Muhammad Tahir Ul Qamar

List of Publications by Citations

87 papers	1,664 citations	20 h-index	38 g-index
100 ext. papers	2,416 ext. citations	4.7 avg, IF	5.8 L-index

#	Paper	IF	Citations
87	Structural basis of SARS-CoV-2 3CL and anti-COVID-19 drug discovery from medicinal plants. *Journal of Pharmaceutical Analysis*, **2020**, 10, 313-319	14	477
86	Epitope-based peptide vaccine design and target site depiction against Middle East Respiratory Syndrome Coronavirus: an immune-informatics study. *Journal of Translational Medicine*, **2019**, 17, 362	8.5	93
85	Pharmacoinformatics and molecular dynamics simulation studies reveal potential covalent and FDA-approved inhibitors of SARS-CoV-2 main protease 3CL. *Journal of Biomolecular Structure and Dynamics*, **2021**, 39, 4936-4948	3.6	71
84	Computational screening of medicinal plant phytochemicals to discover potent pan-serotype inhibitors against dengue virus. *Scientific Reports*, **2019**, 9, 1433	4.9	61
83	Promising terpenes as SARS-CoV-2 spike receptor-binding domain (RBD) attachment inhibitors to the human ACE2 receptor: Integrated computational approach. *Journal of Molecular Liquids*, **2020**, 320, 114493	6	46
82	Designing of a next generation multiepitope based vaccine (MEV) against SARS-COV-2: Immunoinformatics and in silico approaches. *PLoS ONE*, **2020**, 15, e0244176	3.7	43
81	MPD3: a useful medicinal plants database for drug designing. *Natural Product Research*, **2017**, 31, 1228-1236	2.3	42
80	Reverse vaccinology assisted designing of multiepitope-based subunit vaccine against SARS-CoV-2. *Infectious Diseases of Poverty*, **2020**, 9, 132	10.4	38
79	Discovery of human coronaviruses pan-papain-like protease inhibitors using computational approaches. *Journal of Pharmaceutical Analysis*, **2020**, 10, 546-559	14	35
78	Designing multi-epitope vaccine against Staphylococcus aureus by employing subtractive proteomics, reverse vaccinology and immuno-informatics approaches. *Computers in Biology and Medicine*, **2021**, 132, 104389	7	33
77	Peptide vaccine against chikungunya virus: immuno-informatics combined with molecular docking approach. *Journal of Translational Medicine*, **2018**, 16, 298	8.5	31
76	Multiepitope-Based Subunit Vaccine Design and Evaluation against Respiratory Syncytial Virus Using Reverse Vaccinology Approach. *Vaccines*, **2020**, 8,	5.3	29
75	Molecular Docking Based Screening of Plant Flavonoids as Dengue NS1 Inhibitors. *Bioinformation*, **2014**, 10, 460-5	1.1	27
74	MAPS Database: Medicinal plant Activities, Phytochemical and Structural Database. *Bioinformation*, **2013**, 9, 993-5	1.1	27
73	Silencing of Chemosensory Protein Gene NlugCSP8 by RNAi Induces Declining Behavioral Responses of. *Frontiers in Physiology*, **2018**, 9, 379	4.6	25
72	Discovery of Novel Dengue NS2B/NS3 Protease Inhibitors Using Pharmacophore Modeling and Molecular Docking Based Virtual Screening of the ZINC Database. *International Journal of Pharmacology*, **2016**, 12, 621-632	0.7	25
71	Antiviral phytochemicals identification from Azadirachta indica leaves against HCV NS3 protease: an in silico approach. *Natural Product Research*, **2016**, 30, 1866-9	2.3	23

