transcription factor binding motifs from DNA-binding domains, chromatin accessibility and gene expression data. Nucleic Acids Research, 2017, 45, 5666-5677.	14.5	12
46	Modeling gene regulation from paired expression and chromatin accessibility data. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4914-E4923.	7.1	167
47	COSINE: non-seeding method for mapping long noisy sequences. Nucleic Acids Research, 2017, 45, e132-e132.	14.5	4
48	A 41.3/26.7 pJ per Neuron Weight RBM Processor Supporting On-Chip Learning/Inference for IoT Applications. IEEE Journal of Solid-State Circuits, 2017, 52, 2601-2612.	5.4	16
49	Simultaneous inference of phenotype-associated genes and relevant tissues from GWAS data via Bayesian integration of multiple tissue-specific gene networks. Journal of Molecular Cell Biology, 2017, 9, 436-452.	3.3	10
50	Scalable multi-sample single-cell data analysis by Partition-Assisted Clustering and Multiple Alignments of Networks. PLoS Computational Biology, 2017, 13, e1005875.	3.2	18
51	Convergence rates of a partition based Bayesian multivariate density estimation method. Advances in Neural Information Processing Systems, 2017, 30, 4738-4746.	2.8	1
52	A 41.3pJ/26.7pJ per neuron weight RBM processor for on-chip learning/inference applications. , 2016, , .		1
53	Simultaneous dimension reduction and adjustment for confounding variation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14662-14667.	7.1	42
54	Modeling the causal regulatory network by integrating chromatin accessibility and transcriptome data. National Science Review, 2016, 3, 240-251.	9.5	14

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55	Computational Aspects of Optional PÃ³lya Tree. Journal of Computational and Graphical Statistics, 2016, 25, 301-320.	1.7	4
56	The primate-specific noncoding RNA HPAT5 regulates pluripotency during human preimplantation development and nuclear reprogramming. Nature Genetics, 2016, 48, 44-52.	21.4	153
57	Stable 5-Hydroxymethylcytosine (5hmC) Acquisition Marks Gene Activation During Chondrogenic Differentiation. Journal of Bone and Mineral Research, 2016, 31, 524-534.	2.8	48
58	Density Estimation via Discrepancy Based Adaptive Sequential Partition. Advances in Neural Information Processing Systems, 2016, 29, 1091-1099.	2.8	6
59	Genome-Wide Mapping of DNA Hydroxymethylation in Osteoarthritic Chondrocytes. Arthritis and Rheumatology, 2015, 67, 2129-2140.	5.6	37
60	Leveraging long read sequencing from a single individual to provide a comprehensive resource for benchmarking variant calling methods. Scientific Reports, 2015, 5, 14493.	3.3	12
61	MetaSV: an accurate and integrative structural-variant caller for next generation sequencing. Bioinformatics, 2015, 31, 2741-2744.	4.1	131
62	VarSim: a high-fidelity simulation and validation framework for high-throughput genome sequencing with cancer applications. Bioinformatics, 2015, 31, 1469-1471.	4.1	59
63	Characterization of fusion genes and the significantly expressed fusion isoforms in breast cancer by hybrid sequencing. Nucleic Acids Research, 2015, 43, e116-e116.	14.5	104
64	A Hardware-Efficient Sigmoid Function With Adjustable Precision for a Neural Network System. IEEE Transactions on Circuits and Systems II: Express Briefs, 2015, 62, 1073-1077.	3.0	52
65	An ensemble approach to accurately detect somatic mutations using SomaticSeq. Genome Biology, 2015, 16, 197.	8.8	93
66	Learning regulatory programs by threshold SVD regression. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15675-15680.	7.1	21
67	Density estimation on multivariate censored data with optional Polya tree. Biostatistics, 2014, 15, 182-195.	1.5	7
68	Human tRNA synthetase catalytic nulls with diverse functions. Science, 2014, 345, 328-332.	12.6	101
69	Modeling stochastic noise in gene regulatory systems. Quantitative Biology, 2014, 2, 1-29.	0.5	11
