

Ali Sharifi-Zarchi

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

814
citations

567281

15
h-index

552781

26
g-index

49
all docs

49
docs citations

49
times ranked

1375
citing authors

#	ARTICLE	IF	CITATIONS
1	A Universal and Robust Integrated Platform for the Scalable Production of Human Cardiomyocytes From Pluripotent Stem Cells. <i>Stem Cells Translational Medicine</i> , 2015, 4, 1482-1494.	3.3	104
2	DNA methylation regulates discrimination of enhancers from promoters through a H3K4me1-H3K4me3 seesaw mechanism. <i>BMC Genomics</i> , 2017, 18, 964.	2.8	80
3	Inhibition of TGF β 2 Signaling Promotes Ground State Pluripotency. <i>Stem Cell Reviews and Reports</i> , 2014, 10, 16-30.	5.6	60
4	Small RNA Sequencing Reveals Dlk1-Dio3 Locus-Embedded MicroRNAs as Major Drivers of Ground-State Pluripotency. <i>Stem Cell Reports</i> , 2017, 9, 2081-2096.	4.8	45
5	Draft genome of <i>Dugesia japonica</i> provides insights into conserved regulatory elements of the brain restriction gene <i>nou-darake</i> in planarians. <i>Zoological Letters</i> , 2018, 4, 24.	1.3	38
6	Treatment of Human Embryonic Stem Cells with Different Combinations of Priming and Inducing Factors Toward Definitive Endoderm. <i>Stem Cells and Development</i> , 2013, 22, 1419-1432.	2.1	34
7	Analysis of gene expression profiles and protein-protein interaction networks in multiple tissues of systemic sclerosis. <i>BMC Medical Genomics</i> , 2019, 12, 199.	1.5	34
8	Machine Learning and Network Analysis of Molecular Dynamics Trajectories Reveal Two Chains of Red/Ox-specific Residue Interactions in Human Protein Disulfide Isomerase. <i>Scientific Reports</i> , 2017, 7, 3666.	3.3	33
9	DeePathology: Deep Multi-Task Learning for Inferring Molecular Pathology from Cancer Transcriptome. <i>Scientific Reports</i> , 2019, 9, 16526.	3.3	32
10	Proteome Analysis of Ground State Pluripotency. <i>Scientific Reports</i> , 2016, 5, 17985.	3.3	31
11	PIAS2-mediated blockade of IFN- β signaling: a basis for sporadic Parkinson disease dementia. <i>Molecular Psychiatry</i> , 2021, 26, 6083-6099.	7.9	30
12	MicroRNA profiling reveals important functions of miR-125b and let-7a during human retinal pigment epithelial cell differentiation. <i>Experimental Eye Research</i> , 2020, 190, 107883.	2.6	20
13	Whole genome sequencing of SARS-CoV2 strains circulating in Iran during five waves of pandemic. <i>PLoS ONE</i> , 2022, 17, e0267847.	2.5	20
14	StrongestPath: a Cytoscape application for protein-protein interaction analysis. <i>BMC Bioinformatics</i> , 2021, 22, 352.	2.6	19
15	Down-Regulation of miR-200c and Up-Regulation of miR-30c Target both Stemness and Metastasis Genes in Breast Cancer. <i>Cell Journal</i> , 2020, 21, 467-478.	0.2	17
16	The assessment of efficient representation of drug features using deep learning for drug repositioning. <i>BMC Bioinformatics</i> , 2019, 20, 577.	2.6	16
17	An integrated analysis to predict microRNAs targeting both stemness and metastasis in breast cancer stem cells. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 2442-2456.	3.6	15
18	Defining microRNA signatures of hair follicular stem and progenitor cells in healthy and androgenic alopecia patients. <i>Journal of Dermatological Science</i> , 2021, 101, 49-57.	1.9	15

