

Vijay Kumar

List of Publications by Year in descending order

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69
papers

1,683
citations

257357

24
h-index

345118

36
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73
all docs

73
docs citations

73
times ranked

1864
citing authors

#	ARTICLE	IF	CITATIONS
1	Targeting SARS-CoV-2 nucleocapsid oligomerization: Insights from molecular docking and molecular dynamics simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 2430-2443.	2.0	29
2	COVID-19 associated nervous system manifestations. <i>Sleep Medicine</i> , 2022, 91, 231-236.	0.8	19
3	Structural dissection of TDP-43. , 2022, , 27-44.		0
4	In-cell NMR spectroscopy: A tool to study cellular structure biology. , 2022, , 267-276.		0
5	Insights into the structure and dynamics of SARS-CoV-2 spike glycoprotein double mutant L452R-E484Q. <i>3 Biotech</i> , 2022, 12, 87.	1.1	5
6	Computational Insights of Unfolding of N-Terminal Domain of TDP-43 Reveal the Conformational Heterogeneity in the Unfolding Pathway. <i>Frontiers in Molecular Neuroscience</i> , 2022, 15, 822863.	1.4	3
7	Frustration analysis of TBK1 missense mutations reported in ALS/FTD and cancer patients. <i>3 Biotech</i> , 2022, 12, .	1.1	4
8	Structural heterogeneity in RNA recognition motif 2 (RRM2) of TAR DNA-binding protein 43 (TDP-43): clue to amyotrophic lateral sclerosis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 357-367.	2.0	19
9	Brain Disease Network Analysis to Elucidate the Neurological Manifestations of COVID-19. <i>Molecular Neurobiology</i> , 2021, 58, 1875-1893.	1.9	37
10	Artificial intelligence-driven drug repurposing and structural biology for SARS-CoV-2. <i>Current Research in Pharmacology and Drug Discovery</i> , 2021, 2, 100042.	1.7	22
11	Simultaneous Inhibition of SARS-CoV-2 Entry Pathways by Cyclosporine. <i>ACS Chemical Neuroscience</i> , 2021, 12, 930-944.	1.7	20
12	SARS-CoV-2 spike protein interactions with amyloidogenic proteins: Potential clues to neurodegeneration. <i>Biochemical and Biophysical Research Communications</i> , 2021, 554, 94-98.	1.0	98
13	The structural, functional, and dynamic effect of Tau tubulin kinase1 upon a mutation: A neurodegenerative hotspot. <i>Journal of Cellular Biochemistry</i> , 2021, 122, 1653-1664.	1.2	11
14	Genomics-guided identification of potential modulators of SARS-CoV-2 entry proteases, TMPRSS2 and Cathepsins B/L. <i>PLoS ONE</i> , 2021, 16, e0256141.	1.1	12
15	Molecular interactions between C9ORF72 and SMCR8: A local energetic frustration perspective. <i>Biochemical and Biophysical Research Communications</i> , 2021, 570, 1-7.	1.0	4
16	Targeting cathepsins: A potential link between COVID-19 and associated neurological manifestations. <i>Heliyon</i> , 2021, 7, e08089.	1.4	11
17	Genomics-guided targeting of stress granule proteins G3BP1/2 to inhibit SARS-CoV-2 propagation. <i>International Journal of Biological Macromolecules</i> , 2021, 190, 636-648.	3.6	13
18	A molecular journey to check the conformational dynamics of tau tubulin kinase 2 mutations associated with Alzheimer's disease. <i>RSC Advances</i> , 2021, 11, 1320-1331.	1.7	12

