R K Brojen Singh

List of Publications by Year
in descending order

60 papers	770 citations	623699 14 h-index	642715 23 g-index
72 all docs	72 docs citations	72 times ranked	993 citing authors

#	Article	IF	Citations
1	Identification of key regulators in Sarcoidosis through multidimensional systems biological approach. Scientific Reports, 2022, 12, 1236.	3.3	4
2	Network Theoretical Approach to Explore Factors Affecting Signal Propagation and Stability in Dementiaâ€™s Protein-Protein Interaction Network. Biomolecules, 2022, 12, 451.	4.0	11
3	Network medicine in ovarian cancer: topological properties to drug discovery. Briefings in Bioinformatics, 2022, 23, .	6.5	7
4	CDK1 and HSP90AA1 Appear as the Novel Regulatory Genes in Non-Small Cell Lung Cancer: A Bioinformatics Approach. Journal of Personalized Medicine, 2022, 12, 393.	2.5	17
5	Troxerutin-Mediated Complement Pathway Inhibition is a Disease-Modifying Treatment for Inflammatory Arthritis. Frontiers in Cell and Developmental Biology, 2022, 10, 845457.	3.7	0
6	Identification of Potential Key Genes in Prostate Cancer with Gene Expression, Pivotal Pathways and Regulatory Networks Analysis Using Integrated Bioinformatics Methods. Genes, 2022, 13, 655.	2.4	10
7	Identification of key proteins in hostâ€"pathogen interactions between Mycobacterium tuberculosis and Homo sapiens: A systematic network theoretical approach. Healthcare Analytics, 2022, 2, 100052.	4.3	8
8	Functional genomics tools for studying microbe-mediated stress tolerance in plants. , 2022, , 175-204.		1
9	Elevated Vulnerability of Chronic Leukemia Patients to COVID-19 Infection: A Systems Biology Approach. Dr Sulaiman Al Habib Medical Journal, 2022, 4, 32-45.	0.8	1
10	Design of an epitope-based peptide vaccine against the SARS-CoV-2: a vaccine-informatics approach. Briefings in Bioinformatics, 2021, 22, 1309-1323.	6.5	28
11	Brain Disease Network Analysis to Elucidate the Neurological Manifestations of COVID-19. Molecular Neurobiology, 2021, 58, 1875-1893.	4.0	37
12	Noise and delay can shape distribution functions in stochastic reaction dynamics. Nonlinear Dynamics, 2021, 105, 797-811.	5.2	3
13	Interplay of cellular states: Role of delay as control mechanism. Physica A: Statistical Mechanics and Its Applications, 2021, 572, 125869.	2.6	6
14	Multilevel systems biology analysis of lung transcriptomics data identifies key miRNAs and potential miRNA target genes for SARS-CoV-2 infection. Computers in Biology and Medicine, 2021, 135, 104570.	7.0	31
15	Diversity of SARS-CoV-2 isolates driven by pressure and health index. Epidemiology and Infection, 2021, 149, e38.	2.1	5
16	Transition and identification of pathological states in p53 dynamics for therapeutic intervention. Scientific Reports, 2021, 11, 2349.	3.3	1
17	Identifying the natural polyphenol catechin as a multi-targeted agent against SARS-CoV-2 for the plausible therapy of COVID-19: an integrated computational approach. Briefings in Bioinformatics, 2021, 22, 1346-1360.	6.5	62
18	Alzheimerâ€™s Disease: An Overview of Major Hypotheses and Therapeutic Options in Nanotechnology. Nanomaterials, 2021, 11, 59.	4.1	14

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19	Network-based identification of miRNAs and transcription factors and in silico drug screening targeting Î³-secretase involved in Alzheimer's disease. Heliyon, 2021, 7, e08502.	3.2	4
20	A Bioinformatics Approach to Identifying Potential Biomarkers for Cryptosporidium parvum: A Coccidian Parasite Associated with Fetal Diarrhea. Vaccines, 2021, 9, 1427.	4.4	4
21	Kinless hubs are potential target genes in prostate cancer network. Genomics, 2020, 112, 5227-5239.	2.9	16
22	Molecular crosstalk: Notch can manipulate Hes1 and miR-9 behavior. Journal of Theoretical Biology, 2020, 504, 110404.	1.7	3
23	Stochastic approach to study control strategies of Covid-19 pandemic in India. Epidemiology and Infection, 2020, 148, e200.	2.1	4
24	Stochastic method to control Mycobacterium tuberculosis epidemic. Computational Biology and Chemistry, 2020, 87, 107250.	2.3	1
25	Differential levels of Alpha-1-inhibitor III, Immunoglobulin heavy chain variable region, and Hypertrophied skeletal muscle protein GTF3 in rat mammary tumorigenesis. Biochimie, 2020, 174, 57-68.	2.6	1
26	Development and rigorous validation of antimalarial predictive models using machine learning approaches. SAR and QSAR in Environmental Research, 2019, 30, 543-560.	2.2	14
27	Identification of key regulators in prostate cancer from gene expression datasets of patients. Scientific Reports, 2019, 9, 16420.	3.3	19
28	In silico characterization of hypothetical proteins from Orientia tsutsugamushi str. Karp uncovers virulence genes. Heliyon, 2019, 5, e02734.	3.2	10
29	Hamiltonian energy as an efficient approach to identify the significant key regulators in biological networks. PLoS ONE, 2019, 14, e0221463.	2.5	2
30	Identification and Classification of Differentially Expressed Genes and Network Meta-Analysis Reveals Potential Molecular Signatures Associated With Tuberculosis. Frontiers in Genetics, 2019, 10, 932.	2.3	26
31	Organization in complex brain networks: Energy distributions and phase shift. Journal of Theoretical Biology, 2019, 476, 30-35.	1.7	1
32	Universality in stochastic enzymatic futile cycle. Applied Mathematical Modelling, 2019, 74, 658-667.	4.2	2
33	<i>In Vitro</i> and <i>In Silico</i> Evaluation of Betulin on Calcium Oxalate Crystal Formation. Journal of the American College of Nutrition, 2019, 38, 586-596.	1.8	9
34	Draft genome sequence of Dichelobacter nodosus JKS-07 serogroup E from India. Journal of Global Antimicrobial Resistance, 2019, 16, 199-201.	2.2	0
35	Methodology of predicting novel key regulators in ovarian cancer network: a network theoretical approach. BMC Cancer, 2019, 19, 1129.	2.6	20
36	Neuronal communication: Stochastic neuron dynamics and multi-synchrony states. AEU - International Journal of Electronics and Communications, 2019, 100, 75-85.	2.9	5

