Rajanish Giri

List of Publications by Year
in descending order

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78 papers	1,925 citations	346980 22 h-index	355658 38 g-index
93 all docs	93 docs citations	93 times ranked	2454 citing authors

#	Article	IF	Citations
1	An insight into SARS-CoV-2 membrane protein interaction with spike, envelope, and nucleocapsid proteins. Journal of Biomolecular Structure and Dynamics, 2023, 41, 1062-1071.	2.0	18
2	Reprofiling of approved drugs against SARS-CoV-2 main protease: an in-silico study. Journal of Biomolecular Structure and Dynamics, 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. Journal of Biomolecular Structure and Dynamics, 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. Journal of Biomolecular Structure and Dynamics, 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 1242â€“1273) in isolation. Virology, 2022, 566, 42-55.	1.1	14
6	Transactivation domain of Adenovirus Early Region 1A (E1A): Investigating folding dynamics and aggregation. Current Research in Structural Biology, 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. RSC Advances, 2022, 12, 5648-5655.	1.7	11
9	Intrinsic disorder in proteins associated with oxidative stress-induced JNK signaling. Cellular and Molecular Life Sciences, 2022, 79, 202.	2.4	9
10	Functional inhibition of c-Myc using novel inhibitors identified through â€œhot spotâ€•targeting.. Journal of Biological Chemistry, 2022, , 101898.	1.6	5
11	Role of structural disorder in the multi-functionality of flavivirus proteins. Expert Review of Proteomics, 2022, 19, 183-196.	1.3	1
12	Structural dynamics of Zika virus NS1 via a reductionist approach reveal the disordered nature of its Î²-roll domain in isolation. Virology, 2022, 573, 72-83.	1.1	3
13	Polysaccharides like pentagalloylglucose, parishin a and stevioside inhibits the viral entry by binding the Zika virus envelope protein. Journal of Biomolecular Structure and Dynamics, 2021, 39, 6008-6020.	2.0	3
14	Investigating into the molecular interactions of flavonoids targeting NS2B-NS3 protease from ZIKA virus through in-silico approaches. Journal of Biomolecular Structure and Dynamics, 2021, 39, 272-284.	2.0	26
15	Understanding COVID-19 via comparative analysis of dark proteomes of SARS-CoV-2, human SARS and bat SARS-like coronaviruses. Cellular and Molecular Life Sciences, 2021, 78, 1655-1688.	2.4	92
16	Molecular Dynamic Simulation of Intrinsically Disordered Proteins and Relevant Forcefields. , 2021, , 317-333.		1
17	SARS-CoV-2 NSP1 C-terminal (residues 131â€“180) is an intrinsically disordered region in isolation. Current Research in Virological Science, 2021, 2, 100007.	1.8	23
18	Experiments and simulation on ZIKV NS2B-NS3 protease reveal its complex folding. Virology, 2021, 556, 110-123.	1.1	4

