

Suza Mohammad Nur

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

217
citations

1307366

7
h-index

1199470

12
g-index

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all docs

12
docs citations

12
times ranked

356
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic regulation of RNA sensors: Sentinels of immune response. <i>Seminars in Cancer Biology</i> , 2022, 83, 413-421.	4.3	4
2	Epigenetics of Triple-Negative Breast Cancer via Natural Compounds. <i>Current Medicinal Chemistry</i> , 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. <i>Metabolites</i> , 2022, 12, 267.	1.3	3
4	Computational Identification of Druggable Bioactive Compounds from <i>Catharanthus roseus</i> and <i>Avicennia marina</i> against Colorectal Cancer by Targeting Thymidylate Synthase. <i>Molecules</i> , 2022, 27, 2089.	1.7	19
5	Nutritive vitamins as epidrugs. <i>Critical Reviews in Food Science and Nutrition</i> , 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. <i>International Journal of Biological Macromolecules</i> , 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. <i>Nutrients</i> , 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. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 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. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 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. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 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. <i>Drug Target Insights</i> , 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. <i>Journal of Young Pharmacists</i> , 2013, 5, 46-49.	0.1	15