Suyu Mei

List of Publications by Year
in descending order

21 papers	460 citations	840776 11 h-index	752698 20 g-index
21 all docs	21 docs citations	21 times ranked	449 citing authors

#	Article	IF	Citations
1	Multi-kernel transfer learning based on Chou's PseAAC formulation for protein submitochondria localization. Journal of Theoretical Biology, 2012, 293, 121-130.	1.7	95
2	Gene ontology based transfer learning for protein subcellular localization. BMC Bioinformatics, 2011, 12, 44.	2.6	59
3	Probability Weighted Ensemble Transfer Learning for Predicting Interactions between HIV-1 and Human Proteins. PLoS ONE, 2013, 8, e79606.	2.5	48
4	Amino acid classification based spectrum kernel fusion for protein subnuclear localization. BMC Bioinformatics, 2010, 11, S17.	2.6	38
5	Multi-Label Multi-Kernel Transfer Learning for Human Protein Subcellular Localization. PLoS ONE, 2012, 7, e37716.	2.5	37
6	AdaBoost Based Multi-Instance Transfer Learning for Predicting Proteome-Wide Interactions between Salmonella and Human Proteins. PLoS ONE, 2014, 9, e110488.	2.5	30
7	A novel one-class SVM based negative data sampling method for reconstructing proteome-wide HTLV-human protein interaction networks. Scientific Reports, 2015, 5, 8034.	3.3	25
8	A machine learning framework for predicting drugâ€“drug interactions. Scientific Reports, 2021, 11, 17619.	3.3	19
9	SVM ensemble based transfer learning for large-scale membrane proteins discrimination. Journal of Theoretical Biology, 2014, 340, 105-110.	1.7	15
10	Multi-label multi-instance transfer learning for simultaneous reconstruction and cross-talk modeling of multiple human signaling pathways. BMC Bioinformatics, 2015, 16, 417.	2.6	14
11	A Multi-Label Learning Framework for Drug Repurposing. Pharmaceutics, 2019, 11, 466.	4.5	14
12	In silico unravelling pathogen-host signaling cross-talks via pathogen mimicry and human protein-protein interaction networks. Computational and Structural Biotechnology Journal, 2020, 18, 100-113.	4.1	12
13	Computational reconstruction of proteome-wide protein interaction networks between HTLV retroviruses and Homo sapiens. BMC Bioinformatics, 2014, 15, 245.	2.6	11
14	Transferring knowledge of bacterial protein interaction networks to predict pathogen targeted human genes and immune signaling pathways: a case study on M. tuberculosis. BMC Genomics, 2018, 19, 505.	2.8	11
15	Computational discovery of Epstein-Barr virus targeted human genes and signalling pathways. Scientific Reports, 2016, 6, 30612.	3.3	9
16	In Silico Enhancing M. tuberculosis Protein Interaction Networks in STRING To Predict Drug-Resistance Pathways and Pharmacological Risks. Journal of Proteome Research, 2018, 17, 1749-1760.	3.7	8
17	A computational framework for distinguishing directversusindirect interactions in human functional proteinâ€“protein interaction networks. Integrative Biology (United Kingdom), 2017, 9, 595-606.	1.3	7
18	Neglog: Homology-Based Negative Data Sampling Method for Genome-Scale Reconstruction of Human Proteinâ€“Protein Interaction Networks. International Journal of Molecular Sciences, 2019, 20, 5075.	4.1	6

#	Article	IF	Citations
19	A framework combines supervised learning and dense subgraphs discovery to predict protein complexes. Frontiers of Computer Science, 2022, 16, 1.	2.4	1
20	A machine learning framework for predicting synergistic and antagonistic drug combinatorial efficacy. Journal of Mathematical Chemistry, 2022, 60, 752-769.	1.5	1
21	A Computational Framework for Predicting Direct Contacts and Substructures within Protein Complexes. Biomolecules, 2019, 9, 656.	4.0	0