Shoudan Liang

List of Publications by Year
in descending order

45 papers	4,198 citations	279798 23 h-index	289244 40 g-index
45 all docs	45 docs citations	45 times ranked	6701 citing authors

#	Article	IF	Citations
1	Digital Restriction Enzyme Analysis of Methylation (DREAM). Methods in Molecular Biology, 2018, 1708, 247-265.	0.9	11
2	Caloric restriction delays age-related methylation drift. Nature Communications, 2017, 8, 539.	12.8	204
3	Local sequence and sequencing depth dependent accuracy of RNA-seq reads. BMC Bioinformatics, 2017, 18, 364.	2.6	8
4	*TET2* Mutations Affect Non-CpG Island DNA Methylation at Enhancers and Transcription Factor–Binding Sites in Chronic Myelomonocytic Leukemia. Cancer Research, 2015, 75, 2833-2843.	0.9	80
5	PAND: A Distribution to Identify Functional Linkage from Networks with Preferential Attachment Property. PLoS ONE, 2015, 10, e0127968.	2.5	1
6	SOX9 Regulates Multiple Genes in Chondrocytes, Including Genes Encoding ECM Proteins, ECM Modification Enzymes, Receptors, and Transporters. PLoS ONE, 2014, 9, e107577.	2.5	86
7	BM-SNP: A Bayesian Model for SNP Calling Using High Throughput Sequencing Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 1038-1044.	3.0	3
8	TET1 is a maintenance DNA demethylase that prevents methylation spreading in differentiated cells. Nucleic Acids Research, 2014, 42, 6956-6971.	14.5	108
9	Age-related epigenetic drift in the pathogenesis of MDS and AML. Genome Research, 2014, 24, 580-591.	5.5	76
10	A role for BMP-induced homeobox gene *MIXL1* in acute myelogenous leukemia and identification of type I BMP receptor as a potential target for therapy. Oncotarget, 2014, 5, 12675-12693.	1.8	19
11	The epigenome of AML stem and progenitor cells. Epigenetics, 2013, 8, 92-104.	2.7	38
12	A Bayesian Graphical Model for ChIP-Seq Data on Histone Modifications. Journal of the American Statistical Association, 2013, 108, 69-80.	3.1	23
13	Nonparametric Bayesian Bi-Clustering for Next Generation Sequencing Count Data. Bayesian Analysis, 2013, 8, 759-780.	3.0	12
14	Modeling a Lethal Prostate Cancer Variant with Small-Cell Carcinoma Features. Clinical Cancer Research, 2012, 18, 666-677.	7.0	125
15	Conserved DNA methylation patterns in healthy blood cells and extensive changes in leukemia measured by a new quantitative technique. Epigenetics, 2012, 7, 1368-1378.	2.7	66
16	The postnatal role of Sox9 in cartilage. Journal of Bone and Mineral Research, 2012, 27, 2511-2525.	2.8	143
17	A Bayesian model for SNP discovery based on next-generation sequencing data. , 2012, 2012, 42-45.		1
18	SINE Retrotransposons Cause Epigenetic Reprogramming of Adjacent Gene Promoters. Molecular Cancer Research, 2012, 10, 1332-1342.	3.4	73

#	Article	IF	Citations
19	BM-BC: a Bayesian method of base calling for Solexa sequence data. BMC Bioinformatics, 2012, 13, S6.	2.6	5
20	Dnmt3a is essential for hematopoietic stem cell differentiation. Nature Genetics, 2012, 44, 23-31.	21.4	916
21	Aberrant DNA Methylation Is Associated with Disease Progression, Resistance to Imatinib and Shortened Survival in Chronic Myelogenous Leukemia. PLoS ONE, 2011, 6, e22110.	2.5	97
22	BM-Map: Bayesian Mapping of Multireads for Next-Generation Sequencing Data. Biometrics, 2011, 67, 1215-1224.	1.4	23
23	Neuroendocrine prostate cancer xenografts with large‐cell and small‐cell features derived from a single patient's tumor: Morphological, immunohistochemical, and gene expression profiles. Prostate, 2011, 71, 846-856.	2.3	68
24	Genome-Wide Analysis of Epigenetic Modifications. Journal of Computer Science and Technology, 2010, 25, 35-41.	1.5	1
25	Genome architecture marked by retrotransposons modulates predisposition to DNA methylation in cancer. Genome Research, 2010, 20, 1369-1382.	5.5	78
26	Widespread and tissue specific age-related DNA methylation changes in mice. Genome Research, 2010, 20, 332-340.	5.5	466
27	Identification of SOX9 Interaction Sites in the Genome of Chondrocytes. PLoS ONE, 2010, 5, e10113.	2.5	81
28	Analysis of epigenetic modifications by next generation sequencing. , 2009, 2009, 6730.		3
29	Digital Restriction Enzyme Analysis of Methylation (DREAM) by Next Generation Sequencing Yields High Resolution Maps of DNA Methylation.. Blood, 2009, 114, 567-567.	1.4	2
30	Local Network Topology in Human Protein Interaction Data Predicts Functional Association. PLoS ONE, 2009, 4, e6410.	2.5	21
31	LFA-1 Regulates CD8 + T Cell Activation and Immune Signal Network.. Blood, 2009, 114, 1641-1641.	1.4	0
32	Genomics as a Tool for Antigen Discovery in Allogeneic Stem Cell Transplantation: Identification of the Minor Antigen T4A through Donor/Patient Polymorphism Disparities. Blood, 2008, 112, 3907-3907.	1.4	8
33	Predicting protein functions from redundancies in large-scale protein interaction networks. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12579-12583.	7.1	265
34	Phase diagram of the two-chain Hubbard model. Physical Review B, 1999, 59, 2587-2590.	3.2	10
35	Charge and spin dynamics of the Hubbard chains. Physica C: Superconductivity and Its Applications, 1999, 328, 200-206.	1.2	0
36	Continuum Approximations to the Hückel Spectrum of Fullerenes. International Journal of Modern Physics B, 1997, 11, 1607-1617.	2.0	2

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37	Advantage and limitation of density matrix renormalization group method. Journal of Superconductivity and Novel Magnetism, 1995, 8, 551-554.	0.5	0
38	Correlation energy hierarchy in two dimensional Hubbard model. Journal of Physics and Chemistry of Solids, 1995, 56, 1729-1731.	4.0	1
39	Density-matrix renormalization-group studies of the alternating Hubbard model. Physical Review B, 1995, 51, 10287-10292.	3.2	19
40	Approximate diagonalization using the density matrix renormalization-group method: A two-dimensional-systems perspective. Physical Review B, 1994, 49, 9214-9217.	3.2	83
41	Effect of randomness on the Mott state. Physical Review Letters, 1993, 71, 4377-4380.	7.8	26
42	Monte Carlo calculations of the correlation functions for Heisenberg spin chains at $T=0$. Physical Review Letters, 1990, 64, 1597-1600.	7.8	96
43	Existence of Néel order at $T=0$ in the spin-1/2 antiferromagnetic Heisenberg model on a square lattice. Physical Review B, 1990, 42, 6555-6560.	3.2	79
44	Random-walk simulations of flow in Hele Shaw cells. Physical Review A, 1986, 33, 2663-2674.	2.5	97
45	Viscous flows in two dimensions. Reviews of Modern Physics, 1986, 58, 977-999.	45.6	674