

# Venkata S K Mattaparthi

## List of Publications by Year in descending order

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Version: 2024-02-01

47  
papers

649  
citations

932766

10  
h-index

610482

24  
g-index

49  
all docs

49  
docs citations

49  
times ranked

1098  
citing authors

#	ARTICLE	IF	CITATIONS
1	Lysozyme. <i>Advances in Protein Chemistry and Structural Biology</i> , 2011, 84, 63-111.	1.0	205
2	PAMAM Dendrimerâ€™Drug Interactions: Effect of pH on the Binding and Release Pattern. <i>Journal of Physical Chemistry B</i> , 2012, 116, 4370-4376.	1.2	100
3	Excellent N-fixing and P-solubilizing traits in earthworm gut-isolated bacteria: A vermicompost based assessment with vegetable market waste and rice straw feed mixtures. <i>Bioresource Technology</i> , 2016, 222, 165-174.	4.8	92
4	Daboxin P, a Major Phospholipase A2 Enzyme from the Indian <i>Daboia russelii russelii</i> Venom Targets Factor X and Factor Xa for Its Anticoagulant Activity. <i>PLoS ONE</i> , 2016, 11, e0153770.	1.1	26
5	Chemical system biology approach to identify multi-targeting FDA inhibitors for treating COVID-19 and associated health complications. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 9543-9567.	2.0	19
6	Bis- and mixed-ligand copper(II) complexes of nalidixic acid the antibacterial drug: Mode of nalidixate coordination determines DNA binding and cleavage and cytotoxicity. <i>Inorganica Chimica Acta</i> , 2020, 504, 119450.	1.2	15
7	DNA Assisted Self-Assembly of PAMAM Dendrimers. <i>Journal of Physical Chemistry B</i> , 2014, 118, 11805-11815.	1.2	14
8	Computational investigation on the effect of Oleuropein aglycone on the $\beta$ -synuclein aggregation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 1259-1270.	2.0	14
9	$\beta$ , 25-dihydroxy Vitamin D3 containing fractions of <i>Catharanthus roseus</i> leaf aqueous extract inhibit preadipocyte differentiation and induce lipolysis in 3T3-L1 cells. <i>BMC Complementary and Alternative Medicine</i> , 2019, 19, 338.	3.7	12
10	Potential of mean force and molecular dynamics study on the transient interactions between $\beta$ and $\beta^2$ synuclein that drive inhibition of $\beta$ -synuclein aggregation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 3342-3353.	2.0	11
11	Structure of DNA-functionalized dendrimer nanoparticles. <i>Soft Matter</i> , 2012, 8, 1893-1900.	1.2	10
12	In <i>in silico</i> investigation on the inhibition of $A\beta_{42}$ aggregation by $A\beta_{40}$ peptide by potential of mean force study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 741-752.	2.0	10
13	Structure-Based Virtual Screening of High-Affinity ATP-Competitive Inhibitors Against Human Lemur Tyrosine Kinase-3 (LMTK3) Domain: A Novel Therapeutic Target for Breast Cancer. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 527-541.	2.2	10
14	Consequences of Heterogeneous Crowding on an Enzymatic Reaction: A Residence Time Monte Carlo Approach. <i>ACS Omega</i> , 2019, 4, 727-736.	1.6	8
15	Computational Investigation on the p53â€™MDM2 Interaction Using the Potential of Mean Force Study. <i>ACS Omega</i> , 2020, 5, 8449-8462.	1.6	8
16	Investigation on the Molecular Interactions Stabilizing the Structure of $\beta$ -synuclein Fibril: An <i>In silico</i> Study. <i>Central Nervous System Agents in Medicinal Chemistry</i> , 2017, 17, 209-218.	0.5	8
17	Molecular dynamics simulation of HIV-protease with polarizable and non-polarizable force fields. <i>Indian Journal of Physics</i> , 2009, 83, 81-90.	0.9	7
18	A novel approach to segregate and identify functional loop regions in protein structures using their Ramachandran maps. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 900-916.	1.5	7

