

# Junbai Wang

## List of Publications by Year in descending order

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Version: 2024-02-01

64  
papers

1,510  
citations

304743

22  
h-index

330143

37  
g-index

67  
all docs

67  
docs citations

67  
times ranked

2503  
citing authors

#	ARTICLE	IF	CITATIONS
1	Hotspots of transcription factor colocalization in the genome of <i>Drosophila melanogaster</i> . Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 12027-12032.	7.1	182
2	Clustering of the SOM easily reveals distinct gene expression patterns: results of a reanalysis of lymphoma study. BMC Bioinformatics, 2002, 3, 36.	2.6	99
3	Array Comparative Genomic Hybridization Reveals Distinct DNA Copy Number Differences between Gastrointestinal Stromal Tumors and Leiomyosarcomas. Cancer Research, 2006, 66, 8984-8993.	0.9	97
4	Tumor classification and marker gene prediction by feature selection and fuzzy c-means clustering using microarray data. BMC Bioinformatics, 2003, 4, 60.	2.6	80
5	High Resolution Detection and Analysis of CpG Dinucleotides Methylation Using MBD-Seq Technology. PLoS ONE, 2011, 6, e22226.	2.5	69
6	Temporal dynamic reorganization of 3D chromatin architecture in hormone-induced breast cancer and endocrine resistance. Nature Communications, 2019, 10, 1522.	12.8	66
7	Frequent somatic mutations of <i>KMT2D</i> and <i>MLL2</i> and <i>CARD11</i> genes in primary cold agglutinin disease. British Journal of Haematology, 2018, 183, 838-842.	2.5	53
8	NEIL3-Dependent Regulation of Cardiac Fibroblast Proliferation Prevents Myocardial Rupture. Cell Reports, 2017, 18, 82-92.	6.4	45
9	Interleukin-33 Drives a Proinflammatory Endothelial Activation That Selectively Targets Nonquiescent Cells. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, e47-55.	2.4	44
10	Immunomodulatory Effects of the <i>Agaricus blazei</i> Murrill-Based Mushroom Extract AndoSan in Patients with Multiple Myeloma Undergoing High Dose Chemotherapy and Autologous Stem Cell Transplantation: A Randomized, Double Blinded Clinical Study. BioMed Research International, 2015, 2015, 1-11.	1.9	44
11	M-CGH: analysing microarray-based CGH experiments. BMC Bioinformatics, 2004, 5, 74.	2.6	41
12	Splenic Marginal Zone Lymphoma with Villous Lymphocytes Shows On-Going Immunoglobulin Gene Mutations. American Journal of Pathology, 2003, 162, 681-689.	3.8	39
13	Inhibition of Endothelial NOTCH1 Signaling Attenuates Inflammation by Reducing Cytokine-Mediated Histone Acetylation at Inflammatory Enhancers. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 854-869.	2.4	37
14	Genome-wide analysis uncovers high frequency, strong differential chromosomal interactions and their associated epigenetic patterns in E2-mediated gene regulation. BMC Genomics, 2013, 14, 70.	2.8	34
15	MtDNA depleted PC3 cells exhibit Warburg effect and cancer stem cell features. Oncotarget, 2016, 7, 40297-40313.	1.8	34
16	A new framework for identifying combinatorial regulation of transcription factors: A case study of the yeast cell cycle. Journal of Biomedical Informatics, 2007, 40, 707-725.	4.3	31
17	POLD2 and KSP37 (FGFBP2) Correlate Strongly with Histology, Stage and Outcome in Ovarian Carcinomas. PLoS ONE, 2010, 5, e13837.	2.5	31
18	Clinical Relevance of Multidrug Resistance Gene Expression in Ovarian Serous Carcinoma Effusions. Molecular Pharmaceutics, 2011, 8, 2080-2088.	4.6	31

