Sihyun Ham

List of Publications by Year
in descending order

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46	1,148	430874	395702
papers	citations	18 h-index	33 g-index

50	50	50	1648
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Mutation effects on FAS1 domain 4 based on structure and solubility. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2022, 1870, 140746.	2.3	0
2	Time-dependent communication between multiple amino acids during protein folding. Chemical Science, 2021, 12, 5944-5951.	7.4	7
3	Site-Specific Backbone and Side-Chain Contributions to Thermodynamic Stabilizing Forces of the WW Domain. Journal of Physical Chemistry B, 2021, 125, 7108-7116.	2.6	4
4	Atomic Level Investigations of Early Aggregation of Tau43 in Water <scp>II</scp>. <scp>Tau43â€Aî²42</scp> vs. <scp>Tau43â€</scp>Tau43 <scp>Dimerizations</scp>. Bulletin of the Korean Chemical Society, 2021, 42, 1126-1133.	1.9	2
5	Atomic Level Investigations of Early Aggregation of Tau43 in Water I. Conformational Propensity of Monomeric Tau43. Bulletin of the Korean Chemical Society, 2021, 42, 1134-1142.	1.9	0
6	Local environment effects on charged mutations for developing aggregation-resistant monoclonal antibodies. Scientific Reports, 2020, 10, 21191.	3.3	0
7	Effect of linker on the binding free energy of stapled p53/HDM2 complex. PLoS ONE, 2020, 15, e0232613.	2.5	2
8	Effect of linker on the binding free energy of stapled p53/HDM2 complex. , 2020, 15, e0232613.		0
9	Effect of linker on the binding free energy of stapled p53/HDM2 complex. , 2020, 15, e0232613.		0
10	Effect of linker on the binding free energy of stapled p53/HDM2 complex. , 2020, 15, e0232613.		0
11	Effect of linker on the binding free energy of stapled p53/HDM2 complex. , 2020, 15, e0232613.		0
12	Effect of linker on the binding free energy of stapled p53/HDM2 complex. , 2020, 15, e0232613.		0
13	Effect of linker on the binding free energy of stapled p53/HDM2 complex. , 2020, 15, e0232613.		0
14	Diverse Structural Conversion and Aggregation Pathways of AlzheimerÊ¼s Amyloid-Î² (1â€“40). ACS Nano, 2019, 13, 8766-8783.	14.6	33
15	Explicit Characterization of the Free Energy Landscape of pKIDâ€“KIX Coupled Folding and Binding. ACS Central Science, 2019, 5, 1342-1351.	11.3	19
16	Folding Free Energy Landscape of Ordered and Intrinsically Disordered Proteins. Scientific Reports, 2019, 9, 14927.	3.3	32
17	Characterizing the structural and thermodynamic properties of Aî²42 and Aî²40. Biochemical and Biophysical Research Communications, 2019, 510, 442-448.	2.1	19
18	A New Computational Method for Proteinâ€“Ligand Binding Thermodynamics. Bulletin of the Korean Chemical Society, 2019, 40, 180-185.	1.9	1