70	Prediction of Protein-Protein Interactions by Evidence Combining Methods. *International Journal of Molecular Sciences*, **2016**, 17,	6.3	22
69	Functional Analysis of the Chemosensory Protein MsepCSP8 From the Oriental Armyworm. *Frontiers in Physiology*, **2018**, 9, 872	4.6	21
68	Investigating the molecular mechanism of staphylococcal DNA gyrase inhibitors: A combined ligand-based and structure-based resources pipeline. *Journal of Molecular Graphics and Modelling*, **2018**, 85, 122-129	2.8	21
67	Computer Aided Screening of Phytochemicals from Garcinia against the Dengue NS2B/NS3 Protease. *Bioinformation*, **2014**, 10, 115-8	1.1	17
66	Potential of plant alkaloids as dengue ns3 protease inhibitors: Molecular docking and simulation approach. *Bangladesh Journal of Pharmacology*, **2014**, 9,	0.6	16
65	Discovery of selective inhibitors for cyclic AMP response element-binding protein: a combined ligand and structure-based resources pipeline. *Anti-Cancer Drugs*, **2019**, 30, 363-373	2.4	16
64	Characterization of a novel cotton MYB gene, GhMYB108-like responsive to abiotic stresses. *Molecular Biology Reports*, **2020**, 47, 1573-1581	2.8	15
63	The critical role of p16/Rb pathway in the inhibition of GH3 cell cycle induced by T-2 toxin. *Toxicology*, **2018**, 400-401, 28-39	4.4	15
62	Screening of medicinal plant phytochemicals as natural antagonists of p53-MDM2 interaction to reactivate p53 functioning. *Anti-Cancer Drugs*, **2017**, 28, 1032-1038	2.4	15
61	Integrated Core Proteomics, Subtractive Proteomics, and Immunoinformatics Investigation to Unveil a Potential Multi-Epitope Vaccine against Schistosomiasis. *Vaccines*, **2021**, 9,	5.3	15
60	Development of a Novel Multi-Epitope Vaccine Against Crimean-Congo Hemorrhagic Fever Virus: An Integrated Reverse Vaccinology, Vaccine Informatics and Biophysics Approach. *Frontiers in Immunology*, **2021**, 12, 669812	8.4	15
59	Designing of a next generation multiepitope based vaccine (MEV) against SARS-COV-2: Immunoinformatics andin silicoapproaches		14
58	Immuno-Informatics Analysis of Pakistan-Based HCV Subtype-3a for Chimeric Polypeptide Vaccine Design. *Vaccines*, **2021**, 9,	5.3	14
57	Pan-vaccinomics approach towards a universal vaccine candidate against WHO priority pathogens to address growing global antibiotic resistance. *Computers in Biology and Medicine*, **2021**, 136, 104705	7	14
56	Discovery of anti-MERS-CoV small covalent inhibitors through pharmacophore modeling, covalent docking and molecular dynamics simulation. *Journal of Molecular Liquids*, **2021**, 330, 115699	6	13
55	Genome-Wide Bioinformatics Analysis of Aquaporin Gene Family in Maize (Zea mays L.). *Journal of Phylogenetics & Evolutionary Biology*, **2018**, 06,		13
54	Comparative Studies of the Dynamics Effects of BAY60-2770 and BAY58-2667 Binding with Human and Bacterial H-NOX Domains. *Molecules*, **2018**, 23,	4.8	13
53	ppsPCP: a plant presence/absence variants scanner and pan-genome construction pipeline. *Bioinformatics*, **2019**, 35, 4156-4158	7.2	12

