

Achuthsankar S Nair

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

666
citations

840776

11
h-index

642732

23
g-index

58
all docs

58
docs citations

58
times ranked

763
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>In silico</i> screening and epitope mapping of leptospiral outer membrane proteinâ€”Lsa46. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 26-44.	3.5	4
2	Exploring the potent inhibitor Î²-stigmasterol from <i>Pittosporum dasycaulon</i> Miq. leaves against snake venom phospholipase A2 protein through <i>in vitro</i> and molecular dynamics behavior approach. <i>Toxin Reviews</i> , 2023, 42, 85-98.	3.4	2
3	Potential protease inhibitors and their combinations to block SARS-CoV-2. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 903-917.	3.5	15
4	Rutaretin1â€²-(6â€³-sinapoylglucoside): promising inhibitor of COVID 19 m ^{pro} catalytic dyad from the leaves of <i>Pittosporum dasycaulon</i> miq (Pittosporaceae). <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 12557-12573.	3.5	4
5	Bioinformatics screening of ETV4 transcription factor oncogenes and identifying smallâ€molecular anticancer drugs. <i>Chemical Biology and Drug Design</i> , 2022, 99, 277-285.	3.2	3
6	Identification of potential lead compounds against BACE1 through in-silico screening of phytochemicals of Medhya rasayana plants for Alzheimer's disease management. <i>Computers in Biology and Medicine</i> , 2022, 145, 105422.	7.0	4
7	Fingerprint-based similarity search identified <i>p</i> -anisidine as an anticancer agent in HeLa and a prospective phytochemical ETV1 transcription factor inhibitor. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 4973-4980.	3.5	2
8	Beijing genotype dominance among circulating Mycobacterium tuberculosis in patients with pulmonary tuberculosis in Belarus. <i>International Journal of Mycobacteriology</i> , 2021, 9, 19.	0.6	11
9	Molecular docking and molecular dynamics simulation identify a novel Radicol derivative that predicts exclusive binding to Plasmodium falciparum Topoisomerase VIB. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, , 1-13.	3.5	9
10	Identification of Hub Genes and Key Pathways Associated with Anti-VEGF Resistant Glioblastoma Using Gene Expression Data Analysis. <i>Biomolecules</i> , 2021, 11, 403.	4.0	12
11	Green synthesis and characterization of zinc oxide nanoparticles using Cayratia pedata leaf extract. <i>Biochemistry and Biophysics Reports</i> , 2021, 26, 100995.	1.3	142
12	Complete chloroplast genome of the medicinal plant <i>Evolvulus alsinoides</i> : comparative analysis, identification of mutational hotspots and evolutionary dynamics with species of Solanales. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1867-1884.	3.1	3
13	Synthesis and Characterization of Zinc Oxide Nanoparticles Using <i>Acacia caesia</i> Bark Extract and Its Photocatalytic and Antimicrobial Activities. <i>Catalysts</i> , 2021, 11, 1507.	3.5	25
14	High Quality Draft Genome of <i>Arogyapacha</i> (<i>Trichopus zeylanicus</i>), an Important Medicinal Plant Endemic to Western Ghats of India. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2395-2404.	1.8	9
15	SPARK-MSNA: Efficient algorithm on Apache Spark for aligning multiple similar DNA/RNA sequences with supervised learning. <i>Scientific Reports</i> , 2019, 9, 6631.	3.3	7
16	Molecular docking and dynamic studies of crepside E beta glucopyranoside as an inhibitor of snake venom PLA2. <i>Journal of Molecular Modeling</i> , 2019, 25, 88.	1.8	9
17	Glu-108 in <i>Saccharomyces cerevisiae</i> Rad51 Is Critical for DNA Damage-Induced Nuclear Function. <i>MSphere</i> , 2019, 4, .	2.9	4
18	The Complete Chloroplast Genome of <i>Trichopus zeylanicus</i> , And Phylogenetic Analysis with <i>Dioscoreales</i> . <i>Plant Genome</i> , 2019, 12, 1-11.	2.8	17

