

Ali Salehzadeh-Yazdi

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

25
papers

543
citations

11
h-index

23
g-index

31
ext. papers

733
ext. citations

4.8
avg, IF

3.58
L-index

#	Paper	IF	Citations
25	Computational Models for Clinical Applications in Personalized Medicine-Guidelines and Recommendations for Data Integration and Model Validation.. <i>Journal of Personalized Medicine</i> , 2022 , 12,	3.6	2
24	Exploring the Metabolic Heterogeneity of Cancers: A Benchmark Study of Context-Specific Models. <i>Journal of Personalized Medicine</i> , 2021 , 11,	3.6	5
23	A Metabolic Model of Intestinal Secretions: The Link between Human Microbiota and Colorectal Cancer Progression. <i>Metabolites</i> , 2021 , 11,	5.6	2
22	Omics Integration Analyses Reveal the Early Evolution of Malignancy in Breast Cancer. <i>Cancers</i> , 2020 , 12,	6.6	1
21	GEMtractor: extracting views into genome-scale metabolic models. <i>Bioinformatics</i> , 2020 , 36, 3281-3282	7.2	0
20	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. <i>BMJ Open</i> , 2020 , 10, e039560	3	1
19	Enzyme-Constrained Models and Omics Analysis of <i>Streptomyces coelicolor</i> Reveal Metabolic Changes that Enhance Heterologous Production. <i>IScience</i> , 2020 , 23, 101525	6.1	15
18	Unveiling network-based functional features through integration of gene expression into protein networks. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018 , 1864, 2349-2359	6.9	12
17	Evolution of computational models in BioModels Database and the Physiome Model Repository. <i>BMC Systems Biology</i> , 2018 , 12, 53	3.5	1
16	A systematic survey of centrality measures for protein-protein interaction networks. <i>BMC Systems Biology</i> , 2018 , 12, 80	3.5	73
15	Comprehensive functional enrichment analysis of male infertility. <i>Scientific Reports</i> , 2017 , 7, 15778	4.9	11
14	Meta-Analysis of Gene Expression Profiles in Acute Promyelocytic Leukemia Reveals Involved Pathways. <i>International Journal of Hematology-Oncology and Stem Cell Research</i> , 2017 , 11, 1-12	0.5	5
13	Impairment of DNA Methylation Maintenance Is the Main Cause of Global Demethylation in Naive Embryonic Stem Cells. <i>Molecular Cell</i> , 2016 , 62, 848-861	17.6	129
12	Evolution of Centrality Measurements for the Detection of Essential Proteins in Biological Networks. <i>Frontiers in Physiology</i> , 2016 , 7, 375	4.6	37
11	Cancerome: A hidden informative subnetwork of the diseasesome. <i>Computers in Biology and Medicine</i> , 2016 , 76, 173-7	7	3
10	Alterations in cancer cell metabolism: the Warburg effect and metabolic adaptation. <i>Genomics</i> , 2015 , 105, 275-81	4.3	66
9	CentiServer: A Comprehensive Resource, Web-Based Application and R Package for Centrality Analysis. <i>PLoS ONE</i> , 2015 , 10, e0143111	3.7	51

8	Computational analysis of reciprocal association of metabolism and epigenetics in the budding yeast: a genome-scale metabolic model (GSMM) approach. <i>PLoS ONE</i> , 2014 , 9, e111686	3.7	9
7	Computational structure analysis of biomacromolecule complexes by interface geometry. <i>Computational Biology and Chemistry</i> , 2013 , 47, 16-23	3.6	6
6	HomoTarget: a new algorithm for prediction of microRNA targets in Homo sapiens. <i>Genomics</i> , 2013 , 101, 94-100	4.3	22
5	Controllability in cancer metabolic networks according to drug targets as driver nodes. <i>PLoS ONE</i> , 2013 , 8, e79397	3.7	44
4	Integration of Metabolic Knowledge for Genome-Scale Metabolic Reconstruction 2013 , 1023-1048		
3	Computational analysis of RNA-protein interaction interfaces via the Voronoi diagram. <i>Journal of Theoretical Biology</i> , 2012 , 293, 55-64	2.3	3
2	CytoKavosh: a cytoscape plug-in for finding network motifs in large biological networks. <i>PLoS ONE</i> , 2012 , 7, e43287	3.7	10
1	A systematic survey of centrality measures for protein-protein interaction networks		3