Jian

List of Publications by Year
in descending order

81 papers	10,892 citations	76326 40 h-index	58581 82 g-index
88 all docs	88 docs citations	88 times ranked	19103 citing authors

#	Article	IF	Citations
1	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	12.6	1,283
2	Analyses of pig genomes provide insight into porcine demography and evolution. Nature, 2012, 491, 393-398.	27.8	1,190
3	The yak genome and adaptation to life at high altitude. Nature Genetics, 2012, 44, 946-949.	21.4	708
4	A community effort to assess and improve drug sensitivity prediction algorithms. Nature Biotechnology, 2014, 32, 1202-1212.	17.5	653
5	The 4D nucleome project. Nature, 2017, 549, 219-226.	27.8	579
6	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	27.8	541
7	The human body at cellular resolution: the NIH Human Biomolecular Atlas Program. Nature, 2019, 574, 187-192.	27.8	393
8	Finding the missing honey bee genes: lessons learned from a genome upgrade. BMC Genomics, 2014, 15, 86.	2.8	375
9	Transcriptional regulation of autophagy by an FXR–CREB axis. Nature, 2014, 516, 108-111.	27.8	342
10	The Genome 10K Project: A Way Forward. Annual Review of Animal Biosciences, 2015, 3, 57-111.	7.4	294
11	Mapping 3D genome organization relative to nuclear compartments using TSA-Seq as a cytological ruler. Journal of Cell Biology, 2018, 217, 4025-4048.	5.2	275
12	Reconstructing contiguous regions of an ancestral genome. Genome Research, 2006, 16, 1557-1565.	5.5	246
13	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.	7.1	237
14	Draft genome sequence of the Tibetan antelope. Nature Communications, 2013, 4, 1858.	12.8	229
15	Mulan: Multiple-sequence local alignment and visualization for studying function and evolution. Genome Research, 2005, 15, 184-194.	5.5	218
16	A Rewritable, Random-Access DNA-Based Storage System. Scientific Reports, 2015, 5, 14138.	3.3	214
17	DawnRank: discovering personalized driver genes in cancer. Genome Medicine, 2014, 6, 56.	8.2	207
18	CHANGE-seq reveals genetic and epigenetic effects on CRISPR–Cas9 genome-wide activity. Nature Biotechnology, 2020, 38, 1317-1327.	17.5	149

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19	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.	7.1	141
20	A natural antisense lncRNA controls breast cancer progression by promoting tumor suppressor gene mRNA stability. PLoS Genetics, 2018, 14, e1007802.	3.5	135
21	Fasting-induced FGF21 signaling activates hepatic autophagy and lipid degradation via JMJD3 histone demethylase. Nature Communications, 2020, 11, 807.	12.8	127
22	Reference-assisted chromosome assembly. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1785-1790.	7.1	124
23	Genome-wide adaptive complexes to underground stresses in blind mole rats Spalax. Nature Communications, 2014, 5, 3966.	12.8	124
24	BLESS: Bloom filter-based error correction solution for high-throughput sequencing reads. Bioinformatics, 2014, 30, 1354-1362.	4.1	113
25	Alignathon: a competitive assessment of whole-genome alignment methods. Genome Research, 2014, 24, 2077-2089.	5.5	102
26	Revealing Hi-C subcompartments by imputing inter-chromosomal chromatin interactions. Nature Communications, 2019, 10, 5069.	12.8	102
27	Reconstruction and evolutionary history of eutherian chromosomes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5379-E5388.	7.1	94
28	Cactus Graphs for Genome Comparisons. Journal of Computational Biology, 2011, 18, 469-481.	1.6	93
29	Predicting enhancer€promoter interaction from genomic sequence with deep neural networks. Quantitative Biology, 2019, 7, 122-137.	0.5	84
30	The infinite sites model of genome evolution. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14254-14261.	7.1	79
31	Multiscale and integrative single-cell Hi-C analysis with Higashi. Nature Biotechnology, 2022, 40, 254-261.	17.5	75
32	FusionHunter: identifying fusion transcripts in cancer using paired-end RNA-seq. Bioinformatics, 2011, 27, 1708-1710.	4.1	73
33	A network-assisted co-clustering algorithm to discover cancer subtypes based on gene expression. BMC Bioinformatics, 2014, 15, 37.	2.6	68
34	SPIN reveals genome-wide landscape of nuclear compartmentalization. Genome Biology, 2021, 22, 36.	8.8	61
35	Identifying gene regulatory network rewiring using latent differential graphical models. Nucleic Acids Research, 2016, 44, e140-e140.	14.5	56
36	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.	2.5	56

