

# Tao Jiang

## List of Publications by Year in Descending Order

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**Version:** 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

79  
papers

1,573  
citations

22  
h-index

37  
g-index

81  
ext. papers

2,010  
ext. citations

4.5  
avg, IF

4.91  
L-index

#	Paper	IF	Citations
79	Modeling multi-species RNA modification through multi-task curriculum learning. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 3719-3734	20.1	4
78	Enhancement and Imputation of Peak Signal Enables Accurate Cell-Type Classification in scATAC-seq. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 658352	4.5	1
77	FINER: enhancing the prediction of tissue-specific functions of isoforms by refining isoform interaction networks. <i>NAR Genomics and Bioinformatics</i> , <b>2021</b> , 3, lqab057	3.7	0
76	DeepLPI: a multimodal deep learning method for predicting the interactions between lncRNAs and protein isoforms. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 24	3.6	7
75	Riboexp: an interpretable reinforcement learning framework for ribosome density modeling. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	1
74	Facile Fabrication of Multilayer Stretchable Electronics via a Two-mode Mechanical Cutting Process. <i>ACS Nano</i> , <b>2021</b> ,	16.7	2
73	A novel machine learning framework for automated biomedical relation extraction from large-scale literature repositories. <i>Nature Machine Intelligence</i> , <b>2020</b> , 2, 347-355	22.5	8
72	A simulated annealing approach for resolution guided homogeneous cryo-electron microscopy image selection. <i>Quantitative Biology</i> , <b>2020</b> , 8, 51-63	3.9	1
71	Dysregulation of Hypothalamic Gene Expression and the Oxytocinergic System by Soybean Oil Diets in Male Mice. <i>Endocrinology</i> , <b>2020</b> , 161,	4.8	3
70	DeepPASTA: deep neural network based polyadenylation site analysis. <i>Bioinformatics</i> , <b>2019</b> , 35, 4577-4585	9.5	13
69	NeoDTI: neural integration of neighbor information from a heterogeneous network for discovering new drug-target interactions. <i>Bioinformatics</i> , <b>2019</b> , 35, 104-111	7.2	97
68	DIFFUSE: predicting isoform functions from sequences and expression profiles via deep learning. <i>Bioinformatics</i> , <b>2019</b> , 35, i284-i294	7.2	14
67	SCALE method for single-cell ATAC-seq analysis via latent feature extraction. <i>Nature Communications</i> , <b>2019</b> , 10, 4576	17.4	70
66	DeepIsoFun: a deep domain adaptation approach to predict isoform functions. <i>Bioinformatics</i> , <b>2019</b> , 35, 2535-2544	7.2	12
65	DeepHINT: understanding HIV-1 integration via deep learning with attention. <i>Bioinformatics</i> , <b>2019</b> , 35, 1660-1667	7.2	26
64	TAPAS: tool for alternative polyadenylation site analysis. <i>Bioinformatics</i> , <b>2018</b> , 34, 2521-2529	7.2	30
63	FreePSI: an alignment-free approach to estimating exon-inclusion ratios without a reference transcriptome. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, e11	20.1	1

