Wing Hung Wong

List of Publications by Year
in descending order

172	23,063	16451 64	8630 146
papers	citations	h-index	g-index

176	176	176	31713
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Calculation of Posterior Distributions by Data Augmentation. Journal of the American Statistical Association, 1987, 82, 528-540.	3.1	3,022
2	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
3	Extensive and divergent circadian gene expression in liver and heart. Nature, 2002, 417, 78-83.	27.8	1,391
4	FoxOs Are Lineage-Restricted Redundant Tumor Suppressors and Regulate Endothelial Cell Homeostasis. Cell, 2007, 128, 309-323.	28.9	952
5	Sequential Imputations and Bayesian Missing Data Problems. Journal of the American Statistical Association, 1994, 89, 278-288.	3.1	665
6	An integrated software system for analyzing ChIP-chip and ChIP-seq data. Nature Biotechnology, 2008, 26, 1293-1300.	17.5	662
7	p53 and Pten control neural and glioma stem/progenitor cell renewal and differentiation. Nature, 2008, 455, 1129-1133.	27.8	658
8	Issues in cDNA microarray analysis: quality filtering, channel normalization, models of variations and assessment of gene effects. Nucleic Acids Research, 2001, 29, 2549-2557.	14.5	494
9	SMAD4-dependent barrier constrains prostate cancer growth and metastatic progression. Nature, 2011, 470, 269-273.	27.8	462
10	FoxOs Cooperatively Regulate Diverse Pathways Governing Neural Stem Cell Homeostasis. Cell Stem Cell, 2009, 5, 540-553.	11.1	418
11	Activation of Innate Immunity Is Required for Efficient Nuclear Reprogramming. Cell, 2012, 151, 547-558.	28.9	329
12	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
13	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
14	Detection of splice junctions from paired-end RNA-seq data by SpliceMap. Nucleic Acids Research, 2010, 38, 4570-4578.	14.5	300
15	Expression Profiling of Serous Low Malignant Potential, Low-Grade, and High-Grade Tumors of the Ovary. Cancer Research, 2005, 65, 10602-10612.	0.9	298
16	Transitive functional annotation by shortest-path analysis of gene expression data. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12783-12788.	7.1	295
17	Novel mechanisms of T-cell and dendritic cell activation revealed by profiling of psoriasis on the 63,100-element oligonucleotide array. Physiological Genomics, 2003, 13, 69-78.	2.3	282
18	A genome-scale analysis of the cis-regulatory circuitry underlying sonic hedgehog-mediated patterning of the mammalian limb. Genes and Development, 2008, 22, 2651-2663.	5.9	269

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19	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
20	The Multiple-Try Method and Local Optimization in Metropolis Sampling. Journal of the American Statistical Association, 2000, 95, 121-134.	3.1	245
21	Profile Likelihood and Conditionally Parametric Models. Annals of Statistics, 1992, 20, 1768.	2.6	243
22	Convergence Rate of Sieve Estimates. Annals of Statistics, 1994, 22, 580.	2.6	243
23	A Gene Signature Predictive for Outcome in Advanced Ovarian Cancer Identifies a Survival Factor: Microfibril-Associated Glycoprotein 2. Cancer Cell, 2009, 16, 521-532.	16.8	230
24	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
25	Insights into the multistep transformation of MGUS to myeloma using microarray expression analysis. Blood, 2003, 102, 4504-4511.	1.4	212
26	mSin3A corepressor regulates diverse transcriptional networks governing normal and neoplastic growth and survival. Genes and Development, 2005, 19, 1581-1595.	5.9	201
27	Tight Clustering: A Resampling-Based Approach for Identifying Stable and Tight Patterns in Data. Biometrics, 2005, 61, 10-16.	1.4	198
28	Molecular diversity of astrocytes with implications for neurological disorders. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8384-8389.	7.1	193
29	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
30	Real-Parameter Evolutionary Monte Carlo With Applications to Bayesian Mixture Models. Journal of the American Statistical Association, 2001, 96, 653-666.	3.1	172
31	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
32	The Estimation of the Hazard Function from Randomly Censored Data by the Kernel Method. Annals of Statistics, 1983, 11, 989.	2.6	161
33	CRISPR Activation Screens Systematically Identify Factors that Drive Neuronal Fate and Reprogramming. Cell Stem Cell, 2018, 23, 758-771.e8.	11.1	161
34	Evolutionary Monte Carlo for protein folding simulations. Journal of Chemical Physics, 2001, 115, 3374-3380.	3.0	158
35	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
36	Probability Inequalities for Likelihood Ratios and Convergence Rates of Sieve MLES. Annals of Statistics, 1995, 23, 339.	2.6	157

