

Jinfeng Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

832
citations

516710

16
h-index

552781

26
g-index

51
all docs

51
docs citations

51
times ranked

1430
citing authors

#	ARTICLE	IF	CITATIONS
1	Differentially Expressed Transcripts and Dysregulated Signaling Pathways and Networks in African American Breast Cancer. PLoS ONE, 2013, 8, e82460.	2.5	77
2	Differential Nuclease Sensitivity Profiling of Chromatin Reveals Biochemical Footprints Coupled to Gene Expression and Functional DNA Elements in Maize. Plant Cell, 2014, 26, 3883-3893.	6.6	72
3	Bayesian inference of protein-protein interactions from biological literature. Bioinformatics, 2009, 25, 1536-1542.	4.1	68
4	Fast Protein Loop Sampling and Structure Prediction Using Distance-Guided Sequential Chain-Growth Monte Carlo Method. PLoS Computational Biology, 2014, 10, e1003539.	3.2	49
5	ProDCoNN: Protein design using a convolutional neural network. Proteins: Structure, Function and Bioinformatics, 2020, 88, 819-829.	2.6	45
6	Tumoral expression of drug and xenobiotic metabolizing enzymes in breast cancer patients of different ethnicities with implications to personalized medicine. Scientific Reports, 2017, 7, 4747.	3.3	35
7	Extracting chemical-protein interactions from literature using sentence structure analysis and feature engineering. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	32
8	The regulatory landscape of early maize inflorescence development. Genome Biology, 2020, 21, 165.	8.8	32
9	Coordinated Upregulation of Mitochondrial Biogenesis and Autophagy in Breast Cancer Cells: The Role of Dynamin Related Protein-1 and Implication for Breast Cancer Treatment. Oxidative Medicine and Cellular Longevity, 2016, 2016, 1-10.	4.0	31
10	Overview of the BioCreative VI Precision Medicine Track: mining protein interactions and mutations for precision medicine. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	30
11	Integrated Bio-Entity Network: A System for Biological Knowledge Discovery. PLoS ONE, 2011, 6, e21474.	2.5	29
12	Immune landscape of human prostate cancer: immune evasion mechanisms and biomarkers for personalized immunotherapy. BMC Cancer, 2020, 20, 572.	2.6	25
13	Dysregulated gene expression predicts tumor aggressiveness in African-American prostate cancer patients. Scientific Reports, 2018, 8, 16335.	3.3	23
14	Automatic extraction of protein-protein interactions using grammatical relationship graph. BMC Medical Informatics and Decision Making, 2018, 18, 42.	3.0	23
15	Subgrouping breast cancer patients based on immune evasion mechanisms unravels a high involvement of transforming growth factor-beta and decoy receptor 3. PLoS ONE, 2018, 13, e0207799.	2.5	21
16	Integrative Comparison of mRNA Expression Patterns in Breast Cancers from Caucasian and Asian Americans with Implications for Precision Medicine. Cancer Research, 2017, 77, 423-433.	0.9	20
17	The native cisrome and sequence motif families of the maize ear. PLoS Genetics, 2021, 17, e1009689.	3.5	19
18	Context-Specific Protein Network Miner - An Online System for Exploring Context-Specific Protein Interaction Networks from the Literature. PLoS ONE, 2012, 7, e34480.	2.5	18