52	Pharmacoinformatics and Molecular Dynamic Simulation Studies Reveal Potential Inhibitors of SARS-CoV-2 Main Protease 3CLpro		11
51	Towards A Novel Multi-Epitopes Chimeric Vaccine for Simulating Strong Immune Responses and Protection against. *International Journal of Environmental Research and Public Health*, **2021**, 18,	4.6	10
50	Mutational Landscape of Pirin and Elucidation of the Impact of Most Detrimental Missense Variants That Accelerate the Breast Cancer Pathways: A Computational Modelling Study. *Frontiers in Molecular Biosciences*, **2021**, 8, 692835	5.6	10
49	Molecular Docking and Simulation Studies of Antidiabetic Agents Devised from Hypoglycemic Polypeptide-P of. *BioMed Research International*, **2021**, 2021, 5561129	3	10
48	Comparative analysis of miniature inverted-repeat transposable elements (MITEs) and long terminal repeat (LTR) retrotransposons in six Citrus species. *BMC Plant Biology*, **2019**, 19, 140	5.3	9
47	Anticancer potential of phytochemicals against breast cancer: Molecular docking and simulation approach. *Bangladesh Journal of Pharmacology*, **2014**, 9,	0.6	9
46	A chemosensory protein MsepCSP5 involved in chemoreception of oriental armyworm. *International Journal of Biological Sciences*, **2018**, 14, 1935-1949	11.2	9
45	A deep learning model based on sparse auto-encoder for prioritizing cancer-related genes and drug target combinations. *Carcinogenesis*, **2019**, 40, 624-632	4.6	8
44	Structural Basis of SARS-CoV-2 3CLpro and Anti-COVID-19 Drug Discovery from Medicinal Plants		8
43	STATISTICAL ANALYSIS OF RISK FACTORS AFFECTING THE PROGNOSIS OF BILIARY ATRESIA IN INFANTS. *Matrix Science Pharma*, **2017**, 1, 20-24	0.8	8
42	Designing a Multi-Epitope Vaccine against by Employing Integrated Core Proteomics, Immuno-Informatics and In Silico Approaches. *Biology*, **2021**, 10,	4.9	8
41	Structural probing of HapR to identify potent phytochemicals to control Vibrio cholera through integrated computational approaches. *Computers in Biology and Medicine*, **2021**, 138, 104929	7	8
40	SARS-CoV-2: An Update on Genomics, Risk Assessment, Potential Therapeutics and Vaccine Development. *International Journal of Environmental Research and Public Health*, **2021**, 18,	4.6	8
39	Designing a Recombinant Vaccine against Using Immunoinformatics Approach.. *Vaccines*, **2022**, 10,	5.3	7
38	Designing of a multi-epitopes-based peptide vaccine against rift valley fever virus and its validation through integrated computational approaches.. *Computers in Biology and Medicine*, **2021**, 141, 105151	7	7
37	Pan-genome: A promising resource for noncoding RNA discovery in plants. *Plant Genome*, **2020**, 13, e20046	4.4	7
36	Structural insight into the binding pattern and interaction mechanism of chemotherapeutic agents with Sorcin by docking and molecular dynamic simulation. *Colloids and Surfaces B: Biointerfaces*, **2021**, 208, 112098	6	7
35	Network Pharmacology Approach for Medicinal Plants: Review and Assessment. *Pharmaceuticals*, **2022**, 15, 572	5.2	7

34	Discovery of Potential Antiviral Compounds against Hendra Virus by Targeting Its Receptor-Binding Protein (G) Using Computational Approaches.. *Molecules*, **2022**, 27,	4.8	6
33	Structural modeling and conserved epitopes prediction against SARS-COV-2 structural proteins for vaccine development		6
32	Discovery of Novel Inhibitors From Medicinal Plants for V-Domain Ig Suppressor of T-Cell Activation. *Frontiers in Molecular Biosciences*, **2021**, 8, 716735	5.6	6
31	Designing of a Recombinant Multi-Epitopes Based Vaccine against Using Bioinformatics and Immunoinformatics Approaches.. *International Journal of Environmental Research and Public Health*, **2022**, 19,	4.6	6
30	Probing the structural basis of Citrus phytochrome B using computational modelling and molecular dynamics simulation approaches. *Journal of Molecular Liquids*, **2021**, 340, 116895	6	5
29	Synthesis, antimicrobial, anticancer activities, PASS prediction, molecular docking, molecular dynamics and pharmacokinetic studies of designed methyl ED-glucopyranoside esters. *Journal of Molecular Structure*, **2022**, 1260, 132761	3.4	5
28	Identification and Analysis of Micro-Exon Genes in the Rice Genome. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	4
27	Coronavirus Disease 2019 Assosiated Pneumonia in China: Current Status and Future Prospects		4
26	Identification of immunodominant epitopes in allelic variants VK210 and VK247 of Plasmodium Vivax Circumsporozoite immunogen. *Infection, Genetics and Evolution*, **2021**, 96, 105120	4.5	4
25	QTL Mapping for Abiotic Stresses in Cereals **2020**, 229-251		4
24	Effectiveness of Conventional Crop Improvement Strategies vs. Omics **2020**, 253-284		4
23	Designing of a Novel Multi-Antigenic Epitope-Based Vaccine against E. hormaechei: An Intergraded Reverse Vaccinology and Immunoinformatics Approach. *Vaccines*, **2022**, 10, 665	5.3	4
22	Vaccinomics to Design a Multi-Epitopes Vaccine for .. *International Journal of Environmental Research and Public Health*, **2022**, 19,	4.6	4
21	Analysis of and X and Y chromosome transcriptome highlights reproductive driver genes. *Oncotarget*, **2017**, 8, 54416-54433	3.3	3
20	High-quality reference genome sequences of two coconut cultivars provide insights into evolution of monocot chromosomes and differentiation of fiber content and plant height. *Genome Biology*, **2021**, 22, 304	18.3	3
19	A NOVEL STRUCTURAL AND FUNCTIONAL INSIGHT INTO CHLOROPLAST-ENCODED CENTRAL SUBUNIT OF DARK-OPERATED PROTOCHLOROPHYLLIDE OXIDOREDUCTASE (DPOR) OF PLANTS. *Pakistan Journal of Agricultural Sciences*, **2017**, 54, 395-406	1.5	3
18	Role of Biotechnology in Climate Resilient Agriculture **2020**, 339-365		3
17	Conserved Imprinted Genes between Intra-Subspecies and Inter-Subspecies Are Involved in Energy Metabolism and Seed Development in Rice. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	3

