

Qi Zhao

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2256966/publications.pdf>

Version: 2024-02-01

68
papers

3,431
citations

218677

26
h-index

149698

56
g-index

68
all docs

68
docs citations

68
times ranked

2560
citing authors

#	ARTICLE	IF	CITATIONS
1	Inferring Gene Regulatory Networks Using the Improved Markov Blanket Discovery Algorithm. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2022, 14, 168-181.	3.6	46
2	Corrigendum to "Predicting lncRNA-miRNA interactions based on interactome network and graphlet interaction" [Genomics 113 (2021) 874-880]. <i>Genomics</i> , 2022, 114, e1-e7.	2.9	0
3	Tissue specific prediction of N6-methyladenine sites based on an ensemble of multi-input hybrid neural network. <i>Biocell</i> , 2022, 46, 1105-1121.	0.7	3
4	CITEMOXMBD: A flexible single-cell multimodal omics analysis framework to reveal the heterogeneity of immune cells. <i>RNA Biology</i> , 2022, 19, 290-304.	3.1	10
5	Modulation of lncRNA H19 enhances resveratrol-inhibited cancer cell proliferation and migration by regulating endoplasmic reticulum stress. <i>Journal of Cellular and Molecular Medicine</i> , 2022, 26, 2205-2217.	3.6	25
6	Identification of miRNA-disease associations via deep forest ensemble learning based on autoencoder. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	60
7	Editorial: Computational Predictions, Dynamic Tracking, and Evolutionary Analysis of Antibiotic Resistance Through the Mining of Microbial Genomes and Metagenomic Data. <i>Frontiers in Microbiology</i> , 2022, 13, 880967.	3.5	1
8	De Novo design of potential inhibitors against SARS-CoV-2 Mpro. <i>Computers in Biology and Medicine</i> , 2022, 147, 105728.	7.0	6
9	A deep learning method for predicting metabolite-disease associations via graph neural network. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	119
10	Recent advances on the machine learning methods in predicting ncRNA-protein interactions. <i>Molecular Genetics and Genomics</i> , 2021, 296, 243-258.	2.1	5
11	Predicting lncRNA-miRNA interactions based on interactome network and graphlet interaction. <i>Genomics</i> , 2021, 113, 874-880.	2.9	64
12	lncRNA MALAT1 participates in metformin inhibiting the proliferation of breast cancer cell. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 7135-7145.	3.6	31
13	Circular RNAs and complex diseases: from experimental results to computational models. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	116
14	Using Network Distance Analysis to Predict lncRNA-miRNA Interactions. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2021, 13, 535-545.	3.6	126
15	The role of YTH domain containing 2 in epigenetic modification and immune infiltration of pan-cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 8615-8627.	3.6	20
16	Identification of Claudin-6 as a Molecular Biomarker in Pan-Cancer Through Multiple Omics Integrative Analysis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 726656.	3.7	22
17	A Novel Cost-Effective Controller Placement Scheme for Software-Defined Vehicular Networks. <i>IEEE Internet of Things Journal</i> , 2021, 8, 14080-14093.	8.7	9
18	Melatonin inhibiting the survival of human gastric cancer cells under ER stress involving autophagy and Ras-Raf-MAPK signalling. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 1480-1492.	3.6	59

