Menglong Li

List of Publications by Year
in descending order

86 papers	1,826 citations	516710 16 h-index	289244 40 g-index
86 all docs	86 docs citations	86 times ranked	3366 citing authors

#	Article	IF	Citations
1	A Transfer-Learning-Based Deep Convolutional Neural Network for Predicting Leukemia-Related Phosphorylation Sites from Protein Primary Sequences. International Journal of Molecular Sciences, 2022, 23, 1741.	4.1	5
2	Structure-Activity Relationship (SAR) Model for Predicting Teratogenic Risk of Antiseizure Medications in Pregnancy by Using Support Vector Machine. Frontiers in Pharmacology, 2022, 13, 747935.	3.5	3
3	Quantitative Structureâ€“Activity Relationship (QSAR) Model for the Severity Prediction of Drug-Induced Rhabdomyolysis by Using Random Forest. Chemical Research in Toxicology, 2021, 34, 514-521.	3.3	10
4	The Power of Matrix Factorization: Methods for Deconvoluting Genetic Heterogeneous Data at Expression Level. Current Bioinformatics, 2021, 15, 841-853.	1.5	4
5	Prediction of Synergistic Drug Combinations for Prostate Cancer by Transcriptomic and Network Characteristics. Frontiers in Pharmacology, 2021, 12, 634097.	3.5	10
6	Prediction of diseaseâ€associated functional variants in noncoding regions through a comprehensive analysis by integrating datasets and features. Human Mutation, 2021, 42, 667-684.	2.5	0
7	Comparative Analysis for the Performance of Long-Read-Based Structural Variation Detection Pipelines in Tandem Repeat Regions. Frontiers in Pharmacology, 2021, 12, 658072.	3.5	3
8	SBTD: A Novel Method for Detecting Topological Associated Domains from Hi-C Data. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 638-651.	3.6	1
9	Predicting HIV drug resistance using weighted machine learning method at target protein sequence-level. Molecular Diversity, 2021, 25, 1541-1551.	3.9	7
10	Identification of Disease-specific Single Amino Acid Polymorphisms Using a Simple Random Forest at Protein-level. Current Bioinformatics, 2021, 16, 1278-1287.	1.5	0
11	A Multiple Comprehensive Analysis of scATAC-seq Based on Auto-Encoder and Matrix Decomposition. Symmetry, 2021, 13, 1467.	2.2	2
12	Comprehensive characterization of pathological stageâ€related genes of papillary thyroid cancer along with survival prediction. Journal of Cellular and Molecular Medicine, 2021, 25, 8390-8404.	3.6	2
13	Coupling complementary strategy to flexible graph neural network for quick discovery of coformer in diverse co-crystal materials. Nature Communications, 2021, 12, 5950.	12.8	37
14	Identification of Hub lncRNAs Along With lncRNA-miRNA-mRNA Network for Effective Diagnosis and Prognosis of Papillary Thyroid Cancer. Frontiers in Pharmacology, 2021, 12, 748867.	3.5	5
15	GFICLEE: ultrafast tree-based phylogenetic profile method inferring gene function at the genomic-wide level. BMC Genomics, 2021, 22, 774.	2.8	2
16	Drug-induced QT Prolongation Atlas (DIQTA) for enhancing cardiotoxicity management. Drug Discovery Today, 2021, , .	6.4	10
17	ExoceRNA atlas: A database of cancer ceRNAs in human blood exosomes. Life Sciences, 2020, 257, 118092.	4.3	6
18	autoBioSeqpy: A Deep Learning Tool for the Classification of Biological Sequences. Journal of Chemical Information and Modeling, 2020, 60, 3755-3764.	5.4	17

