

# Jian

## List of Publications by Year in descending order

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Version: 2024-02-01

81  
papers

10,892  
citations

76196

40  
h-index

58464

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. <i>Science</i> , 2007, 316, 222-234.	6.0	1,283
2	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	13.7	1,190
3	The yak genome and adaptation to life at high altitude. <i>Nature Genetics</i> , 2012, 44, 946-949.	9.4	708
4	A community effort to assess and improve drug sensitivity prediction algorithms. <i>Nature Biotechnology</i> , 2014, 32, 1202-1212.	9.4	653
5	The 4D nucleome project. <i>Nature</i> , 2017, 549, 219-226.	13.7	579
6	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	13.7	541
7	The human body at cellular resolution: the NIH Human Biomolecular Atlas Program. <i>Nature</i> , 2019, 574, 187-192.	13.7	393
8	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014, 15, 86.	1.2	375
9	Transcriptional regulation of autophagy by an FXR-CREB axis. <i>Nature</i> , 2014, 516, 108-111.	13.7	342
10	The Genome 10K Project: A Way Forward. <i>Annual Review of Animal Biosciences</i> , 2015, 3, 57-111.	3.6	294
11	Mapping 3D genome organization relative to nuclear compartments using TSA-Seq as a cytological ruler. <i>Journal of Cell Biology</i> , 2018, 217, 4025-4048.	2.3	275
12	Reconstructing contiguous regions of an ancestral genome. <i>Genome Research</i> , 2006, 16, 1557-1565.	2.4	246
13	RNA interference knockdown of <i>DNA methyl-transferase 3</i> affects gene alternative splicing in the honey bee. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12750-12755.	3.3	237
14	Draft genome sequence of the Tibetan antelope. <i>Nature Communications</i> , 2013, 4, 1858.	5.8	229
15	Mulan: Multiple-sequence local alignment and visualization for studying function and evolution. <i>Genome Research</i> , 2005, 15, 184-194.	2.4	218
16	A Rewritable, Random-Access DNA-Based Storage System. <i>Scientific Reports</i> , 2015, 5, 14138.	1.6	214
17	DawnRank: discovering personalized driver genes in cancer. <i>Genome Medicine</i> , 2014, 6, 56.	3.6	207
18	CHANGE-seq reveals genetic and epigenetic effects on CRISPR-Cas9 genome-wide activity. <i>Nature Biotechnology</i> , 2020, 38, 1317-1327.	9.4	149

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19	Neuromolecular responses to social challenge: Common mechanisms across mouse, stickleback fish, and honey bee. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17929-17934.	3.3	141
20	A natural antisense lncRNA controls breast cancer progression by promoting tumor suppressor gene mRNA stability. <i>PLoS Genetics</i> , 2018, 14, e1007802.	1.5	135
21	Fasting-induced FGF21 signaling activates hepatic autophagy and lipid degradation via JMJD3 histone demethylase. <i>Nature Communications</i> , 2020, 11, 807.	5.8	127
22	Reference-assisted chromosome assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1785-1790.	3.3	124
23	Genome-wide adaptive complexes to underground stresses in blind mole rats <i>Spalax</i> . <i>Nature Communications</i> , 2014, 5, 3966.	5.8	124
24	BLESS: Bloom filter-based error correction solution for high-throughput sequencing reads. <i>Bioinformatics</i> , 2014, 30, 1354-1362.	1.8	113
25	Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , 2014, 24, 2077-2089.	2.4	102
26	Revealing Hi-C subcompartments by imputing inter-chromosomal chromatin interactions. <i>Nature Communications</i> , 2019, 10, 5069.	5.8	102
27	Reconstruction and evolutionary history of eutherian chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5379-E5388.	3.3	94
28	Cactus Graphs for Genome Comparisons. <i>Journal of Computational Biology</i> , 2011, 18, 469-481.	0.8	93
29	Predicting enhancer-promoter interaction from genomic sequence with deep neural networks. <i>Quantitative Biology</i> , 2019, 7, 122-137.	0.3	84
30	The infinite sites model of genome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14254-14261.	3.3	79
31	Multiscale and integrative single-cell Hi-C analysis with Higashi. <i>Nature Biotechnology</i> , 2022, 40, 254-261.	9.4	75
32	FusionHunter: identifying fusion transcripts in cancer using paired-end RNA-seq. <i>Bioinformatics</i> , 2011, 27, 1708-1710.	1.8	73
33	A network-assisted co-clustering algorithm to discover cancer subtypes based on gene expression. <i>BMC Bioinformatics</i> , 2014, 15, 37.	1.2	68
34	SPIN reveals genome-wide landscape of nuclear compartmentalization. <i>Genome Biology</i> , 2021, 22, 36.	3.8	61
35	Identifying gene regulatory network rewiring using latent differential graphical models. <i>Nucleic Acids Research</i> , 2016, 44, e140-e140.	6.5	56
36	Ancient DNA Analysis of Mid-Holocene Individuals from the Northwest Coast of North America Reveals Different Evolutionary Paths for Mitogenomes. <i>PLoS ONE</i> , 2013, 8, e66948.	1.1	56