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37	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.	7.8	54
38	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.	5.5	53
39	Fasting-induced JMJD3 histone demethylase epigenetically activates mitochondrial fatty acid Î²-oxidation. Journal of Clinical Investigation, 2018, 128, 3144-3159.	8.2	52
40	DUPCAR: Reconstructing Contiguous Ancestral Regions with Duplications. Journal of Computational Biology, 2008, 15, 1007-1027.	1.6	51
41	Personalized Ovarian Cancer Disease Surveillance and Detection of Candidate Therapeutic Drug Target in Circulating Tumor DNA. Neoplasia, 2014, 16, 97-W29.	5.3	45
42	CRISPR/Cas9-mediated knock-in of an optimized TetO repeat for live cell imaging of endogenous loci. Nucleic Acids Research, 2018, 46, e100-e100.	14.5	45
43	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.	7.1	43
44	Allele-Specific Quantification of Structural Variations in Cancer Genomes. Cell Systems, 2016, 3, 21-34.	6.2	41
45	AhR and SHP regulate phosphatidylcholine and S-adenosylmethionine levels in the one-carbon cycle. Nature Communications, 2018, 9, 540.	12.8	41
46	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. Genome Research, 2019, 29, 576-589.	5.5	39
47	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.	2.5	38
48	The 3D Genome Structure of Single Cells. Annual Review of Biomedical Data Science, 2021, 4, 21-41.	6.5	38
49	PSAR: measuring multiple sequence alignment reliability by probabilistic sampling. Nucleic Acids Research, 2011, 39, 6359-6368.	14.5	35
50	Low-input and multiplexed microfluidic assay reveals epigenomic variation across cerebellum and prefrontal cortex. Science Advances, 2018, 4, eaar8187.	10.3	35
51	Intestinal FGF15/19 physiologically repress hepatic lipogenesisÂin the late fed-state by activating SHP and DNMT3A. Nature Communications, 2020, 11, 5969.	12.8	35
52	ADAR2 regulates RNA stability by modifying access of decay-promoting RNA-binding proteins. Nucleic Acids Research, 2017, 45, gkw1304.	14.5	34
53	Liver ChIP-seq analysis in FGF19-treated mice reveals SHP as a global transcriptional partner of SREBP-2. Genome Biology, 2015, 16, 268.	8.8	33
54	TrueSight: a new algorithm for splice junction detection using RNA-seq. Nucleic Acids Research, 2013, 41, e51-e51.	14.5	31

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55	Comparing 3D Genome Organization in Multiple Species Using Phylo-HMRF. Cell Systems, 2019, 8, 494-505.e14.	6.2	27
56	Tracing the Evolution of Lineage-Specific Transcription Factor Binding Sites in a Birth-Death Framework. PLoS Computational Biology, 2014, 10, e1003771.	3.2	25
57	PSIP1/p75 promotes tumorigenicity in breast cancer cells by promoting the transcription of cell cycle genes. Carcinogenesis, 2017, 38, 966-975.	2.8	25
58	MicroRNAâ€210 Promotes Bile Acidâ€"Induced Cholestatic Liver Injury by Targeting Mixedâ€Lineage Leukemiaâ€4 Methyltransferase in Mice. Hepatology, 2020, 71, 2118-2134.	7.3	21
59	Continuous-Trait Probabilistic Model for Comparing Multi-species Functional Genomic Data. Cell Systems, 2018, 7, 208-218.e11.	6.2	20
60	MATCHA: Probing Multi-way Chromatin Interaction with Hypergraph Representation Learning. Cell Systems, 2020, 10, 397-407.e5.	6.2	18
61	PSAR-Align: improving multiple sequence alignment using probabilistic sampling. Bioinformatics, 2014, 30, 1010-1012.	4.1	16
62	LncRNA-mediated regulation of <i>SOX9</i> expression in basal subtype breast cancer cells. Rna, 2020, 26, 175-185.	3.5	16
63	Selective clonal persistence of human retroviruses in vivo: Radial chromatin organization, integration site, and host transcription. Science Advances, 2022, 8, eabm6210.	10.3	15
64	Antagonism between splicing and microprocessor complex dictates the serum-induced processing of lnc-MIRHG for efficient cell cycle reentry. Rna, 2020, 26, 1603-1620.	3.5	12
65	Privacy Challenges of Genomic Big Data. Advances in Experimental Medicine and Biology, 2017, 1028, 139-148.	1.6	11
66	MOCHI enables discovery of heterogeneous interactome modules in 3D nucleome. Genome Research, 2020, 30, 227-238.	5.5	10
67	Greedy Selection of Species for Ancestral State Reconstruction on Phylogenies: Elimination Is Better than Insertion. PLoS ONE, 2010, 5, e8985.	2.5	9
68	Replication Timing Becomes Intertwined with 3D Genome Organization. Cell, 2019, 176, 681-684.	28.9	9
69	TIGER: tiled iterative genome assembler. BMC Bioinformatics, 2012, 13, S18.	2.6	8
70	Correlating cellular features with gene expression using CCA. , 2018, , .		7
71	Comparative Analysis of Brain and Fat Body Gene Splicing Patterns in the Honey Bee, <i>Apis mellifera</i>. G3: Genes, Genomes, Genetics, 2019, 9, 1055-1063.	1.8	5
72	Reconstructing the History of Large-Scale Genomic Changes: Biological Questions and Computational Challenges. Journal of Computational Biology, 2011, 18, 879-893.	1.6	4

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73	Biomedical Informatics and Computational Biology for High-Throughput Data Analysis. Scientific World Journal, The, 2014, 2014, 1-2.	2.1	4
74	Toward Recovering Allele-specific Cancer Genome Graphs. Journal of Computational Biology, 2018, 25, 624-636.	1.6	4
75	UnSplicer: mapping spliced RNA-seq reads in compact genomes and filtering noisy splicing. Nucleic Acids Research, 2014, 42, e25-e25.	14.5	3
76	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.	2.8	3
77	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.	2.0	2
78	Reconstructing ancestral gene orders with duplications guided by synteny level genome reconstruction. BMC Bioinformatics, 2016, 17, 414.	2.6	2
79	Assessing the contribution of tumor mutational phenotypes to cancer progression risk. PLoS Computational Biology, 2021, 17, e1008777.	3.2	2
80	Modern BLAST Programs. , 2010, , 3-19.		2
81	Rapid development of bioinformatics education in China. Journal of Biological Education, 2003, 37, 75-78.	1.5	1