Silvina Matysiak

List of Publications by Year
in descending order

40	1,034	516215 16	414034 32
papers	citations	h-index	g-index

41	41	41	1263
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Assessment of physiological environment on neurodegenerative peptide aggregation. Biophysical Journal, 2022, 121, 352a.	0.2	0
2	Recovery of enzyme structure and activity following rehydration from ionic liquid. Physical Chemistry Chemical Physics, 2022, , .	1.3	2
3	Load-Bearing Nanostructures in Composites of Chitosan with Anionic Surfactants: Implications for Programmable Mechanomaterials. ACS Applied Nano Materials, 2022, 5, 6463-6473.	2.4	7
4	Effects of applied surface-tension on membrane-assisted AÎ² aggregation. Physical Chemistry Chemical Physics, 2021, 23, 20627-20633.	1.3	5
5	Dual Mechanism of Ionic Liquid-Induced Protein Unfolding. Biophysical Journal, 2021, 120, 201a.	0.2	0
6	Dual mechanism of ionic liquid-induced protein unfolding. Physical Chemistry Chemical Physics, 2020, 22, 19779-19786.	1.3	17
7	Microscopic Picture of Calcium-Assisted Lipid Demixing and Membrane Remodeling Using Multiscale Simulations. Journal of Physical Chemistry B, 2020, 124, 7327-7335.	1.2	6
8	Tuning Allostery through Integration of Disorder to Order with a Residue Network. Biochemistry, 2020, 59, 790-801.	1.2	6
9	Pathways of amyloid-beta absorption and aggregation in a membranous environment. Physical Chemistry Chemical Physics, 2019, 21, 8559-8568.	1.3	16
10	Computational insights into lipid assisted peptide misfolding and aggregation in neurodegeneration. Physical Chemistry Chemical Physics, 2019, 21, 22679-22694.	1.3	14
11	Superrepression through Altered Corepressorâ€“Activated Protein:Protein Interactions. Biochemistry, 2018, 57, 1119-1129.	1.2	6
12	Looking at the Disordered Proteins through the Computational Microscope. ACS Central Science, 2018, 4, 534-542.	5.3	46
13	How Hydrophobic Hydration Destabilizes Surfactant Micelles at Low Temperature: A Coarse-Grained Simulation Study. Langmuir, 2018, 34, 12590-12599.	1.6	7
14	Mesoporous Encapsulated Chiral Nanogold for Use in Enantioselective Reactions. Angewandte Chemie - International Edition, 2018, 57, 16791-16795.	7.2	91
15	Mesoporous Encapsulated Chiral Nanogold for Use in Enantioselective Reactions. Angewandte Chemie, 2018, 130, 17033-17037.	1.6	14
16	Protein:Protein Interactions Control Sensitivity of a Transcription Response to Input Signal. Biophysical Journal, 2018, 114, 69a.	0.2	0
17	Effect of pH on chitosan hydrogel polymer network structure. Chemical Communications, 2017, 53, 7373-7376.	2.2	69
18	Quantifying the Relationship between Monovalent Cation Size and Lipid Domain Formation in Anionic-Zwitterionic Mixed Lipid Bilayers. Biophysical Journal, 2017, 112, 520a-521a.	0.2	0

#	Article	IF	Citations
19	Interplay between Conformational Heterogeneity and Hydration in the Folding Landscape of a Designed Three-Helix Bundle. Journal of Physical Chemistry B, 2017, 121, 2731-2738.	1.2	3
20	Influence of Monovalent Cation Size on Nanodomain Formation in Anionicâ€“Zwitterionic Mixed Bilayers. Journal of Physical Chemistry B, 2017, 121, 787-799.	1.2	11
21	Long Distance Modulation of Disorder-to-Order Transitions in Protein Allostery. Biochemistry, 2017, 56, 4478-4488.	1.2	12
22	Effect of lipid head group interactions on membrane properties and membrane-induced cationic Î²-hairpin folding. Physical Chemistry Chemical Physics, 2016, 18, 17836-17850.	1.3	19
23	Acetylation within the First 17 Residues of Huntingtin Exon 1 Alters Aggregation and Lipid Binding. Biophysical Journal, 2016, 111, 349-362.	0.2	55
24	Interplay between the hydrophobic effect and dipole interactions in peptide aggregation at interfaces. Physical Chemistry Chemical Physics, 2016, 18, 2449-2458.	1.3	16
25	Interplay of Dynamical Properties between Ionic Liquids and Ionic Surfactants: Mechanism and Aggregation. Journal of Physical Chemistry B, 2015, 119, 9925-9932.	1.2	8
26	The Effects of Flanking Sequences in the Interaction of Polyglutamine Peptides with a Membrane Bilayer. Journal of Physical Chemistry B, 2014, 118, 6368-6379.	1.2	25
27	Effects of Sequence and Solvation on the Temperature-Pressure Conformational Landscape of Proteinlike Heteropolymers. Physical Review Letters, 2013, 111, 058103.	2.9	9
28	Length and Sequence Dependence in the Association of Htt Protein with Lipid Bilayers. Biophysical Journal, 2013, 104, 431a.	0.2	0
29	Multiscale Simulation of Liquid Water Using a Four-to-One Mapping for Coarse-Graining. Journal of Chemical Theory and Computation, 2013, 9, 5168-5175.	2.3	19
30	Thermal Stability of Hydrophobic Helical Oligomers: A Lattice Simulation Study in Explicit Water. Journal of Physical Chemistry B, 2012, 116, 9963-9970.	1.2	0
31	Phase Behavior of a Lattice Hydrophobic Oligomer in Explicit Water. Journal of Physical Chemistry B, 2012, 116, 9540-9548.	1.2	3
32	Role of Hydrophobic Hydration in Protein Stability: A 3D Water-Explicit Protein Model Exhibiting Cold and Heat Denaturation. Journal of Physical Chemistry B, 2012, 116, 8095-8104.	1.2	52
33	Direct Characterization of Hydrophobic Hydration during Cold and Pressure Denaturation. Journal of Physical Chemistry B, 2012, 116, 5342-5348.	1.2	25
34	Dissecting the Energetics of Hydrophobic Hydration of Polypeptides. Journal of Physical Chemistry B, 2011, 115, 14859-14865.	1.2	34
35	Mapping folding energy landscapes with theory and experiment. Archives of Biochemistry and Biophysics, 2008, 469, 29-33.	1.4	17
36	Adaptive resolution simulation of liquid water. Journal of Physics Condensed Matter, 2007, 19, 292201.	0.7	85

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37	Minimalist Protein Model as a Diagnostic Tool for Misfolding and Aggregation. Journal of Molecular Biology, 2006, 363, 297-308.	2.0	56
38	Dynamics of Polymer Translocation through Nanopores: Theory Meets Experiment. Physical Review Letters, 2006, 96, 118103.	2.9	119
39	Balancing energy and entropy: A minimalist model for the characterization of protein folding landscapes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10141-10146.	3.3	96
40	Optimal Combination of Theory and Experiment for the Characterization of the Protein Folding Landscape of S6: How Far Can a Minimalist Model Go?. Journal of Molecular Biology, 2004, 343, 235-248.	2.0	64