

Shoudan Liang

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

4,198
citations

279701

23
h-index

289141

40
g-index

45
all docs

45
docs citations

45
times ranked

6701
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Dnmt3a is essential for hematopoietic stem cell differentiation. <i>Nature Genetics</i> , 2012, 44, 23-31. | 9.4 | 916 |
| 2 | Viscous flows in two dimensions. <i>Reviews of Modern Physics</i> , 1986, 58, 977-999. | 16.4 | 674 |
| 3 | Widespread and tissue specific age-related DNA methylation changes in mice. <i>Genome Research</i> , 2010, 20, 332-340. | 2.4 | 466 |
| 4 | Predicting protein functions from redundancies in large-scale protein interaction networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12579-12583. | 3.3 | 265 |
| 5 | Caloric restriction delays age-related methylation drift. <i>Nature Communications</i> , 2017, 8, 539. | 5.8 | 204 |
| 6 | The postnatal role of Sox9 in cartilage. <i>Journal of Bone and Mineral Research</i> , 2012, 27, 2511-2525. | 3.1 | 143 |
| 7 | Modeling a Lethal Prostate Cancer Variant with Small-Cell Carcinoma Features. <i>Clinical Cancer Research</i> , 2012, 18, 666-677. | 3.2 | 125 |
| 8 | TET1 is a maintenance DNA demethylase that prevents methylation spreading in differentiated cells. <i>Nucleic Acids Research</i> , 2014, 42, 6956-6971. | 6.5 | 108 |
| 9 | Random-walk simulations of flow in Hele Shaw cells. <i>Physical Review A</i> , 1986, 33, 2663-2674. | 1.0 | 97 |
| 10 | Aberrant DNA Methylation Is Associated with Disease Progression, Resistance to Imatinib and Shortened Survival in Chronic Myelogenous Leukemia. <i>PLoS ONE</i> , 2011, 6, e22110. | 1.1 | 97 |
| 11 | Monte Carlo calculations of the correlation functions for Heisenberg spin chains at $T=0$. <i>Physical Review Letters</i> , 1990, 64, 1597-1600. | 2.9 | 96 |
| 12 | SOX9 Regulates Multiple Genes in Chondrocytes, Including Genes Encoding ECM Proteins, ECM Modification Enzymes, Receptors, and Transporters. <i>PLoS ONE</i> , 2014, 9, e107577. | 1.1 | 86 |
| 13 | Approximate diagonalization using the density matrix renormalization-group method: A two-dimensional-systems perspective. <i>Physical Review B</i> , 1994, 49, 9214-9217. | 1.1 | 83 |
| 14 | Identification of SOX9 Interaction Sites in the Genome of Chondrocytes. <i>PLoS ONE</i> , 2010, 5, e10113. | 1.1 | 81 |
| 15 | TET2 Mutations Affect Non-CpG Island DNA Methylation at Enhancers and Transcription Factor Binding Sites in Chronic Myelomonocytic Leukemia. <i>Cancer Research</i> , 2015, 75, 2833-2843. | 0.4 | 80 |
| 16 | Existence of Néel order at $T=0$ in the spin-1/2 antiferromagnetic Heisenberg model on a square lattice. <i>Physical Review B</i> , 1990, 42, 6555-6560. | 1.1 | 79 |
| 17 | Genome architecture marked by retrotransposons modulates predisposition to DNA methylation in cancer. <i>Genome Research</i> , 2010, 20, 1369-1382. | 2.4 | 78 |
| 18 | Age-related epigenetic drift in the pathogenesis of MDS and AML. <i>Genome Research</i> , 2014, 24, 580-591. | 2.4 | 76 |

