

Mohammad Taghizadeh

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.

10
papers

214
citations

6
h-index

10
g-index

10
ext. papers

236
ext. citations

3
avg, IF

2.93
L-index

#	Paper	IF	Citations
10	Protein-protein interaction networks (PPI) and complex diseases. <i>Gastroenterology and Hepatology From Bed To Bench</i> , 2014 , 7, 17-31	1.2	92
9	Network-based analysis of differentially expressed genes in cerebrospinal fluid (CSF) and blood reveals new candidate genes for multiple sclerosis. <i>PeerJ</i> , 2016 , 4, e2775	3.1	40
8	Identification of new key genes for type 1 diabetes through construction and analysis of protein-protein interaction networks based on blood and pancreatic islet transcriptomes. <i>Journal of Diabetes</i> , 2017 , 9, 764-777	3.8	36
7	Identification of common key genes and pathways between type 1 diabetes and multiple sclerosis using transcriptome and interactome analysis. <i>Endocrine</i> , 2020 , 68, 81-92	4	15
6	Effects of silica nanoparticle supported ionic liquid as additive on thermal reversibility of human carbonic anhydrase II. <i>International Journal of Biological Macromolecules</i> , 2012 , 51, 933-8	7.9	13
5	Network analysis of membranous glomerulonephritis based on metabolomics data. <i>Molecular Medicine Reports</i> , 2018 , 18, 4197-4212	2.9	9
4	SDRL: a sequence-dependent protein side-chain rotamer library. <i>Molecular BioSystems</i> , 2015 , 11, 2000-7		4
3	Modified β -casein restores thermal reversibility of human carbonic anhydrase II: the salt bridge mechanism. <i>Biotechnology and Applied Biochemistry</i> , 2013 , 60, 298-304	2.8	3
2	Centrality Analysis of Protein-Protein Interaction Networks and Molecular Docking Prioritize Potential Drug-Targets in Type 1 Diabetes. <i>Iranian Journal of Pharmaceutical Research</i> , 2020 , 19, 121-134 ^{1.1}		2
1	Variability of the Cyclin-Dependent Kinase 2 Flexibility Without Significant Change in the Initial Conformation of the Protein or Its Environment; a Computational Study. <i>Iranian Journal of Biotechnology</i> , 2016 , 14, 1-12	1	0