70	Early role for IL-6 signalling during generation of induced pluripotent stem cells revealed by heterokaryon RNA-Seq. Nature Cell Biology, 2013, 15, 1244-1252.	10.3	88
71	Personalized prediction of first-cycle in vitro fertilization success. Fertility and Sterility, 2013, 99, 1905-1911.	1.0	41
72	RNA sequencing reveals a diverse and dynamic repertoire of the <i>Xenopus tropicalis</i> transcriptome over development. Genome Research, 2013, 23, 201-216.	5.5	128

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73	Genomic responses in mouse models poorly mimic human inflammatory diseases. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3507-3512.	7.1	2,518
74	An Oct4-Sox2-Nanog network controls developmental progression in the pre-implantation mouse embryo. Molecular Systems Biology, 2013, 9, 632.	7.2	60
75	Multivariate Density Estimation by Bayesian Sequential Partitioning. Journal of the American Statistical Association, 2013, 108, 1402-1410.	3.1	39
76	Modeling kinetic rate variation in third generation DNA sequencing data to detect putative modifications to DNA bases. Genome Research, 2013, 23, 129-141.	5.5	99
77	Simultaneous Isoform Discovery and Quantification from RNA-Seq. Statistics in Biosciences, 2013, 5, 100-118.	1.2	18
78	Characterization of the human ESC transcriptome by hybrid sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4821-30.	7.1	316
79	A Sparse Transmission Disequilibrium Test for Haplotypes Based on Bradley-Terry Graphs. Human Heredity, 2012, 73, 52-61.	0.8	3
80	Neural-specific Sox2 input and differential Gli-binding affinity provide context and positional information in Shh-directed neural patterning. Genes and Development, 2012, 26, 2802-2816.	5.9	158
81	Activation of Innate Immunity Is Required for Efficient Nuclear Reprogramming. Cell, 2012, 151, 547-558.	28.9	329
82	Predicting personalized multiple birth risks after in vitro fertilization—double embryo transfer. Fertility and Sterility, 2012, 98, 69-76.	1.0	17
83	Six2 and Wnt Regulate Self-Renewal and Commitment of Nephron Progenitors through Shared Gene Regulatory Networks. Developmental Cell, 2012, 23, 637-651.	7.0	229
84	The Analysis of ChIP-Seq Data. Methods in Enzymology, 2011, 497, 51-73.	1.0	19
85	A New FACS Approach Isolates hESC Derived Endoderm Using Transcription Factors. PLoS ONE, 2011, 6, e17536.	2.5	23
86	SMAD4-dependent barrier constrains prostate cancer growth and metastatic progression. Nature, 2011, 470, 269-273.	27.8	462
87	Coupling Optional \mathcal{P}^3 Trees and the Two Sample Problem. Journal of the American Statistical Association, 2011, 106, 1553-1565.	3.1	34
88	Human transcriptome array for high-throughput clinical studies. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3707-3712.	7.1	122
89	Completely phased genome sequencing through chromosome sorting. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12-17.	7.1	93
90	Optional \mathcal{P}^3 tree and Bayesian inference. Annals of Statistics, 2010, 38, .	2.6	46

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91	An "almost exhaustive" search-based sequential permutation method for detecting epistasis in disease association studies. <i>Genetic Epidemiology</i> , 2010, 34, 434-443.	1.3	12
92	Hedgehog pathway-regulated gene networks in cerebellum development and tumorigenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9736-9741.	7.1	109
93	Detection of splice junctions from paired-end RNA-seq data by SpliceMap. <i>Nucleic Acids Research</i> , 2010, 38, 4570-4578.	14.5	300
94	Analysis of factorial time-course microarrays with application to a clinical study of burn injury. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9923-9928.	7.1	62
95	Modeling Co-Expression across Species for Complex Traits: Insights to the Difference of Human and Mouse Embryonic Stem Cells. <i>PLoS Computational Biology</i> , 2010, 6, e1000707.	3.2	24