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37	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
38	The primate-specific noncoding RNA HPAT5 regulates pluripotency during human preimplantation development and nuclear reprogramming. Nature Genetics, 2016, 48, 44-52.	21.4	153
39	Analyzing high-density oligonucleotide gene expression array data. Journal of Cellular Biochemistry, 2001, 80, 192-202.	2.6	148
40	On Ï^-Learning. Journal of the American Statistical Association, 2003, 98, 724-734.	3.1	142
41	Inferring Loss-of-Heterozygosity from Unpaired Tumors Using High-Density Oligonucleotide SNP Arrays. PLoS Computational Biology, 2006, 2, e41.	3.2	140
42	Functional annotation and network reconstruction through cross-platform integration of microarray data. Nature Biotechnology, 2005, 23, 238-243.	17.5	137
43	MetaSV: an accurate and integrative structural-variant caller for next generation sequencing. Bioinformatics, 2015, 31, 2741-2744.	4.1	131
44	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
45	Equi-energy sampler with applications in statistical inference and statistical mechanics. Annals of Statistics, 2006, 34, 1581.	2.6	129
46	RNA sequencing reveals a diverse and dynamic repertoire of the Xenopus tropicalis transcriptome over development. Genome Research, 2013, 23, 201-216.	5.5	128
47	Learning Causal Bayesian Network Structures From Experimental Data. Journal of the American Statistical Association, 2008, 103, 778-789.	3.1	123
48	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
49	Hedgehog pathway-regulated gene networks in cerebellum development and tumorigenesis. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9736-9741.	7.1	109
50	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
51	GoSurfer. Applied Bioinformatics, 2004, 3, 261-264.	1.6	101
52	Human tRNA synthetase catalytic nulls with diverse functions. Science, 2014, 345, 328-332.	12.6	101
53	DeepTACT: predicting 3D chromatin contacts via bootstrapping deep learning. Nucleic Acids Research, 2019, 47, e60-e60.	14.5	101
54	Unsupervised clustering and epigenetic classification of single cells. Nature Communications, 2018, 9, 2410.	12.8	100

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55	QuatNet: Quaternion-Based Head Pose Estimation With Multiregression Loss. IEEE Transactions on Multimedia, 2019, 21, 1035-1046.	7.2	100
56	Rejection Control and Sequential Importance Sampling. Journal of the American Statistical Association, 1998, 93, 1022-1031.	3.1	99
57	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
58	A Novel and Critical Role for Oct4 as a Regulator of the Maternal-Embryonic Transition. PLoS ONE, 2008, 3, e4109.	2.5	99
59	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
60	An ensemble approach to accurately detect somatic mutations using SomaticSeq. Genome Biology, 2015, 16, 197.	8.8	93
61	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
62	MADS: A new and improved method for analysis of differential alternative splicing by exon-tiling microarrays. Rna, 2008, 14, 1470-1479.	3.5	86
63	Recombinatoric exploration of novel folded structures: A heteropolymer-based model of protein evolutionary landscapes. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 809-814.	7.1	85
64	ChipInfo: software for extracting gene annotation and gene ontology information for microarray analysis. Nucleic Acids Research, 2003, 31, 3483-3486.	14.5	84
65	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
66	Comprehensive, integrated, and phased whole-genome analysis of the primary ENCODE cell line K562. Genome Research, 2019, 29, 472-484.	5.5	78
67	TFAP2C- and p63-Dependent Networks Sequentially Rearrange Chromatin Landscapes to Drive Human Epidermal Lineage Commitment. Cell Stem Cell, 2019, 24, 271-284.e8.	11.1	76
68	scJoint integrates atlas-scale single-cell RNA-seq and ATAC-seq data with transfer learning. Nature Biotechnology, 2022, 40, 703-710.	17.5	70
69	Integrated functional genomic analyses of Klinefelter and Turner syndromes reveal global network effects of altered X chromosome dosage. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 4864-4873.	7.1	66
70	Analysis of factorial time-course microarrays with application to a clinical study of burn injury. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9923-9928.	7.1	62
71	An Oct4â€Sall4â€Nanog network controls developmental progression in the preâ€implantation mouse embryo. Molecular Systems Biology, 2013, 9, 632.	7.2	60
72	A comparative analysis of genome-wide chromatin immunoprecipitation data for mammalian transcription factors. Nucleic Acids Research, 2006, 34, e146-e146.	14.5	59

