

Udhaya Kumar S

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

828
citations

623574

14
h-index

526166

27
g-index

43
all docs

43
docs citations

43
times ranked

705
citing authors

#	ARTICLE	IF	CITATIONS
1	The Rise and Impact of COVID-19 in India. <i>Frontiers in Medicine</i> , 2020, 7, 250.	1.2	100
2	Analysis of Differentially Expressed Genes and Molecular Pathways in Familial Hypercholesterolemia Involved in Atherosclerosis: A Systematic and Bioinformatics Approach. <i>Frontiers in Genetics</i> , 2020, 11, 734.	1.1	82
3	PSO-based feature selection and neighborhood rough set-based classification for BCI multiclass motor imagery task. <i>Neural Computing and Applications</i> , 2017, 28, 3239-3258.	3.2	75
4	Integrative Bioinformatics Approaches to Map Potential Novel Genes and Pathways Involved in Ovarian Cancer. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 391.	2.0	72
5	Dysregulation of Signaling Pathways Due to Differentially Expressed Genes From the B-Cell Transcriptomes of Systemic Lupus Erythematosus Patients – A Bioinformatics Approach. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 276.	2.0	57
6	Involvement of Essential Signaling Cascades and Analysis of Gene Networks in Diabesity. <i>Genes</i> , 2020, 11, 1256.	1.0	32
7	A systemic approach to explore the mechanisms of drug resistance and altered signaling cascades in extensively drug-resistant tuberculosis. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021, 127, 343-364.	1.0	30
8	Network analysis of transcriptomics data for the prediction and prioritization of membrane-associated biomarkers for idiopathic pulmonary fibrosis (IPF) by bioinformatics approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021, 123, 241-273.	1.0	29
9	Hybrid rough-bijjective soft set classification system. <i>Neural Computing and Applications</i> , 2018, 29, 67-78.	3.2	28
10	Molecular dynamics, residue network analysis, and cross-correlation matrix to characterize the deleterious missense mutations in GALE causing galactosemia III. <i>Cell Biochemistry and Biophysics</i> , 2021, 79, 201-219.	0.9	23
11	Comprehensive in silico screening and molecular dynamics studies of missense mutations in Sjogren-Larsson syndrome associated with the ALDH3A2 gene. <i>Advances in Protein Chemistry and Structural Biology</i> , 2020, 120, 349-377.	1.0	21
12	Structure-Based Virtual Screening to Identify Novel Potential Compound as an Alternative to Remdesivir to Overcome the RdRp Protein Mutations in SARS-CoV-2. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 645216.	1.6	20
13	An extensive computational approach to analyze and characterize the functional mutations in the galactose-1-phosphate uridyl transferase (GALT) protein responsible for classical galactosemia. <i>Computers in Biology and Medicine</i> , 2020, 117, 103583.	3.9	19
14	Mutational landscape of K-Ras substitutions at 12th position-a systematic molecular dynamics approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 1571-1585.	2.0	16
15	An integrative analysis to distinguish between emphysema (EML) and alpha-1 antitrypsin deficiency-related emphysema (ADL) – A systems biology approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021, 127, 315-342.	1.0	16
16	A review of novel coronavirus disease (COVID-19): based on genomic structure, phylogeny, current shreds of evidence, candidate vaccines, and drug repurposing. <i>3 Biotech</i> , 2021, 11, 198.	1.1	15
17	Computational investigation to identify potent inhibitors of the GTPase-Kirsten RAt sarcoma virus (K-Ras) mutants G12C and G12D. <i>Computers in Biology and Medicine</i> , 2021, 139, 104946.	3.9	15
18	A review of bioinformatics tools and web servers in different microarray platforms used in cancer research. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, , 85-164.	1.0	15

