

Muhammad Tahir Ul Qamar

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Designing a Recombinant Vaccine against Using Immunoinformatics Approach.. <i>Vaccines</i> , 2022 , 10,	5.3	7
86	Discovery of Potential Antiviral Compounds against Hendra Virus by Targeting Its Receptor-Binding Protein (G) Using Computational Approaches.. <i>Molecules</i> , 2022 , 27,	4.8	6
85	Mechanism Associated with Brassinosteroids Crosstalk with Gibberellic Acid in Plants 2022 , 101-115		
84	Designing of a Recombinant Multi-Epitopes Based Vaccine against Using Bioinformatics and Immunoinformatics Approaches.. <i>International Journal of Environmental Research and Public Health</i> , 2022 , 19,	4.6	6
83	Whole Proteome-Based Therapeutic Targets Annotation and Designing of Multi-Epitope-Based Vaccines against the Gram-Negative XDR- Bacterium.. <i>Vaccines</i> , 2022 , 10,	5.3	1
82	Synthesis, antimicrobial, anticancer activities, PASS prediction, molecular docking, molecular dynamics and pharmacokinetic studies of designed methyl ED-glucopyranoside esters. <i>Journal of Molecular Structure</i> , 2022 , 1260, 132761	3.4	5
81	Designing of a Novel Multi-Antigenic Epitope-Based Vaccine against E. hormaechei: An Intergraded Reverse Vaccinology and Immunoinformatics Approach. <i>Vaccines</i> , 2022 , 10, 665	5.3	4
80	Design of a Multi-Epitope Vaccine against Tropheryma whipplei Using Immunoinformatics and Molecular Dynamics Simulation Techniques. <i>Vaccines</i> , 2022 , 10, 691	5.3	3
79	Network Pharmacology Approach for Medicinal Plants: Review and Assessment. <i>Pharmaceuticals</i> , 2022 , 15, 572	5.2	7
78	Vaccinomics to Design a Multi-Epitopes Vaccine for .. <i>International Journal of Environmental Research and Public Health</i> , 2022 , 19,	4.6	4
77	Structural Elucidation of Rift Valley Fever Virus L Protein towards the Discovery of Its Potential Inhibitors. <i>Pharmaceuticals</i> , 2022 , 15, 659	5.2	3
76	In Silico Analysis and Functional Characterization of Antimicrobial and Insecticidal Vicilin From Moth Bean (Vigna aconitifolia (Jacq.) Marechal) Seeds. <i>Molecules</i> , 2022 , 27, 3251	4.8	0
75	Pharmacoinformatics and molecular dynamics simulation studies reveal potential covalent and FDA-approved inhibitors of SARS-CoV-2 main protease 3CL. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 4936-4948	3.6	71
74	High-quality reference genome sequences of two coconut cultivars provide insights into evolution of monocot chromosomes and differentiation of fiber content and plant height. <i>Genome Biology</i> , 2021 , 22, 304	18.3	3
73	Designing of a multi-epitopes-based peptide vaccine against rift valley fever virus and its validation through integrated computational approaches.. <i>Computers in Biology and Medicine</i> , 2021 , 141, 105151	7	7
72	Designing a Multi-Epitope Vaccine against by Employing Integrated Core Proteomics, Immuno-Informatics and In Silico Approaches. <i>Biology</i> , 2021 , 10,	4.9	8
71	Discovery of Novel Inhibitors From Medicinal Plants for V-Domain Ig Suppressor of T-Cell Activation. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 716735	5.6	6

70	Towards A Novel Multi-Epitopes Chimeric Vaccine for Simulating Strong Immune Responses and Protection against. <i>International Journal of Environmental Research and Public Health</i> , 2021 , 18,	4.6	10
69	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. <i>Vaccines</i> , 2021 , 9,	5.3	1
68	Structural probing of HapR to identify potent phytochemicals to control <i>Vibrio cholera</i> through integrated computational approaches. <i>Computers in Biology and Medicine</i> , 2021 , 138, 104929	7	8