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73	VarSim: a high-fidelity simulation and validation framework for high-throughput genome sequencing with cancer applications. Bioinformatics, 2015, 31, 1469-1471.	4.1	59
74	Simultaneous deep generative modelling and clustering of single-cell genomic data. Nature Machine Intelligence, 2021, 3, 536-544.	16.0	59
75	Role of Epidermal Growth Factor Receptor Signaling in RAS-Driven Melanoma. Molecular and Cellular Biology, 2005, 25, 4176-4188.	2.3	58
76	DC3 is a method for deconvolution and coupled clustering from bulk and single-cell genomics data. Nature Communications, 2019, 10, 4613.	12.8	57
77	Probe Selection and Expression Index Computation of Affymetrix Exon Arrays. PLoS ONE, 2006, 1, e88.	2.5	57
78	Xrare: a machine learning method jointly modeling phenotypes and genetic evidence for rare disease diagnosis. Genetics in Medicine, 2019, 21, 2126-2134.	2.4	56
79	The use of oscillatory signals in the study of genetic networks. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7063-7068.	7.1	53
80	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
81	Assessing the Conservation of Mammalian Gene Expression Using High-Density Exon Arrays. Molecular Biology and Evolution, 2007, 24, 1283-1285.	8.9	49
82	Stable 5-Hydroxymethylcytosine (5hmC) Acquisition Marks Gene Activation During Chondrogenic Differentiation. Journal of Bone and Mineral Research, 2016, 31, 524-534.	2.8	48
83	Detect and adjust for population stratification in population-based association study using genomic control markers: an application of Affymetrix GenechipÂ® Human Mapping 10K array. European Journal of Human Genetics, 2004, 12, 1001-1006.	2.8	47
84	Estimation of genotype error rate using samples with pedigree informationâ€"an application on the GeneChip Mapping 10K array. Genomics, 2004, 84, 623-630.	2.9	47
85	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
86	Optional PÃ³lya tree and Bayesian inference. Annals of Statistics, 2010, 38, .	2.6	46
87	Haplotype-resolved and integrated genome analysis of the cancer cell line HepG2. Nucleic Acids Research, 2019, 47, 3846-3861.	14.5	45
88	Sampling motifs on phylogenetic trees. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 9481-9486.	7.1	43
89	Reliable prediction of transcription factor binding sites by phylogenetic verification. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16945-16950.	7.1	43
90	Chromatin accessibility landscape and regulatory network of high-altitude hypoxia adaptation. Nature Communications, 2020, 11, 4928.	12.8	43

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91	Isolation and Transcriptional Profiling of Purified Hepatic Cells Derived from Human Embryonic Stem Cells. Stem Cells, 2008, 26, 2032-2041.	3.2	42
92	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
93	Personalized prediction of first-cycle in vitro fertilization success. Fertility and Sterility, 2013, 99, 1905-1911.	1.0	41
94	On Maximum Likelihood Estimation in Infinite Dimensional Parameter Spaces. Annals of Statistics, 1991, 19, 603.	2.6	40
95	Multivariate Density Estimation by Bayesian Sequential Partitioning. Journal of the American Statistical Association, 2013, 108, 1402-1410.	3.1	39
96	Determination of Local Statistical Significance of Patterns in Markov Sequences with Application to Promoter Element Identification. Journal of Computational Biology, 2004, 11, 1-14.	1.6	38
97	Genomeâ€Wide Mapping of DNA Hydroxymethylation in Osteoarthritic Chondrocytes. Arthritis and Rheumatology, 2015, 67, 2129-2140.	5.6	37
98	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
99	Deep phenotyping to predict live birth outcomes in in vitro fertilization. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 13570-13575.	7.1	36
100	CRISPhieRmix: a hierarchical mixture model for CRISPR pooled screens. Genome Biology, 2018, 19, 159.	8.8	36
101	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
102	Time course regulatory analysis based on paired expression and chromatin accessibility data. Genome Research, 2020, 30, 622-634.	5.5	35
103	An Application of Imputation to an Estimation Problem in Grouped Lifetime Analysis. Technometrics, 1987, 29, 23-32.	1.9	34
104	Coupling Optional PÃ³lya Trees and the Two Sample Problem. Journal of the American Statistical Association, 2011, 106, 1553-1565.	3.1	34
105	Array comparative genome hybridization for tumor classification and gene discovery in mouse models of malignant melanoma. Cancer Research, 2003, 63, 5352-6.	0.9	34
106	Computational Biology: Toward Deciphering Gene Regulatory Information in Mammalian Genomes. Biometrics, 2006, 62, 645-663.	1.4	31
107	Defining Human Embryo Phenotypes by Cohort-Specific Prognostic Factors. PLoS ONE, 2008, 3, e2562.	2.5	29
108	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