#	ARTICLE	IF	CITATIONS
19	Predicting human disease-associated circRNAs based on locality-constrained linear coding. <i>Genomics</i> , 2020, 112, 1335-1342.	2.9	40
20	A path-based computational model for long non-coding RNA-protein interaction prediction. <i>Genomics</i> , 2020, 112, 1754-1760.	2.9	9
21	Predicting lncRNA-miRNA interactions based on logistic matrix factorization with neighborhood regularized. <i>Knowledge-Based Systems</i> , 2020, 191, 105261.	7.1	115
22	Current Computational Models for Prediction of the Varied Interactions Related to Protein - Part 2. <i>Protein and Peptide Letters</i> , 2020, 27, 347-347.	0.9	0
23	MicroRNAs Associated With Colon Cancer: New Potential Prognostic Markers and Targets for Therapy. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 176.	4.1	28
24	Editorial: Bioinformatics in Microbiota. <i>Frontiers in Microbiology</i> , 2020, 11, 100.	3.5	5
25	Recent Advances on the Machine Learning Methods in Identifying Phage Virion Proteins. <i>Current Bioinformatics</i> , 2020, 15, 657-661.	1.5	3
26	Integrating Bipartite Network Projection and KATZ Measure to Identify Novel CircRNA-Disease Associations. <i>IEEE Transactions on Nanobioscience</i> , 2019, 18, 578-584.	3.3	90
27	Computational Model Development of Drug-Target Interaction Prediction: A Review. <i>Current Protein and Peptide Science</i> , 2019, 20, 492-494.	1.4	23
28	QSAR modelling study of the bioconcentration factor and toxicity of organic compounds to aquatic organisms using machine learning and ensemble methods. <i>Ecotoxicology and Environmental Safety</i> , 2019, 179, 71-78.	6.0	40
29	Predicting the cytotoxicity of chemicals using ensemble learning methods and molecular fingerprints. <i>Journal of Applied Toxicology</i> , 2019, 39, 1366-1377.	2.8	23
30	MicroRNAs and complex diseases: from experimental results to computational models. <i>Briefings in Bioinformatics</i> , 2019, 20, 515-539.	6.5	507
31	Study on the Mechanisms of Active Compounds in Traditional Chinese Medicine for the Treatment of Influenza Virus by Virtual Screening. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018, 10, 320-328.	3.6	13
32	EGBMMDA: Extreme Gradient Boosting Machine for MiRNA-Disease Association prediction. <i>Cell Death and Disease</i> , 2018, 9, 3.	6.3	256
33	BNPMDA: Bipartite Network Projection for MiRNA-Disease Association prediction. <i>Bioinformatics</i> , 2018, 34, 3178-3186.	4.1	307
34	HLPI-Ensemble: Prediction of human lncRNA-protein interactions based on ensemble strategy. <i>RNA Biology</i> , 2018, 15, 1-10.	3.1	101
35	HNGRNMF: Heterogeneous Network-based Graph Regularized Nonnegative Matrix Factorization for predicting events of microbe-disease associations. , 2018, , .		6
36	Current Computational Models for Prediction of the Varied Interactions Related to Protein - PART 1. <i>Protein and Peptide Letters</i> , 2018, 25, 806-806.	0.9	0

#	ARTICLE	IF	CITATIONS
37	Developing Novel Computational Techniques for Medicine and Pharmacy. <i>Current Topics in Medicinal Chemistry</i> , 2018, 18, 947-948.	2.1	2
38	The Bipartite Network Projection-Recommended Algorithm for Predicting Long Non-coding RNA-Protein Interactions. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 13, 464-471.	5.1	74
39	Identifying and Exploiting Potential miRNA-Disease Associations With Neighborhood Regularized Logistic Matrix Factorization. <i>Frontiers in Genetics</i> , 2018, 9, 303.	2.3	10
40	Predicting Drug-Induced Liver Injury Using Ensemble Learning Methods and Molecular Fingerprints. <i>Toxicological Sciences</i> , 2018, 165, 100-107.	3.1	65
41	IRWNRLPI: Integrating Random Walk and Neighborhood Regularized Logistic Matrix Factorization for lncRNA-Protein Interaction Prediction. <i>Frontiers in Genetics</i> , 2018, 9, 239.	2.3	83
42	SSCMDA: spy and super cluster strategy for MiRNA-disease association prediction. <i>Oncotarget</i> , 2018, 9, 1826-1842.	1.8	10
43	RWLPAP: Random Walk for lncRNA-protein Associations Prediction. <i>Protein and Peptide Letters</i> , 2018, 25, 830-837.	0.9	25
44	Resonance in an ensemble of excitable reaction-diffusion systems under spatially periodic force. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2017, 467, 184-191.	2.6	10
45	A novel computational model based on super-disease and miRNA for potential miRNA-disease association prediction. <i>Molecular BioSystems</i> , 2017, 13, 1202-1212.	2.9	47
46	CarcinoPred-EL: Novel models for predicting the carcinogenicity of chemicals using molecular fingerprints and ensemble learning methods. <i>Scientific Reports</i> , 2017, 7, 2118.	3.3	153
47	LPI-ETSLP: lncRNA-protein interaction prediction using eigenvalue transformation-based semi-supervised link prediction. <i>Molecular BioSystems</i> , 2017, 13, 1781-1787.	2.9	64
48	LPI-NRLMF: lncRNA-protein interaction prediction by neighborhood regularized logistic matrix factorization. <i>Oncotarget</i> , 2017, 8, 103975-103984.	1.8	35
49	Virtual screening approach to identifying influenza virus neuraminidase inhibitors using molecular docking combined with machine-learning-based scoring function. <i>Oncotarget</i> , 2017, 8, 83142-83154.	1.8	40
50	The interaction between NOLC1 and IAV NS1 protein promotes host cell apoptosis and reduces virus replication. <i>Oncotarget</i> , 2017, 8, 94519-94527.	1.8	9
51	PCPA protects against monocrotaline-induced pulmonary arterial remodeling in rats: potential roles of connective tissue growth factor. <i>Oncotarget</i> , 2017, 8, 111642-111655.	1.8	8
52	Computational Prediction of Influenza Neuraminidase Inhibitors Using Machine Learning Algorithms and Recursive Feature Elimination Method. <i>Lecture Notes in Computer Science</i> , 2017, , 344-349.	1.3	2
53	Effect of Dynamic Interaction between microRNA and Transcription Factor on Gene Expression. <i>BioMed Research International</i> , 2016, 2016, 1-10.	1.9	21
54	Stochastic modeling suggests that noise reduces differentiation efficiency by inducing a heterogeneous drug response in glioma differentiation therapy. <i>BMC Systems Biology</i> , 2016, 10, 73.	3.0	8