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19	Multi-models in predicting RNA solvent accessibility exhibit the contribution from none-sequential attributes and providing a globally stable modeling strategy. Chemometrics and Intelligent Laboratory Systems, 2020, 205, 104100.	3.5	2
20	Improving Model Performance on the Stratification of Breast Cancer Patients by Integrating Multiscale Genomic Features. BioMed Research International, 2020, 2020, 1-12.	1.9	1
21	Uncovering the prognostic gene signatures for the improvement of risk stratification in cancers by using deep learning algorithm coupled with wavelet transform. BMC Bioinformatics, 2020, 21, 195.	2.6	4
22	An effective seven-CpG-based signature to predict survival in renal clear cell carcinoma by integrating DNA methylation and gene expression. Life Sciences, 2020, 243, 117289.	4.3	6
23	Drug-Induced Rhabdomyolysis Atlas (DIRA) for idiosyncratic adverse drug reaction management. Drug Discovery Today, 2019, 24, 9-15.	6.4	22
24	Transcriptome Analysis Identifies Piwi-Interacting RNAs as Prognostic Markers for Recurrence of Prostate Cancer. Frontiers in Genetics, 2019, 10, 1018.	2.3	12
25	A Machine Learning-Based QSAR Model for Benzimidazole Derivatives as Corrosion Inhibitors by Incorporating Comprehensive Feature Selection. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 738-747.	3.6	27
26	Molecular Mechanism Regarding Allosteric Modulation of Ligand Binding and the Impact of Mutations on Dimerization for CCR5 Homodimer. Journal of Chemical Information and Modeling, 2019, 59, 1965-1976.	5.4	15
27	Genetic Contexts Characterize Dynamic Histone Modification Patterns Among Cell Types. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 698-710.	3.6	1
28	Comparative Analysis for the Performance of Variant Calling Pipelines on Detecting the de novo Mutations in Humans. Frontiers in Pharmacology, 2019, 10, 358.	3.5	12
29	Probing the Druggablility on the Interface of the Proteinâ€“Protein Interaction and Its Allosteric Regulation Mechanism on the Drug Screening for the CXCR4 Homodimer. Frontiers in Pharmacology, 2019, 10, 1310.	3.5	5
30	Narrowing the Gap Between In Vitro and In Vivo Genetic Profiles by Deconvoluting Toxicogenomic Data In Silico. Frontiers in Pharmacology, 2019, 10, 1489.	3.5	8
31	Use multiscale simulation to explore the effects of the homodimerizations between different conformation states on the activation and allosteric pathway for the Î¼-opioid receptor. Physical Chemistry Chemical Physics, 2018, 20, 13485-13496.	2.8	16
32	Postâ€modified nonâ€negative matrix factorization for deconvoluting the gene expression profiles of specific cell types from heterogeneous clinical samples based on RNAâ€sequencing data. Journal of Chemometrics, 2018, 32, e2929.	1.3	5
33	The landscape of miRNA-related ceRNA networks for marking different renal cell carcinoma subtypes. Briefings in Bioinformatics, 2018, , .	6.5	5
34	Individually double minimum-distance definition of proteinâ€“RNA binding residues and application to structure-based prediction. Journal of Computer-Aided Molecular Design, 2018, 32, 1363-1373.	2.9	5
35	Bipartite network analysis reveals metabolic gene expression profiles that are highly associated with the clinical outcomes of acute myeloid leukemia. Computational Biology and Chemistry, 2017, 67, 150-157.	2.3	8
36	Functional annotation of sixty-five type-2 diabetes risk SNPs and its application in risk prediction. Scientific Reports, 2017, 7, 43709.	3.3	4