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19	Conformational sampling and structure prediction of multiple interacting loops in soluble and α -barrel membrane proteins using multi-loop distance-guided chain-growth Monte Carlo method. <i>Bioinformatics</i> , 2015, 31, 2646-2652.	4.1	16
20	IMID: integrated molecular interaction database. <i>Bioinformatics</i> , 2012, 28, 747-749.	4.1	15
21	Protein Surface Matching by Combining Local and Global Geometric Information. <i>PLoS ONE</i> , 2012, 7, e40540.	2.5	14
22	PIMiner: a web tool for extraction of protein interactions from biomedical literature. <i>International Journal of Data Mining and Bioinformatics</i> , 2013, 7, 450.	0.1	13
23	Personalized chemotherapy selection for breast cancer using gene expression profiles. <i>Scientific Reports</i> , 2017, 7, 43294.	3.3	13
24	DNA Methyltransferase 3A Is Involved in the Sustained Effects of Chronic Stress on Synaptic Functions and Behaviors. <i>Cerebral Cortex</i> , 2021, 31, 1998-2012.	2.9	11
25	Super-delta: a new differential gene expression analysis procedure with robust data normalization. <i>BMC Bioinformatics</i> , 2017, 18, 582.	2.6	10
26	MatchMixer: a cross-platform normalization method for gene expression data integration. <i>Bioinformatics</i> , 2020, 36, 2486-2491.	4.1	10
27	iSeg: an efficient algorithm for segmentation of genomic and epigenomic data. <i>BMC Bioinformatics</i> , 2018, 19, 131.	2.6	9
28	Genetic factors associated with cancer racial disparity – an integrative study across twenty-one cancer types. <i>Molecular Oncology</i> , 2020, 14, 2775-2786.	4.6	8
29	Cytochrome P450-2D6: A novel biomarker in liver cancer health disparity. <i>PLoS ONE</i> , 2021, 16, e0257072.	2.5	8
30	RASS: a web server for RNA alignment in the joint sequence-structure space. <i>Nucleic Acids Research</i> , 2014, 42, W377-W381.	14.5	7
31	Mixture of logistic models and an ensemble approach for protein-protein interaction extraction. , 2011, , .		6
32	Triage of documents containing protein interactions affected by mutations using an NLP based machine learning approach. <i>BMC Genomics</i> , 2020, 21, 773.	2.8	6
33	Chromatin structure profile data from DNS-seq: Differential nuclease sensitivity mapping of four reference tissues of B73 maize (<i>Zea mays</i> L). <i>Data in Brief</i> , 2018, 20, 358-363.	1.0	5
34	Super-delta2: an enhanced differential expression analysis procedure for multi-group comparisons of RNA-seq data. <i>Bioinformatics</i> , 2021, 37, 2627-2636.	4.1	5
35	Structure-based RNA Function Prediction Using Elastic Shape Analysis. , 2011, , .		4
36	Distance-Guided Forward and Backward Chain-Growth Monte Carlo Method for Conformational Sampling and Structural Prediction of Antibody CDR-H3 Loops. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 380-388.	5.3	4

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37	Extraction of protein-protein interactions using natural language processing based pattern matching. , 2017, , .		4
38	Maximizing the reusability of gene expression data by predicting missing metadata. PLoS Computational Biology, 2020, 16, e1007450.	3.2	4
39	An efficient multiple protein structure comparison method and its application to structure clustering and outlier detection. , 2013, , .		3
40	FTIP: an accurate and efficient method for global protein surface comparison. Bioinformatics, 2020, 36, 3056-3063.	4.1	2
41	Biological Network Inference With GRASP: A Bayesian Network Structure Learning Method Using Adaptive Sequential Monte Carlo. Frontiers in Genetics, 2021, 12, 764020.	2.3	1
42	Identifying county-level factors for female breast cancer incidence rate through a large-scale population study. Applied Geography, 2020, 125, 102324.	3.7	0
43	Maximizing the reusability of gene expression data by predicting missing metadata. , 2020, 16, e1007450.		0
44	Maximizing the reusability of gene expression data by predicting missing metadata. , 2020, 16, e1007450.		0
45	Maximizing the reusability of gene expression data by predicting missing metadata. , 2020, 16, e1007450.		0
46	Maximizing the reusability of gene expression data by predicting missing metadata. , 2020, 16, e1007450.		0
47	Maximizing the reusability of gene expression data by predicting missing metadata. , 2020, 16, e1007450.		0
48	Maximizing the reusability of gene expression data by predicting missing metadata. , 2020, 16, e1007450.		0