Yazdan Asgari

List of Publications by Citations

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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.

32 319 9 17 g-index

38 421 3.4 3.52 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
32	Alterations in cancer cell metabolism: the Warburg effect and metabolic adaptation. <i>Genomics</i> , 2015 , 105, 275-81	4.3	66
31	CentiServer: A Comprehensive Resource, Web-Based Application and R Package for Centrality Analysis. <i>PLoS ONE</i> , 2015 , 10, e0143111	3.7	51
30	Controllability in cancer metabolic networks according to drug targets as driver nodes. <i>PLoS ONE</i> , 2013 , 8, e79397	3.7	44
29	Metabolic cancer biology: structural-based analysis of cancer as a metabolic disease, new sights and opportunities for disease treatment. <i>Seminars in Cancer Biology</i> , 2015 , 30, 21-9	12.7	31
28	Computer simulation study of the Levy flight process. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2009 , 388, 1509-1514	3.3	19
27	Network-based approach reveals Y chromosome influences prostate cancer susceptibility. <i>Computers in Biology and Medicine</i> , 2014 , 54, 24-31	7	17
26	Identification of candidate genes and proteins in aging skeletal muscle (sarcopenia) using gene expression and structural analysis. <i>PeerJ</i> , 2018 , 6, e5239	3.1	15
25	Obtaining critical point and shift exponent for the anisotropic two-layer Ising and Potts models: Cellular automata approach. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2008 , 387, 1937-1946	3.3	9
24	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
23	iMM1865: A New Reconstruction of Mouse Genome-Scale Metabolic Model. <i>Scientific Reports</i> , 2020 , 10, 6177	4.9	6
22	Reconstruction and Analysis of Cattle Metabolic Networks in Normal and Acidosis Rumen Tissue. <i>Animals</i> , 2020 , 10,	3.1	6
21	A network analysis of angiogenesis/osteogenesis-related growth factors in bone tissue engineering based on in-vitro and in-vivo data: A systems biology approach. <i>Tissue and Cell</i> , 2021 , 72, 101553	2.7	6
20	Exploring candidate biomarkers for lung and prostate cancers using gene expression and flux variability analysis. <i>Integrative Biology (United Kingdom)</i> , 2018 , 10, 113-120	3.7	5
19	MGL_3741 gene contributes to pathogenicity of Malassezia globosa in pityriasis versicolor. <i>Mycoses</i> , 2018 , 61, 938-944	5.2	5
18	CONSTRUCTING THE CRITICAL CURVE FOR THE TWO-LAYER POTTS MODEL USING CELLULAR AUTOMATA. <i>Journal of Theoretical and Computational Chemistry</i> , 2006 , 05, 141-150	1.8	5
17	Paclitaxel resistance resulted in a stem-like state in triple-negative breast cancer: A systems biology approach. <i>Meta Gene</i> , 2020 , 26, 100800	0.7	4
16	A systematic review of long non-coding RNAs with a potential role in breast cancer. <i>Mutation Research - Reviews in Mutation Research</i> , 2021 , 787, 108375	7	4

