

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	abc4pwm: affinity based clustering for position weight matrices in applications of DNA sequence analysis. BMC Bioinformatics, 2022, 23, 83.	2.6	1
2	Integrating whole genome sequencing, methylation, gene expression, topologically associated domain information in regulatory mutation prediction: A study of follicular lymphoma. Computational and Structural Biotechnology Journal, 2022, 20, 1726-1742.	4.1	1
3	Nuclear IL-33 restrains the early conversion of fibroblasts to an extracellular matrix-secreting phenotype. Scientific Reports, 2021, 11, 108.	3.3	17
4	Hi-C profiling of cancer spheroids identifies 3D-growth-specific chromatin interactions in breast cancer endocrine resistance. Clinical Epigenetics, 2021, 13, 175.	4.1	10
5	HMST-Seq-Analyzer: A new python tool for differential methylation and hydroxymethylation analysis in various DNA methylation sequencing data. Computational and Structural Biotechnology Journal, 2020, 18, 2877-2889.	4.1	4
6	The 3D genomic landscape of differential response to EGFR/HER2 inhibition in endocrine-resistant breast cancer cells. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194631.	1.9	10
7	Modeling and analysis of Hi-C data by HiSIF identifies characteristic promoter-distal loops. Genome Medicine, 2020, 12, 69.	8.2	8
8	IGAP-integrative genome analysis pipeline reveals new gene regulatory model associated with nonspecific TF-DNA binding affinity. Computational and Structural Biotechnology Journal, 2020, 18, 1270-1286.	4.1	1
9	Exploring the potential effect of paricalcitol on markers of inflammation in de novo renal transplant recipients. PLoS ONE, 2020, 15, e0243759.	2.5	1
10	Title is missing!. , 2020, 15, e0243759.		0
11	Title is missing!. , 2020, 15, e0243759.		0
12	Title is missing!. , 2020, 15, e0243759.		0
13	Title is missing!. , 2020, 15, e0243759.		0
14	BayesPI-BAR2: A New Python Package for Predicting Functional Non-coding Mutations in Cancer Patient Cohorts. Frontiers in Genetics, 2019, 10, 282.	2.3	5
15	Temporal dynamic reorganization of 3D chromatin architecture in hormone-induced breast cancer and endocrine resistance. Nature Communications, 2019, 10, 1522.	12.8	66
16	Three-dimensional analysis reveals altered chromatin interaction by enhancer inhibitors harbors TCF7L2-regulated cancer gene signature. Journal of Cellular Biochemistry, 2019, 120, 3056-3070.	2.6	9
17	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
18	Frequent somatic mutations of <i>KMT2D</i> (<i>MLL2</i>) and <i>CARD11</i> genes in primary cold agglutinin disease. British Journal of Haematology, 2018, 183, 838-842.	2.5	53

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19	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
20	NEIL3-Dependent Regulation of Cardiac Fibroblast Proliferation Prevents Myocardial Rupture. <i>Cell Reports</i> , 2017, 18, 82-92.	6.4	45
21	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
22	Metabolic reprogramming is associated with flavopiridol resistance in prostate cancer DU145 cells. <i>Scientific Reports</i> , 2017, 7, 5081.	3.3	23
23	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
24	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
25	MtDNA depleted PC3 cells exhibit Warburg effect and cancer stem cell features. <i>Oncotarget</i> , 2016, 7, 40297-40313.	1.8	34
26	Integrated study to infer dynamic protein-gene interactions in human p53 regulatory networks. , 2015, , .		0
27	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
28	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. <i>BioMed Research International</i> , 2015, 2015, 1-11.	1.9	44
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	Mitochondrial DNA Deficiency in Ovarian Cancer Cells and Cancer Stem Cell-like Properties. <i>Anticancer Research</i> , 2015, 35, 3743-53.	1.1	4
31	Biomedical Informatics and Computational Biology for High-Throughput Data Analysis. <i>Scientific World Journal</i> , The, 2014, 2014, 1-2.	2.1	4
32	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
33	Characterizing a collective and dynamic component of chromatin immunoprecipitation enrichment profiles in yeast. <i>BMC Genomics</i> , 2014, 15, 494.	2.8	2
34	Genome-wide analysis uncovers high frequency, strong differential chromosomal interactions and their associated epigenetic patterns in E2-mediated gene regulation. <i>BMC Genomics</i> , 2013, 14, 70.	2.8	34
35	Systems Biology Studies of Gene Network and Cell Signaling Pathway in Cancer Research. <i>Translational Bioinformatics</i> , 2013, , 109-129.	0.0	0
36	Interleukin-33 Drives a Proinflammatory Endothelial Activation That Selectively Targets Nonquiescent Cells. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013, 33, e47-55.	2.4	44