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37	A postprandial <sc>FGF</sc> 19â€™<sc>SHP</sc> â€™<sc>LSD</sc> 1 regulatory axisÂmediates epigenetic repression of hepaticÂautophagy. EMBO Journal, 2017, 36, 1755-1769.	3.5	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.	2.4	53
39	Fasting-induced JMJD3 histone demethylase epigenetically activates mitochondrial fatty acid ð²-oxidation. Journal of Clinical Investigation, 2018, 128, 3144-3159.	3.9	52
40	DUPCAR: Reconstructing Contiguous Ancestral Regions with Duplications. Journal of Computational Biology, 2008, 15, 1007-1027.	0.8	51
41	Personalized Ovarian Cancer Disease Surveillance and Detection of Candidate Therapeutic Drug Target in Circulating Tumor DNA. Neoplasia, 2014, 16, 97-W29.	2.3	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.	6.5	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.	3.3	43
44	Allele-Specific Quantification of Structural Variations in Cancer Genomes. Cell Systems, 2016, 3, 21-34.	2.9	41
45	AhR and SHP regulate phosphatidylcholine and S-adenosylmethionine levels in the one-carbon cycle. Nature Communications, 2018, 9, 540.	5.8	41
46	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. Genome Research, 2019, 29, 576-589.	2.4	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.	1.1	38
48	The 3D Genome Structure of Single Cells. Annual Review of Biomedical Data Science, 2021, 4, 21-41.	2.8	38
49	PSAR: measuring multiple sequence alignment reliability by probabilistic sampling. Nucleic Acids Research, 2011, 39, 6359-6368.	6.5	35
50	Low-input and multiplexed microfluidic assay reveals epigenomic variation across cerebellum and prefrontal cortex. Science Advances, 2018, 4, eaar8187.	4.7	35
51	Intestinal FGF15/19 physiologically repress hepatic lipogenesisÂin the late fed-state by activating SHP and DNMT3A. Nature Communications, 2020, 11, 5969.	5.8	35
52	ADAR2 regulates RNA stability by modifying access of decay-promoting RNA-binding proteins. Nucleic Acids Research, 2017, 45, gkw1304.	6.5	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.	3.8	33
54	TrueSight: a new algorithm for splice junction detection using RNA-seq. Nucleic Acids Research, 2013, 41, e51-e51.	6.5	31

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55	Comparing 3D Genome Organization in Multiple Species Using Phylo-HMRF. <i>Cell Systems</i> , 2019, 8, 494-505.e14.	2.9	27
56	Tracing the Evolution of Lineage-Specific Transcription Factor Binding Sites in a Birth-Death Framework. <i>PLoS Computational Biology</i> , 2014, 10, e1003771.	1.5	25
57	PSIP1/p75 promotes tumorigenicity in breast cancer cells by promoting the transcription of cell cycle genes. <i>Carcinogenesis</i> , 2017, 38, 966-975.	1.3	25
58	MicroRNA-210 Promotes Bile Acid-Induced Cholestatic Liver Injury by Targeting Mixed-Lineage Leukemia-4 Methyltransferase in Mice. <i>Hepatology</i> , 2020, 71, 2118-2134.	3.6	21
59	Continuous-Trait Probabilistic Model for Comparing Multi-species Functional Genomic Data. <i>Cell Systems</i> , 2018, 7, 208-218.e11.	2.9	20
60	MATCHA: Probing Multi-way Chromatin Interaction with Hypergraph Representation Learning. <i>Cell Systems</i> , 2020, 10, 397-407.e5.	2.9	18
61	PSAR-Align: improving multiple sequence alignment using probabilistic sampling. <i>Bioinformatics</i> , 2014, 30, 1010-1012.	1.8	16
62	LncRNA-mediated regulation of <i>SOX9</i> expression in basal subtype breast cancer cells. <i>Rna</i> , 2020, 26, 175-185.	1.6	16
63	Selective clonal persistence of human retroviruses in vivo: Radial chromatin organization, integration site, and host transcription. <i>Science Advances</i> , 2022, 8, eabm6210.	4.7	15
64	Antagonism between splicing and microprocessor complex dictates the serum-induced processing of lnc-MIRHG for efficient cell cycle reentry. <i>Rna</i> , 2020, 26, 1603-1620.	1.6	12
65	Privacy Challenges of Genomic Big Data. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1028, 139-148.	0.8	11
66	MOCHI enables discovery of heterogeneous interactome modules in 3D nucleome. <i>Genome Research</i> , 2020, 30, 227-238.	2.4	10
67	Greedy Selection of Species for Ancestral State Reconstruction on Phylogenies: Elimination Is Better than Insertion. <i>PLoS ONE</i> , 2010, 5, e8985.	1.1	9
68	Replication Timing Becomes Intertwined with 3D Genome Organization. <i>Cell</i> , 2019, 176, 681-684.	13.5	9
69	TIGER: tiled iterative genome assembler. <i>BMC Bioinformatics</i> , 2012, 13, S18.	1.2	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> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1055-1063.	0.8	5
72	Reconstructing the History of Large-Scale Genomic Changes: Biological Questions and Computational Challenges. <i>Journal of Computational Biology</i> , 2011, 18, 879-893.	0.8	4

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73	Biomedical Informatics and Computational Biology for High-Throughput Data Analysis. Scientific World Journal, The, 2014, 2014, 1-2.	0.8	4
74	Toward Recovering Allele-specific Cancer Genome Graphs. Journal of Computational Biology, 2018, 25, 624-636.	0.8	4
75	UnSplicer: mapping spliced RNA-seq reads in compact genomes and filtering noisy splicing. Nucleic Acids Research, 2014, 42, e25-e25.	6.5	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.	1.3	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.	0.9	2
78	Reconstructing ancestral gene orders with duplications guided by synteny level genome reconstruction. BMC Bioinformatics, 2016, 17, 414.	1.2	2
79	Assessing the contribution of tumor mutational phenotypes to cancer progression risk. PLoS Computational Biology, 2021, 17, e1008777.	1.5	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.	0.8	1