

Umesh Kalathiya

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

509
citations

1039880

9
h-index

713332

21
g-index

32
all docs

32
docs citations

32
times ranked

820
citing authors

#	ARTICLE	IF	CITATIONS
1	The emerging landscape of single-molecule protein sequencing technologies. <i>Nature Methods</i> , 2021, 18, 604-617.	9.0	198
2	Highly Conserved Homotrimer Cavity Formed by the SARS-CoV-2 Spike Glycoprotein: A Novel Binding Site. <i>Journal of Clinical Medicine</i> , 2020, 9, 1473.	1.0	73
3	Nonsense-Mediated mRNA Decay: Pathologies and the Potential for Novel Therapeutics. <i>Cancers</i> , 2020, 12, 765.	1.7	33
4	Structural, functional, and stability change predictions in human telomerase upon specific point mutations. <i>Scientific Reports</i> , 2019, 9, 8707.	1.6	23
5	Structure-based design and evaluation of novel N-phenyl-1H-indol-2-amine derivatives for fat mass and obesity-associated (FTO) protein inhibition. <i>Computational Biology and Chemistry</i> , 2016, 64, 414-425.	1.1	21
6	Multivalent Display of SARS-CoV-2 Spike (RBD Domain) of COVID-19 to Nanomaterial, Protein Ferritin Nanocages. <i>Biomolecules</i> , 2021, 11, 297.	1.8	20
7	Functional Interfaces, Biological Pathways, and Regulations of Interferon-Related DNA Damage Resistance Signature (IRDS) Genes. <i>Biomolecules</i> , 2021, 11, 622.	1.8	18
8	Insights into the Effects of Cancer Associated Mutations at the UPF2 and ATP-Binding Sites of NMD Master Regulator: UPF1. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5644.	1.8	13
9	Structural and dynamic changes adopted by EmrE, multidrug transporter protein—Studies by molecular dynamics simulation. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 2065-2074.	1.4	11
10	Molecular Modeling and Evaluation of Novel Dibenzopyrrole Derivatives as Telomerase Inhibitors and Potential Drug for Cancer Therapy. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 1196-1207.	1.9	9
11	Viruses, cancer and non-self recognition. <i>Open Biology</i> , 2021, 11, 200348.	1.5	9
12	Structural determinants of peptide-dependent TAP1-TAP2 transit passage targeted by viral proteins and altered by cancer-associated mutations. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5072-5091.	1.9	9
13	The Elephant Evolved p53 Isoforms that Escape MDM2-Mediated Repression and Cancer. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9
14	Identification of 1 <i>H</i> -indene-(1,3,5,6)-tetrol derivatives as potent pancreatic lipase inhibitors using molecular docking and molecular dynamics approach. <i>Biotechnology and Applied Biochemistry</i> , 2016, 63, 765-778.	1.4	8
15	Recognition Dynamics of Cancer Mutations on the ERp57-Tapasin Interface. <i>Cancers</i> , 2020, 12, 737.	1.7	8
16	Interfaces with Structure Dynamics of the Workhorses from Cells Revealed through Cross-Linking Mass Spectrometry (CLMS). <i>Biomolecules</i> , 2021, 11, 382.	1.8	8
17	Drug repositioning against COVID-19: a first line treatment. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 12812-12826.	2.0	8
18	Molecular Determinants and Specificity of mRNA with Alternatively-Spliced UPF1 Isoforms, Influenced by an Insertion in the “Regulatory Loop”™. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12744.	1.8	7

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19	The structurally similar TRFH domain of TRF1 and TRF2 dimers shows distinct behaviour towards TIN2. Archives of Biochemistry and Biophysics, 2018, 642, 52-62.	1.4	5
20	Molecular basis and quantitative assessment of TRF1 and TRF2 protein interactions with TIN2 and Apollo peptides. European Biophysics Journal, 2017, 46, 171-187.	1.2	4
21	Comparative molecular dynamics study of dimeric and monomeric forms of HIV-1 protease in ligand bound and unbound state. General Physiology and Biophysics, 2017, 36, 141-154.	0.4	2
22	MOLECULAR DOCKING STUDIES TOWARDS DEVELOPMENT OF NOVEL GLY-PHE ANALOGS FOR POTENTIAL INHIBITION OF CATHEPSIN C (DIPEPTIDYL PEPTIDASE I). International Journal for Computational Biology, 2014, 3, 3.	0.1	2
23	Molecular basis and potential activity of HIV-1 reverse transcriptase toward trimethylamine-based compounds. Biotechnology and Applied Biochemistry, 2017, 64, 810-826.	1.4	1
24	Inhibiting Activity of HIV-1: Protease, Reverse Transcriptase and Integrase All Together by Novel Compounds Using Computational Approaches. International Journal of Bioscience, Biochemistry, Bioinformatics (IJBBB), 0, , 448-457.	0.2	1
25	COMPUTER-AIDED DESIGN OF ORGANOPHOSPHORUS INHIBITORS OF UREASE. International Journal for Computational Biology, 2014, 3, 31.	0.1	1
26	SiMiSnoRNA: Collection of siRNA, miRNA, and snoRNA database for RNA interference / SiMiSnoRNA: RNA Interferans'ın siRNA, miRNA ve snoRNA veritabanında depolanan siRNA, miRNA, and snoRNA koleksiyonları. Turkish Journal of Biochemistry, 2015, 40, .	0.3	0
27	Extracting functional groups of ALLINI to design derivatives of FDA-approved drugs: Inhibition of HIV-1 integrase. Biotechnology and Applied Biochemistry, 2018, 65, 594-607.	1.4	0
28	Structural analysis and predicting effects of natural mutations on telomerase. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C276-C276.	0.0	0
29	Molecular basis of TRF proteins and their interactions with peptides. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C174-C174.	0.0	0
30	Self-derived peptides from the SARS-CoV-2 spike glycoprotein disrupting shaping and stability of the homotrimer unit. Biomedicine and Pharmacotherapy, 2022, 151, 113190.	2.5	0