Jian

List of Publications by Year
in descending order

81 papers	10,892 citations	87401 40 h-index	66518 82 g-index
88 all docs	88 docs citations	88 times ranked	21379 citing authors

#	ARTICLE	IF	CITATIONS
1	Multiscale and integrative single-cell Hi-C analysis with Higashi. Nature Biotechnology, 2022, 40, 254-261.	9.4	75
2	Selective clonal persistence of human retroviruses in vivo: Radial chromatin organization, integration site, and host transcription. Science Advances, 2022, 8, eabm6210.	4.7	15
3	SPIN reveals genome-wide landscape of nuclear compartmentalization. Genome Biology, 2021, 22, 36.	3.8	61
4	Assessing the contribution of tumor mutational phenotypes to cancer progression risk. PLoS Computational Biology, 2021, 17, e1008777.	1.5	2
5	The 3D Genome Structure of Single Cells. Annual Review of Biomedical Data Science, 2021, 4, 21-41.	2.8	38
6	TSA-seq reveals a largely conserved genome organization relative to nuclear speckles with small position changes tightly correlated with gene expression changes. Genome Research, 2021, 31, 251-264.	2.4	53
7	MicroRNAâ€210 Promotes Bile Acidâ€"Induced Cholestatic Liver Injury by Targeting Mixedâ€Lineage Leukemiaâ€4 Methyltransferase in Mice. Hepatology, 2020, 71, 2118-2134.	3.6	21
8	LncRNA-mediated regulation of <i>SOX9</i> expression in basal subtype breast cancer cells. Rna, 2020, 26, 175-185.	1.6	16
9	MOCHI enables discovery of heterogeneous interactome modules in 3D nucleome. Genome Research, 2020, 30, 227-238.	2.4	10
10	Neural Network Deconvolution Method for Resolving Pathway-Level Progression of Tumor Clonal Expression Programs With Application to Breast Cancer Brain Metastases. Frontiers in Physiology, 2020, 11, 1055.	1.3	3
11	Antagonism between splicing and microprocessor complex dictates the serum-induced processing of lnc-MIRHG for efficient cell cycle reentry. Rna, 2020, 26, 1603-1620.	1.6	12
12	Intestinal FGF15/19 physiologically repress hepatic lipogenesisÂin the late fed-state by activating SHP and DNMT3A. Nature Communications, 2020, 11, 5969.	5.8	35
13	CHANGE-seq reveals genetic and epigenetic effects on CRISPRâ€"Cas9 genome-wide activity. Nature Biotechnology, 2020, 38, 1317-1327.	9.4	149
14	MATCHA: Probing Multi-way Chromatin Interaction with Hypergraph Representation Learning. Cell Systems, 2020, 10, 397-407.e5.	2.9	18
15	Fasting-induced FGF21 signaling activates hepatic autophagy and lipid degradation via JMJD3 histone demethylase. Nature Communications, 2020, 11, 807.	5.8	127
16	Predicting enhancerâ€promoter interaction from genomic sequence with deep neural networks. Quantitative Biology, 2019, 7, 122-137.	0.3	84
17	The human body at cellular resolution: the NIH Human Biomolecular Atlas Program. Nature, 2019, 574, 187-192.	13.7	393
18	Revealing Hi-C subcompartments by imputing inter-chromosomal chromatin interactions. Nature Communications, 2019, 10, 5069.	5.8	102