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37	Fractal rules in brain networks: Signatures of self-organization. Journal of Theoretical Biology, 2018, 437, 58-66.	1.7	6
38	Exploring novel key regulators in breast cancer network. PLoS ONE, 2018, 13, e0198525.	2.5	20
39	Isolation and genome analysis of a lytic *Pasteurella multocida* Bacteriophage PMP-GAD-IND. Letters in Applied Microbiology, 2018, 67, 244-253.	2.2	4
40	Assessment of the key regulatory genes and their Interologs for Turner Syndrome employing network approach. Scientific Reports, 2018, 8, 10091.	3.3	26
41	Pharmacokinetic and Molecular Docking Studies of Plant-Derived Natural Compounds to Exploring Potential Anti-Alzheimer Activity. , 2018, , 217-238.		14
42	Stochastic synchronization of neurons: the topological impacts. Bioinformation, 2018, 14, 504-510.	0.5	1
43	Complex multifractal nature in Mycobacterium tuberculosis genome. Scientific Reports, 2017, 7, 46395.	3.3	7
44	Recent trends in ZikV research: A step away from cure. Biomedicine and Pharmacotherapy, 2017, 91, 1152-1159.	5.6	25
45	Potential entry inhibitors of the envelope protein (E2) of Chikungunya virus: in silico structural modeling, docking and molecular dynamic studies. VirusDisease, 2017, 28, 39-49.	2.0	18
46	Control of apoptosis by SMAR1. Molecular BioSystems, 2017, 13, 350-362.	2.9	14
47	Dynamical states, possibilities and propagation of stress signal. Scientific Reports, 2017, 7, 40596.	3.3	11
48	Identification of Inference Genes in Breast Cancer Network. Journal of Biosciences and Medicines, 2017, 05, 29-42.	0.2	2
49	From ZikV genome to vaccine: *in silico* approach for the epitope‐based peptide vaccine against Zika virus envelope glycoprotein. Immunology, 2016, 149, 386-399.	4.4	98
50	Identification of key regulators and their controlling mechanism in a combinatorial apoptosis network: a systems biology approach. Molecular BioSystems, 2016, 12, 3357-3369.	2.9	7
51	Scaling in topological properties of brain networks. Scientific Reports, 2016, 6, 24926.	3.3	21
52	Bifurcation in Cell Cycle Dynamics Regulated by p53. PLoS ONE, 2015, 10, e0129620.	2.5	7
53	Dynamics of p53 and Wnt cross talk. Computational Biology and Chemistry, 2015, 59, 55-66.	2.3	10
54	Apoptosis regulatory protein–protein interaction demonstrates hierarchical scale-free fractal network. Briefings in Bioinformatics, 2015, 16, 675-699.	6.5	24

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55	Ordering Dynamics in Neuron Activity Pattern Model: An Insight to Brain Functionality. PLoS ONE, 2015, 10, e0141463.	2.5	8
56	Evolutionary Trace Analysis of p53 Protein: A Statistical Analysis of Conserved Amino Acids in p53 Protein. Journal of Bioinformatics and Intelligent Control, 2014, 3, 194-201.	0.2	0
57	Switching p53 states by calcium: dynamics and interaction of stress systems. Molecular BioSystems, 2013, 9, 508.	2.9	13
58	The Dynamics of Stress p53-Mdm2 Network Regulated by p300 and HDAC1. PLoS ONE, 2013, 8, e52736.	2.5	14
59	Intercellular Synchronization of Coupled Smooth Muscle Cells via Ca^{2+} Propagation. Journal of Nanoscience and Nanotechnology, 2012, 12, 8303-8315.	0.9	3
60	Non-Markovian process with variable memory functions. Ricerche Di Matematica, 0, , 1.	1.0	0