LIST OF PUBLICATIONS

Calculation of the Critical Point for Two-Layer Ising and Potts Models Using Cellular Automata. <i>Lecture Notes in Computer Science</i> , 2004 , 709-718	0.9	3
Analysis of the enzyme network involved in cattle milk production using graph theory. <i>Molecular Biology Research Communications</i> , 2015 , 4, 93-103	1.6	3
Network analysis reveals essential proteins that regulate sodium-iodide symporter expression in anaplastic thyroid carcinoma. <i>Scientific Reports</i> , 2020 , 10, 21440	4.9	3
Expression Analysis of Long Non-Coding RNAs Related With FOXM1, GATA3, FOXA1 and ESR1 in Breast Tissues. <i>Frontiers in Oncology</i> , 2021 , 11, 671418	5.3	3
SCAN-Toolbox: Structural COBRA Add-oN (SCAN) for Analysing Large Metabolic Networks. <i>Current Bioinformatics</i> , 2018 , 13, 100-107	4.7	1
Binder design for targeting SARS-CoV-2 spike protein: An in silico perspective. <i>Gene Reports</i> , 2022 , 26, 101452	1.4	1
Flux variability analysis reveals a tragedy of commons in cancer cells. SN Applied Sciences, 2020, 2, 1	1.8	1
Unveiling the structure of GPI-anchored protein of Malassezia globosa and its pathogenic role in pityriasis versicolor. <i>Journal of Molecular Modeling</i> , 2021 , 27, 246	2	O
Thioredoxin is a potential pathogenesis attribute of Malassezia globosa and Malassezia sympodialis in pityriasis versicolor. <i>Gene Reports</i> , 2019 , 17, 100468	1.4	
Integration of Metabolic Knowledge for Genome-Scale Metabolic Reconstruction 2013 , 1023-1048		
Constructing mRNA, miRNA, circRNA and lncRNA regulatory network by Analysis of microarray data in breast cancer. <i>Gene Reports</i> , 2022 , 26, 101510	1.4	
Lattice Gas Automata Simulation of 2D Site-Percolation Diffusion: Configuration Dependence of the Theoretically Expected Crossover of Diffusion Regime. <i>Lecture Notes in Computer Science</i> , 2008 , 274	l-281	
New Biomarkers Based on Smoking-Related Phenotypes for Smoking Cessation Outcomes of Nicotine Replacement Therapy: A Prospective Study <i>Basic and Clinical Neuroscience</i> , 2021 , 12, 639-650	1.4	
On the possibility of oscillating in the Ebola virus dynamics and investigating the effect of the lifetime of T lymphocytes <i>PLoS ONE</i> , 2022 , 17, e0265065	3.7	
Screening of candidate genes associated with high titer production of oncolytic measles virus based on systems biology approach <i>Virus Genes</i> , 2022 , 1	2.3	
	Analysis of the enzyme network involved in cattle milk production using graph theory. <i>Molecular Biology Research Communications</i> , 2015, 4, 93-103 Network analysis reveals essential proteins that regulate sodium-iodide symporter expression in anaplastic thyroid carcinoma. <i>Scientific Reports</i> , 2020, 10, 21440 Expression Analysis of Long Non-Coding RNAs Related With FOXM1, GATA3, FOXA1 and ESR1 in Breast Tissues. <i>Frontiers in Oncology</i> , 2021, 11, 671418 SCAN-Toolbox: Structural COBRA Add-oN (SCAN) for Analysing Large Metabolic Networks. <i>Current Bioinformatics</i> , 2018, 13, 100-107 Binder design for targeting SARS-CoV-2 spike protein: An in silico perspective. <i>Gene Reports</i> , 2022, 26, 101452 Flux variability analysis reveals a tragedy of commons in cancer cells. <i>SN Applied Sciences</i> , 2020, 2, 1 Unveiling the structure of GPI-anchored protein of Malassezia globosa and its pathogenic role in pityriasis versicolor. <i>Journal of Molecular Modeling</i> , 2021, 27, 246 Thioredoxin is a potential pathogenesis attribute of Malassezia globosa and Malassezia sympodialis in pityriasis versicolor. <i>Gene Reports</i> , 2019, 17, 100468 Integration of Metabolic Knowledge for Genome-Scale Metabolic Reconstruction 2013, 1023-1048 Constructing mRNA, miRNA, circRNA and IncRNA regulatory network by Analysis of microarray data in breast cancer. <i>Gene Reports</i> , 2022, 26, 101510 Lattice Gas Automata Simulation of 2D Site-Percolation Diffusion: Configuration Dependence of the Theoretically Expected Crossover of Diffusion Regime. <i>Lecture Notes in Computer Science</i> , 2008, 274 New Biomarkers Based on Smoking-Related Phenotypes for Smoking Cessation Outcomes of Nicotine Replacement Therapy: A Prospective Study. <i>Basic and Clinical Neuroscience</i> , 2021, 12, 639-650 On the possibility of oscillating in the Ebola virus dynamics and investigating the effect of the lifetime of T lymphocytes. <i>PLoS ONE</i> , 2022, 17, e0265065	Analysis of the enzyme network involved in cattle milk production using graph theory. Molecular Biology Research Communications, 2015, 4, 93-103 Network analysis reveals essential proteins that regulate sodium-iodide symporter expression in anaplastic thyroid carcinoma. Scientific Reports, 2020, 10, 21440 Expression Analysis of Long Non-Coding RNAs Related With FOXM1, GATA3, FOXA1 and ESR1 in Breast Tissues. Frontiers in Oncology, 2021, 11, 671418 SCAN-Toolbox: Structural COBRA Add-oN (SCAN) for Analysing Large Metabolic Networks. Current Bioinformatics, 2018, 13, 100-107 Binder design for targeting SARS-CoV-2 spike protein: An in silico perspective. Gene Reports, 2022, 26, 101452 Lunveiling the structure of GPI-anchored protein of Malassezia globosa and its pathogenic role in pityriasis versicolor. Journal of Molecular Modeling, 2021, 27, 246 Thioredoxin is a potential pathogenesis attribute of Malassezia globosa and Malassezia sympodialis in pityriasis versicolor. Gene Reports, 2019, 17, 100468 Integration of Metabolic Knowledge for Genome-Scale Metabolic Reconstruction 2013, 1023-1048 Constructing mRNA, miRNA, circRNA and IncRNA regulatory network by Analysis of microarray data in breast cancer. Gene Reports, 2022, 26, 101510 Lattice Gas Automata Simulation of 2D Site-Percolation Diffusion: Configuration Dependence of the Theoretically Expected Crossover of Diffusion Regime. Lecture Notes in Computer Science, 2008, 274-281 New Biomarkers Based on Smoking-Related Phenotypes for Smoking Cessation Outcomes of Nicotine Replacement Therapy: A Prospective Study. Basic and Clinical Neuroscience, 2021, 12, 639-650 On the possibility of oscillating in the Ebola virus dynamics and investigating the effect of the lifetime of T lymphocytes PLos ONE, 2022, 17, e0265065 Screening of candidate genes associated with high titer production of oncolytic measles virus