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19	Comparative Evaluation of Human Dental Pulp and Follicle Stem Cell Commitment. <i>Cell Journal</i> , 2017, 18, 609-618.	0.2	15
20	Downregulation of Extracellular Matrix and Cell Adhesion Molecules in Cumulus Cells of Infertile Polycystic Ovary Syndrome Women with and without Insulin Resistance. <i>Cell Journal</i> , 2019, 21, 35-42.	0.2	15
21	Genome-wide DNA methylation profiling in ectopic and eutopic of endometrial tissues. <i>Journal of Assisted Reproduction and Genetics</i> , 2019, 36, 1743-1752.	2.5	14
22	Cell Identity Codes: Understanding Cell Identity from Gene Expression Profiles using Deep Neural Networks. <i>Scientific Reports</i> , 2019, 9, 2342.	3.3	14
23	Blockage of the Epithelial-to-Mesenchymal Transition Is Required for Embryonic Stem Cell Derivation. <i>Stem Cell Reports</i> , 2017, 9, 1275-1290.	4.8	12
24	An integrative Bayesian network approach to highlight key drivers in systemic lupus erythematosus. <i>Arthritis Research and Therapy</i> , 2020, 22, 156.	3.5	11
25	Increased robustness of early embryogenesis through collective decision-making by key transcription factors. <i>BMC Systems Biology</i> , 2015, 9, 23.	3.0	9
26	Pan-cancer analysis of microRNA expression profiles highlights microRNAs enriched in normal body cells as effective suppressors of multiple tumor types: A study based on TCGA database. <i>PLoS ONE</i> , 2022, 17, e0267291.	2.5	7
27	Genome-Wide Distribution of Nascent Transcripts in Sperm DNA, Products of a Late Wave of General Transcription. <i>Cells</i> , 2019, 8, 1196.	4.1	6
28	The metabolic network model of primed/naive human embryonic stem cells underlines the importance of oxidation-reduction potential and tryptophan metabolism in primed pluripotency. <i>Cell and Bioscience</i> , 2019, 9, 71.	4.8	6
29	Temporal activation of LRH $\hat{\epsilon}$ 1 and RAR $\hat{\epsilon}$ 3 in human pluripotent stem cells induces a functional na \tilde{v} e $\hat{\epsilon}$ like state. <i>EMBO Reports</i> , 2020, 21, e47533.	4.5	6
30	DNA-RNA Hybrid (R-Loop): From a Unified Picture of the Mammalian Telomere to the Genome-Wide Profile. <i>Cells</i> , 2021, 10, 1556.	4.1	6
31	Common-Deadline Lazy Bureaucrat Scheduling Problems. <i>Lecture Notes in Computer Science</i> , 2003, , 59-66.	1.3	6
32	Expression and Function of C1orf132 Long-Noncoding RNA in Breast Cancer Cell Lines and Tissues. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6768.	4.1	5
33	Graph Traversal Edit Distance and Extensions. <i>Journal of Computational Biology</i> , 2020, 27, 317-329.	1.6	4
34	miR-361-5p as a promising qRT-PCR internal control for tumor and normal breast tissues. <i>PLoS ONE</i> , 2021, 16, e0253009.	2.5	4
35	Determination of genetic characterization and circulation pattern of Respiratory Syncytial Virus (RSV) in children with a respiratory infection, Tehran, Iran, during 2018-2019. <i>Virus Research</i> , 2021, 305, 198564.	2.2	4
36	Evaluation of the Ankylosing Spondylitis Transcriptome for Oxidative Phosphorylation Pathway: The Shared Pathway with Neurodegenerative Diseases. <i>Iranian Journal of Allergy, Asthma and Immunology</i> , 2021, 20, 563-573.	0.4	4

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37	A novel panel of blood-based microRNAs capable of discrimination between benign breast disease and breast cancer at early stages. <i>RNA Biology</i> , 2021, 18, 747-756.	3.1	4
38	Transversals in long rectangular arrays. <i>Discrete Mathematics</i> , 2006, 306, 3011-3013.	0.7	3
39	Enhanced Waddington landscape model with cell-cell communication can explain molecular mechanisms of self-organization. <i>Bioinformatics</i> , 2019, 35, 4081-4088.	4.1	3
40	Dysregulation of ribosome-related genes in ankylosing spondylitis: a systems biology approach and experimental method. <i>BMC Musculoskeletal Disorders</i> , 2021, 22, 789.	1.9	3
41	Natural Biased Coin Encoded in the Genome Determines Cell Strategy. <i>PLoS ONE</i> , 2014, 9, e103569.	2.5	3
42	PyGTED: Python Application for Computing Graph Traversal Edit Distance. <i>Journal of Computational Biology</i> , 2020, 27, 436-439.	1.6	2
43	A novel metabolic disorder in the degradation pathway of endogenous methanol due to a mutation in the gene of alcohol dehydrogenase. <i>Clinical Biochemistry</i> , 2021, 90, 66-72.	1.9	2
44	Downregulation of <i>ITM2A</i> Gene Expression in Macrophages of Patients with Ankylosing Spondylitis. <i>International Archives of Allergy and Immunology</i> , 2021, 182, 1113-1121.	2.1	2
45	GTED: Graph Traversal Edit Distance. <i>Lecture Notes in Computer Science</i> , 2018, , 37-53.	1.3	1
46	ARYANA: Aligning Reads by Yet Another Approach. <i>BMC Bioinformatics</i> , 2014, 15, S12.	2.6	0