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19	Insights into the SARS-CoV-2-Mediated Alteration in the Stress Granule Protein Regulatory Networks in Humans. <i>Pathogens</i> , 2021, 10, 1459.	1.2	9
20	Delineating the Aggregation-Prone Hotspot Regions (Peptides) in the Human Cu/Zn Superoxide Dismutase 1. <i>ACS Omega</i> , 2021, 6, 33985-33994.	1.6	1
21	Impact of Gln94Glu mutation on the structure and function of protection of telomere 1, a cause of cutaneous familial melanoma. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 1514-1524.	2.0	29
22	Characterization of heterogeneous intermediate ensembles on the guanidinium chloride-induced unfolding pathway of β^2 -lactoglobulin. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 1042-1053.	2.0	4
23	Virtual high-throughput screening of natural compounds in-search of potential inhibitors for protection of telomeres 1 (POT1). <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 4625-4634.	2.0	32
24	Impact of amino acid substitution in the kinase domain of Bruton tyrosine kinase and its association with X-linked agammaglobulinemia. <i>International Journal of Biological Macromolecules</i> , 2020, 164, 2399-2408.	3.6	18
25	Neurological manifestations of COVID-19: available evidences and a new paradigm. <i>Journal of NeuroVirology</i> , 2020, 26, 619-630.	1.0	75
26	Targeting hub genes and pathways of innate immune response in COVID-19: A network biology perspective. <i>International Journal of Biological Macromolecules</i> , 2020, 163, 1-8.	3.6	72
27	Folding/Unfolding Pattern and Stability of Intramolecular G-Quadruplex Structure by Myoinositol. <i>Biophysical Journal</i> , 2020, 118, 220a.	0.2	0
28	Insights into the biased activity of dextromethorphan and haloperidol towards SARS-CoV-2 NSP6: in silico binding mechanistic analysis. <i>Journal of Molecular Medicine</i> , 2020, 98, 1659-1673.	1.7	39
29	Insights into the DNA binding induced thermal stabilization of transcription factor FOXP3. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 2219-2229.	2.0	8
30	Structural Analysis and Conformational Dynamics of STN1 Gene Mutations Involved in Coat Plus Syndrome. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 41.	1.6	53
31	Delineating the effect of mutations on the conformational dynamics of N-terminal domain of TDP-43. <i>Biophysical Chemistry</i> , 2019, 250, 106174.	1.5	21
32	Investigating architecture and structure-function relationships in cold shock DNA-binding domain family using structural genomics-based approach. <i>International Journal of Biological Macromolecules</i> , 2019, 133, 484-494.	3.6	17
33	Structural and functional impact of non-synonymous SNPs in the CST complex subunit TEN1: structural genomics approach. <i>Bioscience Reports</i> , 2019, 39, .	1.1	17
34	Mechanism and implications of traditional Chinese medicine in amyotrophic lateral sclerosis therapy. <i>Journal of Proteins and Proteomics</i> , 2019, 10, 131.	1.0	3
35	Investigation of deleterious effects of nsSNPs in the <i>POT1</i> gene: a structural genomics-based approach to understand the mechanism of cancer development. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 10281-10294.	1.2	32
36	Exploring the aggregation-prone regions from structural domains of human TDP-43. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 286-296.	1.1	27

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37	Amyotrophic Lateral Sclerosis: Current Therapeutic Perspectives. , 2019, , 207-224.		2
38	Comparative analysis of thermal unfolding simulations of RNA recognition motifs (RRMs) of TAR DNA-binding protein 43 (TDP-43). Journal of Biomolecular Structure and Dynamics, 2019, 37, 178-194.	2.0	27
39	TFE-induced local unfolding and fibrillation of SOD1: bridging the experiment and simulation studies. Biochemical Journal, 2018, 475, 1701-1719.	1.7	24
40	Phosphorylation-induced changes in the energetic frustration in human Tank binding kinase 1. Journal of Theoretical Biology, 2018, 449, 14-22.	0.8	16
41	Alterations in local stability and dynamics of A4V SOD1 in the presence of trifluoroethanol. Biopolymers, 2018, 109, e23102.	1.2	31
42	Solvent sensitivity of protein aggregation in Cu, Zn superoxide dismutase: a molecular dynamics simulation study. Journal of Biomolecular Structure and Dynamics, 2018, 36, 2605-2617.	2.0	19
43	Sequence, structure and evolutionary analysis of cold shock domain proteins, a member of OB fold family. Journal of Evolutionary Biology, 2018, 31, 1903-1917.	0.8	25
44	Systems Biology of RNA-Binding Proteins in Amyotrophic Lateral Sclerosis. RNA Technologies, 2018, , 59-75.	0.2	0
45	Elucidation of the structural stability and dynamics of heterogeneous intermediate ensembles in unfolding pathway of the N-terminal domain of TDP-43. RSC Advances, 2018, 8, 19835-19845.	1.7	21
46	Protein aggregation, misfolding and consequential human neurodegenerative diseases. International Journal of Neuroscience, 2017, 127, 1047-1057.	0.8	44
47	Towards understanding cellular structure biology: In-cell NMR. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 547-557.	1.1	17
48	Fas-activated serine/threonine kinase: Structure and function. Gene Reports, 2017, 8, 117-127.	0.4	6
49	Computing disease-linked SOD1 mutations: deciphering protein stability and patient-phenotype relations. Scientific Reports, 2017, 7, 4678.	1.6	34
50	Exploring Missense Mutations in Tyrosine Kinases Implicated with Neurodegeneration. Molecular Neurobiology, 2017, 54, 5085-5106.	1.9	8
51	Unraveling the Role of RNA Mediated Toxicity of C9orf72 Repeats in C9-FTD/ALS. Frontiers in Neuroscience, 2017, 11, 711.	1.4	46
52	Therapeutic progress in amyotrophic lateral sclerosis-beginning to learning. European Journal of Medicinal Chemistry, 2016, 121, 903-917.	2.6	59
53	Protein aggregation and neurodegenerative diseases: From theory to therapy. European Journal of Medicinal Chemistry, 2016, 124, 1105-1120.	2.6	120
54	Structural insight into C9orf72 hexanucleotide repeat expansions: Towards new therapeutic targets in FTD-ALS. Neurochemistry International, 2016, 100, 11-20.	1.9	25