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37	Functional dissection of human targets for KSHV-encoded miRNAs using network analysis. Scientific Reports, 2017, 7, 3159.	3.3	4
38	A sequence-based computational method for prediction of MoRFs. RSC Advances, 2017, 7, 18937-18945.	3.6	8
39	Exploring functions of long noncoding RNAs across multiple cancers through co-expression network. Scientific Reports, 2017, 7, 754.	3.3	41
40	Distinguishing the disease-associated SNPs based on composition frequency analysis. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 459-467.	3.6	4
41	Effective prediction of bacterial type IV secreted effectors by combined features of both C-termini and N-termini. Journal of Computer-Aided Molecular Design, 2017, 31, 1029-1038.	2.9	21
42	Expression dynamics and relations with nearby genes of rat transposable elements across 11 organs, 4 developmental stages and both sexes. BMC Genomics, 2017, 18, 666.	2.8	6
43	A New Network-Based Strategy for Predicting the Potential miRNA-mRNA Interactions in Tumorigenesis. International Journal of Genomics, 2017, 2017, 1-11.	1.6	5
44	Computational identifying and characterizing circular RNAs and their associated genes in hepatocellular carcinoma. PLoS ONE, 2017, 12, e0174436.	2.5	18
45	Mutation status coupled with RNA-sequencing data can efficiently identify important non-significantly mutated genes serving as diagnostic biomarkers of endometrial cancer. BMC Bioinformatics, 2017, 18, 472.	2.6	5
46	Expression profiling and functional annotation of noncoding genes across 11 distinct organs in rat development. Scientific Reports, 2016, 6, 38575.	3.3	4
47	A Combination of Chemometrics and Quantum Mechanics Methods Applied to Analysis of Femtosecond Transient Absorption Spectrum of Ortho-Nitroaniline. Scientific Reports, 2016, 6, 19364.	3.3	8
48	Molecular mechanism of carbon nanotube to activate Subtilisin Carlsberg in polar and non-polar organic media. Scientific Reports, 2016, 6, 36838.	3.3	9
49	A facile strategy applied to simultaneous qualitative-detection on multiple components of mixture samples: a joint study of infrared spectroscopy and multi-label algorithms on PBX explosives. RSC Advances, 2016, 6, 4713-4722.	3.6	1
50	Unfolding mechanism of thrombin-binding aptamer revealed by molecular dynamics simulation and Markov State Model. Scientific Reports, 2016, 6, 24065.	3.3	21
51	Exploring the mechanism of F282L mutation-caused constitutive activity of GPCR by a computational study. Physical Chemistry Chemical Physics, 2016, 18, 29412-29422.	2.8	11
52	Use of network model to explore dynamic and allosteric properties of three GPCR homodimers. RSC Advances, 2016, 6, 106327-106339.	3.6	12
53	A new strategy for exploring the hierarchical structure of cancers by adaptively partitioning functional modules from gene expression network. Scientific Reports, 2016, 6, 28720.	3.3	13
54	Dissecting the regulation rules of cancer-related miRNAs based on network analysis. Scientific Reports, 2016, 6, 34172.	3.3	9