67	Identification of immunodominant epitopes in allelic variants VK210 and VK247 of <i>Plasmodium Vivax</i> Circumsporozoite immunogen. <i>Infection, Genetics and Evolution</i> , 2021 , 96, 105120	4.5	4
66	Immuno-Informatics Analysis of Pakistan-Based HCV Subtype-3a for Chimeric Polypeptide Vaccine Design. <i>Vaccines</i> , 2021 , 9,	5.3	14
65	Advances in guide RNA design for editing plant genomes using CRISPR-Cas systems 2021 , 147-174		
64	Appraisal of MsepCSP14 for chemosensory functions in <i>Mythimna separata</i> . <i>Insect Science</i> , 2021 ,	3.6	2
63	Advances in guide RNA design for editing plant genomes using CRISPR-Cas systems 2021 , 147-174		
62	Designing multi-epitope vaccine against <i>Staphylococcus aureus</i> by employing subtractive proteomics, reverse vaccinology and immuno-informatics approaches. <i>Computers in Biology and Medicine</i> , 2021 , 132, 104389	7	33
61	The effects of genotypes and media composition on callogenesis, regeneration and cell suspension culture of chamomile (L.). <i>PeerJ</i> , 2021 , 9, e11464	3.1	1
60	Discovery of anti-MERS-CoV small covalent inhibitors through pharmacophore modeling, covalent docking and molecular dynamics simulation. <i>Journal of Molecular Liquids</i> , 2021 , 330, 115699	6	13
59	Mutational Landscape of Pirin and Elucidation of the Impact of Most Detrimental Missense Variants That Accelerate the Breast Cancer Pathways: A Computational Modelling Study. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 692835	5.6	10
58	Integrated Core Proteomics, Subtractive Proteomics, and Immunoinformatics Investigation to Unveil a Potential Multi-Epitope Vaccine against Schistosomiasis. <i>Vaccines</i> , 2021 , 9,	5.3	15
57	Development of a Novel Multi-Epitope Vaccine Against Crimean-Congo Hemorrhagic Fever Virus: An Integrated Reverse Vaccinology, Vaccine Informatics and Biophysics Approach. <i>Frontiers in Immunology</i> , 2021 , 12, 669812	8.4	15
56	SARS-CoV-2: An Update on Genomics, Risk Assessment, Potential Therapeutics and Vaccine Development. <i>International Journal of Environmental Research and Public Health</i> , 2021 , 18,	4.6	8
55	Pan-vaccinomics approach towards a universal vaccine candidate against WHO priority pathogens to address growing global antibiotic resistance. <i>Computers in Biology and Medicine</i> , 2021 , 136, 104705	7	14
54	Molecular Docking and Simulation Studies of Antidiabetic Agents Devised from Hypoglycemic Polypeptide-P of. <i>BioMed Research International</i> , 2021 , 2021, 5561129	3	10
53	Potential Application of CRISPR/Cas9 System to Engineer Abiotic Stress Tolerance in Plants. <i>Protein and Peptide Letters</i> , 2021 , 28, 861-877	1.9	3

52	Probing the structural basis of Citrus phytochrome B using computational modelling and molecular dynamics simulation approaches. <i>Journal of Molecular Liquids</i> , 2021 , 340, 116895	6	5
51	Structural insight into the binding pattern and interaction mechanism of chemotherapeutic agents with Sorcin by docking and molecular dynamic simulation. <i>Colloids and Surfaces B: Biointerfaces</i> , 2021 , 208, 112098	6	7
50	Multiepitope-Based Subunit Vaccine Design and Evaluation against Respiratory Syncytial Virus Using Reverse Vaccinology Approach. <i>Vaccines</i> , 2020 , 8,	5.3	29
49	Structural basis of SARS-CoV-2 3CL and anti-COVID-19 drug discovery from medicinal plants. <i>Journal of Pharmaceutical Analysis</i> , 2020 , 10, 313-319	14	477
48	Characterization of a novel cotton MYB gene, GhMYB108-like responsive to abiotic stresses. <i>Molecular Biology Reports</i> , 2020 , 47, 1573-1581	2.8	15