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|----|---|-----|-----------|
| 19 | SINE Retrotransposons Cause Epigenetic Reprogramming of Adjacent Gene Promoters. <i>Molecular Cancer Research</i> , 2012, 10, 1332-1342. | 1.5 | 73 |
| 20 | Neuroendocrine prostate cancer xenografts with largeâ€cell and smallâ€cell features derived from a single patient's tumor: Morphological, immunohistochemical, and gene expression profiles. <i>Prostate</i> , 2011, 71, 846-856. | 1.2 | 68 |
| 21 | Conserved DNA methylation patterns in healthy blood cells and extensive changes in leukemia measured by a new quantitative technique. <i>Epigenetics</i> , 2012, 7, 1368-1378. | 1.3 | 66 |
| 22 | The epigenome of AML stem and progenitor cells. <i>Epigenetics</i> , 2013, 8, 92-104. | 1.3 | 38 |
| 23 | Effect of randomness on the Mott state. <i>Physical Review Letters</i> , 1993, 71, 4377-4380. | 2.9 | 26 |
| 24 | BM-Map: Bayesian Mapping of Multireads for Next-Generation Sequencing Data. <i>Biometrics</i> , 2011, 67, 1215-1224. | 0.8 | 23 |
| 25 | A Bayesian Graphical Model for ChIP-Seq Data on Histone Modifications. <i>Journal of the American Statistical Association</i> , 2013, 108, 69-80. | 1.8 | 23 |
| 26 | Local Network Topology in Human Protein Interaction Data Predicts Functional Association. <i>PLoS ONE</i> , 2009, 4, e6410. | 1.1 | 21 |
| 27 | Density-matrix renormalization-group studies of the alternating Hubbard model. <i>Physical Review B</i> , 1995, 51, 10287-10292. | 1.1 | 19 |
| 28 | A role for BMP-induced homeobox gene <i>MIXL1</i> in acute myelogenous leukemia and identification of type I BMP receptor as a potential target for therapy. <i>Oncotarget</i> , 2014, 5, 12675-12693. | 0.8 | 19 |
| 29 | Nonparametric Bayesian Bi-Clustering for Next Generation Sequencing Count Data. <i>Bayesian Analysis</i> , 2013, 8, 759-780. | 1.6 | 12 |
| 30 | Digital Restriction Enzyme Analysis of Methylation (DREAM). <i>Methods in Molecular Biology</i> , 2018, 1708, 247-265. | 0.4 | 11 |
| 31 | Phase diagram of the two-chain Hubbard model. <i>Physical Review B</i> , 1999, 59, 2587-2590. | 1.1 | 10 |
| 32 | Local sequence and sequencing depth dependent accuracy of RNA-seq reads. <i>BMC Bioinformatics</i> , 2017, 18, 364. | 1.2 | 8 |
| 33 | Genomics as a Tool for Antigen Discovery in Allogeneic Stem Cell Transplantation: Identification of the Minor Antigen T4A through Donor/Patient Polymorphism Disparities. <i>Blood</i> , 2008, 112, 3907-3907. | 0.6 | 8 |
| 34 | BM-BC: a Bayesian method of base calling for Solexa sequence data. <i>BMC Bioinformatics</i> , 2012, 13, S6. | 1.2 | 5 |
| 35 | Analysis of epigenetic modifications by next generation sequencing. , 2009, 2009, 6730. | | 3 |
| 36 | BM-SNP: A Bayesian Model for SNP Calling Using High Throughput Sequencing Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 1038-1044. | 1.9 | 3 |

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|----|--|-----|-----------|
| 37 | Continuum Approximations to the Hückel Spectrum of Fullerenes. International Journal of Modern Physics B, 1997, 11, 1607-1617. | 1.0 | 2 |
| 38 | Digital Restriction Enzyme Analysis of Methylation (DREAM) by Next Generation Sequencing Yields High Resolution Maps of DNA Methylation.. Blood, 2009, 114, 567-567. | 0.6 | 2 |
| 39 | Correlation energy hierarchy in two dimensional Hubbard model. Journal of Physics and Chemistry of Solids, 1995, 56, 1729-1731. | 1.9 | 1 |
| 40 | Genome-Wide Analysis of Epigenetic Modifications. Journal of Computer Science and Technology, 2010, 25, 35-41. | 0.9 | 1 |
| 41 | A Bayesian model for SNP discovery based on next-generation sequencing data. , 2012, 2012, 42-45. | | 1 |
| 42 | PAND: A Distribution to Identify Functional Linkage from Networks with Preferential Attachment Property. PLoS ONE, 2015, 10, e0127968. | 1.1 | 1 |
| 43 | Advantage and limitation of density matrix renormalization group method. Journal of Superconductivity and Novel Magnetism, 1995, 8, 551-554. | 0.5 | 0 |
| 44 | Charge and spin dynamics of the Hubbard chains. Physica C: Superconductivity and Its Applications, 1999, 328, 200-206. | 0.6 | 0 |
| 45 | LFA-1 Regulates CD8 + T Cell Activation and Immune Signal Network.. Blood, 2009, 114, 1641-1641. | 0.6 | 0 |