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19	Temporal VEGFA responsive genes in HUVECs: Gene signatures and potential ligands/receptors fine-tuning angiogenesis. <i>Journal of Cell Communication and Signaling</i> , 2019, 13, 561-571.	3.4	9
20	An Approach to Reveal the Possible Underlying Mechanisms Inherent to <i>Oecophylla smaragdina</i> as a Biocontrol Agent. <i>Proceedings of the National Academy of Sciences India Section B - Biological Sciences</i> , 2019, 89, 313-319.	1.0	0
21	Mathematical modelling of nonlinear dynamics generated from modular interconnections in cellular SOS response system. <i>Nonlinear Dynamics</i> , 2018, 93, 643-652.	5.2	1
22	Effect of Transducer Positioning in Active Noise Control. , 2018, , .		0
23	RBLOSUM performs better than CorBLOSUM with lesser error per query. <i>BMC Research Notes</i> , 2018, 11, 328.	1.4	1
24	HYPO: A Database of Human Hypothetical Proteins. <i>Protein and Peptide Letters</i> , 2018, 25, 799-803.	0.9	1
25	Computational study of HUB™ microRNA in human cardiac diseases. <i>Bioinformatics</i> , 2017, 13, 17-20.	0.5	4
26	Function annotation of peptides generated from the non-coding regions of <i>D. melanogaster</i> genome. <i>Bioinformatics</i> , 2016, 12, 202-208.	0.5	4
27	Effect of retroactivity in the dynamics of mixed feedback loop. , 2016, , .		1
28	NGS read data compression using parallel computing algorithm. , 2015, , .		1
29	Computational identification of novel microRNAs and their targets in the malarial vector, <i>Anopheles stephensi</i> . <i>Systems and Synthetic Biology</i> , 2015, 9, 11-17.	1.0	5
30	In silico study of peptide inhibitors against BACE 1. <i>Systems and Synthetic Biology</i> , 2015, 9, 67-72.	1.0	7
31	Predicting stable functional peptides from the intergenic space of <i>E. coli</i> . <i>Systems and Synthetic Biology</i> , 2015, 9, 135-140.	1.0	1
32	Heat Stress-Induced Cup9-Dependent Transcriptional Regulation of <i>SIR2</i> . <i>Molecular and Cellular Biology</i> , 2015, 35, 437-450.	2.3	12
33	Making novel proteins from pseudogenes. <i>Bioinformatics</i> , 2015, 31, 33-39.	4.1	18
34	Compression of Large genomic datasets using COMRAD on Parallel Computing Platform. <i>Bioinformatics</i> , 2015, 11, 267-271.	0.5	2
35	A bio-sequence k-mer frequency counter (kFC). , 2014, , .		1
36	Decahydroquinolines from the venom of a formicine ant, <i>Oecophylla smaragdina</i> . <i>Toxicon</i> , 2014, 92, 50-53.	1.6	2

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37	Studies on neutralizing effect of Ophiorrhiza mungos root extract against Daboia russelii venom. Journal of Ethnopharmacology, 2014, 151, 543-547.	4.1	29
38	Identifying pseudogenes from hypothetical proteins for making synthetic proteins. Systems and Synthetic Biology, 2014, 8, 169-171.	1.0	6
39	Cell Phenomena Are Reminiscent of Electric Circuits. IEEE Potentials, 2013, 32, 32-35.	0.3	0
40	Bagging with CTD – A Novel Signature for the Hierarchical Prediction of Secreted Protein Trafficking in Eukaryotes. Genomics, Proteomics and Bioinformatics, 2013, 11, 385-390.	6.9	3
41	A Novel Algorithm for Hub Protein Identification in H.Sapiens Using Global Amino Acid Features. Advances in Intelligent Systems and Computing, 2013, , 13-22.	0.6	0
42	A Novel Algorithm for Prediction of Hub Proteins from Primary Structure in Eukaryotic Proteome Using Dipeptide Compositional Skew Information and Amino Acid Sequence Likeness. , 2012, , 33-40.		0
43	Virtual screening for NS5B inhibitors of Hepatitis C virus. Nature Precedings, 2012, , .	0.1	0
44	Looking for a sequence based allostery definition: A statistical journey at different resolution scales. Journal of Theoretical Biology, 2012, 304, 211-218.	1.7	8
45	A Novel Algorithm for Hub Protein Identification in Prokaryotic Proteome Using Di-Peptide Composition and Hydrophobicity Ratio. Communications in Computer and Information Science, 2012, , 204-211.	0.5	0
46	Classification of proteins in intracellular and secretory pathway using global descriptors of amino acid sequence. , 2011, , .		0
47	Composition, Transition and Distribution (CTD) — A dynamic feature for predictions based on hierarchical structure of cellular sorting. , 2011, , .		41
48	Application of Recurrence Quantification Analysis (RQA) in Biosequence Pattern Recognition. Communications in Computer and Information Science, 2011, , 284-293.	0.5	4
49	Identification and analysis of novel microRNAs from fragile sites of human cervical cancer: Computational and experimental approach. Genomics, 2011, 97, 333-340.	2.9	20
50	Lacunarity Analysis of Protein Sequences Reveal Fractal Like Behavior of Amino Acid Distributions. Communications in Computer and Information Science, 2011, , 320-327.	0.5	0
51	Sequence signatures of allosteric proteins towards rational design. Systems and Synthetic Biology, 2010, 4, 271-280.	1.0	9
52	MTar: a computational microRNA target prediction architecture for human transcriptome. BMC Bioinformatics, 2010, 11, S2.	2.6	55
53	Protein location prediction using atomic composition and global features of the amino acid sequence. Biochemical and Biophysical Research Communications, 2010, 391, 1670-1674.	2.1	19
54	Fractality of numeric and symbolic sequences. IEEE Potentials, 2010, 29, 36-39.	0.3	4

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55	A coding measure scheme employing electron-ion interaction pseudopotential (EIIP). <i>Bioinformation</i> , 2006, 1, 197-202.	0.5	107
56	Are categorical periodograms and indicator sequences of genomes spectrally equivalent?. <i>In Silico Biology</i> , 2006, 6, 215-22.	0.9	2
57	A computational-cum-experimental study provides some clues on the druggable binding site and design of anticancer therapeutics on ETV1 transcription factor oncoprotein. <i>Molecular Systems Design and Engineering</i> , 0, , .	3.4	1