47	Designing of a next generation multiepitope based vaccine (MEV) against SARS-COV-2: Immunoinformatics and in silico approaches. <i>PLoS ONE</i> , 2020 , 15, e0244176	3.7	43
46	QTL Mapping for Abiotic Stresses in Cereals 2020 , 229-251		4
45	Role of Biotechnology in Climate Resilient Agriculture 2020 , 339-365		3
44	Discovery of human coronaviruses pan-papain-like protease inhibitors using computational approaches. <i>Journal of Pharmaceutical Analysis</i> , 2020 , 10, 546-559	14	35
43	Promising terpenes as SARS-CoV-2 spike receptor-binding domain (RBD) attachment inhibitors to the human ACE2 receptor: Integrated computational approach. <i>Journal of Molecular Liquids</i> , 2020 , 320, 114493	6	46
42	Effectiveness of Conventional Crop Improvement Strategies vs. Omics 2020 , 253-284		4
41	Pan-genome: A promising resource for noncoding RNA discovery in plants. <i>Plant Genome</i> , 2020 , 13, e200446	4.4	7
40	Reverse vaccinology assisted designing of multiepitope-based subunit vaccine against SARS-CoV-2. <i>Infectious Diseases of Poverty</i> , 2020 , 9, 132	10.4	38
39	Conserved Imprinted Genes between Intra-Subspecies and Inter-Subspecies Are Involved in Energy Metabolism and Seed Development in Rice. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	3
38	Identification and Analysis of Micro-Exon Genes in the Rice Genome. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	4
37	Comparative analysis of miniature inverted-repeat transposable elements (MITEs) and long terminal repeat (LTR) retrotransposons in six Citrus species. <i>BMC Plant Biology</i> , 2019 , 19, 140	5.3	9
36	ppsPCP: a plant presence/absence variants scanner and pan-genome construction pipeline. <i>Bioinformatics</i> , 2019 , 35, 4156-4158	7.2	12
35	A deep learning model based on sparse auto-encoder for prioritizing cancer-related genes and drug target combinations. <i>Carcinogenesis</i> , 2019 , 40, 624-632	4.6	8

34	Computational screening of medicinal plant phytochemicals to discover potent pan-serotype inhibitors against dengue virus. <i>Scientific Reports</i> , 2019 , 9, 1433	4.9	61
33	Epitope-based peptide vaccine design and target site depiction against Middle East Respiratory Syndrome Coronavirus: an immune-informatics study. <i>Journal of Translational Medicine</i> , 2019 , 17, 362	8.5	93
32	Discovery of selective inhibitors for cyclic AMP response element-binding protein: a combined ligand and structure-based resources pipeline. <i>Anti-Cancer Drugs</i> , 2019 , 30, 363-373	2.4	16
31	The critical role of p16/Rb pathway in the inhibition of GH3 cell cycle induced by T-2 toxin. <i>Toxicology</i> , 2018 , 400-401, 28-39	4.4	15
30	Silencing of Chemosensory Protein Gene NlugCSP8 by RNAi Induces Declining Behavioral Responses of. <i>Frontiers in Physiology</i> , 2018 , 9, 379	4.6	25
29	Functional Analysis of the Chemosensory Protein MsepCSP8 From the Oriental Armyworm. <i>Frontiers in Physiology</i> , 2018 , 9, 872	4.6	21
28	Investigating the molecular mechanism of staphylococcal DNA gyrase inhibitors: A combined ligand-based and structure-based resources pipeline. <i>Journal of Molecular Graphics and Modelling</i> , 2018 , 85, 122-129	2.8	21
27	Inference of Transcriptional Regulation from Expression Data Using Model Integration. <i>Current Bioinformatics</i> , 2018 , 13, 426-434	4.7	1
26	A chemosensory protein MsepCSP5 involved in chemoreception of oriental armyworm. <i>International Journal of Biological Sciences</i> , 2018 , 14, 1935-1949	11.2	9
25	Genome-Wide Bioinformatics Analysis of Aquaporin Gene Family in Maize (<i>Zea mays</i> L.). <i>Journal of Phylogenetics & Evolutionary Biology</i> , 2018 , 06,		13