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19	MArray: analysing single, replicated or reversed microarray experiments. <i>Bioinformatics</i> , 2002, 18, 1139-1140.	4.1	30
20	MGraph: graphical models for microarray data analysis. <i>Bioinformatics</i> , 2003, 19, 2210-2211.	4.1	29
21	New probabilistic graphical models for genetic regulatory networks studies. <i>Journal of Biomedical Informatics</i> , 2005, 38, 443-455.	4.3	27
22	Plasminogen activator inhibitor-1 increases the expression of VEGF in human glioma cells. <i>Experimental Cell Research</i> , 2004, 294, 130-139.	2.6	23
23	Comprehensive genome-wide transcription factor analysis reveals that a combination of high affinity and low affinity DNA binding is needed for human gene regulation. <i>BMC Genomics</i> , 2015, 16, S12.	2.8	23
24	Metabolic reprogramming is associated with flavopiridol resistance in prostate cancer DU145 cells. <i>Scientific Reports</i> , 2017, 7, 5081.	3.3	23
25	Computational Biology of Genome Expression and Regulation—A Review of Microarray Bioinformatics. <i>Journal of Environmental Pathology, Toxicology and Oncology</i> , 2008, 27, 157-179.	1.2	22
26	Adhesion molecule protein signature in ovarian cancer effusions is prognostic of patient outcome. <i>Cancer</i> , 2012, 118, 1543-1553.	4.1	21
27	BayesPI - a new model to study protein-DNA interactions: a case study of condition-specific protein binding parameters for Yeast transcription factors. <i>BMC Bioinformatics</i> , 2009, 10, 345.	2.6	18
28	Integrative whole-genome sequence analysis reveals roles of regulatory mutations in BCL6 and BCL2 in follicular lymphoma. <i>Scientific Reports</i> , 2017, 7, 7040.	3.3	18
29	BayesPI-BAR: a new biophysical model for characterization of regulatory sequence variations. <i>Nucleic Acids Research</i> , 2015, 43, gkv733.	14.5	17
30	Nuclear IL-33 restrains the early conversion of fibroblasts to an extracellular matrix-secreting phenotype. <i>Scientific Reports</i> , 2021, 11, 108.	3.3	17
31	Early introduction of oral paricalcitol in renal transplant recipients. An open-label randomized study. <i>Transplant International</i> , 2017, 30, 827-840.	1.6	16
32	Neutralization and charge transfer in H <sup>+</sup> -H <sup>+</sup> - and H <sup>+</sup> -H collisions. <i>Journal of Physics B: Atomic, Molecular and Optical Physics</i> , 2000, 33, 241-249.	1.5	15
33	Quantitative model for inferring dynamic regulation of the tumour suppressor gene p53. <i>BMC Bioinformatics</i> , 2010, 11, 36.	2.6	14
34	Low levels of monoclonal small B cells in the bone marrow of patients with diffuse large B-cell lymphoma of activated B-cell type but not of germinal center B-cell type. <i>Haematologica</i> , 2010, 95, 1334-1341.	3.5	13
35	An integrated approach to infer dynamic protein-gene interactions—A case study of the human P53 protein. <i>Methods</i> , 2016, 110, 3-13.	3.8	12
36	The 3D genomic landscape of differential response to EGFR/HER2 inhibition in endocrine-resistant breast cancer cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194631.	1.9	10