96	Deep phenotyping to predict live birth outcomes in in vitro fertilization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 13570-13575.	7.1	36
97	Dissecting Early Differentially Expressed Genes in a Mixture of Differentiating Embryonic Stem Cells. <i>PLoS Computational Biology</i> , 2009, 5, e1000607.	3.2	13
98	ChIP-Seq of transcription factors predicts absolute and differential gene expression in embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21521-21526.	7.1	312
99	Using high-density exon arrays to profile gene expression in closely related species. <i>Nucleic Acids Research</i> , 2009, 37, e90-e90.	14.5	17
100	A Gene Signature Predictive for Outcome in Advanced Ovarian Cancer Identifies a Survival Factor: Microfibril-Associated Glycoprotein 2. <i>Cancer Cell</i> , 2009, 16, 521-532.	16.8	230
101	FoxOs Cooperatively Regulate Diverse Pathways Governing Neural Stem Cell Homeostasis. <i>Cell Stem Cell</i> , 2009, 5, 540-553.	11.1	418
102	Isolation and Transcriptional Profiling of Purified Hepatic Cells Derived from Human Embryonic Stem Cells. <i>Stem Cells</i> , 2008, 26, 2032-2041.	3.2	42
103	p53 and Pten control neural and glioma stem/progenitor cell renewal and differentiation. <i>Nature</i> , 2008, 455, 1129-1133.	27.8	658
104	An integrated software system for analyzing ChIP-chip and ChIP-seq data. <i>Nature Biotechnology</i> , 2008, 26, 1293-1300.	17.5	662
105	Learning Causal Bayesian Network Structures From Experimental Data. <i>Journal of the American Statistical Association</i> , 2008, 103, 778-789.	3.1	123
106	Optimal discovery of a stochastic genetic network. , 2008, , .		1
107	A genome-scale analysis of the <i>cis</i> -regulatory circuitry underlying sonic hedgehog-mediated patterning of the mammalian limb. <i>Genes and Development</i> , 2008, 22, 2651-2663.	5.9	269
108	MADS: A new and improved method for analysis of differential alternative splicing by exon-tiling microarrays. <i>Rna</i> , 2008, 14, 1470-1479.	3.5	86

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109	Defining Human Embryo Phenotypes by Cohort-Specific Prognostic Factors. PLoS ONE, 2008, 3, e2562.	2.5	29
110	A Novel and Critical Role for Oct4 as a Regulator of the Maternal-Embryonic Transition. PLoS ONE, 2008, 3, e4109.	2.5	99
111	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
112	Evolutionary Monte Carlo Methods for Clustering. Journal of Computational and Graphical Statistics, 2007, 16, 855-876.	1.7	6
113	Assessing the Conservation of Mammalian Gene Expression Using High-Density Exon Arrays. Molecular Biology and Evolution, 2007, 24, 1283-1285.	8.9	49
114	FoxOs Are Lineage-Restricted Redundant Tumor Suppressors and Regulate Endothelial Cell Homeostasis. Cell, 2007, 128, 309-323.	28.9	952
115	Is the future biology Shakespearean or Newtonian?. Molecular BioSystems, 2006, 2, 411.	2.9	6
116	Estimation of the Loss of an Estimate. , 2006, , 491-506.		0
117	Equi-energy sampler with applications in statistical inference and statistical mechanics. Annals of Statistics, 2006, 34, 1581.	2.6	129
118	Computational Biology: Toward Deciphering Gene Regulatory Information in Mammalian Genomes. Biometrics, 2006, 62, 645-663.	1.4	31
119	A comparative analysis of genome-wide chromatin immunoprecipitation data for mammalian transcription factors. Nucleic Acids Research, 2006, 34, e146-e146.	14.5	59
120	Inferring Loss-of-Heterozygosity from Unpaired Tumors Using High-Density Oligonucleotide SNP Arrays. PLoS Computational Biology, 2006, 2, e41.	3.2	140
121	A study of density of states and ground states in hydrophobic-hydrophilic protein folding models by equi-energy sampling. Journal of Chemical Physics, 2006, 124, 244903.	3.0	28
122	Probe Selection and Expression Index Computation of Affymetrix Exon Arrays. PLoS ONE, 2006, 1, e88.	2.5	57