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19	Bridged Î±-helix mimetic small molecules. Chemical Communications, 2019, 55, 13311-13314.	4.1	9
20	Role of electrostatic interactions in determining the G-quadruplex structures. Chemical Physics Letters, 2018, 693, 216-221.	2.6	2
21	Examining a Thermodynamic Order Parameter of Protein Folding. Scientific Reports, 2018, 8, 7148.	3.3	6
22	Computer Simulations of Intrinsically Disordered Proteins. Annual Review of Physical Chemistry, 2017, 68, 117-134.	10.8	68
23	Dynamics of Hydration Water Plays a Key Role in Determining the Binding Thermodynamics of Protein Complexes. Scientific Reports, 2017, 7, 8744.	3.3	52
24	Structure of Full-Length SMC and Rearrangements Required for Chromosome Organization. Molecular Cell, 2017, 67, 334-347.e5.	9.7	151
25	New Computational Approach for External Entropy in Proteinâ€“Protein Binding. Journal of Chemical Theory and Computation, 2016, 12, 2509-2516.	5.3	12
26	Anomalous Dynamics of Water Confined in Proteinâ€“Protein and Proteinâ€“DNA Interfaces. Journal of Physical Chemistry Letters, 2016, 7, 3967-3972.	4.6	35
27	A Cyclized Helixâ€Loopâ€Helix Peptide as a Molecular Scaffold for the Design of Inhibitors of Intracellular Proteinâ€“Protein Interactions by Epitope and Arginine Grafting. Angewandte Chemie - International Edition, 2016, 55, 10612-10615.	13.8	38
28	A Cyclized Helixâ€Loopâ€Helix Peptide as a Molecular Scaffold for the Design of Inhibitors of Intracellular Proteinâ€“Protein Interactions by Epitope and Arginine Grafting. Angewandte Chemie, 2016, 128, 10770-10773.	2.0	6
29	Structural and Thermodynamic Characteristics of Amyloidogenic Intermediates of Î²-2-Microglobulin. Scientific Reports, 2015, 5, 13631.	3.3	12
30	Thermodynamic-Ensemble Independence of Solvation Free Energy. Journal of Chemical Theory and Computation, 2015, 11, 378-380.	5.3	16
31	Structural versus energetic approaches for protein conformational entropy. Chemical Physics Letters, 2015, 627, 90-95.	2.6	3
32	Distinct Role of Hydration Water in Protein Misfolding and Aggregation Revealed by Fluctuating Thermodynamics Analysis. Accounts of Chemical Research, 2015, 48, 956-965.	15.6	68
33	Dissecting Protein Configurational Entropy into Conformational and Vibrational Contributions. Journal of Physical Chemistry B, 2015, 119, 12623-12631.	2.6	23
34	Different Functional and Structural Characteristics between ApoA-I and ApoA-4 in Lipid-Free and Reconstituted HDL State: ApoA-4 Showed Less Anti-Atherogenic Activity. Molecules and Cells, 2015, 38, 573-579.	2.6	12
35	Interaction with the Surrounding Water Plays a Key Role in Determining the Aggregation Propensity of Proteins. Angewandte Chemie - International Edition, 2014, 53, 3961-3964.	13.8	87
36	Siteâ€directed analysis on protein hydrophobicity. Journal of Computational Chemistry, 2014, 35, 1364-1370.	3.3	20

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37	Protein Folding Thermodynamics: A New Computational Approach. Journal of Physical Chemistry B, 2014, 118, 5017-5025.	2.6	18
38	Structural heterogeneity in familial Alzheimer's disease mutants of amyloid-beta peptides. Molecular BioSystems, 2013, 9, 997.	2.9	37
39	Conformational Entropy of Intrinsically Disordered Protein. Journal of Physical Chemistry B, 2013, 117, 5503-5509.	2.6	25
40	Elucidating the Molecular Origin of Hydrolysis Energy of Pyrophosphate in Water. Journal of Chemical Theory and Computation, 2012, 8, 2239-2246.	5.3	16
41	Impact of chemical heterogeneity on protein self-assembly in water. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7636-7641.	7.1	109
42	Structural and Thermodynamic Investigations on the Aggregation and Folding of Acylphosphatase by Molecular Dynamics Simulations and Solvation Free Energy Analysis. Journal of the American Chemical Society, 2011, 133, 7075-7083.	13.7	37
43	Atomic decomposition of the protein solvation free energy and its application to amyloid-beta protein in water. Journal of Chemical Physics, 2011, 135, 034506.	3.0	35
44	Characterizing amyloidâ€beta protein misfolding from molecular dynamics simulations with explicit water. Journal of Computational Chemistry, 2011, 32, 349-355.	3.3	77
45	Configurational entropy of protein: A combined approach based on molecular simulation and integral-equation theory of liquids. Chemical Physics Letters, 2011, 504, 225-229.	2.6	29
46	Tren-spaced rhodamine and pyrene fluorophores: Excimer modulation with metal ion complexation. Supramolecular Chemistry, 2009, 21, 135-141.	1.2	11