Umesh Kalathiya

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1320605/publications.pdf

Version: 2024-02-01

30	509	1040056	713466
papers	citations	9	21
		h-index	g-index

32	32	32	820
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The emerging landscape of single-molecule protein sequencing technologies. Nature Methods, 2021, 18, 604-617.	19.0	198
2	Highly Conserved Homotrimer Cavity Formed by the SARS-CoV-2 Spike Glycoprotein: A Novel Binding Site. Journal of Clinical Medicine, 2020, 9, 1473.	2.4	73
3	Nonsense-Mediated mRNA Decay: Pathologies and the Potential for Novel Therapeutics. Cancers, 2020, 12, 765.	3.7	33
4	Structural, functional, and stability change predictions in human telomerase upon specific point mutations. Scientific Reports, 2019, 9, 8707.	3.3	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. Computational Biology and Chemistry, 2016, 64, 414-425.	2.3	21
6	Multivalent Display of SARS-CoV-2 Spike (RBD Domain) of COVID-19 to Nanomaterial, Protein Ferritin Nanocages. Biomolecules, 2021, 11, 297.	4.0	20
7	Functional Interfaces, Biological Pathways, and Regulations of Interferon-Related DNA Damage Resistance Signature (IRDS) Genes. Biomolecules, 2021, 11, 622.	4.0	18
8	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, 5644.	4.1	13
9	Structural and dynamic changes adopted by EmrE, multidrug transporter proteinâ€"Studies by molecular dynamics simulation. Biochimica Et Biophysica Acta - Biomembranes, 2015, 1848, 2065-2074.	2.6	11
10	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, 1196-1207.	3.0	9
11	Viruses, cancer and non-self recognition. Open Biology, 2021, 11, 200348.	3.6	9
12	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.	4.1	9
13	The Elephant Evolved p53 Isoforms that Escape MDM2-Mediated Repression and Cancer. Molecular Biology and Evolution, 2022, 39, .	8.9	9
14	Identification of 1Hâ€indeneâ€(1,3,5,6)â€tetrol derivatives as potent pancreatic lipase inhibitors using molecular docking and molecular dynamics approach. Biotechnology and Applied Biochemistry, 2016, 63, 765-778.	3.1	8
15	Recognition Dynamics of Cancer Mutations on the ERp57-Tapasin Interface. Cancers, 2020, 12, 737.	3.7	8
16	Interfaces with Structure Dynamics of the Workhorses from Cells Revealed through Cross-Linking Mass Spectrometry (CLMS). Biomolecules, 2021, 11, 382.	4.0	8
17	Drug repositioning against COVID-19: a first line treatment. Journal of Biomolecular Structure and Dynamics, 2022, 40, 12812-12826.	3.5	8
18	Molecular Determinants and Specificity of mRNA with Alternatively-Spliced UPF1 Isoforms, Influenced by an Insertion in the â€˜Regulatory Loopâ€™. International Journal of Molecular Sciences, 2021, 22, 12744.	4.1	7

#	Article	IF	Citations
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.	3.0	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.	2.2	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.	0.9	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 HIVâ€1 reverse transcriptase toward trimethylamineâ€based compounds. Biotechnology and Applied Biochemistry, 2017, 64, 810-826.	3.1	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 InterferansÄ± iÃ§in siRNA, miRNA ve snoRNA veritabanÄ±nda depolanan siRNA, miRNA, and snoRNA koleksiyonlarÄ±. Turkish Journal of Biochemistry, 2015, 40, .	0.5	0
27	Extracting functional groups of ALLINI to design derivatives of FDAâ€approved drugs: Inhibition of HIVâ€1 integrase. Biotechnology and Applied Biochemistry, 2018, 65, 594-607.	3.1	0
28	Structural analysis and predicting effects of natural mutations on telomerase. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C276-C276.	0.1	0
29	Molecular basis of TRF proteins and their interactions with peptides. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C174-C174.	0.1	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.	5.6	0