Anum Munir

List of Publications by Year
in descending order

30 papers	138 citations	1478505 6 h-index	1281871 11 g-index
30 all docs	30 docs citations	30 times ranked	255 citing authors

#	Article	IF	Citations
1	nCOV-19 peptides mass fingerprinting identification, binding, and blocking of inhibitors flavonoids and anthraquinone of <i>Moringa oleifera</i> and hydroxychloroquine. Journal of Biomolecular Structure and Dynamics, 2021, 39, 4089-4099.	3.5	31
2	Subtractive Proteome Mining Approach towards Unique Putative Drug Targets Identification for Salmonella typhimurium. Infectious Disorders - Drug Targets, 2021, 20, 884-892.	0.8	1
3	Gene expression profiling utilizing extremely sensitive CDNA arrays and enrichment-based network study of major bone cancer genes. Journal of Research in Medical Sciences, 2021, 26, 49.	0.9	0
4	In-silico network-based analysis of drugs used against COVID-19: Human well-being study. Saudi Journal of Biological Sciences, 2021, 28, 2029-2039.	3.8	2
5	In silico analysis of quranic and prophetic medicinals plants for the treatment of infectious viral diseases including corona virus. Saudi Journal of Biological Sciences, 2021, 28, 3137-3151.	3.8	18
6	Identification of differentially expressed genes and pathways crosstalk analysis in Rheumatoid and Osteoarthritis using next-generation sequencing and protein-protein networks. Saudi Journal of Biological Sciences, 2021, 28, 4656-4663.	3.8	4
7	Proteomic Analysis of Medicinal Plant Calotropis Gigantea by In Silico Peptide Mass Fingerprinting. Current Computer-Aided Drug Design, 2021, 17, 254-265.	1.2	3
8	Synthesized Drug from Medicinal Plant phytochemicals Effectively Targets ECM1 Gene Mutations in Ulcerative Colitis. Letters in Drug Design and Discovery, 2021, 18, .	0.7	0
9	In silico authentication of amygdalin as a potent anticancer compound in the bitter kernels of family Rosaceae. Saudi Journal of Biological Sciences, 2020, 27, 2444-2451.	3.8	17
10	Modeling of apoptosis through gene interaction network and analysis of gene expression pattern. Meta Gene, 2020, 25, 100730.	0.6	2
11	Repositioning of strongly integrated drugs against achromatopsia (CNGB3). Journal of King Saud University - Science, 2020, 32, 1793-1811.	3.5	6
12	Effect of Modified Aspirin and Isoxsuprine Analogs on Ischemic Heart Disease. Advances in Pharmacology and Pharmacy, 2020, 8, 31-40.	0.2	1
13	In silico Structure Prediction and Functional Annotation of Ananas comosus Hypothetical Protein OAY63476.1. International Journal Bioautomation, 2020, 24, 349-358.	0.3	0
14	De-Novo Ligand Design against Mutated Huntington Gene by Ligand-based Pharmacophore Modeling Approach. Current Computer-Aided Drug Design, 2020, 16, 134-144.	1.2	1
15	In silico T-cell and B-cell Epitope Based Vaccine Design Against Alphavirus Strain of Chikungunya. Infectious Disorders - Drug Targets, 2020, 20, 523-530.	0.8	2
16	Computational approach to design potential siRNA for CDKN2A gene silencing in melanoma through RNA interference. Gene Reports, 2019, 17, 100469.	0.8	0
17	Mathematical Modeling and Docking of Medicinal Plants and Synthetic Drugs to Determine Their Effects on Abnormal Expression of Cholinesterase and Acetyl Cholinesterase Proteins in Alzheimer. Lecture Notes in Computer Science, 2019, , 111-127.	1.3	0
18	Single-Cell Omics in CVDs. , 2019, , 129-152.		1

#	Article	IF	Citations
19	Design and Synthesis of Novel Inhibitor against Ser121 and Val122 Mutations in P53 Cancer Gene. Advances in Pharmacology and Pharmacy, 2019, 7, 63-70.	0.2	5
20	Proteome Mining for the Identification of Putative Drug Targets For Human Pathogen Clostridium Tetani. Current Bioinformatics, 2019, 14, 532-540.	1.5	19
21	Treatment against Mutation of PIK3CA Gene Involved in Lung Cancer by Structure Base Pharmacophore Modeling, Virtual Screening and Molecular Docking. Advances in Pharmacology and Pharmacy, 2019, 7, 71-84.	0.2	0
22	Computational Prediction of Tumor-Specific Antigens as Potential Vaccine Candidates against Germ-line Mutations in Endometrial Cancer. Advances in Pharmacology and Pharmacy, 2019, 7, 55-62.	0.2	0
23	Clustering based drug-drug interaction networks for possible repositioning of drugs against EGFR mutations: Clustering based DDI networks for EGFR mutations. Computational Biology and Chemistry, 2018, 75, 24-31.	2.3	8
24	Evaluation of the whole body physiologically based pharmacokinetic (WB-PBPK) modeling of drugs. Journal of Theoretical Biology, 2018, 451, 1-9.	1.7	0
25	Silver nanoparticles conjugated with Neurotrophin 3 upregulate myelin gene transcription pathway. Journal of Theoretical Biology, 2018, 459, 111-118.	1.7	2
26	Computational design of small interfering RNAs and small hairpin RNAs to silence mutated P53 gene expressions. Informatics in Medicine Unlocked, 2018, 12, 1-5.	3.4	2
27	Repurposing of Modified Alpidem and Propoxyphene to Cure AURKA, BCAS1, GNAS and MLH1 Gene Mutations in Colorectal Cancer. Drug Designing: Open Access, 2017, 06, .	0.2	2
28	In-Silico Identification of Novel Resistant Genes for Fungal Pathogen Fusarium oxysporum f. sp. cubense Race 4: Causative Agent of Banana Vascular Wilt Disease. Journal of Plant Biochemistry & Physiology, 2017, 05, .	0.5	1
29	Structure-Based Pharmacophore Modeling, Virtual Screening and Molecular docking for the Treatment of ESR1 Mutations in Breast Cancer. Drug Designing: Open Access, 2016, 05, .	0.2	9
30	Computational drug ZINPIP-Analog an ultimate solution to cure conserved domains of mutant EGFR, ALK and BRAF Proteins in NSCLC. International Current Pharmaceutical Journal, 2015, 4, 396-401.	0.3	1