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55	Delineating the relationship between amyotrophic lateral sclerosis and frontotemporal dementia: Sequence and structure-based predictions. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 1742-1754.	1.8	22
56	Kinetic and Structural Studies on the Interactions of Heparin and Proteins of Human Seminal Plasma using Surface Plasmon Resonance. <i>Protein and Peptide Letters</i> , 2012, 19, 795-803.	0.4	4
57	Purification and characterization of a native zinc-binding high molecular weight multiprotein complex from human seminal plasma. <i>Journal of Separation Science</i> , 2011, 34, 1076-1083.	1.3	8
58	Proteomic analysis of heparin-binding proteins from human seminal plasma: a step towards identification of molecular markers of male fertility. <i>Journal of Biosciences</i> , 2009, 34, 899-908.	0.5	61
59	Purification and preliminary X-ray crystallographic studies of β^2 -microseminoprotein from human seminal plasma. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 518-521.	0.7	3
60	Strategy for sensitive and specific detection of molecular forms of PSA based on 2DE and kinetic analysis: A step towards diagnosis of prostate cancer. <i>Clinica Chimica Acta</i> , 2009, 403, 17-22.	0.5	16
61	Proteomic analysis of human amniotic fluid from Rh ⁺ pregnancy. <i>Prenatal Diagnosis</i> , 2008, 28, 102-108.	1.1	18
62	Purification and characterization of zinc β^2 -glycoprotein-prolactin inducible protein complex from human seminal plasma. <i>Journal of Separation Science</i> , 2008, 31, 2318-2324.	1.3	32
63	Heparin-binding proteins of human seminal plasma: purification and characterization. <i>Molecular Reproduction and Development</i> , 2008, 75, 1767-1774.	1.0	28
64	Crystal Structure of the Novel Complex Formed between Zinc β^2 -Glycoprotein (ZAG) and Prolactin-Inducible Protein (PIP) from Human Seminal Plasma. <i>Journal of Molecular Biology</i> , 2008, 384, 663-672.	2.0	65
65	Comparative Studies on the Aggregation Behavior of HBPs from Human Seminal Plasma by Dynamic Light Scattering. <i>Protein and Peptide Letters</i> , 2008, 15, 633-639.	0.4	2
66	Proteomic approach for purification of seminal plasma proteins involved in tumor proliferation. <i>Journal of Separation Science</i> , 2007, 30, 1979-1988.	1.3	33
67	Structure-guided design of peptidic ligand for human prostate specific antigen. <i>Journal of Peptide Science</i> , 2007, 13, 849-855.	0.8	41
68	Structural Model of Human PSA: A Target for Prostate Cancer Therapy. <i>Chemical Biology and Drug Design</i> , 2007, 70, 261-267.	1.5	39
69	Towards Understanding the Relationship Between ER Stress and Unfolded Protein Response in Amyotrophic Lateral Sclerosis. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	1.7	8