Maria Stepanova

List of Publications by Year
in descending order

21	297	933264 10	887953 17
papers	citations	h-index	g-index

23	23	23	402
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Prion protein with a mutant N-terminal octarepeat region undergoes cobalamin-dependent assembly into highâ€“molecular weight complexes. Journal of Biological Chemistry, 2022, 298, 101770.	1.6	4
2	Aggregation of AÎ²40/42 chains in the presence of cyclic neuropeptides investigated by molecular dynamics simulations. PLoS Computational Biology, 2021, 17, e1008771.	1.5	5
3	Surface Plasmon-Driven Reversible Transformation of DNA-Bound Methylene Blue Detected In Situ by SERS. Plasmonics, 2020, 15, 427-434.	1.8	5
4	Interaction of AÎ²1â^'42 chains and fibrillary seeds studied by allâ€atom molecular dynamics simulations. Computational and Mathematical Methods, 2020, , e1138.	0.3	0
5	Combining molecular dynamics simulations and experimental analyses in protein misfolding. Advances in Protein Chemistry and Structural Biology, 2019, 118, 33-110.	1.0	9
6	Destabilizing polymorphism in cervid prion protein hydrophobic core determines prion conformation and conversion efficiency. PLoS Pathogens, 2017, 13, e1006553.	2.1	29
7	Understanding the dynamics of monomeric, dimeric, and tetrameric Î±â€synuclein structures in water. FEBS Open Bio, 2016, 6, 666-686.	1.0	14
8	Surface Enhanced Raman Spectroscopy Detection of Biomolecules Using EBL Fabricated Nanostructured Substrates. Journal of Visualized Experiments, 2015, , .	0.2	16
9	Programmed self-assembly of microscale components using biomolecular recognition through the avidinâ€“biotin interaction. Journal of Vacuum Science and Technology B:Nanotechnology and Microelectronics, 2014, 32, 06F301.	0.6	0
10	Understanding Interactions of Functionalized Nanoparticles with Proteins: A Case Study on Lactate Dehydrogenase. Small, 2014, 10, 2006-2021.	5.2	33
11	Molecular mechanisms in the selective basal activation of pyrabactin receptor 1: Comparative analysis of mutants. FEBS Open Bio, 2014, 4, 496-509.	1.0	3
12	Molecular Mechanisms in the Activation of Abscisic Acid Receptor PYR1. PLoS Computational Biology, 2013, 9, e1003114.	1.5	17
13	Conformational modes in biomolecules: Dynamics and approximate invariance. Physical Review E, 2012, 85, 020901.	0.8	11
14	Exploring the essential collective dynamics of interacting proteins: Application to prion protein dimers. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1847-1865.	1.5	14
15	Identification of dynamic structural domains in proteins, analysis of local bond flexibility and application for interpretation of NMR experiments. Molecular Simulation, 2011, 37, 729-732.	0.9	3
16	Comparative analysis of essential collective dynamics and NMR-derived flexibility profiles in evolutionarily diverse prion proteins. Prion, 2011, 5, 188-200.	0.9	22
17	Effects of Temperature on the p53-DNA Binding Interactions and Their Dynamical Behavior: Comparing the Wild Type to the R248Q Mutant. PLoS ONE, 2011, 6, e27651.	1.1	39
18	Selfâ€Consistent Field Modeling of Threeâ€Dimensional Morphologies of Branched Lipid Surfactant at Airâ€Water Interface. Macromolecular Theory and Simulations, 2010, 19, 228-239.	0.6	3

#	Article	IF	Citations
19	Dynamics of essential collective motions in proteins: Theory. Physical Review E, 2007, 76, 051918.	0.8	62
20	Fabrication and Atomistic Modeling of Ion-Etch Nanostructures on Substrates. Materials Research Society Symposia Proceedings, 2004, 849, 7.	0.1	0
21	SOS Simulation of Sputtered Nanoripples. Materials Research Society Symposia Proceedings, 2003, 777, 841.	0.1	0