62	Improved Approximation Algorithms for the Maximum Happy Vertices and Edges Problems. <i>Algorithmica</i> , <b>2018</b> , 80, 1412-1438	0.9	15
61	Constructing tissue-specific transcriptional regulatory networks via a Markov random field. <i>BMC Genomics</i> , <b>2018</b> , 19, 884	4.5	5
60	A deep boosting based approach for capturing the sequence binding preferences of RNA-binding proteins from high-throughput CLIP-seq data. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e129	20.1	17
59	Analysis of Ribosome Stalling and Translation Elongation Dynamics by Deep Learning. <i>Cell Systems</i> , <b>2017</b> , 5, 212-220.e6	10.6	39
58	TITER: predicting translation initiation sites by deep learning. <i>Bioinformatics</i> , <b>2017</b> , 33, i234-i242	7.2	44
57	SDEAP: a splice graph based differential transcript expression analysis tool for population data. <i>Bioinformatics</i> , <b>2016</b> , 32, 3593-3602	7.2	2
56	TransComb: genome-guided transcriptome assembly via combing junctions in splicing graphs. <i>Genome Biology</i> , <b>2016</b> , 17, 213	18.3	40
55	Differential regulation enrichment analysis via the integration of transcriptional regulatory network and gene expression data. <i>Bioinformatics</i> , <b>2015</b> , 31, 563-71	7.2	15
54	Improved Approximation Algorithms for the Maximum Happy Vertices and Edges Problems. <i>Lecture Notes in Computer Science</i> , <b>2015</b> , 159-170	0.9	12
53	Differential gene expression analysis using coexpression and RNA-Seq data. <i>Bioinformatics</i> , <b>2013</b> , 29, 2153-61	7.2	19
52	An Efficient Algorithm for Haplotype Inference on Pedigrees with a Small Number of Recombinants. <i>Algorithmica</i> , <b>2012</b> , 62, 951-981	0.9	2
51	An efficient algorithm for haplotype inference on pedigrees with recombinations and mutations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2012</b> , 9, 12-25	3	8
50	A linear-time algorithm for reconstructing zero-recombinant haplotype configuration on a pedigree. <i>BMC Bioinformatics</i> , <b>2012</b> , 13 Suppl 17, S19	3.6	3
49	Transcriptome assembly and isoform expression level estimation from biased RNA-Seq reads. <i>Bioinformatics</i> , <b>2012</b> , 28, 2914-21	7.2	68
48	IsoLasso: a LASSO regression approach to RNA-Seq based transcriptome assembly. <i>Journal of Computational Biology</i> , <b>2011</b> , 18, 1693-707	1.7	100
47	Workshop: Transcriptome assembly from RNA-Seq data: Objectives, algorithms and challenges <b>2011</b> ,		2
46	Inference of isoforms from short sequence reads. <i>Journal of Computational Biology</i> , <b>2011</b> , 18, 305-21	1.7	41
45	Inferring haplotypes from genotypes on a pedigree with mutations, genotyping errors and missing alleles. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2011</b> , 9, 339-65	1	4

44	Some Algorithmic Challenges in Genome-Wide Ortholog Assignment. <i>Journal of Computer Science and Technology</i> , <b>2010</b> , 25, 42-52	1.7	8
43	A linear-time algorithm for reconstructing zero-recombinant haplotype configuration on pedigrees without mating loops. <i>Journal of Combinatorial Optimization</i> , <b>2010</b> , 19, 217-240	0.9	5
42	Beyond evolutionary trees. <i>Natural Computing</i> , <b>2010</b> , 9, 421-435	1.3	0
41	MSOAR 2.0: Incorporating tandem duplications into ortholog assignment based on genome rearrangement. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 10	3.6	46
40	Efficient Algorithms for Reconstructing Zero-Recombinant Haplotypes on a Pedigree Based on Fast Elimination of Redundant Linear Equations. <i>SIAM Journal on Computing</i> , <b>2009</b> , 38, 2198-2219	1.1	7
39	A survey on haplotyping algorithms for tightly linked markers. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2008</b> , 6, 241-59	1	14
38	Clustering of main orthologs for multiple genomes. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2008</b> , 6, 573-84	1	9
37	A New Model of Multi-Marker Correlation for Genome-Wide Tag SNP Selection <b>2008</b> ,		3
36	Complexity and approximation of the minimum recombinant haplotype configuration problem. <i>Theoretical Computer Science</i> , <b>2007</b> , 378, 316-330	1.1	13
35	Average-case analysis of QuickSort and Binary Insertion Tree height using incompressibility. <i>Information Processing Letters</i> , <b>2007</b> , 103, 45-51	0.8	3
34	MSOAR: a high-throughput ortholog assignment system based on genome rearrangement. <i>Journal of Computational Biology</i> , <b>2007</b> , 14, 1160-75	1.7	60
33	CLUSTERING OF MAIN ORTHOLOGS FOR MULTIPLE GENOMES <b>2007</b> ,		2
32	LEARNING POSITION WEIGHT MATRICES FROM SEQUENCE AND EXPRESSION DATA <b>2007</b> ,		3
31	AN IMPROVED GIBBS SAMPLING METHOD FOR MOTIF DISCOVERY VIA SEQUENCE WEIGHTING <b>2006</b> ,		2
30	A Parsimony Approach to Genome-Wide Ortholog Assignment. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 578-594	0.9	8
29	Assignment of orthologous genes via genome rearrangement. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2005</b> , 2, 302-15	3	101
28	A class of edit kernels for SVMs to predict translation initiation sites in eukaryotic mRNAs. <i>Journal of Computational Biology</i> , <b>2005</b> , 12, 702-18	1.7	41
27	Computing the minimum recombinant haplotype configuration from incomplete genotype data on a pedigree by integer linear programming. <i>Journal of Computational Biology</i> , <b>2005</b> , 12, 719-39	1.7	62

