

Faryal Mehwish Awan

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

2,973
citations

394421

19
h-index

526287

27
g-index

33
all docs

33
docs citations

33
times ranked

3833
citing authors

#	ARTICLE	IF	CITATIONS
1	Induction of tumor apoptosis through a circular RNA enhancing Foxo3 activity. <i>Cell Death and Differentiation</i> , 2017, 24, 357-370.	11.2	521
2	Identifying and Characterizing circRNA-Protein Interaction. <i>Theranostics</i> , 2017, 7, 4183-4191.	10.0	467
3	A Circular RNA Binds To and Activates AKT Phosphorylation and Nuclear Localization Reducing Apoptosis and Enhancing Cardiac Repair. <i>Theranostics</i> , 2017, 7, 3842-3855.	10.0	297
4	A circular RNA promotes tumorigenesis by inducing c-myc nuclear translocation. <i>Cell Death and Differentiation</i> , 2017, 24, 1609-1620.	11.2	252
5	A circular RNA circ-DNMT1 enhances breast cancer progression by activating autophagy. <i>Oncogene</i> , 2018, 37, 5829-5842.	5.9	222
6	The Circular RNA Interacts with STAT3, Increasing Its Nuclear Translocation and Wound Repair by Modulating Dnmt3a and miR-17 Function. <i>Molecular Therapy</i> , 2017, 25, 2062-2074.	8.2	201
7	Identification of putative vaccine candidates against <i>Helicobacter pylori</i> exploiting exoproteome and secretome: A reverse vaccinology based approach. <i>Infection, Genetics and Evolution</i> , 2015, 32, 280-291.	2.3	180
8	Pangenome and immuno-proteomics analysis of <i>Acinetobacter baumannii</i> strains revealed the core peptide vaccine targets. <i>BMC Genomics</i> , 2016, 17, 732.	2.8	100
9	Enhanced breast cancer progression by mutant p53 is inhibited by the circular RNA circ-Ccnb1. <i>Cell Death and Differentiation</i> , 2018, 25, 2195-2208.	11.2	100
10	The circular RNA circ-Ccnb1 dissociates Ccnb1/Cdk1 complex suppressing cell invasion and tumorigenesis. <i>Cancer Letters</i> , 2019, 459, 216-226.	7.2	84
11	Designing Multi-Epitope Vaccines to Combat Emerging Coronavirus Disease 2019 (COVID-19) by Employing Immuno-Informatics Approach. <i>Frontiers in Immunology</i> , 2020, 11, 1663.	4.8	79
12	Exploring NS3/4A, NS5A and NS5B proteins to design conserved subunit multi-epitope vaccine against HCV utilizing immunoinformatics approaches. <i>Scientific Reports</i> , 2018, 8, 16107.	3.3	77
13	The Circular RNA circSKA3 Binds Integrin β 21 to Induce Invadopodium Formation Enhancing Breast Cancer Invasion. <i>Molecular Therapy</i> , 2020, 28, 1287-1298.	8.2	66
14	YAP Circular RNA, circYap, Attenuates Cardiac Fibrosis via Binding with Tropomyosin-4 and Gamma-Actin Decreasing Actin Polymerization. <i>Molecular Therapy</i> , 2021, 29, 1138-1150.	8.2	62
15	Mutation-Structure-Function Relationship Based Integrated Strategy Reveals the Potential Impact of Deleterious Missense Mutations in Autophagy Related Proteins on Hepatocellular Carcinoma (HCC): A Comprehensive Informatics Approach. <i>International Journal of Molecular Sciences</i> , 2017, 18, 139.	4.1	54
16	The emerging role and significance of circular RNAs in viral infections and antiviral immune responses: possible implication as theranostic agents. <i>RNA Biology</i> , 2021, 18, 1-15.	3.1	45
17	Innovations in Genomics and Big Data Analytics for Personalized Medicine and Health Care: A Review. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4645.	4.1	45
18	Identification of Circulating Biomarker Candidates for Hepatocellular Carcinoma (HCC): An Integrated Prioritization Approach. <i>PLoS ONE</i> , 2015, 10, e0138913.	2.5	35

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19	MicroRNA pharmacogenomics based integrated model of miR-17-92 cluster in sorafenib resistant HCC cells reveals a strategy to forestall drug resistance. <i>Scientific Reports</i> , 2017, 7, 11448.	3.3	31
20	In-silico analysis of claudin-5 reveals novel putative sites for post-translational modifications: Insights into potential molecular determinants of blood-brain barrier breach during HIV-1 infiltration. <i>Infection, Genetics and Evolution</i> , 2014, 27, 355-365.	2.3	15
21	Inhibitory Potential of Phytochemicals on Interleukin-6-Mediated T-Cell Reduction in COVID-19 Patients: A Computational Approach. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222110214.	2.0	10
22	Model of the adaptive immune response system against HCV infection reveals potential immunomodulatory agents for combination therapy. <i>Scientific Reports</i> , 2018, 8, 8874.	3.3	9
23	Identification of drug resistance and immune-driven variations in hepatitis C virus (HCV) NS3/4A, NS5A and NS5B regions reveals a new approach toward personalized medicine. <i>Antiviral Research</i> , 2017, 137, 112-124.	4.1	8
24	The Impact of Mutations on the Pathogenic and Antigenic Activity of SARS-CoV-2 during the First Wave of the COVID-19 Pandemic: A Comprehensive Immunoinformatics Analysis. <i>Vaccines</i> , 2021, 9, 1410.	4.4	5
25	Modeling and analysis of innate immune responses induced by the host cells against hepatitis C virus infection. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 544-559.	1.3	4
26	Structure-Function Mutational Analysis and Prediction of the Potential Impact of High Risk Non-Synonymous Single-Nucleotide Polymorphism on Poliovirus 2A Protease Stability Using Comprehensive Informatics Approaches. <i>Genes</i> , 2018, 9, 228.	2.4	2
27	Formal Modeling of the Key Determinants of Hepatitis C Virus (HCV) Induced Adaptive Immune Response Network: An Integrative Approach to Map the Cellular and Cytokine-Mediated Host Immune Regulations. <i>Lecture Notes in Computer Science</i> , 2018, , 635-649.	1.3	1
28	Systems-Level Understanding of Single-Cell Omics. , 2019, , 433-456.		0
29	A Multi-Method and Structure-Based In Silico Vaccine Designing Against <i>Helicobacter pylori</i> Employing Immuno-Informatics Approach. <i>Current Proteomics</i> , 2021, 18, 237-247.	0.3	0
30	The HOPE for Pandora's Box of artificial circular RNA immunogenicity. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 28, 640-642.	5.1	0