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19	Comparing 3D Genome Organization in Multiple Species Using Phylo-HMRF. Cell Systems, 2019, 8, 494-505.e14.	2.9	27
20	Comparative Analysis of Brain and Fat Body Gene Splicing Patterns in the Honey Bee, *Apis mellifera*. G3: Genes, Genomes, Genetics, 2019, 9, 1055-1063.	0.8	5
21	Replication Timing Becomes Intertwined with 3D Genome Organization. Cell, 2019, 176, 681-684.	13.5	9
22	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. Genome Research, 2019, 29, 576-589.	2.4	39
23	Low-input and multiplexed microfluidic assay reveals epigenomic variation across cerebellum and prefrontal cortex. Science Advances, 2018, 4, eaar8187.	4.7	35
24	Toward Recovering Allele-specific Cancer Genome Graphs. Journal of Computational Biology, 2018, 25, 624-636.	0.8	4
25	AhR and SHP regulate phosphatidylcholine and S-adenosylmethionine levels in the one-carbon cycle. Nature Communications, 2018, 9, 540.	5.8	41
26	Fasting-induced JMJD3 histone demethylase epigenetically activates mitochondrial fatty acid Î²-oxidation. Journal of Clinical Investigation, 2018, 128, 3144-3159.	3.9	52
27	A natural antisense lncRNA controls breast cancer progression by promoting tumor suppressor gene mRNA stability. PLoS Genetics, 2018, 14, e1007802.	1.5	135
28	Correlating cellular features with gene expression using CCA. , 2018, , .		7
29	Continuous-Trait Probabilistic Model for Comparing Multi-species Functional Genomic Data. Cell Systems, 2018, 7, 208-218.e11.	2.9	20
30	Mapping 3D genome organization relative to nuclear compartments using TSA-Seq as a cytological ruler. Journal of Cell Biology, 2018, 217, 4025-4048.	2.3	275
31	CRISPR/Cas9-mediated knock-in of an optimized TetO repeat for live cell imaging of endogenous loci. Nucleic Acids Research, 2018, 46, e100-e100.	6.5	45
32	A postprandial <scp>FGF</scp> 19â€•<scp>SHP</scp> â€•<scp>LSD</scp> 1 regulatory axisÂmediates epigenetic repression of hepaticÂautophagy. EMBO Journal, 2017, 36, 1755-1769.	3.5	54
33	PSIP1/p75 promotes tumorigenicity in breast cancer cells by promoting the transcription of cell cycle genes. Carcinogenesis, 2017, 38, 966-975.	1.3	25
34	Reconstruction and evolutionary history of eutherian chromosomes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5379-E5388.	3.3	94
35	The 4D nucleome project. Nature, 2017, 549, 219-226.	13.7	579
36	Privacy Challenges of Genomic Big Data. Advances in Experimental Medicine and Biology, 2017, 1028, 139-148.	0.8	11

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37	ADAR2 regulates RNA stability by modifying access of decay-promoting RNA-binding proteins. Nucleic Acids Research, 2017, 45, gkw1304.	6.5	34
38	Identifying gene regulatory network rewiring using latent differential graphical models. Nucleic Acids Research, 2016, 44, e140-e140.	6.5	56
39	Allele-Specific Quantification of Structural Variations in Cancer Genomes. Cell Systems, 2016, 3, 21-34.	2.9	41
40	Reconstructing ancestral gene orders with duplications guided by synteny level genome reconstruction. BMC Bioinformatics, 2016, 17, 414.	1.2	2
41	A Rewritable, Random-Access DNA-Based Storage System. Scientific Reports, 2015, 5, 14138.	1.6	214
42	Liver ChIP-seq analysis in FGF19-treated mice reveals SHP as a global transcriptional partner of SREBP-2. Genome Biology, 2015, 16, 268.	3.8	33
43	The Genome 10K Project: A Way Forward. Annual Review of Animal Biosciences, 2015, 3, 57-111.	3.6	294
44	Single-molecule analysis reveals widespread structural variation in multiple myeloma. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7689-7694.	3.3	43
45	Cross-species DNA copy number analyses identifies multiple 1q21-q23 subtype-specific driver genes for breast cancer. Breast Cancer Research and Treatment, 2015, 152, 347-356.	1.1	38
46	Biomedical Informatics and Computational Biology for High-Throughput Data Analysis. Scientific World Journal, The, 2014, 2014, 1-2.	0.8	4
47	Tracing the Evolution of Lineage-Specific Transcription Factor Binding Sites in a Birth-Death Framework. PLoS Computational Biology, 2014, 10, e1003771.	1.5	25
48	Alignathon: a competitive assessment of whole-genome alignment methods. Genome Research, 2014, 24, 2077-2089.	2.4	102
49	Neuromolecular responses to social challenge: Common mechanisms across mouse, stickleback fish, and honey bee. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17929-17934.	3.3	141
50	UnSplicer: mapping spliced RNA-seq reads in compact genomes and filtering noisy splicing. Nucleic Acids Research, 2014, 42, e25-e25.	6.5	3
51	Finding the missing honey bee genes: lessons learned from a genome upgrade. BMC Genomics, 2014, 15, 86.	1.2	375
52	A network-assisted co-clustering algorithm to discover cancer subtypes based on gene expression. BMC Bioinformatics, 2014, 15, 37.	1.2	68
53	BLESS: Bloom filter-based error correction solution for high-throughput sequencing reads. Bioinformatics, 2014, 30, 1354-1362.	1.8	113
54	PSAR-Align: improving multiple sequence alignment using probabilistic sampling. Bioinformatics, 2014, 30, 1010-1012.	1.8	16

