

Prateek Kumar

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

618
citations

643344

15
h-index

843174

20
g-index

50
all docs

50
docs citations

50
times ranked

742
citing authors

#	ARTICLE	IF	CITATIONS
1	An insight into SARS-CoV-2 membrane protein interaction with spike, envelope, and nucleocapsid proteins. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 1062-1071.	2.0	18
2	Reprofiling of approved drugs against SARS-CoV-2 main protease: an in-silico study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 3170-3184.	2.0	20
3	Quercetin acts as a P-gp modulator via impeding signal transduction from nucleotide-binding domain to transmembrane domain. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 4507-4515.	2.0	23
4	One microsecond MD simulations of the SARS-CoV-2 main protease and hydroxychloroquine complex reveal the intricate nature of binding. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 10763-10770.	2.0	2
5	Microsecond simulations and CD spectroscopy reveals the intrinsically disordered nature of SARS-CoV-2 spike-C-terminal cytoplasmic tail (residues 1242-1273) in isolation. <i>Virology</i> , 2022, 566, 42-55.	1.1	14
6	Transactivation domain of Adenovirus Early Region 1A (E1A): Investigating folding dynamics and aggregation. <i>Current Research in Structural Biology</i> , 2022, 4, 29-40.	1.1	1
7	Computational methods to study intrinsically disordered proteins. , 2022, , 489-504.		3
8	Mitoxantrone dihydrochloride, an FDA approved drug, binds with SARS-CoV-2 NSP1 C-terminal. <i>RSC Advances</i> , 2022, 12, 5648-5655.	1.7	11
9	Functional inhibition of c-Myc using novel inhibitors identified through α hot spot-targeting.. <i>Journal of Biological Chemistry</i> , 2022, , 101898.	1.6	5
10	Role of structural disorder in the multi-functionality of flavivirus proteins. <i>Expert Review of Proteomics</i> , 2022, 19, 183-196.	1.3	1
11	Structural dynamics of Zika virus NS1 via a reductionist approach reveal the disordered nature of its β -roll domain in isolation. <i>Virology</i> , 2022, 573, 72-83.	1.1	3
12	Polysaccharides like pentagalloylglucose, parishin a and stevioside inhibits the viral entry by binding the Zika virus envelope protein. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 6008-6020.	2.0	3
13	Investigating into the molecular interactions of flavonoids targeting NS2B-NS3 protease from ZIKA virus through <i>in-silico</i> approaches. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 272-284.	2.0	26
14	Understanding COVID-19 via comparative analysis of dark proteomes of SARS-CoV-2, human SARS and bat SARS-like coronaviruses. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 1655-1688.	2.4	92
15	Molecular Dynamic Simulation of Intrinsically Disordered Proteins and Relevant Forcefields. , 2021, , 317-333.		1
16	SARS-CoV-2 NSP1 C-terminal (residues 131-180) is an intrinsically disordered region in isolation. <i>Current Research in Virological Science</i> , 2021, 2, 100007.	1.8	23
17	Anti-tuberculosic thionamide antibiotics show antioxidative and neuronal cytoprotective nature by inhibiting amyloid formation in human insulin and amyloid β -42. <i>Journal of Molecular Liquids</i> , 2021, 326, 115396.	2.3	6
18	Experiments and simulation on ZIKV NS2B-NS3 protease reveal its complex folding. <i>Virology</i> , 2021, 556, 110-123.	1.1	4

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19	Identification of Naturally Occurring Antiviral Molecules for SARS-CoV-2 Mitigation. The Open Covid Journal, 2021, 1, 38-46.	0.4	7
20	Analysis of the dark proteome of Chandipura virus reveals maximum propensity for intrinsic disorder in phosphoprotein. Scientific Reports, 2021, 11, 13253.	1.6	8
21	A novel inhibitor L755507 efficiently blocks c-Myc's MAX heterodimerization and induces apoptosis in cancer cells. Journal of Biological Chemistry, 2021, 297, 100903.	1.6	13
22	Salvianolic acid B noncovalently interacts with disordered c-Myc: a computational and spectroscopic-based study. Future Medicinal Chemistry, 2021, 13, 1341-1352.	1.1	4
23	In silico screening of Pueraria tuberosa (PTY-2) for targeting COVID-19 by countering dual targets Mpro and TMPRSS2. Journal of Biomolecular Structure and Dynamics, 2021, , 1-14.	2.0	2
24	Conformational dynamics of 13 amino acids long NSP11 of SARS-CoV-2 under membrane mimetics and different solvent conditions. Microbial Pathogenesis, 2021, 158, 105041.	1.3	26
25	Investigating the conformational dynamics of SARS-CoV-2 NSP6 protein with emphasis on non-transmembrane 91-112 & 231-290 regions. Microbial Pathogenesis, 2021, 161, 105236.	1.3	8
26	Targeting the NTPase site of Zika virus NS3 helicase for inhibitor discovery. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4827-4837.	2.0	11
27	The dark side of Alzheimer's disease: unstructured biology of proteins from the amyloid cascade signaling pathway. Cellular and Molecular Life Sciences, 2020, 77, 4163-4208.	2.4	23
28	Understanding the penetrance of intrinsic protein disorder in rotavirus proteome. International Journal of Biological Macromolecules, 2020, 144, 892-908.	3.6	24
29	Bisindolemethane derivatives as highly potent anticancer agents: Synthesis, medicinal activity evaluation, cell-based compound discovery, and computational target predictions. Computers in Biology and Medicine, 2020, 116, 103574.	3.9	9
30	Identification of peptidomimetic compounds as potential inhibitors against MurA enzyme of <i>Mycobacterium tuberculosis</i> . Journal of Biomolecular Structure and Dynamics, 2020, 38, 4997-5013.	2.0	17
31	Zika virus NS4A cytosolic region (residues 1-48) is an intrinsically disordered domain and folds upon binding to lipids. Virology, 2020, 550, 27-36.	1.1	25
32	Unlike dengue virus, the conserved 14-23 residues in N-terminal region of Zika virus capsid is not involved in lipid interactions. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183440.	1.4	13
33	Small molecule inhibitors possibly targeting the rearrangement of Zika virus envelope protein. Antiviral Research, 2020, 182, 104876.	1.9	11
34	Exploring the SARS-CoV-2 structural proteins for multi-epitope vaccine development: an in-silico approach. Expert Review of Vaccines, 2020, 19, 887-898.	2.0	19
35	Japanese encephalitis virus - exploring the dark proteome and disorder-function paradigm. FEBS Journal, 2020, 287, 3751-3776.	2.2	18
36	Unstructured Biology of Proteins from Ubiquitin-Proteasome System: Roles in Cancer and Neurodegenerative Diseases. Biomolecules, 2020, 10, 796.	1.8	17

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37	Folding and structural polymorphism of p53 C-terminal domain: One peptide with many conformations. Archives of Biochemistry and Biophysics, 2020, 684, 108342.	1.4	24
38	Targeting the nsp2 Cysteine Protease of Chikungunya Virus Using FDA Approved Library and Selected Cysteine Protease Inhibitors. Pathogens, 2019, 8, 128.	1.2	17
39	The dark proteome of cancer: Intrinsic disorder and functionality of HIF-1 α along with its interacting proteins. Progress in Molecular Biology and Translational Science, 2019, 166, 371-403.	0.9	25