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	Structure of Full-Length SMC and Rearrangements Required for Chromosome Organization. Molecular Cell, 2017, 67, 334-347.e5.	9.7	151
2	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
3	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
4	Characterizing amyloidâ€beta protein misfolding from molecular dynamics simulations with explicit water. Journal of Computational Chemistry, 2011, 32, 349-355.	3.3	77
5	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
6	Computer Simulations of Intrinsically Disordered Proteins. Annual Review of Physical Chemistry, 2017, 68, 117-134.	10.8	68
7	Dynamics of Hydration Water Plays a Key Role in Determining the Binding Thermodynamics of Protein Complexes. Scientific Reports, 2017, 7, 8744.	3.3	52
8	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
9	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
10	Structural heterogeneity in familial Alzheimer's disease mutants of amyloid-beta peptides. Molecular BioSystems, 2013, 9, 997.	2.9	37
11	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
12	Anomalous Dynamics of Water Confined in Proteinâ€“Protein and Proteinâ€“DNA Interfaces. Journal of Physical Chemistry Letters, 2016, 7, 3967-3972.	4.6	35
13	Diverse Structural Conversion and Aggregation Pathways of AlzheimerÊ¼s Amyloid-Î² (1â€“40). ACS Nano, 2019, 13, 8766-8783.	14.6	33
14	Folding Free Energy Landscape of Ordered and Intrinsically Disordered Proteins. Scientific Reports, 2019, 9, 14927.	3.3	32
15	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
16	Conformational Entropy of Intrinsically Disordered Protein. Journal of Physical Chemistry B, 2013, 117, 5503-5509.	2.6	25
17	Dissecting Protein Configurational Entropy into Conformational and Vibrational Contributions. Journal of Physical Chemistry B, 2015, 119, 12623-12631.	2.6	23
18	Siteâ€directed analysis on protein hydrophobicity. Journal of Computational Chemistry, 2014, 35, 1364-1370.	3.3	20

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19	Explicit Characterization of the Free Energy Landscape of pKIDâ€“KIX Coupled Folding and Binding. ACS Central Science, 2019, 5, 1342-1351.	11.3	19
20	Characterizing the structural and thermodynamic properties of AÎ²42 and AÎ²40. Biochemical and Biophysical Research Communications, 2019, 510, 442-448.	2.1	19
21	Protein Folding Thermodynamics: A New Computational Approach. Journal of Physical Chemistry B, 2014, 118, 5017-5025.	2.6	18
22	Elucidating the Molecular Origin of Hydrolysis Energy of Pyrophosphate in Water. Journal of Chemical Theory and Computation, 2012, 8, 2239-2246.	5.3	16
23	Thermodynamic-Ensemble Independence of Solvation Free Energy. Journal of Chemical Theory and Computation, 2015, 11, 378-380.	5.3	16
24	Structural and Thermodynamic Characteristics of Amyloidogenic Intermediates of Î²-2-Microglobulin. Scientific Reports, 2015, 5, 13631.	3.3	12
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	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
27	Tren-spaced rhodamine and pyrene fluorophores: Excimer modulation with metal ion complexation. Supramolecular Chemistry, 2009, 21, 135-141.	1.2	11
28	Bridged Î±-helix mimetic small molecules. Chemical Communications, 2019, 55, 13311-13314.	4.1	9
29	Time-dependent communication between multiple amino acids during protein folding. Chemical Science, 2021, 12, 5944-5951.	7.4	7
30	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
31	Examining a Thermodynamic Order Parameter of Protein Folding. Scientific Reports, 2018, 8, 7148.	3.3	6
32	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
33	Structural versus energetic approaches for protein conformational entropy. Chemical Physics Letters, 2015, 627, 90-95.	2.6	3
34	Role of electrostatic interactions in determining the G-quadruplex structures. Chemical Physics Letters, 2018, 693, 216-221.	2.6	2
35	Effect of linker on the binding free energy of stapled p53/HDM2 complex. PLoS ONE, 2020, 15, e0232613.	2.5	2
36	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

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37	A New Computational Method for Proteinâ€“Ligand Binding Thermodynamics. Bulletin of the Korean Chemical Society, 2019, 40, 180-185.	1.9	1
38	Local environment effects on charged mutations for developing aggregation-resistant monoclonal antibodies. