Gia G Maisuradze

List of Publications by Year
in descending order

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37 papers	1,311 citations	430874 18 h-index	377865 34 g-index
37 all docs	37 docs citations	37 times ranked	1403 citing authors

#	Article	IF	Citations
1	Probing Protein Aggregation Using the Coarse-Grained UNRES Force Field. Methods in Molecular Biology, 2022, 2340, 79-104.	0.9	1
2	Mechanistic Kinetic Model Reveals How Amyloidogenic Hydrophobic Patches Facilitate the Amyloid-Î² Fibril Elongation. ACS Chemical Neuroscience, 2022, 13, 987-1001.	3.5	4
3	How Useful can the Voigt Profile be in Protein Folding Processes?. Protein Journal, 2021, 40, 140-147.	1.6	1
4	Investigation of Phosphorylation-Induced Folding of an Intrinsically Disordered Protein by Coarse-Grained Molecular Dynamics. Journal of Chemical Theory and Computation, 2021, 17, 3203-3220.	5.3	11
5	Missense Mutations Modify the Conformational Ensemble of the Î±-Synuclein Monomer Which Exhibits a Two-Phase Characteristic. Frontiers in Molecular Biosciences, 2021, 8, 786123.	3.5	9
6	Tribute to Harold A. Scheraga. Journal of Physical Chemistry B, 2020, 124, 10301-10302.	2.6	0
7	Curvature and Torsion of Protein Main Chain as Local Order Parameters of Protein Unfolding. Journal of Physical Chemistry B, 2020, 124, 4391-4398.	2.6	9
8	New Insights into Folding, Misfolding, and Nonfolding Dynamics of a WW Domain. Journal of Physical Chemistry B, 2020, 124, 3855-3872.	2.6	4
9	Statistical Model To Decipher Protein Folding/Unfolding at a Local Scale. Journal of Physical Chemistry B, 2018, 122, 3540-3549.	2.6	6
10	From a Highly Disordered to a Metastable State: Uncovering Insights of Î±-Synuclein. ACS Chemical Neuroscience, 2018, 9, 1051-1065.	3.5	22
11	Lysosomal enzyme tripeptidyl peptidase 1 destabilizes fibrillar AÎ² by multiple endoproteolytic cleavages within the Î²-sheet domain. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1493-1498.	7.1	33
12	Dependence of the Formation of Tau and AÎ² Peptide Mixed Aggregates on the Secondary Structure of the N-Terminal Region of AÎ². Journal of Physical Chemistry B, 2018, 122, 7049-7056.	2.6	22
13	Sequence-, structure-, and dynamics-based comparisons of structurally homologous CheY-like proteins. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1578-1583.	7.1	24
14	Elucidating Important Sites and the Mechanism for Amyloid Fibril Formation by Coarse-Grained Molecular Dynamics. ACS Chemical Neuroscience, 2017, 8, 201-209.	3.5	32
15	Eliminating a Protein Folding Intermediate by Tuning a Local Hydrophobic Contact. Journal of Physical Chemistry B, 2017, 121, 3276-3284.	2.6	5
16	Microscopic Physics-Based Models of Proteins and Nucleic Acids. , 2017, , 67-120.		1
17	New Insights into Protein (Un)Folding Dynamics. Journal of Physical Chemistry Letters, 2015, 6, 1082-1086.	4.6	20
18	Preventing fibril formation of a protein by selective mutation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13549-13554.	7.1	17

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19	Kinks, loops, and protein folding, with protein A as an example. Journal of Chemical Physics, 2014, 140, 025101.	3.0	18
20	Folding kinetics of WW domains with the united residue force field for bridging microscopic motions and experimental measurements. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18243-18248.	7.1	36
21	Accounting for a mirror-image conformation as a subtle effect in protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8458-8463.	7.1	19
22	Local vs Global Motions in Protein Folding. Journal of Chemical Theory and Computation, 2013, 9, 2907-2921.	5.3	18
23	Simulation of the Opening and Closing of Hsp70 Chaperones by Coarse-Grained Molecular Dynamics. Journal of Chemical Theory and Computation, 2012, 8, 1750-1764.	5.3	63
24	Hidden Protein Folding Pathways in Free-Energy Landscapes Uncovered by Network Analysis. Journal of Chemical Theory and Computation, 2012, 8, 1176-1189.	5.3	13
25	Effects of Mutation, Truncation, and Temperature on the Folding Kinetics of a WW Domain. Journal of Molecular Biology, 2012, 420, 350-365.	4.2	17
26	Anomalous diffusion and dynamical correlation between the side chains and the main chain of proteins in their native state. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10346-10351.	7.1	29
27	Determination of sideâ€chainâ€rotamer and sideâ€chain and backbone virtualâ€bondâ€stretching potentials of mean force from AM1 energy surfaces of terminallyâ€blocked aminoâ€acid residues, for coarseâ€grained simulations of protein structure and folding. II. Results, comparison with statistical potentials, and implementation in the UNRES force field. Journal of Computational Chemistry, 2010, 31, 1154-1167.	3.3	36
28	Nonexponential decay of internal rotational correlation functions of native proteins and self-similar structural fluctuations. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19844-19849.	7.1	28
29	Investigation of Protein Folding by Coarse-Grained Molecular Dynamics with the UNRES Force Field. Journal of Physical Chemistry A, 2010, 114, 4471-4485.	2.5	91
30	Evidence, from Simulations, of a Single State with Residual Native Structure at the Thermal Denaturation Midpoint of a Small Globular Protein. Journal of the American Chemical Society, 2010, 132, 9444-9452.	13.7	31
31	Relation between Free Energy Landscapes of Proteins and Dynamics. Journal of Chemical Theory and Computation, 2010, 6, 583-595.	5.3	132
32	How Adequate are One- and Two-Dimensional Free Energy Landscapes for Protein Folding Dynamics?. Physical Review Letters, 2009, 102, 238102.	7.8	48
33	Principal Component Analysis for Protein Folding Dynamics. Journal of Molecular Biology, 2009, 385, 312-329.	4.2	331
34	How main-chains of proteins explore the free-energy landscape in native states. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 19708-19713.	7.1	52
35	Free energy landscape of a biomolecule in dihedral principal component space: Sampling convergence and correspondence between structures and minima. Proteins: Structure, Function and Bioinformatics, 2007, 67, 569-578.	2.6	107
36	Theory of inhomogeneous environmental gaussian broadening of resonance Raman excitation profiles for polyatomic molecules in solution. Journal of Raman Spectroscopy, 1989, 20, 359-365.	2.5	14

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37	Wild-Type Î±-Synuclein and Variants Occur in Different Disordered Dimers and Pre-Fibrillar Conformations in Early Stage of Aggregation. Frontiers in Molecular Biosciences, 0, 9, .	3.5	7