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19	Naturally Occurring Bioactives as Antivirals: Emphasis on Coronavirus Infection. Frontiers in Pharmacology, 2021, 12, 575877.	1.6	18
20	Identification of Naturally Occurring Antiviral Molecules for SARS-CoV-2 Mitigation. The Open Covid Journal, 2021, 1, 38-46.	0.4	7
21	Analysis of the dark proteome of Chandipura virus reveals maximum propensity for intrinsic disorder in phosphoprotein. Scientific Reports, 2021, 11, 13253.	1.6	8
22	A novel inhibitor L755507 efficiently blocks c-Mycâ€“MAX heterodimerization and induces apoptosis in cancer cells. Journal of Biological Chemistry, 2021, 297, 100903.	1.6	13
23	Zika virus capsid anchor forms cytotoxic amyloid-like fibrils. Virology, 2021, 560, 8-16.	1.1	11
24	Salvianolic acid B noncovalently interacts withÂdisordered c-Myc: a computational and spectroscopic-based study. Future Medicinal Chemistry, 2021, 13, 1341-1352.	1.1	4
25	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
26	The role of microRNA-21 in the onset and progression of cancer. Future Medicinal Chemistry, 2021, 13, 1885-1906.	1.1	34
27	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
28	The signal peptide of the amyloid precursor protein forms amyloid-like aggregates and enhances AÎ²42 aggregation. Cell Reports Physical Science, 2021, 2, 100599.	2.8	5
29	Investigating the conformational dynamics of SARS-CoV-2 NSP6 protein with emphasis on non-transmembrane 91â€“112 & 231â€“290 regions. Microbial Pathogenesis, 2021, 161, 105236.	1.3	8
30	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
31	The history of mutational pressure changes during the evolution of adeno-associated viruses: A message to gene therapy and DNA-vaccine vectors designers. Infection, Genetics and Evolution, 2020, 77, 104100.	1.0	9
32	The dark side of Alzheimerâ€™s disease: unstructured biology of proteins from the amyloid cascade signaling pathway. Cellular and Molecular Life Sciences, 2020, 77, 4163-4208.	2.4	23
33	A biscoumarin scaffold as an efficient anti-Zika virus lead with NS3-helicase inhibitory potential: in vitro and in silico investigations. New Journal of Chemistry, 2020, 44, 1872-1880.	1.4	13
34	Folding perspectives of an intrinsically disordered transactivation domain and its single mutation breaking the folding propensity. International Journal of Biological Macromolecules, 2020, 155, 1359-1372.	3.6	7
35	Understanding the penetrance of intrinsic protein disorder in rotavirus proteome. International Journal of Biological Macromolecules, 2020, 144, 892-908.	3.6	24
36	Identification of peptidomimetic compounds as potential inhibitors against MurA enzyme of Mycobacterium tuberculosis. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4997-5013.	2.0	17

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37	Zika virus NS4A N-Terminal region (1-48) acts as a cofactor for inducing NTPase activity of NS3 helicase but not NS3 protease. Archives of Biochemistry and Biophysics, 2020, 695, 108631.	1.4	8
38	Translation-Associated Mutational U-Pressure in the First ORF of SARS-CoV-2 and Other Coronaviruses. Frontiers in Microbiology, 2020, 11, 559165.	1.5	12
39	Zika virus NS4A cytosolic region (residues 1â€“48) is an intrinsically disordered domain and folds upon binding to lipids. Virology, 2020, 550, 27-36.	1.1	25
40	Unlike dengue virus, the conserved 14â€“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
41	Small molecule inhibitors possibly targeting the rearrangement of Zika virus envelope protein. Antiviral Research, 2020, 182, 104876.	1.9	11
42	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
43	Mechanistic Insights into Zika Virus NS3 Helicase Inhibition by Epigallocatechin-3-Gallate. ACS Omega, 2020, 5, 11217-11226.	1.6	25
44	Japanese encephalitis virus â€“ exploring the dark proteome and disorderâ€“function paradigm. FEBS Journal, 2020, 287, 3751-3776.	2.2	18
45	Conformational dynamics of p53ÂN-terminal TAD2 region under different solvent conditions. Archives of Biochemistry and Biophysics, 2020, 689, 108459.	1.4	14
46	Unstructured Biology of Proteins from Ubiquitin-Proteasome System: Roles in Cancer and Neurodegenerative Diseases. Biomolecules, 2020, 10, 796.	1.8	17
47	Folding and structural polymorphism of p53ÂC-terminal domain: One peptide with many conformations. Archives of Biochemistry and Biophysics, 2020, 684, 108342.	1.4	24
48	Amyloid formation by intrinsically disordered trans-activation domain of cMyb. Biochemical and Biophysical Research Communications, 2020, 524, 446-452.	1.0	13
49	Targeting the nsp2 Cysteine Protease of Chikungunya Virus Using FDA Approved Library and Selected Cysteine Protease Inhibitors. Pathogens, 2019, 8, 128.	1.2	17
50	Mammalian antimicrobial peptide protegrinâ€4 self assembles and forms amyloidâ€like aggregates: Assessment of its functional relevance. Journal of Peptide Science, 2019, 25, e3151.	0.8	17
51	The dark proteome of cancer: Intrinsic disorderedness and functionality of HIF-1Î± along with its interacting proteins. Progress in Molecular Biology and Translational Science, 2019, 166, 371-403.	0.9	25
52	The mechanism of phosphatidylcholineâ€induced interference of PAP (248â€286) aggregation. Journal of Peptide Science, 2019, 25, e3152.	0.8	2
53	Deciphering the dark proteome of Chikungunya virus. Scientific Reports, 2018, 8, 5822.	1.6	37
54	E7 oncoprotein of human papillomavirus: Structural dynamics and inhibitor screening study. Gene, 2018, 658, 159-177.	1.0	30