123	Functional annotation and network reconstruction through cross-platform integration of microarray data. Nature Biotechnology, 2005, 23, 238-243.	17.5	137
124	Tight Clustering: A Resampling-Based Approach for Identifying Stable and Tight Patterns in Data. Biometrics, 2005, 61, 10-16.	1.4	198
125	A Small-Molecule Inhibitor of Mps1 Blocks the Spindle-Checkpoint Response to a Lack of Tension on Mitotic Chromosomes. Current Biology, 2005, 15, 1070-1076.	3.9	79
126	Role of Epidermal Growth Factor Receptor Signaling in RAS-Driven Melanoma. Molecular and Cellular Biology, 2005, 25, 4176-4188.	2.3	58

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127	Human Upstream and Mouse Upstream: Databases of Promoter Sequences in the Human and Mouse Genomes. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 220-224.	2.0	0
128	The use of oscillatory signals in the study of genetic networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7063-7068.	7.1	53
129	Sampling motifs on phylogenetic trees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 9481-9486.	7.1	43
130	mSin3A corepressor regulates diverse transcriptional networks governing normal and neoplastic growth and survival. <i>Genes and Development</i> , 2005, 19, 1581-1595.	5.9	201
131	Reliable prediction of transcription factor binding sites by phylogenetic verification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16945-16950.	7.1	43
132	UBIC2 – TOWARDS UBIQUITOUS BIO-INFORMATION COMPUTING: DATA PROTOCOLS, MIDDLEWARE, AND WEB SERVICES FOR HETEROGENEOUS BIOLOGICAL INFORMATION INTEGRATION AND RETRIEVAL. <i>International Journal of Software Engineering and Knowledge Engineering</i> , 2005, 15, 475-485.	0.8	1
133	Expression Profiling of Serous Low Malignant Potential, Low-Grade, and High-Grade Tumors of the Ovary. <i>Cancer Research</i> , 2005, 65, 10602-10612.	0.9	298
134	Determination of Local Statistical Significance of Patterns in Markov Sequences with Application to Promoter Element Identification. <i>Journal of Computational Biology</i> , 2004, 11, 1-14.	1.6	38
135	Molecular diversity of astrocytes with implications for neurological disorders. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 8384-8389.	7.1	193
136	Integrated Analysis of Microarray Data and Gene Function Information. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 106-117.	2.0	12
137	CisModule: De novo discovery of cis-regulatory modules by hierarchical mixture modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12114-12119.	7.1	189
138	Detect and adjust for population stratification in population-based association study using genomic control markers: an application of Affymetrix Genechip® Human Mapping 10K array. <i>European Journal of Human Genetics</i> , 2004, 12, 1001-1006.	2.8	47
139	GoSurfer. <i>Applied Bioinformatics</i> , 2004, 3, 261-264.	1.6	101
140	Estimation of genotype error rate using samples with pedigree information – an application on the GeneChip Mapping 10K array. <i>Genomics</i> , 2004, 84, 623-630.	2.9	47
141	Novel mechanisms of T-cell and dendritic cell activation revealed by profiling of psoriasis on the 63,100-element oligonucleotide array. <i>Physiological Genomics</i> , 2003, 13, 69-78.	2.3	282
142	On $\tilde{\tau}$ -Learning. <i>Journal of the American Statistical Association</i> , 2003, 98, 724-734.	3.1	142
143	Insights into the multistep transformation of MGUS to myeloma using microarray expression analysis. <i>Blood</i> , 2003, 102, 4504-4511.	1.4	212
144	ChipInfo: software for extracting gene annotation and gene ontology information for microarray analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3483-3486.	14.5	84

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145	Array comparative genome hybridization for tumor classification and gene discovery in mouse models of malignant melanoma. <i>Cancer Research</i> , 2003, 63, 5352-6.	0.9	34
