

Kuo Yang

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

625
citations

933447

10
h-index

642732

23
g-index

30
all docs

30
docs citations

30
times ranked

595
citing authors

#	ARTICLE	IF	CITATIONS
1	PDGNet: Predicting Disease Genes Using a Deep Neural Network With Multi-View Features. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 575-584.	3.0	16
2	Link Prediction based on Tensor Decomposition for the Knowledge Graph of COVID-19 Antiviral Drug. Data Intelligence, 2022, 4, 134-148.	1.5	4
3	The TCM Preparation Feilike Mixture for the Treatment of Pneumonia: Network Analysis, Pharmacological Assessment and Silico Simulation. Frontiers in Pharmacology, 2022, 13, 794405.	3.5	6
4	TCMPR: TCM Prescription Recommendation Based on Subnetwork Term Mapping and Deep Learning. BioMed Research International, 2022, 2022, 1-12.	1.9	7
5	Phenonizer: A Fine-Grained Phenotypic Named Entity Recognizer for Chinese Clinical Texts. BioMed Research International, 2022, 2022, 1-12.	1.9	3
6	Decoding multilevel relationships with the human tissue-cell-molecule network. Briefings in Bioinformatics, 2022, 23, .	6.5	7
7	Add-On Chinese Medicine for Coronavirus Disease 2019 (ACCORD): A Retrospective Cohort Study of Hospital Registries. The American Journal of Chinese Medicine, 2021, 49, 543-575.	3.8	21
8	A network-based machine-learning framework to identify both functional modules and disease genes. Human Genetics, 2021, 140, 897-913.	3.8	9
9	FordNet: Recommending traditional Chinese medicine formula via deep neural network integrating phenotype and molecule. Pharmacological Research, 2021, 173, 105752.	7.1	33
10	Efficacy and Safety of TCMI in Patients With Combined Coronary Heart Disease and Heart Failure: A Systematic Review and Network Meta-Analysis. Frontiers in Pharmacology, 2021, 12, 741261.	3.5	4
11	Phenonizer: A fine-grained phenotypic named entity recognizer for Chinese clinical texts. , 2021, , .		0
12	TCMPR: TCM Prescription recommendation based on subnetwork term mapping and deep learning. , 2021, , .		4
13	Integrated Pharmacogenetics Analysis of the Three Fangjis Decoctions for Treating Arrhythmias Based on Molecular Network Patterns. Frontiers in Cardiovascular Medicine, 2021, 8, 726694.	2.4	0
14	Disease phenotype synonymous prediction through network representation learning from PubMed database. Artificial Intelligence in Medicine, 2020, 102, 101745.	6.5	5
15	Topological Analysis of the Language Networks of Ancient Traditional Chinese Medicine Books. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-10.	1.2	0
16	Integrated network analysis of symptom clusters across disease conditions. Journal of Biomedical Informatics, 2020, 107, 103482.	4.3	11
17	Identification of herbal categories active in pain disorder subtypes by machine learning help reveal novel molecular mechanisms of algia. Pharmacological Research, 2020, 156, 104797.	7.1	9
18	Network Patterns of Herbal Combinations in Traditional Chinese Clinical Prescriptions. Frontiers in Pharmacology, 2020, 11, 590824.	3.5	12

#	ARTICLE	IF	CITATIONS
19	Network-based gene prediction for TCM symptoms. , 2020, , .		2
20	Herb Target Prediction Based on Representation Learning of Symptom related Heterogeneous Network. Computational and Structural Biotechnology Journal, 2019, 17, 282-290.	4.1	26
21	HerGePred: Heterogeneous Network Embedding Representation for Disease Gene Prediction. IEEE Journal of Biomedical and Health Informatics, 2019, 23, 1805-1815.	6.3	51
22	SymMap: an integrative database of traditional Chinese medicine enhanced by symptom mapping. Nucleic Acids Research, 2019, 47, D1110-D1117.	14.5	301
23	SNFM: A semi-supervised NMF algorithm for detecting biological functional modules. Mathematical Biosciences and Engineering, 2019, 16, 1933-1948.	1.9	4
24	Overlapping functional modules detection in PPI network with pairwise constrained non-negative matrix tri-factorisation. IET Systems Biology, 2018, 12, 45-54.	1.5	8
25	Heterogeneous network embedding for identifying symptom candidate genes. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 1452-1459.	4.4	25
26	Integrated Modules Analysis to Explore the Molecular Mechanisms of Phlegm-Stasis Cementation Syndrome with Ischemic Heart Disease. Frontiers in Physiology, 2018, 9, 7.	2.8	21
27	Prediction of Molecular Mechanisms for LianXia NingXin Formula: A Network Pharmacology Study. Frontiers in Physiology, 2018, 9, 489.	2.8	16
28	Heterogeneous network propagation for herb target identification. BMC Medical Informatics and Decision Making, 2018, 18, 17.	3.0	7
29	Multistage analysis method for detection of effective herb prescription from clinical data. Frontiers of Medicine, 2018, 12, 206-217.	3.4	13
30	Integrating herb effect similarity for network-based herb target prediction. , 2015, , .		0