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109	A Theory for Dynamic Weighting in Monte Carlo Computation. Journal of the American Statistical Association, 2001, 96, 561-573.	3.1	26
110	Modeling Co-Expression across Species for Complex Traits: Insights to the Difference of Human and Mouse Embryonic Stem Cells. PLoS Computational Biology, 2010, 6, e1000707.	3.2	24
111	A New FACS Approach Isolates hESC Derived Endoderm Using Transcription Factors. PLoS ONE, 2011, 6, e17536.	2.5	23
112	Regulatory analysis of single cell multiome gene expression and chromatin accessibility data with scREG. Genome Biology, 2022, 23, 114.	8.8	22
113	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
114	The Analysis of ChIP-Seq Data. Methods in Enzymology, 2011, 497, 51-73.	1.0	19
115	Simultaneous Isoform Discovery and Quantification from RNA-Seq. Statistics in Biosciences, 2013, 5, 100-118.	1.2	18
116	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
117	Using high-density exon arrays to profile gene expression in closely related species. Nucleic Acids Research, 2009, 37, e90-e90.	14.5	17
118	Predicting personalized multiple birth risks after inÂvitro fertilizationâ€“double embryo transfer. Fertility and Sterility, 2012, 98, 69-76.	1.0	17
119	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
120	Modeling regulatory network topology improves genome-wide analyses of complex human traits. Nature Communications, 2021, 12, 2851.	12.8	17
121	Random Sieve Likelihood and General Regression Models. Journal of the American Statistical Association, 1999, 94, 835-846.	3.1	16
122	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
123	A method for scoring the cell type-specific impacts of noncoding variants in personal genomes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21364-21372.	7.1	16
124	Sensitive detection of tumor mutations from blood and its application to immunotherapy prognosis. Nature Communications, 2021, 12, 4172.	12.8	16
125	Relaxed simulated tempering for VLSI floorplan designs. , 1999, , .		14
126	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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127	Dissecting Early Differentially Expressed Genes in a Mixture of Differentiating Embryonic Stem Cells. PLoS Computational Biology, 2009, 5, e1000607.	3.2	13
128	Integrated Analysis of Microarray Data and Gene Function Information. OMICS A Journal of Integrative Biology, 2004, 8, 106-117.	2.0	12
129	An â€œalmost exhaustiveâ€•searchâ€based sequential permutation method for detecting epistasis in disease association studies. Genetic Epidemiology, 2010, 34, 434-443.	1.3	12
130	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
131	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
132	Sc-compReg enables the comparison of gene regulatory networks between conditions using single-cell data. Nature Communications, 2021, 12, 4763.	12.8	12
133	Modeling stochastic noise in gene regulatory systems. Quantitative Biology, 2014, 2, 1-29.	0.5	11
134	Feature Consistency Training With JPEG Compressed Images. IEEE Transactions on Circuits and Systems for Video Technology, 2020, 30, 4769-4780.	8.3	11
135	Bayesian Analysis in Applications of Hierarchical Models: Issues and Methods. Journal of Educational and Behavioral Statistics, 1996, 21, 131.	1.7	10
136	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
137	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
138	Dynamic weighting in simulations of spin systems. Physics Letters, Section A: General, Atomic and Solid State Physics, 1999, 252, 257-262.	2.1	9
139	Confnet: Predict with Confidence. , 2018, , .		8
140	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
141	Density estimation on multivariate censored data with optional Polya tree. Biostatistics, 2014, 15, 182-195.	1.5	7
142	DeepCAGE: Incorporating Transcription Factors in Genome-Wide Prediction of Chromatin Accessibility. Genomics, Proteomics and Bioinformatics, 2022, 20, 496-507.	6.9	7
143	Is the future biology Shakespearean or Newtonian?. Molecular BioSystems, 2006, 2, 411.	2.9	6
144	Evolutionary Monte Carlo Methods for Clustering. Journal of Computational and Graphical Statistics, 2007, 16, 855-876.	1.7	6

