Umesh Kalathiya

List of Publications by Year
in descending order

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

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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	Drug repositioning against COVID-19: a first line treatment. Journal of Biomolecular Structure and Dynamics, 2022, 40, 12812-12826.	3.5	8
2	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
3	The Elephant Evolved p53 Isoforms that Escape MDM2-Mediated Repression and Cancer. Molecular Biology and Evolution, 2022, 39, .	8.9	9
4	Multivalent Display of SARS-CoV-2 Spike (RBD Domain) of COVID-19 to Nanomaterial, Protein Ferritin Nanocages. Biomolecules, 2021, 11, 297.	4.0	20
5	Viruses, cancer and non-self recognition. Open Biology, 2021, 11, 200348.	3.6	9
6	Interfaces with Structure Dynamics of the Workhorses from Cells Revealed through Cross-Linking Mass Spectrometry (CLMS). Biomolecules, 2021, 11, 382.	4.0	8
7	Functional Interfaces, Biological Pathways, and Regulations of Interferon-Related DNA Damage Resistance Signature (IRDS) Genes. Biomolecules, 2021, 11, 622.	4.0	18
8	The emerging landscape of single-molecule protein sequencing technologies. Nature Methods, 2021, 18, 604-617.	19.0	198
9	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
10	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
11	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
12	Nonsense-Mediated mRNA Decay: Pathologies and the Potential for Novel Therapeutics. Cancers, 2020, 12, 765.	3.7	33
13	Recognition Dynamics of Cancer Mutations on the ERp57-Tapasin Interface. Cancers, 2020, 12, 737.	3.7	8
14	Structural, functional, and stability change predictions in human telomerase upon specific point mutations. Scientific Reports, 2019, 9, 8707.	3.3	23
15	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
16	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
17	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
18	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

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19	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
20	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
21	Structural analysis and predicting effects of natural mutations on telomerase. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C276-C276.	0.1	0
22	Molecular basis of TRF proteins and their interactions with peptides. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C174-C174.	0.1	0
23	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
24	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
25	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
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	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
28	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
29	COMPUTER-AIDED DESIGN OF ORGANOPHOSPHORUS INHIBITORS OF UREASE. International Journal for Computational Biology, 2014, 3, 31.	0.1	1
30	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