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55	Position-specific prediction of methylation sites from sequence conservation based on information theory. Scientific Reports, 2015, 5, 12403.	3.3	22
56	A hybrid method for identification of structural domains. Scientific Reports, 2015, 4, 7476.	3.3	1
57	An eigenvalue transformation technique for predicting drug-target interaction. Scientific Reports, 2015, 5, 13867.	3.3	20
58	A structural dissection of large protein-protein crystal packing contacts. Scientific Reports, 2015, 5, 14214.	3.3	39
59	Domain position prediction based on sequence information by using fuzzy mean operator. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1462-1469.	2.6	0
60	Improving the Understanding of Pathogenesis of Human Papillomavirus 16 via Mapping Protein-Protein Interaction Network. BioMed Research International, 2015, 2015, 1-10.	1.9	8
61	Simultaneous determination of multiple components in explosives using ultraviolet spectrophotometry and a partial least squares method. RSC Advances, 2015, 5, 13021-13027.	3.6	16
62	Probing Immobilization Mechanism of alpha-chymotrypsin onto Carbon Nanotube in Organic Media by Molecular Dynamics Simulation. Scientific Reports, 2015, 5, 9297.	3.3	32
63	Visualizing the topology and re-analyzing the causes of small-world property of amino acid network. , 2015, , .		0
64	Age-related changes in functional connectivity between young adulthood and late adulthood. Analytical Methods, 2015, 7, 4111-4122.	2.7	8
65	A consensus subunit-specific model for annotation of substrate specificity for ABC transporters. RSC Advances, 2015, 5, 42009-42019.	3.6	6
66	Exploring the relationship between hub proteins and drug targets based on GO and intrinsic disorder. Computational Biology and Chemistry, 2015, 56, 41-48.	2.3	12
67	Comparative analysis of oncogenes identified by microarray and RNA-sequencing as biomarkers for clinical prognosis. Biomarkers in Medicine, 2015, 9, 1067-1078.	1.4	12
68	Characteristic wavenumbers of Raman spectra reveal the molecular mechanisms of oral leukoplakia and can help to improve the performance of diagnostic models. Analytical Methods, 2015, 7, 590-597.	2.7	1
69	Predicting the Druggability of Protein-Protein Interactions Based on Sequence and Structure Features of Active Pockets. Current Pharmaceutical Design, 2015, 21, 3051-3061.	1.9	3
70	A Systematic Investigation of Computation Models for Predicting Adverse Drug Reactions (ADRs). PLoS ONE, 2014, 9, e105889.	2.5	14
71	Hierarchically porous nitrogen-rich carbon derived from wheat straw as an ultra-high-rate anode for lithium ion batteries. Journal of Materials Chemistry A, 2014, 2, 9684-9690.	10.3	216
72	Predicting putative adverse drug reaction related proteins based on network topological properties. Analytical Methods, 2014, 6, 2692.	2.7	9

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73	Classification of multi-family enzymes by multi-label machine learning and sequence-based descriptors. Analytical Methods, 2014, 6, 6832.	2.7	8
74	Improving the prediction of chemotherapeutic sensitivity of tumors in breast cancer via optimizing the selection of candidate genes. Computational Biology and Chemistry, 2014, 49, 71-78.	2.3	7
75	Prediction of adverse drug reactions by a network based external link prediction method. Analytical Methods, 2013, 5, 6120.	2.7	21
76	The Effect of Edge Definition of Complex Networks on Protein Structure Identification. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-9.	1.3	4
77	Effective Identification of Gram-Negative Bacterial Type III Secreted Effectors Using Position-Specific Residue Conservation Profiles. PLoS ONE, 2013, 8, e84439.	2.5	27
78	A COMPARATIVE STUDY OF META/PARA SUBSTITUTION EFFECTS ON THE HYDROGEN-BONDED COMPLEX OF ANILINE-H2O: OBSERVATIONS FROM COMPUTATION. Journal of Theoretical and Computational Chemistry, 2011, 10, 567-579.	1.8	2
79	Studying Peptides Biological Activities Based on Multidimensional Descriptors (E) Using Support Vector Regression. International Journal of Peptide Research and Therapeutics, 2010, 16, 111-121.	1.9	10
80	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	17.5	795
81	Ensemble Multivariate Calibration Based on Mutual Information for Food Analysis Using Near-Infrared Spectroscopy. Analytical Letters, 2010, 43, 2640-2651.	1.8	3
82	Solvent effects on isolated formamide and its monohydrated complex: observations from PCM study. New Journal of Chemistry, 2009, 33, 1709.	2.8	12
83	Subspace Regression Ensemble Method Based on Variable Clustering for Near-Infrared Spectroscopic Calibration. Analytical Letters, 2009, 42, 1693-1710.	1.8	14
84	Optimal QSAR Analysis of the Carcinogenic Activity of Aromatic and Heteroaromatic Amines. QSAR and Combinatorial Science, 2008, 27, 543-554.	1.4	4
85	Substituent effects on the hydrogen-bonded complex of anilineâ€“H2O: a computational study. New Journal of Chemistry, 2008, 32, 1060.	2.8	17
86	Method for Infrared Spectral Compression Based on the Embedded Zerotree Wavelet. Spectroscopy Letters, 2005, 38, 171-184.	1.0	1