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145	Extensive and deep sequencing of the Venter/HuRef genome for developing and benchmarking genome analysis tools. Scientific Data, 2018, 5, 180261.	5.3	6
146	Density Estimation via Discrepancy Based Adaptive Sequential Partition. Advances in Neural Information Processing Systems, 2016, 29, 1091-1099.	2.8	6
147	Multiple-Sequence Information Provides Protection against Mis-Specified Potential Energy Functions in the Lattice Model of Proteins. Physical Review Letters, 2000, 85, 5242-5245.	7.8	4
148	Computational Molecular Biology. Journal of the American Statistical Association, 2000, 95, 322-326.	3.1	4
149	Computational Aspects of Optional PÃ³lya Tree. Journal of Computational and Graphical Statistics, 2016, 25, 301-320.	1.7	4
150	COSINE: non-seeding method for mapping long noisy sequences. Nucleic Acids Research, 2017, 45, e132-e132.	14.5	4
151	Molecular dynamic simulation of chaperonin-mediated protein folding. The Protein Journal, 1998, 17, 377-380.	1.1	3
152	A Sparse Transmission Disequilibrium Test for Haplotypes Based on Bradley-Terry Graphs. Human Heredity, 2012, 73, 52-61.	0.8	3
153	Correlation-Based Face Detection for Recognizing Faces in Videos. , 2018, , .		3
154	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
155	Torsional Relaxation for Biopolymers. Journal of Computational Biology, 1998, 5, 655-665.	1.6	2
156	UBIC2 â€" TOWARDS UBIQUITOUS BIO-INFORMATION COMPUTING: DATA PROTOCOLS, MIDDLEWARE, AND WEB SERVICES FOR HETEROGENEOUS BIOLOGICAL INFORMATION INTEGRATION AND RETRIEVAL. International Journal of Software Engineering and Knowledge Engineering, 2005, 15, 475-485.	0.8	1
157	Optimal discovery of a stochastic genetic network. , 2008, , .		1
158	A 41.3pJ/26.7pJ per neuron weight RBM processor for on-chip learning/inference applications. , 2016, , .		1
159	Phased Genome Sequencing Through Chromosome Sorting. Methods in Molecular Biology, 2017, 1551, 171-188.	0.9	1
160	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
161	Detecting Strong Signals in Gene Perturbation Experiments: An Adaptive Approach With Power Guarantee and FDR Control. Journal of the American Statistical Association, 2020, 115, 1747-1755.	3.1	1
162	Mini-Batch Metropolisâ€"Hastings With Reversible SGLD Proposal. Journal of the American Statistical Association, 2022, 117, 386-394.	3.1	1

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163	MIMIC: an optimization method to identify cell type-specific marker panel for cell sorting. Briefings in Bioinformatics, 2021, 22, .	6.5	1
164	Collaborative Multilabel Classification. Journal of the American Statistical Association, 2023, 118, 913-924.	3.1	1
165	Convergence rates of a partition based Bayesian multivariate density estimation method. Advances in Neural Information Processing Systems, 2017, 30, 4738-4746.	2.8	1
166	Human Upstream and Mouse Upstream: Databases of Promoter Sequences in the Human and Mouse Genomes. OMICS A Journal of Integrative Biology, 2005, 9, 220-224.	2.0	0
167	Estimation of the Loss of an Estimate. , 2006, , 491-506.		0
168	A 1.86mJ/Gb/query bit-plane payload machine learning processor in 90nm CMOS. , 2018, , .		0
169	81 INTEGRATED ANALYSIS OF GENE EXPRESSION, DNA METHYLATION AND CHROMATIN ACCESSIBILITY IN A HUMAN IPSC-TO-INDUCED-NEURON MODEL OF THE 15Q13.3 MICRODELETION. European Neuropsychopharmacology, 2019, 29, S105.	0.7	0
170	Coupled Generation. Journal of the American Statistical Association, 2022, 117, 1243-1253.	3.1	0
171	Meta-analysis of peptides to detect protein significance. Statistics and Its Interface, 2020, 13, 465-474.	0.3	0
172	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