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37	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
38	Adhesion molecule protein signature in ovarian cancer effusions is prognostic of patient outcome. <i>Cancer</i> , 2012, 118, 1543-1553.	4.1	21
39	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
40	Clinical Relevance of Multidrug Resistance Gene Expression in Ovarian Serous Carcinoma Effusions. <i>Molecular Pharmaceutics</i> , 2011, 8, 2080-2088.	4.6	31
41	High Resolution Detection and Analysis of CpG Dinucleotides Methylation Using MBD-Seq Technology. <i>PLoS ONE</i> , 2011, 6, e22226.	2.5	69
42	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
43	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
44	Quantitative model for inferring dynamic regulation of the tumour suppressor gene p53. <i>BMC Bioinformatics</i> , 2010, 11, 36.	2.6	14
45	POLD2 and KSP37 (FGFBP2) Correlate Strongly with Histology, Stage and Outcome in Ovarian Carcinomas. <i>PLoS ONE</i> , 2010, 5, e13837.	2.5	31
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	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
48	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
49	A new framework for identifying combinatorial regulation of transcription factors: A case study of the yeast cell cycle. <i>Journal of Biomedical Informatics</i> , 2007, 40, 707-725.	4.3	31
50	Array Comparative Genomic Hybridization Reveals Distinct DNA Copy Number Differences between Gastrointestinal Stromal Tumors and Leiomyosarcomas. <i>Cancer Research</i> , 2006, 66, 8984-8993.	0.9	97
51	Hotspots of transcription factor colocalization in the genome of <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12027-12032.	7.1	182
52	New probabilistic graphical models for genetic regulatory networks studies. <i>Journal of Biomedical Informatics</i> , 2005, 38, 443-455.	4.3	27
53	M-CGH: analysing microarray-based CGH experiments. <i>BMC Bioinformatics</i> , 2004, 5, 74.	2.6	41
54	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

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55	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
56	Splenic Marginal Zone Lymphoma with Villous Lymphocytes Shows On-Going Immunoglobulin Gene Mutations. American Journal of Pathology, 2003, 162, 681-689.	3.8	39
57	MGraph: graphical models for microarray data analysis. Bioinformatics, 2003, 19, 2210-2211.	4.1	29
58	MArray: analysing single, replicated or reversed microarray experiments. Bioinformatics, 2002, 18, 1139-1140.	4.1	30
59	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
60	Neutralization and charge transfer in H ⁺ -H and H-H collisions. Journal of Physics B: Atomic, Molecular and Optical Physics, 2000, 33, 241-249.	1.5	15
61	Left/right capture asymmetry in He ²⁺ -Na(3p-1) collisions: classical versus quantal collision dynamics. Journal of Physics B: Atomic, Molecular and Optical Physics, 2000, 33, L197-L202.	1.5	1
62	Experimental evidence of transfer excitation in Ar ⁶⁺ -He collisions. Journal of Physics B: Atomic, Molecular and Optical Physics, 2000, 33, L171-L178.	1.5	6
63	Spin Anisotropy for Excitation in Collisions between Two One-Electron Atoms. Physical Review Letters, 2000, 85, 1638-1641.	7.8	7
64	Origin of the structures in the excitation cross sections in ion-atom collisions. Physical Review A, 1998, 57, R4086-R4089.	2.5	5