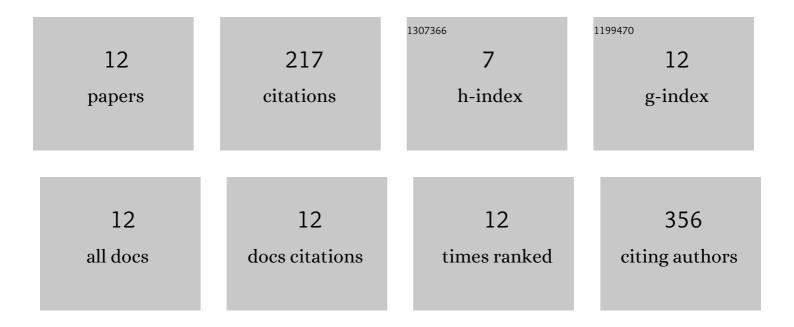
Suza Mohammad Nur

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10804638/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Epigenetic regulation of RNA sensors: Sentinels of immune response. Seminars in Cancer Biology, 2022, 83, 413-421.	4.3	4
2	Epigenetics of Triple-Negative Breast Cancer via Natural Compounds. Current Medicinal Chemistry, 2022, 29, 1436-1458.	1.2	8
3	Untargeted Metabolomics Showed Accumulation of One-Carbon Metabolites to Facilitate DNA Methylation during Extracellular Matrix Detachment of Cancer Cells. Metabolites, 2022, 12, 267.	1.3	3
4	Computational Identification of Druggable Bioactive Compounds from Catharanthus roseus and Avicennia marina against Colorectal Cancer by Targeting Thymidylate Synthase. Molecules, 2022, 27, 2089.	1.7	19
5	Nutritive vitamins as epidrugs. Critical Reviews in Food Science and Nutrition, 2021, 61, 1-13.	5.4	66
6	Spike protein recognizer receptor ACE2 targeted identification of potential natural antiviral drug candidates against SARS-CoV-2. International Journal of Biological Macromolecules, 2021, 191, 1114-1125.	3.6	36
7	Comparative Analysis of the Impact of Urolithins on the Composition of the Gut Microbiota in Normal-Diet Fed Rats. Nutrients, 2021, 13, 3885.	1.7	10
8	Design of Potential RNAi (miRNA and siRNA) Molecules for Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Gene Silencing by Computational Method. Interdisciplinary Sciences, Computational Life Sciences, 2015, 7, 257-265.	2.2	37
9	Design of potential RNAi (miRNA and siRNA) molecules for Middle East respiratory syndrome coronavirus (MERS-CoV) gene silencing by computational method. Interdisciplinary Sciences, Computational Life Sciences, 2014, 7, 257.	2.2	1
10	Design of potential RNAi (miRNA and siRNA) molecules for Middle East respiratory syndrome coronavirus (MERS-CoV) gene silencing by computational method. Interdisciplinary Sciences, Computational Life Sciences, 2014, , .	2.2	2
11	<i>In Silico</i> Molecular Characterization of Cysteine Protease YopT from <i>Yersinia pestis</i> by Homology Modeling and Binding Site Identification. Drug Target Insights, 2014, 8, DTI.S13529.	0.9	16
12	An in silico approach to design potential siRNA molecules for ICP22 (US1) gene silencing of different strains of human herpes simplex 1. Journal of Young Pharmacists, 2013, 5, 46-49.	0.1	15