146	Recombinatoric exploration of novel folded structures: A heteropolymer-based model of protein evolutionary landscapes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 809-814.	7.1	85
147	Transitive functional annotation by shortest-path analysis of gene expression data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12783-12788.	7.1	295
148	Extensive and divergent circadian gene expression in liver and heart. <i>Nature</i> , 2002, 417, 78-83.	27.8	1,391
149	Evolutionary Monte Carlo for protein folding simulations. <i>Journal of Chemical Physics</i> , 2001, 115, 3374-3380.	3.0	158
150	Real-Parameter Evolutionary Monte Carlo With Applications to Bayesian Mixture Models. <i>Journal of the American Statistical Association</i> , 2001, 96, 653-666.	3.1	172
151	Analyzing high-density oligonucleotide gene expression array data. <i>Journal of Cellular Biochemistry</i> , 2001, 80, 192-202.	2.6	148
152	Issues in cDNA microarray analysis: quality filtering, channel normalization, models of variations and assessment of gene effects. <i>Nucleic Acids Research</i> , 2001, 29, 2549-2557.	14.5	494
153	A Theory for Dynamic Weighting in Monte Carlo Computation. <i>Journal of the American Statistical Association</i> , 2001, 96, 561-573.	3.1	26
154	Multiple-Sequence Information Provides Protection against Mis-Specified Potential Energy Functions in the Lattice Model of Proteins. <i>Physical Review Letters</i> , 2000, 85, 5242-5245.	7.8	4
155	The Multiple-Try Method and Local Optimization in Metropolis Sampling. <i>Journal of the American Statistical Association</i> , 2000, 95, 121-134.	3.1	245
156	Computational Molecular Biology. <i>Journal of the American Statistical Association</i> , 2000, 95, 322-326.	3.1	4
157	Dynamic weighting in simulations of spin systems. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 1999, 252, 257-262.	2.1	9
158	Random Sieve Likelihood and General Regression Models. <i>Journal of the American Statistical Association</i> , 1999, 94, 835-846.	3.1	16
159	Relaxed simulated tempering for VLSI floorplan designs. , 1999, , .		14
160	Molecular dynamic simulation of chaperonin-mediated protein folding. <i>The Protein Journal</i> , 1998, 17, 377-380.	1.1	3
161	Rejection Control and Sequential Importance Sampling. <i>Journal of the American Statistical Association</i> , 1998, 93, 1022-1031.	3.1	99
162	Torsional Relaxation for Biopolymers. <i>Journal of Computational Biology</i> , 1998, 5, 655-665.	1.6	2

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163	Bayesian Analysis in Applications of Hierarchical Models: Issues and Methods. Journal of Educational and Behavioral Statistics, 1996, 21, 131.	1.7	10
164	Probability Inequalities for Likelihood Ratios and Convergence Rates of Sieve MLES. Annals of Statistics, 1995, 23, 339.	2.6	157
165	Sequential Imputations and Bayesian Missing Data Problems. Journal of the American Statistical Association, 1994, 89, 278-288.	3.1	665
166	Convergence Rate of Sieve Estimates. Annals of Statistics, 1994, 22, 580.	2.6	243
167	Profile Likelihood and Conditionally Parametric Models. Annals of Statistics, 1992, 20, 1768.	2.6	243
168	On Maximum Likelihood Estimation in Infinite Dimensional Parameter Spaces. Annals of Statistics, 1991, 19, 603.	2.6	40
169	The Calculation of Posterior Distributions by Data Augmentation. Journal of the American Statistical Association, 1987, 82, 528-540.	3.1	3,022
170	An Application of Imputation to an Estimation Problem in Grouped Lifetime Analysis. Technometrics, 1987, 29, 23-32.	1.9	34
171	Data-Based Nonparametric Estimation of the Hazard Function with Applications to Model Diagnostis and Exploratory Analysis. Journal of the American Statistical Association, 1984, 79, 174.	3.1	36
172	The Estimation of the Hazard Function from Randomly Censored Data by the Kernel Method. Annals of Statistics, 1983, 11, 989.	2.6	161