

Suyu Mei

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7037668/publications.pdf>

Version: 2024-02-01

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	A framework combines supervised learning and dense subgraphs discovery to predict protein complexes. <i>Frontiers of Computer Science</i> , 2022, 16, 1.	2.4	1
2	A machine learning framework for predicting synergistic and antagonistic drug combinatorial efficacy. <i>Journal of Mathematical Chemistry</i> , 2022, 60, 752-769.	1.5	1
3	A machine learning framework for predicting drug-drug interactions. <i>Scientific Reports</i> , 2021, 11, 17619.	3.3	19
4	In silico unravelling pathogen-host signaling cross-talks via pathogen mimicry and human protein-protein interaction networks. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 100-113.	4.1	12
5	A Multi-Label Learning Framework for Drug Repurposing. <i>Pharmaceutics</i> , 2019, 11, 466.	4.5	14
6	Neglog: Homology-Based Negative Data Sampling Method for Genome-Scale Reconstruction of Human Protein-Protein Interaction Networks. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5075.	4.1	6
7	A Computational Framework for Predicting Direct Contacts and Substructures within Protein Complexes. <i>Biomolecules</i> , 2019, 9, 656.	4.0	0
8	In Silico Enhancing <i>M. tuberculosis</i> Protein Interaction Networks in STRING To Predict Drug-Resistance Pathways and Pharmacological Risks. <i>Journal of Proteome Research</i> , 2018, 17, 1749-1760.	3.7	8
9	Transferring knowledge of bacterial protein interaction networks to predict pathogen targeted human genes and immune signaling pathways: a case study on <i>M. tuberculosis</i> . <i>BMC Genomics</i> , 2018, 19, 505.	2.8	11
10	A computational framework for distinguishing direct versus indirect interactions in human functional protein-protein interaction networks. <i>Integrative Biology (United Kingdom)</i> , 2017, 9, 595-606.	1.3	7
11	Computational discovery of Epstein-Barr virus targeted human genes and signalling pathways. <i>Scientific Reports</i> , 2016, 6, 30612.	3.3	9
12	Multi-label multi-instance transfer learning for simultaneous reconstruction and cross-talk modeling of multiple human signaling pathways. <i>BMC Bioinformatics</i> , 2015, 16, 417.	2.6	14
13	A novel one-class SVM based negative data sampling method for reconstructing proteome-wide HTLV-human protein interaction networks. <i>Scientific Reports</i> , 2015, 5, 8034.	3.3	25
14	AdaBoost Based Multi-Instance Transfer Learning for Predicting Proteome-Wide Interactions between Salmonella and Human Proteins. <i>PLoS ONE</i> , 2014, 9, e110488.	2.5	30
15	SVM ensemble based transfer learning for large-scale membrane proteins discrimination. <i>Journal of Theoretical Biology</i> , 2014, 340, 105-110.	1.7	15
16	Computational reconstruction of proteome-wide protein interaction networks between HTLV retroviruses and Homo sapiens. <i>BMC Bioinformatics</i> , 2014, 15, 245.	2.6	11
17	Probability Weighted Ensemble Transfer Learning for Predicting Interactions between HIV-1 and Human Proteins. <i>PLoS ONE</i> , 2013, 8, e79606.	2.5	48
18	Multi-Label Multi-Kernel Transfer Learning for Human Protein Subcellular Localization. <i>PLoS ONE</i> , 2012, 7, e37716.	2.5	37

#	ARTICLE	IF	CITATIONS
19	Multi-kernel transfer learning based on Chou's PseAAC formulation for protein submitochondria localization. <i>Journal of Theoretical Biology</i> , 2012, 293, 121-130.	1.7	95
20	Gene ontology based transfer learning for protein subcellular localization. <i>BMC Bioinformatics</i> , 2011, 12, 44.	2.6	59
21	Amino acid classification based spectrum kernel fusion for protein subnuclear localization. <i>BMC Bioinformatics</i> , 2010, 11, S17.	2.6	38