## Sachidanand Singh

List of Publications by Year in descending order

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

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16 papers	163 citations	7 h-index	1125743 13 g-index
16 all docs	16 docs citations	16 times ranked	211 citing authors

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