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37	Hi-C profiling of cancer spheroids identifies 3D-growth-specific chromatin interactions in breast cancer endocrine resistance. <i>Clinical Epigenetics</i> , 2021, 13, 175.	4.1	10
38	Monocytoid B cells: An Enigmatic B cell Subset Showing Evidence of Extrafollicular Immunoglobulin gene Somatic Hypermutation. <i>Scandinavian Journal of Immunology</i> , 2012, 75, 500-509.	2.7	9
39	Three-dimensional analysis reveals altered chromatin interaction by enhancer inhibitors harbors TCF7L2-regulated cancer gene signature. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 3056-3070.	2.6	9
40	Quality versus accuracy: result of a reanalysis of protein-binding microarrays from the DREAM5 challenge by using BayesPI2 including dinucleotide interdependence. <i>BMC Bioinformatics</i> , 2014, 15, 289.	2.6	8
41	Modeling and analysis of Hi-C data by HiSIF identifies characteristic promoter-distal loops. <i>Genome Medicine</i> , 2020, 12, 69.	8.2	8
42	Spin Anisotropy for Excitation in Collisions between Two One-Electron Atoms. <i>Physical Review Letters</i> , 2000, 85, 1638-1641.	7.8	7
43	Experimental evidence of transfer excitation in Ar <sup>6+</sup> -He collisions. <i>Journal of Physics B: Atomic, Molecular and Optical Physics</i> , 2000, 33, L171-L178.	1.5	6
44	Predicting Variation of DNA Shape Preferences in Protein-DNA Interaction in Cancer Cells with a New Biophysical Model. <i>Genes</i> , 2017, 8, 233.	2.4	6
45	Origin of the structures in the excitation cross sections in ion-atom collisions. <i>Physical Review A</i> , 1998, 57, R4086-R4089.	2.5	5
46	The effect of prior assumptions over the weights in BayesPI with application to study protein-DNA interactions from CHIP-based high-throughput data. <i>BMC Bioinformatics</i> , 2010, 11, 412.	2.6	5
47	Computational study of associations between histone modification and protein-DNA binding in yeast genome by integrating diverse information. <i>BMC Genomics</i> , 2011, 12, 172.	2.8	5
48	BayesPI-BAR2: A New Python Package for Predicting Functional Non-coding Mutations in Cancer Patient Cohorts. <i>Frontiers in Genetics</i> , 2019, 10, 282.	2.3	5
49	Biomedical Informatics and Computational Biology for High-Throughput Data Analysis. <i>Scientific World Journal, The</i> , 2014, 2014, 1-2.	2.1	4
50	HMST-Seq-Analyzer: A new python tool for differential methylation and hydroxymethylation analysis in various DNA methylation sequencing data. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2877-2889.	4.1	4
51	Mitochondrial DNA Deficiency in Ovarian Cancer Cells and Cancer Stem Cell-like Properties. <i>Anticancer Research</i> , 2015, 35, 3743-53.	1.1	4
52	Characterizing a collective and dynamic component of chromatin immunoprecipitation enrichment profiles in yeast. <i>BMC Genomics</i> , 2014, 15, 494.	2.8	2
53	Left/right capture asymmetry in He <sup>2+</sup> -Na(3p-1) collisions: classical versus quantal collision dynamics. <i>Journal of Physics B: Atomic, Molecular and Optical Physics</i> , 2000, 33, L197-L202.	1.5	1
54	IGAP-integrative genome analysis pipeline reveals new gene regulatory model associated with nonspecific TF-DNA binding affinity. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1270-1286.	4.1	1

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55	Effective Non-linear Methods for Inferring Genetic Regulation from Time-Series Microarray Gene Expression Data. <i>Methods in Molecular Biology</i> , 2012, 802, 235-246.	0.9	1
56	Exploring the potential effect of paricalcitol on markers of inflammation in de novo renal transplant recipients. <i>PLoS ONE</i> , 2020, 15, e0243759.	2.5	1
57	abc4pwm: affinity based clustering for position weight matrices in applications of DNA sequence analysis. <i>BMC Bioinformatics</i> , 2022, 23, 83.	2.6	1
58	Integrating whole genome sequencing, methylation, gene expression, topologically associated domain information in regulatory mutation prediction: A study of follicular lymphoma. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1726-1742.	4.1	1
59	Systems Biology Studies of Gene Network and Cell Signaling Pathway in Cancer Research. <i>Translational Bioinformatics</i> , 2013, , 109-129.	0.0	0
60	Integrated study to infer dynamic protein-gene interactions in human p53 regulatory networks. , 2015, , .		0
61	Title is missing!. , 2020, 15, e0243759.		0
62	Title is missing!. , 2020, 15, e0243759.		0
63	Title is missing!. , 2020, 15, e0243759.		0
64	Title is missing!. , 2020, 15, e0243759.		0