

Anis Karimpour-Fard

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

3,119
citations

394421

19
h-index

302126

39
g-index

40
all docs

40
docs citations

40
times ranked

5166
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrated analysis of miRNA-mRNA interaction in pediatric dilated cardiomyopathy. <i>Pediatric Research</i> , 2022, 92, 98-108.	2.3	12
2	Amniotic Fluid microRNA in Severe Twin-Twin Transfusion Syndrome Cardiomyopathy Identification of Differences and Predicting Demise. <i>Journal of Cardiovascular Development and Disease</i> , 2022, 9, 37.	1.6	2
3	Circulating cyclic adenosine monophosphate concentrations in milrinone treated paediatric patients after congenital heart surgery. <i>Cardiology in the Young</i> , 2021, 31, 1393-1400.	0.8	1
4	MAP3K7 Loss Drives Enhanced Androgen Signaling and Independently Confers Risk of Recurrence in Prostate Cancer with Joint Loss of CHD1. <i>Molecular Cancer Research</i> , 2021, 19, 1123-1136.	3.4	8
5	Amniotic fluid microRNA profiles in twin-twin transfusion syndrome with and without severe recipient cardiomyopathy. <i>American Journal of Obstetrics and Gynecology</i> , 2021, 225, 439.e1-439.e10.	1.3	5
6	Serum circulating proteins from pediatric patients with dilated cardiomyopathy cause pathologic remodeling and cardiomyocyte stiffness. <i>JCI Insight</i> , 2021, 6, .	5.0	7
7	Serum response factor deletion 5 regulates phospholamban phosphorylation and calcium uptake. <i>Journal of Molecular and Cellular Cardiology</i> , 2021, 159, 28-37.	1.9	1
8	MicroRNA regulation postbleomycin due to the R213G extracellular superoxide dismutase variant is predicted to suppress inflammatory and immune pathways. <i>Physiological Genomics</i> , 2020, 52, 245-254.	2.3	1
9	Circulating microRNAs differentiate Kawasaki Disease from infectious febrile illnesses in childhood. <i>Journal of Molecular and Cellular Cardiology</i> , 2020, 146, 12-18.	1.9	16
10	Analysis of Keloid Response to 5-Fluorouracil Treatment and Long-Term Prevention of Keloid Recurrence. <i>Plastic and Reconstructive Surgery</i> , 2019, 143, 490-494.	1.4	30
11	Origins of Intraindividual Genetic Variation in Human Fetuses. <i>Reproductive Sciences</i> , 2019, 26, 1139-1145.	2.5	0
12	Elevated serum vascular endothelial growth factor and development of cardiac allograft vasculopathy in children. <i>Journal of Heart and Lung Transplantation</i> , 2018, 37, 1075-1082.	0.6	9
13	Phosphodiesterase-5 Is Elevated in Failing Single Ventricle Myocardium and Affects Cardiomyocyte Remodeling In Vitro. <i>Circulation: Heart Failure</i> , 2018, 11, e004571.	3.9	32
14	R213G polymorphism in SOD3 protects against bleomycin-induced inflammation and attenuates induction of proinflammatory pathways. <i>Physiological Genomics</i> , 2018, 50, 807-816.	2.3	9
15	Improved Detection of Circulating miRNAs in Serum and Plasma Following Rapid Heat/Freeze Cycling. <i>MicroRNA (Sharjah, United Arab Emirates)</i> , 2018, 7, 138-147.	1.2	15
16	Myocardial microRNAs associated with reverse remodeling in human heart failure. <i>JCI Insight</i> , 2017, 2, e89169.	5.0	42
17	Pediatric dilated cardiomyopathy hearts display a unique gene expression profile. <i>JCI Insight</i> , 2017, 2, .	5.0	46
18	Amino acids in a targeted versus a non-targeted metabolomics LC-MS/MS assay. Are the results consistent?. <i>Clinical Biochemistry</i> , 2016, 49, 955-961.	1.9	32

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19	A survey of computational tools for downstream analysis of proteomic and other omic datasets. <i>Human Genomics</i> , 2015, 9, 28.	2.9	16
20	Coordinate Loss of <i>MAP3K7</i> and <i>CHD1</i> Promotes Aggressive Prostate Cancer. <i>Cancer Research</i> , 2015, 75, 1021-1034.	0.9	74
21	Circulating microRNA as a biomarker for recovery in pediatric dilated cardiomyopathy. <i>Journal of Heart and Lung Transplantation</i> , 2015, 34, 724-733.	0.6	65
22	Micro-RNA Expression in Hypoplastic Left Heart Syndrome. <i>Journal of Cardiac Failure</i> , 2015, 21, 83-88.	1.7	40
23	Metabolic changes associated with the long winter fast dominate the liver proteome in 13-lined ground squirrels. <i>Physiological Genomics</i> , 2014, 46, 348-361.	2.3	49
24	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.	27.8	320
25	Genome-scale identification and characterization of ethanol tolerance genes in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2013, 15, 124-133.	7.0	52
26	Kidney proteome changes provide evidence for a dynamic metabolism and regional redistribution of plasma proteins during torpor-arousal cycles of hibernation. <i>Physiological Genomics</i> , 2012, 44, 717-727.	2.3	21
27	Temporal analysis of mRNA and miRNA expression in transgenic mice overexpressing Arg- and Gly389 polymorphic variants of the β_1 -adrenergic receptor. <i>Physiological Genomics</i> , 2011, 43, 1294-1306.	2.3	17
28	Metabolic cycles in a circannual hibernator. <i>Physiological Genomics</i> , 2011, 43, 799-807.	2.3	64
29	Skeletal muscle proteomics: carbohydrate metabolism oscillates with seasonal and torpor-arousal physiology of hibernation. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2011, 301, R1440-R1452.	1.8	47
30	Multistate proteomics analysis reveals novel strategies used by a hibernator to precondition the heart and conserve ATP for winter heterothermy. <i>Physiological Genomics</i> , 2011, 43, 1263-1275.	2.3	42
31	A survey of analysis software for array-comparative genomic hybridisation studies to detect copy number variation. <i>Human Genomics</i> , 2010, 4, 421.	2.9	6
32	Rapid profiling of a microbial genome using mixtures of barcoded oligonucleotides. <i>Nature Biotechnology</i> , 2010, 28, 856-862.	17.5	265
33	Predicting protein linkages in bacteria: Which method is best depends on task. <i>BMC Bioinformatics</i> , 2008, 9, 397.	2.6	16
34	The topology of the bacterial co-conserved protein network and its implications for predicting protein function. <i>BMC Genomics</i> , 2008, 9, 313.	2.8	16
35	Gene copy number variation spanning 60 million years of human and primate evolution. <i>Genome Research</i> , 2007, 17, 1266-1277.	5.5	153
36	Cross-species cluster co-conservation: a new method for generating protein interaction networks. <i>Genome Biology</i> , 2007, 8, R185.	9.6	12

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37	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	12.6	1,283
38	Investigation of factors affecting prediction of protein-protein interaction networks by phylogenetic profiling. <i>BMC Genomics</i> , 2007, 8, 393.	2.8	16
39	Lineage-Specific Gene Duplication and Loss in Human and Great Ape Evolution. <i>PLoS Biology</i> , 2004, 2, e207.	5.6	263