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55	Transcriptional regulation of autophagy by an FXRâ€"CREB axis. Nature, 2014, 516, 108-111.	13.7	342
56	DawnRank: discovering personalized driver genes in cancer. Genome Medicine, 2014, 6, 56.	3.6	207
57	A community effort to assess and improve drug sensitivity prediction algorithms. Nature Biotechnology, 2014, 32, 1202-1212.	9.4	653
58	Genome-wide adaptive complexes to underground stresses in blind mole rats Spalax. Nature Communications, 2014, 5, 3966.	5.8	124
59	Personalized Ovarian Cancer Disease Surveillance and Detection of Candidate Therapeutic Drug Target in Circulating Tumor DNA. Neoplasia, 2014, 16, 97-W29.	2.3	45
60	Search for chromosome rearrangements: New approaches toward discovery of novel translocations in head and neck squamous cell carcinoma. Head and Neck, 2013, 35, 831-835.	0.9	2
61	TrueSight: a new algorithm for splice junction detection using RNA-seq. Nucleic Acids Research, 2013, 41, e51-e51.	6.5	31
62	Draft genome sequence of the Tibetan antelope. Nature Communications, 2013, 4, 1858.	5.8	229
63	RNA interference knockdown of <i>DNA methyl-transferase 3</i> affects gene alternative splicing in the honey bee. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12750-12755.	3.3	237
64	Reference-assisted chromosome assembly. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1785-1790.	3.3	124
65	Ancient DNA Analysis of Mid-Holocene Individuals from the Northwest Coast of North America Reveals Different Evolutionary Paths for Mitogenomes. PLoS ONE, 2013, 8, e66948.	1.1	56
66	Analyses of pig genomes provide insight into porcine demography and evolution. Nature, 2012, 491, 393-398.	13.7	1,190
67	TIGER: tiled iterative genome assembler. BMC Bioinformatics, 2012, 13, S18.	1.2	8
68	The yak genome and adaptation to life at high altitude. Nature Genetics, 2012, 44, 946-949.	9.4	708
69	Reconstructing the History of Large-Scale Genomic Changes: Biological Questions and Computational Challenges. Journal of Computational Biology, 2011, 18, 879-893.	0.8	4
70	Cactus Graphs for Genome Comparisons. Journal of Computational Biology, 2011, 18, 469-481.	0.8	93
71	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	13.7	541
72	FusionHunter: identifying fusion transcripts in cancer using paired-end RNA-seq. Bioinformatics, 2011, 27, 1708-1710.	1.8	73

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73	PSAR: measuring multiple sequence alignment reliability by probabilistic sampling. Nucleic Acids Research, 2011, 39, 6359-6368.	6.5	35
74	Greedy Selection of Species for Ancestral State Reconstruction on Phylogenies: Elimination Is Better than Insertion. PLoS ONE, 2010, 5, e8985.	1.1	9
75	Modern BLAST Programs. , 2010, , 3-19.		2
76	The infinite sites model of genome evolution. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14254-14261.	3.3	79
77	DUPCAR: Reconstructing Contiguous Ancestral Regions with Duplications. Journal of Computational Biology, 2008, 15, 1007-1027.	0.8	51
78	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	6.0	1,283
79	Reconstructing contiguous regions of an ancestral genome. Genome Research, 2006, 16, 1557-1565.	2.4	246
80	Mulan: Multiple-sequence local alignment and visualization for studying function and evolution. Genome Research, 2005, 15, 184-194.	2.4	218
81	Rapid development of bioinformatics education in China. Journal of Biological Education, 2003, 37, 75-78.	0.8	1