

Sachidanand Singh

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3624961/publications.pdf>

Version: 2024-02-01

16
papers

163
citations

1307594

7
h-index

1125743

13
g-index

16
all docs

16
docs citations

16
times ranked

211
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene co-expression network analysis for identifying genetic markers in Parkinson's disease - a three-way comparative approach. <i>Genomics</i> , 2019, 111, 819-830.	2.9	37
2	Diagnosis of Arthritis Through Fuzzy Inference System. <i>Journal of Medical Systems</i> , 2012, 36, 1459-1468.	3.6	36
3	Prioritization of potential vaccine candidates and designing a multi-epitope-based subunit vaccine against multidrug-resistant <i>Salmonella Typhi</i> str. CT18: A subtractive proteomics and immunoinformatics approach. <i>Microbial Pathogenesis</i> , 2021, 159, 105150.	2.9	15
4	SVMRFE based approach for prediction of most discriminatory gene target for type II diabetes. <i>Genomics Data</i> , 2017, 12, 28-37.	1.3	13
5	Uncovering potential Drug Targets for Tuberculosis using Protein Networks. <i>Bioinformatics</i> , 2012, 8, 403-406.	0.5	11
6	Molecular Modeling and Network Based Approach in Explaining the Medicinal Properties of <i>Nyctanthes arbor-tristis</i> , <i>Lippia nodiflora</i> for Rheumatoid Arthritis. <i>Journal of Bioinformatics and Intelligent Control</i> , 2014, 3, 31-38.	0.2	10
7	Implying Analytic Measures for Unravelling Rheumatoid Arthritis Significant Proteins Through Drug-Target Interaction. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2016, 8, 122-131.	3.6	8
8	Unwinding the Novel Genes Involved in the Differentiation of Embryonic Stem Cells into Insulin-Producing Cells: A Network-Based Approach. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017, 9, 88-95.	3.6	7
9	Pan-genomic analysis of the species <i>Salmonella enterica</i> : Identification of core essential and putative essential genes. <i>Gene Reports</i> , 2020, 20, 100669.	0.8	5
10	Classifying Rheumatoid Arthritis gene network signatures for identifying key regulatory molecules and their altered pathways by adopting network biology approach. <i>Gene Reports</i> , 2018, 13, 199-211.	0.8	4
11	Putative Target Identification for Gout; A Network Biology Approach. <i>Journal of Bionanoscience</i> , 2013, 7, 649-653.	0.4	4
12	Exploring Functional Diversity and Community Structure of Diazotrophic Endophytic Bacteria Associated with <i>Pennisetum glaucum</i> Growing under Field in a Semi-Arid Region. <i>Land</i> , 2022, 11, 991.	2.9	4
13	<i>Porphyromonas gingivalis</i> resistance and virulence: An integrated functional network analysis. <i>Gene</i> , 2022, 839, 146734.	2.2	4
14	Gene interaction map: a paradigm for identifying significant pathways responsible for rheumatoid arthritis. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2014, 3, 1.	2.1	2
15	Rheumatoid Arthritis Candidate Genes Identification by Investigating Core and Periphery Interaction Structures. <i>SpringerBriefs in Applied Sciences and Technology</i> , 2015, , 87-96.	0.4	2
16	Implying analytic measures for unraveling rheumatoid arthritis significant proteins through drug target interaction. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2015, , .	3.6	1