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19	Identification of potential inhibitors against pathogenic missense mutations of PMM2 using a structure-based virtual screening approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 171-187.	2.0	14
20	Mutations in ARSB in MPS VI patients in India. <i>Molecular Genetics and Metabolism Reports</i> , 2015, 4, 53-61.	0.4	13
21	A computational model revealing the immune-related hub genes and key pathways involved in rheumatoid arthritis (RA). <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, 129, 247-273.	1.0	12
22	Isolation, characterization, and in vitro evaluation of bovine rumen submucosa films of collagen or chitosan-treated collagen. <i>Journal of Biomaterials Applications</i> , 2016, 30, 780-792.	1.2	11
23	Deciphering the Role of Filamin B Calponin-Homology Domain in Causing the Larsen Syndrome, Boomerang Dysplasia, and Atelosteogenesis Type I Spectrum Disorders via a Computational Approach. <i>Molecules</i> , 2020, 25, 5543.	1.7	10
24	Kerala, India's Front Runner in Novel Coronavirus Disease (COVID-19). <i>Frontiers in Medicine</i> , 2020, 7, 355.	1.2	9
25	Molecular dynamics simulations to decipher the structural and functional consequences of pathogenic missense mutations in the galactosylceramidase (GALC) protein causing Krabbe's disease. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 1795-1810.	2.0	8
26	Comparison of potential inhibitors and targeting fat mass and obesity-associated protein causing diabetes through docking and molecular dynamics strategies. <i>Journal of Cellular Biochemistry</i> , 2021, 122, 1625-1638.	1.2	8
27	Investigating mutations at the hotspot position of the ERBB2 and screening for the novel lead compound to treat breast cancer – a computational approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021, 123, 49-71.	1.0	7
28	Unraveling the versatility of CCD4: Metabolic engineering, transcriptomic and computational approaches. <i>Plant Science</i> , 2021, 310, 110991.	1.7	7
29	Computational model to analyze and characterize the functional mutations of NOD2 protein causing inflammatory disorder – Blau syndrome. <i>Advances in Protein Chemistry and Structural Biology</i> , 2020, 120, 379-408.	1.0	7
30	Understanding the activating mechanism of the immune system against COVID-19 by Traditional Indian Medicine: Network pharmacology approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, 129, 275-379.	1.0	7
31	Whole-exome sequencing analysis of NSCLC reveals the pathogenic missense variants from cancer-associated genes. <i>Computers in Biology and Medicine</i> , 2022, 148, 105701.	3.9	7
32	Functional and structural characterization of missense mutations in PAX6 gene. <i>Frontiers in Biology</i> , 2015, 10, 377-385.	0.7	6
33	Znf76 is associated with development of the eyes, midbrain, MHB, and hindbrain in zebrafish embryos. <i>Animal Cells and Systems</i> , 2019, 23, 26-31.	0.8	6
34	Mutations in G6PC2 gene with increased risk for development of type 2 diabetes: Understanding via computational approach. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, 130, 351-373.	1.0	6
35	Integrative ontology and pathway-based approach identifies distinct molecular signatures in transcriptomes of esophageal squamous cell carcinoma. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, , 177-206.	1.0	6
36	Identification of potential inhibitors, conformational dynamics, and mechanistic insights into mutant Kirsten rat sarcoma virus (G13D) driven cancers. <i>Journal of Cellular Biochemistry</i> , 2022, 123, 1467-1480.	1.2	6

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37	Residue interaction networks of K-Ras protein with water molecules identifies the potential role of switch II and P-loop. <i>Computers in Biology and Medicine</i> , 2021, 135, 104597.	3.9	4
38	Computational structural assessment of Breast Cancer type 1 susceptibility protein (BRCA1) and BRCA1-Associated Ring Domain protein 1 (BARD1) mutations on the protein-protein interface. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, 130, 375-397.	1.0	4
39	Computational validation of ABCB1 gene polymorphism and its effect on tacrolimus dose concentration/levels in renal transplant individuals of South India. <i>Computers in Biology and Medicine</i> , 2021, 139, 104971.	3.9	2
40	Investigation of differentially expressed genes and dysregulated pathways involved in multiple sclerosis. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, , 235-259.	1.0	2
41	Spark Based Framework for Breast Cancer Analysis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
42	A computational overview on phylogenetic characterization, pathogenic mutations, and drug targets for Ebola virus disease. <i>Current Opinion in Pharmacology</i> , 2021, 61, 28-35.	1.7	0
43	Siddha Medicine and Computer Modeling: A Treasure for SARS-CoV-2 Treatment. <i>Studies in Systems, Decision and Control</i> , 2022, , 521-541.	0.8	0