#	ARTICLE	IF	CITATIONS
55	Comprehensive Circular RNA Profiling Reveals That hsa_circ_0005075, a New Circular RNA Biomarker, Is Involved in Hepatocellular Carcinoma Development. <i>Medicine (United States)</i> , 2016, 95, e3811.	1.0	306
56	Study of spatial signal transduction in bistable switches. <i>Frontiers of Physics</i> , 2016, 11, 1.	5.0	7
57	Eliminating amplitude death by the asymmetry coupling and process delay in coupled oscillators. <i>European Physical Journal B</i> , 2016, 89, 1.	1.5	4
58	An optimization approach and its application to compare DNA sequences. <i>Journal of Molecular Structure</i> , 2015, 1082, 49-55.	3.6	4
59	Collective dynamics induced by diversity taken from two-point distribution in globally coupled chaotic oscillators. <i>Nonlinear Dynamics</i> , 2014, 75, 17-26.	5.2	6
60	Ubiquitin chain specific auto-ubiquitination triggers sustained oscillation, bistable switches and excitable firing. <i>IET Systems Biology</i> , 2014, 8, 282-292.	1.5	8
61	Complete synchronization induced by disorder in coupled chaotic lattices. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 2013, 377, 370-377.	2.1	42
62	Force exerted on the spiral tip by the heterogeneity in an excitable medium. <i>Europhysics Letters</i> , 2013, 104, 58005.	2.0	18
63	The study of amplitude death in globally delay-coupled nonidentical systems based on order parameter expansion. <i>Chaos</i> , 2012, 22, 023149.	2.5	7
64	Spatial distribution and dose-response relationship for different operation modes in a reaction-diffusion model of the MAPK cascade. <i>Physical Biology</i> , 2011, 8, 055004.	1.8	13
65	Spatiotemporal stochastic resonance in a bistable FitzHugh-Nagumo ring with phase-repulsive coupling. <i>European Physical Journal B</i> , 2011, 84, 299-305.	1.5	9
66	A theoretical modeling for frequency modulation of Ca ²⁺ signal on activation of MAPK cascade. <i>Biophysical Chemistry</i> , 2011, 157, 33-42.	2.8	16
67	Oscillation death in coupled oscillators. <i>Frontiers of Physics in China</i> , 2009, 4, 97-110.	1.0	25
68	Information propagation from IP3 to target protein: A combined model for encoding and decoding of Ca ²⁺ signal. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2009, 388, 4105-4114.	2.6	12