

Ning Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

1,325
citations

394421
19
h-index

361022
35
g-index

61
all docs

61
docs citations

61
times ranked

1785
citing authors

#	ARTICLE	IF	CITATIONS
1	3D Porous Fe_2O_3 @C Nanocomposite as High-Performance Anode Material of Na-ion Batteries. <i>Advanced Energy Materials</i> , 2015, 5, 1401123.	19.5	320
2	A hybrid method for prediction and repositioning of drug Anatomical Therapeutic Chemical classes. <i>Molecular BioSystems</i> , 2014, 10, 868.	2.9	70
3	Classification of cancers based on copy number variation landscapes. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2750-2755.	2.4	65
4	Classifying Ten Types of Major Cancers Based on Reverse Phase Protein Array Profiles. <i>PLoS ONE</i> , 2015, 10, e0123147.	2.5	58
5	Identification of hepatocellular carcinoma related genes with k-th shortest paths in a protein-protein interaction network. <i>Molecular BioSystems</i> , 2013, 9, 2720.	2.9	47
6	Computational prediction and analysis of protein γ -carboxylation sites based on a random forest method. <i>Molecular BioSystems</i> , 2012, 8, 2946.	2.9	46
7	Prediction of Aptamer-Target Interacting Pairs with Pseudo-Amino Acid Composition. <i>PLoS ONE</i> , 2014, 9, e86729.	2.5	41
8	Discriminating Ramos and Jurkat Cells with Image Textures from Diffraction Imaging Flow Cytometry Based on a Support Vector Machine. <i>Current Bioinformatics</i> , 2018, 13, 50-56.	1.5	39
9	Predicting A-to-I RNA Editing by Feature Selection and Random Forest. <i>PLoS ONE</i> , 2014, 9, e110607.	2.5	37
10	Analysis of cellular objects through diffraction images acquired by flow cytometry. <i>Optics Express</i> , 2013, 21, 24819.	3.4	33
11	A method to distinguish between lysine acetylation and lysine ubiquitination with feature selection and analysis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 2479-2490.	3.5	33
12	Polarization imaging and classification of Jurkat T and Ramos B cells using a flow cytometer. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2014, 85, 817-826.	1.5	30
13	Automatic Lung Tumor Segmentation on PET/CT Images Using Fuzzy Markov Random Field Model. <i>Computational and Mathematical Methods in Medicine</i> , 2014, 2014, 1-6.	1.3	28
14	Discriminating between deleterious and neutral non-frameshifting indels based on protein interaction networks and hybrid properties. <i>Molecular Genetics and Genomics</i> , 2015, 290, 343-352.	2.1	28
15	Identification of Lung-Cancer-Related Genes with the Shortest Path Approach in a Protein-Protein Interaction Network. <i>BioMed Research International</i> , 2013, 2013, 1-8.	1.9	26
16	Prediction of the parallel/antiparallel orientation of beta-strands using amino acid pairing preferences and support vector machines. <i>Journal of Theoretical Biology</i> , 2010, 263, 360-368.	1.7	24
17	Computationally identifying virulence factors based on KEGG pathways. <i>Molecular BioSystems</i> , 2013, 9, 1447.	2.9	23
18	Exploring Mouse Protein Function via Multiple Approaches. <i>PLoS ONE</i> , 2016, 11, e0166580.	2.5	22

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19	Prediction of protein N-formylation and comparison with N-acetylation based on a feature selection method. <i>Neurocomputing</i> , 2016, 217, 53-62.	5.9	20
20	Prediction of function changes associated with single-point protein mutations using support vector machines (SVMs). <i>Human Mutation</i> , 2009, 30, 1161-1166.	2.5	18
21	A Novel Method of Predicting Protein Disordered Regions Based on Sequence Features. <i>BioMed Research International</i> , 2013, 2013, 1-8.	1.9	17
22	A quantitative method for measurement of HL-60 cell apoptosis based on diffraction imaging flow cytometry technique. <i>Biomedical Optics Express</i> , 2014, 5, 2172.	2.9	17
23	Prediction of carbamylated lysine sites based on the one-class k-nearest neighbor method. <i>Molecular BioSystems</i> , 2013, 9, 2729.	2.9	16
24	PCAT-1 facilitates breast cancer progression via binding to RACK1 and enhancing oxygen-independent stability of HIF-1 α . <i>Molecular Therapy - Nucleic Acids</i> , 2021, 24, 310-324.	5.1	15
25	Prediction of Multi-Type Membrane Proteins in Human by an Integrated Approach. <i>PLoS ONE</i> , 2014, 9, e93553.	2.5	15
26	An Ensemble Prognostic Model for Colorectal Cancer. <i>PLoS ONE</i> , 2013, 8, e63494.	2.5	14
27	Identification of Influenza A/H7N9 Virus Infection-Related Human Genes Based on Shortest Paths in a Virus-Human Protein Interaction Network. <i>BioMed Research International</i> , 2014, 2014, 1-11.	1.9	14
28	Prediction of S-Nitrosylation Modification Sites Based on Kernel Sparse Representation Classification and mRMR Algorithm. <i>BioMed Research International</i> , 2014, 2014, 1-10.	1.9	14
29	Prediction of the Ebola Virus Infection Related Human Genes Using Protein-Protein Interaction Network. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2017, 20, 638-646.	1.1	14
30	Characterization and analysis of a novel diguanylate cyclase PA0847 from <i>Pseudomonas aeruginosa</i> PAO1. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 655-665.	2.7	13
31	The interstrand amino acid pairs play a significant role in determining the parallel or antiparallel orientation of β -strands. <i>Biochemical and Biophysical Research Communications</i> , 2009, 386, 537-543.	2.1	12
32	Discriminating between Lysine Sumoylation and Lysine Acetylation Using mRMR Feature Selection and Analysis. <i>PLoS ONE</i> , 2014, 9, e107464.	2.5	12
33	Prediction of protein amidation sites by feature selection and analysis. <i>Molecular Genetics and Genomics</i> , 2013, 288, 391-400.	2.1	10
34	From EST to novel spider silk gene identification for production of spidroin-based biomaterials. <i>Scientific Reports</i> , 2017, 7, 13354.	3.3	10
35	Structure of the C-terminal domain of TRADD reveals a novel fold in the death domain superfamily. <i>Scientific Reports</i> , 2017, 7, 7073.	3.3	10
36	Identification of Triple-Negative Breast Cancer Genes and a Novel High-Risk Breast Cancer Prediction Model Development Based on PPI Data and Support Vector Machines. <i>Frontiers in Genetics</i> , 2019, 10, 180.	2.3	10