24	Peptide vaccine against chikungunya virus: immuno-informatics combined with molecular docking approach. <i>Journal of Translational Medicine</i> , 2018 , 16, 298	8.5	31
23	Comparative Studies of the Dynamics Effects of BAY60-2770 and BAY58-2667 Binding with Human and Bacterial H-NOX Domains. <i>Molecules</i> , 2018 , 23,	4.8	13
22	Screening of medicinal plant phytochemicals as natural antagonists of p53-MDM2 interaction to reactivate p53 functioning. <i>Anti-Cancer Drugs</i> , 2017 , 28, 1032-1038	2.4	15
21	MPD3: a useful medicinal plants database for drug designing. <i>Natural Product Research</i> , 2017 , 31, 1228-1236	3.6	42
20	Analysis of and X and Y chromosome transcriptome highlights reproductive driver genes. <i>Oncotarget</i> , 2017 , 8, 54416-54433	3.3	3
19	A NOVEL STRUCTURAL AND FUNCTIONAL INSIGHT INTO CHLOROPLAST-ENCODED CENTRAL SUBUNIT OF DARK-OPERATED PROTOCHLOROPHYLLIDE OXIDOREDUCTASE (DPOR) OF PLANTS. <i>Pakistan Journal of Agricultural Sciences</i> , 2017 , 54, 395-406	1.5	3
18	STATISTICAL ANALYSIS OF RISK FACTORS AFFECTING THE PROGNOSIS OF BILIARY ATRESIA IN INFANTS. <i>Matrix Science Pharma</i> , 2017 , 1, 20-24	0.8	8
17	Antiviral phytochemicals identification from <i>Azadirachta indica</i> leaves against HCV NS3 protease: an in silico approach. <i>Natural Product Research</i> , 2016 , 30, 1866-9	2.3	23

16	Discovery of Novel Dengue NS2B/NS3 Protease Inhibitors Using Pharmacophore Modeling and Molecular Docking Based Virtual Screening of the ZINC Database. <i>International Journal of Pharmacology</i> , 2016 , 12, 621-632	0.7	25
15	Prediction of Protein-Protein Interactions by Evidence Combining Methods. <i>International Journal of Molecular Sciences</i> , 2016 , 17,	6.3	22
14	Anticancer potential of phytochemicals against breast cancer: Molecular docking and simulation approach. <i>Bangladesh Journal of Pharmacology</i> , 2014 , 9,	0.6	9
13	Molecular Modeling and docking of Wheat Hydroquinone Glucosyl transferase by using Hydroquinone, Phenyl phosphorodiamate and n-(n butyl) Phosphorothiocic Triamide as Inhibitors. <i>Bioinformation</i> , 2014 , 10, 124-9	1.1	1
12	Potential of plant alkaloids as dengue ns3 protease inhibitors: Molecular docking and simulation approach. <i>Bangladesh Journal of Pharmacology</i> , 2014 , 9,	0.6	16
11	Molecular Docking Based Screening of Plant Flavonoids as Dengue NS1 Inhibitors. <i>Bioinformation</i> , 2014 , 10, 460-5	1.1	27
10	Computer Aided Screening of Phytochemicals from Garcinia against the Dengue NS2B/NS3 Protease. <i>Bioinformation</i> , 2014 , 10, 115-8	1.1	17
9	Phylogenetic and Comparative Sequence Analysis of Thermostable Alpha Amylases of kingdom Archea, Prokaryotes and Eukaryotes. <i>Bioinformation</i> , 2014 , 10, 443-8	1.1	1
8	Modelling and simulation of mutant alleles of breast cancer metastasis suppressor 1 (BRMS1) gene. <i>Bioinformation</i> , 2014 , 10, 454-9	1.1	2
7	MAPS Database: Medicinal plant Activities, Phytochemical and Structural Database. <i>Bioinformation</i> , 2013 , 9, 993-5	1.1	27
6	Coronavirus Disease 2019 Associated Pneumonia in China: Current Status and Future Prospects		4
5	Structural Basis of SARS-CoV-2 3CLpro and Anti-COVID-19 Drug Discovery from Medicinal Plants		8
4	Pharmacoinformatics and Molecular Dynamic Simulation Studies Reveal Potential Inhibitors of SARS-CoV-2 Main Protease 3CLpro		11
3	A Novel Coronavirus 2019 Linked with Pneumonia in China: Current Status and Future Prospects		2
2	Structural modeling and conserved epitopes prediction against SARS-COV-2 structural proteins for vaccine development		6
1	Designing of a next generation multiepitope based vaccine (MEV) against SARS-COV-2: Immunoinformatics and in silico approaches		14