

# Ning Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

59  
papers

1,325  
citations

393982

19  
h-index

360668

35  
g-index

61  
all docs

61  
docs citations

61  
times ranked

1785  
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	1.2	6
2	PCAT-1 facilitates breast cancer progression via binding to RACK1 and enhancing oxygen-independent stability of HIF-1 $\alpha$ . <i>Molecular Therapy - Nucleic Acids</i> , 2021, 24, 310-324.	2.3	15
3	Structural basis of NF- $\kappa$ 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.	1.6	6
4	Research Progress of Gliomas in Machine Learning. <i>Cells</i> , 2021, 10, 3169.	1.8	8
5	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.	2.2	5
6	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.	0.9	5
7	&lt;p&gt;Characterization and analysis of a novel diguanylate cyclase PA0847 from &lt;em&gt;Pseudomonas aeruginos&lt;/em&gt;a PAO1&lt;/p&gt;. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 655-665.	1.1	13
8	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.	1.1	10
9	Tuberculosis and HIV Coinfection&#x2014;the Challenge in the Prevention, Detection and Treatment of Tuberculosis. <i>Current Bioinformatics</i> , 2019, 14, 91-99.	0.7	3
10	Identification of Novel Breast Cancer Genes based on Gene Expression Profiles and PPI Data. <i>Current Proteomics</i> , 2019, 16, 415-426.	0.1	0
11	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.	1.6	8
12	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.	0.7	39
13	From EST to novel spider silk gene identification for production of spidroin-based biomaterials. <i>Scientific Reports</i> , 2017, 7, 13354.	1.6	10
14	<sup>1</sup> H, <sup>15</sup> N and <sup>13</sup> C chemical shift assignments of the C-terminal domain of TRADD. <i>Biomolecular NMR Assignments</i> , 2017, 11, 281-284.	0.4	3
15	Structure of the C-terminal domain of TRADD reveals a novel fold in the death domain superfamily. <i>Scientific Reports</i> , 2017, 7, 7073.	1.6	10
16	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.	0.6	14
17	Recognizing and Predicting Thioether Bridges Formed by Lanthionine and $\beta$ -Methylanthionine in Lantibiotics Using a Random Forest Approach with Feature Selection. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2017, 20, 582-593.	0.6	7
18	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.	0.6	7

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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.	3.5	20
20	Classification of cancers based on copy number variation landscapes. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2750-2755.	1.1	65
21	Exploring Mouse Protein Function via Multiple Approaches. <i>PLoS ONE</i> , 2016, 11, e0166580.	1.1	22
22	Classifying Ten Types of Major Cancers Based on Reverse Phase Protein Array Profiles. <i>PLoS ONE</i> , 2015, 10, e0123147.	1.1	58
23	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.	2.0	33
24	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.	1.0	28
25	3D Porous $\text{Fe}_2\text{O}_3$ @C Nanocomposite as High-Performance Anode Material of Na $\kern-0.25ex \kern-0.25ex $ on Batteries. <i>Advanced Energy Materials</i> , 2015, 5, 1401123.	10.2	320
26	Predicting A-to-I RNA Editing by Feature Selection and Random Forest. <i>PLoS ONE</i> , 2014, 9, e110607.	1.1	37
27	Identification of <i>Influenza A</i> /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.	0.9	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.	0.9	14
29	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.	1.5	17
30	Novel Computational Methods and Tools in Biomedicine and Biopharmacy. <i>Computational and Mathematical Methods in Medicine</i> , 2014, 2014, 1-2.	0.7	1
31	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.	0.7	28
32	A hybrid method for prediction and repositioning of drug Anatomical Therapeutic Chemical classes. <i>Molecular BioSystems</i> , 2014, 10, 868.	2.9	70
33	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.	1.1	30
34	Prediction of Aptamer-Target Interacting Pairs with Pseudo-Amino Acid Composition. <i>PLoS ONE</i> , 2014, 9, e86729.	1.1	41
35	Prediction of Multi-Type Membrane Proteins in Human by an Integrated Approach. <i>PLoS ONE</i> , 2014, 9, e93553.	1.1	15
36	Discriminating between Lysine Sumoylation and Lysine Acetylation Using mRMR Feature Selection and Analysis. <i>PLoS ONE</i> , 2014, 9, e107464.	1.1	12

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37	Prediction of protein amidation sites by feature selection and analysis. <i>Molecular Genetics and Genomics</i> , 2013, 288, 391-400.	1.0	10
38	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.	1.1	6
39	Computationally identifying virulence factors based on KEGG pathways. <i>Molecular BioSystems</i> , 2013, 9, 1447.	2.9	23
40	Prediction of carbamylated lysine sites based on the one-class k-nearest neighbor method. <i>Molecular BioSystems</i> , 2013, 9, 2729.	2.9	16
41	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
42	Analysis of cellular objects through diffraction images acquired by flow cytometry. <i>Optics Express</i> , 2013, 21, 24819.	1.7	33
43	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.	0.9	26
44	A Novel Method of Predicting Protein Disordered Regions Based on Sequence Features. <i>BioMed Research International</i> , 2013, 2013, 1-8.	0.9	17
45	NURBS: a database of experimental and predicted nuclear receptor binding sites of mouse. <i>Bioinformatics</i> , 2013, 29, 295-297.	1.8	6
46	Statistical Analysis of Terminal Extensions of Protein $\alpha$ -Strand Pairs. <i>Advances in Bioinformatics</i> , 2013, 2013, 1-7.	5.7	5
47	An Ensemble Prognostic Model for Colorectal Cancer. <i>PLoS ONE</i> , 2013, 8, e63494.	1.1	14
48	Prediction and Analysis of Post-Translational Pyruvoyl Residue Modification Sites from Internal Serines in Proteins. <i>PLoS ONE</i> , 2013, 8, e66678.	1.1	7
49	Computational prediction and analysis of protein $\beta$ -carboxylation sites based on a random forest method. <i>Molecular BioSystems</i> , 2012, 8, 2946.	2.9	46
50	Effects of soil stoichiometry of the CaCO <sub>3</sub> /available phosphorus ratio on plant density in <i>Artemisia ordosica</i> communities. <i>Science Bulletin</i> , 2012, 57, 492-499.	1.7	9
51	New insights regarding protein folding as learned from beta-sheets. <i>EXCLI Journal</i> , 2012, 11, 543-55.	0.5	0
52	Studies on the rules of $\beta$ -strand alignment in a protein $\beta$ -sheet structure. <i>Journal of Theoretical Biology</i> , 2011, 285, 69-76.	0.8	5
53	Desktop Software for Patch-Clamp Raw Binary Data Conversion and Preprocessing. <i>Journal of Electrical and Computer Engineering</i> , 2011, 2011, 1-7.	0.6	0
54	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.	0.8	24

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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	Prediction of function changes associated with single-point protein mutations using support vector machines (SVMs). Human Mutation, 2009, 30, 1161-1166.	1.1	18
58	The interstrand amino acid pairs play a significant role in determining the parallel or antiparallel orientation of $\beta^2$ -strands. Biochemical and Biophysical Research Communications, 2009, 386, 537-543.	1.0	12
59	SHEETSPAIR: A Database of Amino Acid Pairs in Protein Sheet Structures. Data Science Journal, 2007, 6, S589-S595.	0.6	7