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37	Effects of soil stoichiometry of the CaCO ₃ /available phosphorus ratio on plant density in <i>Artemisia ordosica</i> communities. <i>Science Bulletin</i> , 2012, 57, 492-499.	1.7	9
38	A fuzzy feature fusion method for auto-segmentation of gliomas with multi-modality diffusion and perfusion magnetic resonance images in radiotherapy. <i>Scientific Reports</i> , 2018, 8, 3231.	3.3	8
39	Research Progress of Gliomas in Machine Learning. <i>Cells</i> , 2021, 10, 3169.	4.1	8
40	Prediction and Analysis of Post-Translational Pyruvoyl Residue Modification Sites from Internal Serines in Proteins. <i>PLoS ONE</i> , 2013, 8, e66678.	2.5	7
41	Recognizing and Predicting Thioether Bridges Formed by Lanthionine and β -Methyllanthionine in Lantibiotics Using a Random Forest Approach with Feature Selection. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2017, 20, 582-593.	1.1	7
42	Computational Prediction of Protein Epsilon Lysine Acetylation Sites Based on a Feature Selection Method. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2017, 20, 629-637.	1.1	7
43	SHEETSPAIR: A Database of Amino Acid Pairs in Protein Sheet Structures. <i>Data Science Journal</i> , 2007, 6, S589-S595.	1.3	7
44	Prediction of protein modification sites of gamma-carboxylation using position specific scoring matrices based evolutionary information. <i>Computational Biology and Chemistry</i> , 2013, 47, 215-220.	2.3	6
45	NURBS: a database of experimental and predicted nuclear receptor binding sites of mouse. <i>Bioinformatics</i> , 2013, 29, 295-297.	4.1	6
46	Structural basis of NF- κ B signaling by the p75 neurotrophin receptor interaction with adaptor protein TRADD through their respective death domains. <i>Journal of Biological Chemistry</i> , 2021, 297, 100916.	3.4	6
47	Identification of WHO II/III Gliomas by 16 Prognostic-related Gene Signatures using Machine Learning Methods. <i>Current Medicinal Chemistry</i> , 2022, 29, 1622-1639.	2.4	6
48	Studies on the rules of β -strand alignment in a protein β -sheet structure. <i>Journal of Theoretical Biology</i> , 2011, 285, 69-76.	1.7	5
49	Statistical Analysis of Terminal Extensions of Protein β -Strand Pairs. <i>Advances in Bioinformatics</i> , 2013, 2013, 1-7.	5.7	5
50	Identification of genes of four malignant tumors and a novel prediction model development based on PPI data and support vector machines. <i>Cancer Gene Therapy</i> , 2020, 27, 715-725.	4.6	5
51	Epigenome-Wide Tobacco-Related Methylation Signature Identification and Their Multilevel Regulatory Network Inference for Lung Adenocarcinoma. <i>BioMed Research International</i> , 2020, 2020, 1-12.	1.9	5
52	¹ H, ¹⁵ N and ¹³ C chemical shift assignments of the C-terminal domain of TRADD. <i>Biomolecular NMR Assignments</i> , 2017, 11, 281-284.	0.8	3
53	Tuberculosis and HIV Coinfection—the Challenge in the Prevention, Detection and Treatment of Tuberculosis. <i>Current Bioinformatics</i> , 2019, 14, 91-99.	1.5	3
54	Novel Computational Methods and Tools in Biomedicine and Biopharmacy. <i>Computational and Mathematical Methods in Medicine</i> , 2014, 2014, 1-2.	1.3	1

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55	Component Vector method and Its Application in Detecting Similarities between Sequences. , 2009, , .		0
56	StrandPairsViewer: A Toolkit for Visualization and Analysis of Amino Acids Pairs in Protein Sheet Structures. , 2009, , .		0
57	Desktop Software for Patch-Clamp Raw Binary Data Conversion and Preprocessing. Journal of Electrical and Computer Engineering, 2011, 2011, 1-7.	0.9	0
58	Identification of Novel Breast Cancer Genes based on Gene Expression Profiles and PPI Data. Current Proteomics, 2019, 16, 415-426.	0.3	0
59	New insights regarding protein folding as learned from beta-sheets. EXCLI Journal, 2012, 11, 543-55.	0.7	0