Umesh Kalathiya

List of Publications by Year in Descending Order

24 papers	241 citations	8 h-index	15 g-index
32 ext. papers	372 ext. citations	4.7 avg, IF	3.71 L-index

#	Paper	IF	Citations
24	Self-derived peptides from the SARS-CoV-2 spike glycoprotein disrupting shaping and stability of the homotrimer unit. *Biomedicine and Pharmacotherapy*, **2022**, 151, 113190	7.5	
23	Molecular Determinants and Specificity of mRNA with Alternatively-Spliced UPF1 Isoforms, Influenced by an Insertion in the WRegulatory LoopW *International Journal of Molecular Sciences*, **2021**, 22,	6.3	3
22	Viruses, cancer and non-self recognition. *Open Biology*, **2021**, 11, 200348	7	2
21	Interfaces with Structure Dynamics of the Workhorses from Cells Revealed through Cross-Linking Mass Spectrometry (CLMS). *Biomolecules*, **2021**, 11,	5.9	1
20	Functional Interfaces, Biological Pathways, and Regulations of Interferon-Related DNA Damage Resistance Signature (IRDS) Genes. *Biomolecules*, **2021**, 11,	5.9	6
19	The emerging landscape of single-molecule protein sequencing technologies. *Nature Methods*, **2021**, 18, 604-617	21.6	60
18	Multivalent Display of SARS-CoV-2 Spike (RBD Domain) of COVID-19 to Nanomaterial, Protein Ferritin Nanocages. *Biomolecules*, **2021**, 11,	5.9	11
17	Drug repositioning against COVID-19: a first line treatment. *Journal of Biomolecular Structure and Dynamics*, **2021**, 1-15	3.6	4
16	Structural determinants of peptide-dependent TAP1-TAP2 transit passage targeted by viral proteins and altered by cancer-associated mutations. *Computational and Structural Biotechnology Journal*, **2021**, 19, 5072-5091	6.8	1
15	Highly Conserved Homotrimer Cavity Formed by the SARS-CoV-2 Spike Glycoprotein: A Novel Binding Site. *Journal of Clinical Medicine*, **2020**, 9,	5.1	55
14	Nonsense-Mediated mRNA Decay: Pathologies and the Potential for Novel Therapeutics. *Cancers*, **2020**, 12,	6.6	18
13	Recognition Dynamics of Cancer Mutations on the ERp57-Tapasin Interface. *Cancers*, **2020**, 12,	6.6	6
12	Structural, functional, and stability change predictions in human telomerase upon specific point mutations. *Scientific Reports*, **2019**, 9, 8707	4.9	15
11	Insights into the Effects of Cancer Associated Mutations at the UPF2 and ATP-Binding Sites of NMD Master Regulator: UPF1. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	5
10	The structurally similar TRFH domain of TRF1 and TRF2 dimers shows distinct behaviour towards TIN2. *Archives of Biochemistry and Biophysics*, **2018**, 642, 52-62	4.1	2
9	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	2.8	
8	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	2.1	1

7	Molecular basis and potential activity of HIV-1 reverse transcriptase toward trimethylamine-based compounds. *Biotechnology and Applied Biochemistry*, **2017**, 64, 810-826	2.8	
6	Molecular basis and quantitative assessment of TRF1 and TRF2 protein interactions with TIN2 and Apollo peptides. *European Biophysics Journal*, **2017**, 46, 171-187	1.9	3
5	Structure-based design and evaluation of novel N-phenyl-1H-indol-2-amine derivatives for fat mass and obesity-associated (FTO) protein inhibition. *Computational Biology and Chemistry*, **2016**, 64, 414-425	3.6	16
4	Identification of 1H-indene-(1,3,5,6)-tetrol derivatives as potent pancreatic lipase inhibitors using molecular docking and molecular dynamics approach. *Biotechnology and Applied Biochemistry*, **2016**, 63, 765-778	2.8	5
3	Structural and dynamic changes adopted by EmrE, multidrug transporter protein--Studies by molecular dynamics simulation. *Biochimica Et Biophysica Acta - Biomembranes*, **2015**, 1848, 2065-74	3.8	10
2	Molecular Modeling and Evaluation of Novel Dibenzopyrrole Derivatives as Telomerase Inhibitors and Potential Drug for Cancer Therapy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2014**, 11, 1196-207	3	8
1	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		2