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19	An <i>in silico</i> approach to understand the structure–function properties of a serine protease (Bacifrinase) from <i>Bacillus cereus</i> and experimental evidence to support the interaction of Bacifrinase with fibrinogen and thrombin. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 622-644.	2.0	7
20	Structural insight into the binding interactions of modeled structure of <i>Arabidopsis thaliana</i> urease with urea: an <i>in silico</i> study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 845-851.	2.0	6
21	Computational investigation on the effects of H50Q and G51D mutations on the $\beta$ -Synuclein aggregation propensity. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 2224-2236.	2.0	6
22	Unveiling the Transient Protein-Protein Interactions that Regulate the Activity of Human Lemur Tyrosine Kinase-3 (LMTK3) Domain by Cyclin Dependent Kinase 5 (CDK5) in Breast Cancer: An <i>in silico</i> Study. <i>Current Proteomics</i> , 2018, 15, .	0.1	5
23	Computational Investigation on Tyrosine to Alanine Mutations Delaying the Early Stage of $\beta$ -Synuclein Aggregation. <i>Current Proteomics</i> , 2017, 14, 31-41.	0.1	5
24	Inhibition of $A\beta_{1-42}$ peptide aggregation using short ss-oligonucleotide as polyions: an <i>in silico</i> approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 1401-1406.	2.0	4
25	Characterizing the Binding Interactions between DNA-Binding Proteins, XPA and XPE: A Molecular Dynamics Approach. <i>ACS Omega</i> , 2018, 3, 15442-15454.	1.6	4
26	Investigation of the probable homo-dimer model of the <i>Xeroderma pigmentosum</i> complementation group A (XPA) protein to represent the DNA-binding core. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 3322-3336.	2.0	4
27	Computational Study on the Role of $\beta$ -Synuclein in Inhibiting the $\beta$ -Synuclein Aggregation. <i>Central Nervous System Agents in Medicinal Chemistry</i> , 2019, 19, 24-30.	0.5	4
28	CONFORMATIONAL DYNAMICS OF HIV-1 PROTEASE: A COMPARATIVE MOLECULAR DYNAMICS SIMULATION STUDY WITH MULTIPLE AMBER FORCE FIELDS. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1250018.	0.3	3
29	Interchain hydrophobic clustering promotes rigidity in HIV-1 protease flap dynamics: new insights from Molecular Dynamics. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 899-915.	2.0	3
30	Comparative Study on the Binding Affinity of Methimazole and Propylthiouracil to Thyroid Peroxidase as an Anti-Thyroid Drug: An <i>In silico</i> Approach. <i>Journal of Molecular Imaging &amp; Dynamics</i> , 2017, 07, .	0.2	3
31	Structural dynamics and interactions of <i>Xeroderma pigmentosum</i> complementation group A (XPA <sub>98-210</sub> ) with damaged DNA. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 3341-3353.	2.0	3
32	A Comparative Study to Elucidate the Inhibitory Mechanism of a 6-Mer Fragment of Amyloid-Beta 42 Peptide as a Potential Therapeutic in Alzheimer's Disease: Insights from Molecular Dynamics Simulations. <i>Current Science</i> , 2018, 114, 1207.	0.4	3
33	Cross-Seeding Interaction Between Amyloid $\beta$ and Tau Protein can Enhance Aggregation. <i>Current Biotechnology</i> , 2017, 6, .	0.2	3
34	Interaction studies of <i>E. coli</i> uracil phosphoribosyltransferase with 5-fluorouracil for potent anti cancer activity. <i>Medicinal Chemistry Research</i> , 2012, 21, 1149-1155.	1.1	2
35	Pressure Induced Conformational Dynamics of HIV-1 Protease: A Molecular Dynamics Simulation Study. , 2008, , .		1
36	Effect of CTerm of human albumin on the aggregation propensity of $A\beta_{1-42}$ peptide: a potential of mean force study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 1334-1342.	2.0	1

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37	Structural Characterization of Amyloid $\beta$ 17-42 Dimer by Potential of Mean Force Analysis: Insights from Molecular Dynamics Simulations. <i>Protein and Peptide Letters</i> , 2017, 24, 650-660.	0.4	1
38	Effect of C-Terminal Truncations on the Aggregation Propensity of $\beta$ -Synuclein - A Potential of Mean Force Study. <i>Journal of Molecular Imaging &amp; Dynamics</i> , 2017, 07, .	0.2	1
39	Unveiling the Transient Protein-Protein Interactions that Modulate the Activity of Estrogen Receptor(ER)- $\beta$ by Human Lemur Tyrosine Kinase-3 (LMTK3) Domain: An In Silico Study. <i>Current Proteomics</i> , 2017, 14, 157-164.	0.1	1
40	Dimerization of C-terminal Truncations of $\beta$ -synuclein and its Effect on the Aggregation Propensity: A Potential of Mean Force Study. <i>Current Chemical Biology</i> , 2018, 12, 191-200.	0.2	1
41	Computational Investigation on the MDM2-Idasanutlin Interaction using the Potential of Mean Force method. <i>Current Chemical Biology</i> , 2021, 15, .	0.2	0
42	Investigations on the Structural Characteristics that Seed the Aggregation of Amyloid- $\beta$ 1-42 Peptide: Insights from Molecular Dynamics Simulations. <i>Current Proteomics</i> , 2016, 13, 172-178.	0.1	0
43	Computational Study of Intermolecular Interactions between $\beta$ -Synuclein Fibrils and Tau Protein Propagating Tau Aggregation. <i>Current Science</i> , 2017, 112, 2219.	0.4	0
44	Kaempferol attenuates COX-2 expression in IL-6-induced macrophages and carrageenan-induced mouse paw edema by targeting STAT3 and NF- $\kappa$ B. <i>Canadian Journal of Biotechnology</i> , 2017, 1, 163-163.	0.3	0
45	Effect of C-terminal truncations on the aggregation propensity of A53E, a familial mutant of $\beta$ -Synuclein: An Insilico Study. <i>International Journal for Computational Biology</i> , 2018, 7, 16.	0.1	0
46	Salient Structural Features of Human Lemur Tyrosine Kinase 3 (LMTK3) Domain from Molecular Dynamics Simulation Study. <i>Current Biotechnology</i> , 2018, 7, 309-316.	0.2	0
47	Effect of Ionic Strength on the Aggregation Propensity of A $\beta$ 1-42 Peptide: An In-silico Study. <i>Current Chemical Biology</i> , 2020, 14, 216-226.	0.2	0