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55	Molecular Recognition Features in Zika Virus Proteome. Journal of Molecular Biology, 2018, 430, 2372-2388.	2.0	58
56	Hydroxychloroquine Inhibits Zika Virus NS2B-NS3 Protease. ACS Omega, 2018, 3, 18132-18141.	1.6	86
57	Role of the glutaredoxin domain and FAD in the stabilization of thioredoxin glutathione reductase. Archives of Biochemistry and Biophysics, 2018, 656, 38-45.	1.4	3
58	Understanding the interactability of chikungunya virus proteinsviamolecular recognition feature analysis. RSC Advances, 2018, 8, 27293-27303.	1.7	23
59	Comprehensive analysis of the catalytic and structural properties of a mu-class glutathione s-transferase from Fasciola gigantica. Scientific Reports, 2017, 7, 17547.	1.6	20
60	Therapeutic Interventions of Cancers Using Intrinsically Disordered Proteins as Drug Targets: c-Myc as Model System. Cancer Informatics, 2017, 16, 117693511769940.	0.9	45
61	Epigallocatechin gallate, an active green tea compound inhibits the Zika virus entry into host cells via binding the envelope protein. International Journal of Biological Macromolecules, 2017, 104, 1046-1054.	3.6	84
62	Mutational Pressure in Zika Virus: Local ADAR-Editing Areas Associated with Pauses in Translation and Replication. Frontiers in Cellular and Infection Microbiology, 2017, 7, 44.	1.8	34
63	Intrinsically Disordered Side of the Zika Virus Proteome. Frontiers in Cellular and Infection Microbiology, 2016, 6, 144.	1.8	83
64	Towards a structural biology of the hydrophobic effect in protein folding. Scientific Reports, 2016, 6, 28285.	1.6	91
65	Molecular Recognition by Templated Folding of an Intrinsically Disordered Protein. Scientific Reports, 2016, 6, 21994.	1.6	87
66	Mechanism of Cyclic AMP Partial Agonism in Protein Kinase G (PKG). Biophysical Journal, 2016, 110, 514a.	0.2	0
67	Optical signaling in biofluids: a nondenaturing photostable molecular probe for serum albumins. Chemical Communications, 2016, 52, 1887-1890.	2.2	46
68	Mechanism of cAMP Partial Agonism in Protein Kinase G (PKG). Journal of Biological Chemistry, 2015, 290, 28631-28641.	1.6	44
69	Tapping the translation potential of cAMP signalling: molecular basis for selectivity in cAMP agonism and antagonism as revealed by NMR. Biochemical Society Transactions, 2014, 42, 302-307.	1.6	16
70	The mechanism of binding of the KIX domain to the mixed lineage leukemia protein and its allosteric role in the recognition of câ€Myb. Protein Science, 2014, 23, 962-969.	3.1	38
71	The kinetics of folding of frataxin. Physical Chemistry Chemical Physics, 2014, 16, 6391.	1.3	17
72	Understanding the frustration arising from the competition between function, misfolding, and aggregation in a globular protein. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14141-14146.	3.3	43

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73	Structure of the transition state for the binding of c-Myb and KIX highlights an unexpected order for a disordered system. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14942-14947.	3.3	99
74	Reassessing the folding of the KIX domain: Evidence for a twoâ€state mechanism. Protein Science, 2012, 21, 1775-1779.	3.1	2
75	Morphogenesis of a protein: folding pathways and the energy landscape1. Biochemical Society Transactions, 2012, 40, 429-432.	1.6	10
76	A folding-after-binding mechanism describes the recognition between the transactivation domain of c-Myb and the KIX domain of the CREB-binding protein. Biochemical and Biophysical Research Communications, 2012, 428, 205-209.	1.0	71
77	Folding pathways of proteins with increasing degree of sequence identities but different structure and function. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17772-17776.	3.3	25
78	GB1 Is Not a Two-State Folder: Identification and Characterization of an On-Pathway Intermediate. Biophysical Journal, 2011, 101, 2053-2060.	0.2	29