Ali Salehzadeh-Yazdi

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Impairment of DNA Methylation Maintenance Is the Main Cause of Global Demethylation in Naive Embryonic Stem Cells. Molecular Cell, 2016, 62, 848-861.	4.5	189
2	A systematic survey of centrality measures for protein-protein interaction networks. BMC Systems Biology, 2018, 12, 80.	3.0	133
3	Alterations in cancer cell metabolism: The Warburg effect and metabolic adaptation. Genomics, 2015, 105, 275-281.	1.3	90
4	CentiServer: A Comprehensive Resource, Web-Based Application and R Package for Centrality Analysis. PLoS ONE, 2015, 10, e0143111.	1.1	85
5	Controllability in Cancer Metabolic Networks According to Drug Targets as Driver Nodes. PLoS ONE, 2013, 8, e79397.	1.1	57
6	Evolution of Centrality Measurements for the Detection of Essential Proteins in Biological Networks. Frontiers in Physiology, 2016, 7, 375.	1.3	56
7	HomoTarget: A new algorithm for prediction of microRNA targets in Homo sapiens. Genomics, 2013, 101, 94-100.	1.3	30
8	Enzyme-Constrained Models and Omics Analysis of Streptomyces coelicolor Reveal Metabolic Changes that Enhance Heterologous Production. IScience, 2020, 23, 101525.	1.9	30
9	Comprehensive functional enrichment analysis of male infertility. Scientific Reports, 2017, 7, 15778.	1.6	27
10	Computational Models for Clinical Applications in Personalized Medicine—Guidelines and Recommendations for Data Integration and Model Validation. Journal of Personalized Medicine, 2022, 12, 166.	1.1	24
11	Unveiling network-based functional features through integration of gene expression into protein networks. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 2349-2359.	1.8	17
12	Computational Analysis of Reciprocal Association of Metabolism and Epigenetics in the Budding Yeast: A Genome-Scale Metabolic Model (GSMM) Approach. PLoS ONE, 2014, 9, e111686.	1.1	12
13	Exploring the Metabolic Heterogeneity of Cancers: A Benchmark Study of Context-Specific Models. Journal of Personalized Medicine, 2021, 11, 496.	1.1	11
14	A Metabolic Model of Intestinal Secretions: The Link between Human Microbiota and Colorectal Cancer Progression. Metabolites, 2021, 11, 456.	1.3	11
15	CytoKavosh: A Cytoscape Plug-In for Finding Network Motifs in Large Biological Networks. PLoS ONE, 2012, 7, e43287.	1.1	11
16	Meta-Analysis of Gene Expression Profiles in Acute Promyelocytic Leukemia Reveals Involved Pathways. International Journal of Hematology-Oncology and Stem Cell Research, 2017, 11, 1-12.	0.3	8
17	Computational structure analysis of biomacromolecule complexes by interface geometry. Computational Biology and Chemistry, 2013, 47, 16-23.	1.1	6
18	Cancerome: A hidden informative subnetwork of the diseasome. Computers in Biology and Medicine, 2016, 76, 173-177.	3.9	6

#	Article	IF	CITATIONS
19	Towards biomarkers for outcomes after pancreatic ductal adenocarcinoma and ischaemic stroke, with focus on (co)-morbidity and ageing/cellular senescence (SASKit): protocol for a prospective cohort study. BMJ Open, 2020, 10, e039560.	0.8	5
20	Computational analysis of RNA–protein interaction interfaces via the Voronoi diagram. Journal of Theoretical Biology, 2012, 293, 55-64.	0.8	4
21	Evolution of computational models in BioModels Database and the Physiome Model Repository. BMC Systems Biology, 2018, 12, 53.	3.0	3
22	Omics Integration Analyses Reveal the Early Evolution of Malignancy in Breast Cancer. Cancers, 2020, 12, 1460.	1.7	1
23	GEMtractor: extracting views into genome-scale metabolic models. Bioinformatics, 2020, 36, 3281-3282.	1.8	1
24	Hubs and Non-hubs in Protein-Protein Interaction Networks: A Biophysical Interpretation. , 2012, , .		0