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16	Potential Application of CRISPR/Cas9 System to Engineer Abiotic Stress Tolerance in Plants. *Protein and Peptide Letters*, **2021**, 28, 861-877	1.9	3
15	Design of a Multi-Epitope Vaccine against Tropheryma whipplei Using Immunoinformatics and Molecular Dynamics Simulation Techniques. *Vaccines*, **2022**, 10, 691	5.3	3
14	Structural Elucidation of Rift Valley Fever Virus L Protein towards the Discovery of Its Potential Inhibitors. *Pharmaceuticals*, **2022**, 15, 659	5.2	3
13	A Novel Coronavirus 2019 Linked with Pneumonia in China: Current Status and Future Prospects		2
12	Modelling and simulation of mutant alleles of breast cancer metastasis suppressor 1 (BRMS1) gene. *Bioinformation*, **2014**, 10, 454-9	1.1	2
11	Appraisal of MsepCSP14 for chemosensory functions in Mythimna separata. *Insect Science*, **2021**,	3.6	2
10	Molecular Modeling and docking of Wheat Hydroquinone Glucosyl transferase by using Hydroquinone, Phenyl phosphorodiamate and n-(n butyl) Phosphorothiocic Triamide as Inhibitors. *Bioinformation*, **2014**, 10, 124-9	1.1	1
9	Phylogenetic and Comparative Sequence Analysis of Thermostable Alpha Amylases of kingdom Archea, Prokaryotes and Eukaryotes. *Bioinformation*, **2014**, 10, 443-8	1.1	1
8	Immunoinformatics and Immunogenetics-Based Design of Immunogenic Peptides Vaccine against the Emerging Tick-Borne Encephalitis Virus (TBEV) and Its Validation through In Silico Cloning and Immune Simulation. *Vaccines*, **2021**, 9,	5.3	1
7	Inference of Transcriptional Regulation from Expression Data Using Model Integration. *Current Bioinformatics*, **2018**, 13, 426-434	4.7	1
6	The effects of genotypes and media composition on callogenesis, regeneration and cell suspension culture of chamomile (L.). *PeerJ*, **2021**, 9, e11464	3.1	1
5	Whole Proteome-Based Therapeutic Targets Annotation and Designing of Multi-Epitope-Based Vaccines against the Gram-Negative XDR- Bacterium.. *Vaccines*, **2022**, 10,	5.3	1
4	In Silico Analysis and Functional Characterization of Antimicrobial and Insecticidal Vicilin from Moth Bean (Vigna aconitifolia (Jacq.) Marechal) Seeds. *Molecules*, **2022**, 27, 3251	4.8	0
3	Advances in guide RNA design for editing plant genomes using CRISPR-Cas systems **2021**, 147-174		
2	Advances in guide RNA design for editing plant genomes using CRISPR-Cas systems **2021**, 147-174		
1	Mechanism Associated with Brassinosteroids Crosstalk with Gibberellic Acid in Plants **2022**, 101-115		