

# I Arnold Emerson

## List of Publications by Year in descending order

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Version: 2024-02-01

19  
papers

101  
citations

1683354

5  
h-index

1473754

9  
g-index

19  
all docs

19  
docs citations

19  
times ranked

150  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular dynamic study on PTEN frameshift mutations in breast cancer provide c2 domain as a potential biomarker. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 3132-3143.	2.0	5
2	Global and regional connectivity analysis of resting-state function MRI brain images using graph theory in Parkinson's disease. <i>International Journal of Neuroscience</i> , 2021, 131, 105-115.	0.8	19
3	Network-based gene deletion analysis identifies candidate genes and molecular mechanism involved in clear cell renal cell carcinoma. <i>Journal of Genetics</i> , 2021, 100, 1.	0.4	4
4	Exploring the conformational dynamics and flexibility of intrinsically disordered HIV-1 Nef protein using molecular dynamic network approaches. <i>3 Biotech</i> , 2021, 11, 156.	1.1	0
5	Computational investigations on the dynamic binding effect of molecular tweezer CLR01 toward intrinsically disordered HIV-1 Nef. <i>Biotechnology and Applied Biochemistry</i> , 2021, 68, 513-530.	1.4	1
6	DCMP: database of cancer mutant protein domains. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	0
7	Network-based gene deletion analysis identifies candidate genes and molecular mechanism involved in clear cell renal cell carcinoma. <i>Journal of Genetics</i> , 2021, 100, .	0.4	0
8	Construction and analysis of brain networks from different neuroimaging techniques. <i>International Journal of Neuroscience</i> , 2020, , 1-22.	0.8	5
9	Gene Prioritization in Parkinson's Disease Using Human Protein-Protein Interaction Network. <i>Journal of Computational Biology</i> , 2020, 27, 1610-1621.	0.8	2
10	Dynamic conformational flexibility and molecular interactions of intrinsically disordered proteins. <i>Journal of Biosciences</i> , 2020, 45, 1.	0.5	13
11	Oncogenomics and CYP450 Implications in Personalized Cancer Therapy. <i>Current Pharmacogenomics and Personalized Medicine</i> , 2020, 17, 104-113.	0.2	0
12	Breast cancer mutation in GATA3 zinc finger 1 induces conformational changes leading to the closer binding of ZnFn2 with a wrapping architecture. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 38, 1-15.	2.0	5
13	Understanding contact patterns of protein structures from protein contact map and investigation of unique patterns in the globin-like folded domains. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 9877-9886.	1.2	4
14	Identification of target genes in cancer diseases using protein-protein interaction networks. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2019, 8, 1.	1.2	3
15	Protein contact maps: A binary depiction of protein 3D structures. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2017, 465, 782-791.	1.2	17
16	An Analysis of Central Residues Between Ligand-Bound and Ligand-Free Protein Structures Based on Network Approach. <i>Protein and Peptide Letters</i> , 2017, 24, 517-527.	0.4	2
17	Detection of Active Site Residues in Bovine Rhodopsin Using Network Analysis. <i>Trends in Bioinformatics</i> , 2015, 8, 63-74.	0.3	5
18	Network analysis of transmembrane protein structures. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2012, 391, 905-916.	1.2	12

#	ARTICLE	IF	CITATIONS
19	A Frame Work for Learning Drug Designing through Molecular Modelling Software Techniques and Biological Databases for Protein-Ligand Interactions. International Journal of Engineering Research in Africa, 0, 27, 111-118.	0.7	4