26	More reliable protein NMR peak assignment via improved 2-interval scheduling. <i>Journal of Computational Biology</i> , <b>2005</b> , 12, 129-46	1.7	4
25	An exact solution for finding minimum recombinant haplotype configurations on pedigrees with missing data by integer linear programming <b>2004</b> ,		20
24	A Further Improved Approximation Algorithm for Breakpoint Graph Decomposition. <i>Journal of Combinatorial Optimization</i> , <b>2004</b> , 8, 183-194	0.9	17
23	The longest common subsequence problem for arc-annotated sequences. <i>Journal of Discrete Algorithms</i> , <b>2004</b> , 2, 257-270		32
22	Efficient inference of haplotypes from genotypes on a pedigree. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2003</b> , 1, 41-69	1	61
21	Minimum Recombinant Haplotype Configuration on Tree Pedigrees. <i>Lecture Notes in Computer Science</i> , <b>2003</b> , 339-353	0.9	18
20	Approximation algorithms for NMR spectral peak assignment. <i>Theoretical Computer Science</i> , <b>2003</b> , 299, 211-229	1.1	16
19	Computational assignment of protein backbone NMR peaks by efficient bounding and filtering. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2003</b> , 1, 387-409	1	4
18	Efficient rule-based haplotyping algorithms for pedigree data <b>2003</b> ,		27
17	More Reliable Protein NMR Peak Assignment via Improved 2-Interval Scheduling. <i>Lecture Notes in Computer Science</i> , <b>2003</b> , 580-592	0.9	1
16	The average-case area of Heilbronn-type triangles*. <i>Random Structures and Algorithms</i> , <b>2002</b> , 20, 206-219	0.8	14
15	The longest common subsequence problem for sequences with nested arc annotations. <i>Journal of Computer and System Sciences</i> , <b>2002</b> , 65, 465-480	1	36
14	. <i>Computing in Science and Engineering</i> , <b>2002</b> , 4, 50-62	1.5	16
13	New applications of the incompressibility method: Part II. <i>Theoretical Computer Science</i> , <b>2000</b> , 235, 59-70	1.1	13
12	Average-case analysis of algorithms using Kolmogorov complexity. <i>Journal of Computer Science and Technology</i> , <b>2000</b> , 15, 402-408	1.7	7
11	A lower bound on the average-case complexity of shellsort. <i>Journal of the ACM</i> , <b>2000</b> , 47, 905-911	2	12
10	The Incompressibility Method. <i>Lecture Notes in Computer Science</i> , <b>2000</b> , 36-53	0.9	
9	Mapping Clones with a Given Ordering or Interleaving. <i>Algorithmica</i> , <b>1998</b> , 21, 262-284	0.9	5

8	Two heads are better than two tapes. <i>Journal of the ACM</i> , <b>1997</b> , 44, 237-256	2	6
7	Approximation algorithms for tree alignment with a given phylogeny. <i>Algorithmica</i> , <b>1996</b> , 16, 302-315	0.9	39
6	DNA sequencing and string learning. <i>Mathematical Systems Theory</i> , <b>1996</b> , 29, 387-405		11
5	An approximation scheme for some Steiner tree problems in the plane. <i>Networks</i> , <b>1996</b> , 28, 187-193	1.6	15
4	Pattern languages with and without erasing. <i>International Journal of Computer Mathematics</i> , <b>1994</b> , 50, 147-163	1.2	44
3	THE STRUCTURE AND COMPLEXITY OF MINIMAL NFA $\bar{\cup}$ OVER A UNARY ALPHABET. <i>International Journal of Foundations of Computer Science</i> , <b>1991</b> , 02, 163-182	0.6	29
2	Orchestrating quartets: approximation and data correction		10
1	DeepHINT: Understanding HIV-1 integration via deep learning with attention		2