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	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
2	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
3	Exploring functions of long noncoding RNAs across multiple cancers through co-expression network. Scientific Reports, 2017, 7, 754.	3.3	41
4	A structural dissection of large protein-protein crystal packing contacts. Scientific Reports, 2015, 5, 14214.	3.3	39
5	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
6	Probing Immobilization Mechanism of alpha-chymotrypsin onto Carbon Nanotube in Organic Media by Molecular Dynamics Simulation. Scientific Reports, 2015, 5, 9297.	3.3	32
7	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
8	Effective Identification of Gram-Negative Bacterial Type III Secreted Effectors Using Position-Specific Residue Conservation Profiles. PLoS ONE, 2013, 8, e84439.	2.5	27
9	Position-specific prediction of methylation sites from sequence conservation based on information theory. Scientific Reports, 2015, 5, 12403.	3.3	22
10	Drug-Induced Rhabdomyolysis Atlas (DIRA) for idiosyncratic adverse drug reaction management. Drug Discovery Today, 2019, 24, 9-15.	6.4	22
11	Prediction of adverse drug reactions by a network based external link prediction method. Analytical Methods, 2013, 5, 6120.	2.7	21
12	Unfolding mechanism of thrombin-binding aptamer revealed by molecular dynamics simulation and Markov State Model. Scientific Reports, 2016, 6, 24065.	3.3	21
13	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
14	An eigenvalue transformation technique for predicting drug-target interaction. Scientific Reports, 2015, 5, 13867.	3.3	20
15	Computational identifying and characterizing circular RNAs and their associated genes in hepatocellular carcinoma. PLoS ONE, 2017, 12, e0174436.	2.5	18
16	Substituent effects on the hydrogen-bonded complex of anilineâ€“H2O: a computational study. New Journal of Chemistry, 2008, 32, 1060.	2.8	17
17	autoBioSeqpy: A Deep Learning Tool for the Classification of Biological Sequences. Journal of Chemical Information and Modeling, 2020, 60, 3755-3764.	5.4	17
18	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

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19	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
20	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
21	Subspace Regression Ensemble Method Based on Variable Clustering for Near-Infrared Spectroscopic Calibration. Analytical Letters, 2009, 42, 1693-1710.	1.8	14
22	A Systematic Investigation of Computation Models for Predicting Adverse Drug Reactions (ADRs). PLoS ONE, 2014, 9, e105889.	2.5	14
23	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
24	Solvent effects on isolated formamide and its monohydrated complex: observations from PCM study. New Journal of Chemistry, 2009, 33, 1709.	2.8	12
25	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
26	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
27	Use of network model to explore dynamic and allosteric properties of three GPCR homodimers. RSC Advances, 2016, 6, 106327-106339.	3.6	12
28	Transcriptome Analysis Identifies Piwi-Interacting RNAs as Prognostic Markers for Recurrence of Prostate Cancer. Frontiers in Genetics, 2019, 10, 1018.	2.3	12
29	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
30	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
31	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
32	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
33	Prediction of Synergistic Drug Combinations for Prostate Cancer by Transcriptomic and Network Characteristics. Frontiers in Pharmacology, 2021, 12, 634097.	3.5	10
34	Drug-induced QT Prolongation Atlas (DIQTA) for enhancing cardiotoxicity management. Drug Discovery Today, 2021, , .	6.4	10
35	Predicting putative adverse drug reaction related proteins based on network topological properties. Analytical Methods, 2014, 6, 2692.	2.7	9
36	Molecular mechanism of carbon nanotube to activate Subtilisin Carlsberg in polar and non-polar organic media. Scientific Reports, 2016, 6, 36838.	3.3	9

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37	Dissecting the regulation rules of cancer-related miRNAs based on network analysis. Scientific Reports, 2016, 6, 34172.	3.3	9
38	Classification of multi-family enzymes by multi-label machine learning and sequence-based descriptors. Analytical Methods, 2014, 6, 6832.	2.7	8
39	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
40	Age-related changes in functional connectivity between young adulthood and late adulthood. Analytical Methods, 2015, 7, 4111-4122.	2.7	8
41	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
42	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
43	A sequence-based computational method for prediction of MoRFs. RSC Advances, 2017, 7, 18937-18945.	3.6	8
44	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
45	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
46	Predicting HIV drug resistance using weighted machine learning method at target protein sequence-level. Molecular Diversity, 2021, 25, 1541-1551.	3.9	7
47	A consensus subunit-specific model for annotation of substrate specificity for ABC transporters. RSC Advances, 2015, 5, 42009-42019.	3.6	6
48	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
49	ExoceRNA atlas: A database of cancer ceRNAs in human blood exosomes. Life Sciences, 2020, 257, 118092.	4.3	6
50	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
51	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
52	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
53	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
54	The landscape of miRNA-related ceRNA networks for marking different renal cell carcinoma subtypes. Briefings in Bioinformatics, 2018, , .	6.5	5

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55	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
56	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
57	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
58	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
59	Optimal QSAR Analysis of the Carcinogenic Activity of Aromatic and Heteroaromatic Amines. QSAR and Combinatorial Science, 2008, 27, 543-554.	1.4	4
60	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
61	Expression profiling and functional annotation of noncoding genes across 11 distinct organs in rat development. Scientific Reports, 2016, 6, 38575.	3.3	4
62	Functional annotation of sixty-five type-2 diabetes risk SNPs and its application in risk prediction. Scientific Reports, 2017, 7, 43709.	3.3	4
63	Functional dissection of human targets for KSHV-encoded miRNAs using network analysis. Scientific Reports, 2017, 7, 3159.	3.3	4
64	Distinguishing the disease-associated SNPs based on composition frequency analysis. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 459-467.	3.6	4
65	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
66	The Power of Matrix Factorization: Methods for Deconvoluting Genetic Heterogeneous Data at Expression Level. Current Bioinformatics, 2021, 15, 841-853.	1.5	4
67	Ensemble Multivariate Calibration Based on Mutual Information for Food Analysis Using Near-Infrared Spectroscopy. Analytical Letters, 2010, 43, 2640-2651.	1.8	3
68	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
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	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
71	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
72	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

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73	A Multiple Comprehensive Analysis of scATAC-seq Based on Auto-Encoder and Matrix Decomposition. Symmetry, 2021, 13, 1467.	2.2	2
74	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
75	GFICLEE: ultrafast tree-based phylogenetic profile method inferring gene function at the genomic-wide level. BMC Genomics, 2021, 22, 774.	2.8	2
76	Method for Infrared Spectral Compression Based on the Embedded Zerotree Wavelet. Spectroscopy Letters, 2005, 38, 171-184.	1.0	1
77	A hybrid method for identification of structural domains. Scientific Reports, 2015, 4, 7476.	3.3	1
78	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
79	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
80	Genetic Contexts Characterize Dynamic Histone Modification Patterns Among Cell Types. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 698-710.	3.6	1
81	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
82	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
83	Domain position prediction based on sequence information by using fuzzy mean operator. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1462-1469.	2.6	0
84	Visualizing the topology and re-analyzing the causes of small-world property of amino acid network. , 2015, , .		0
85	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
86	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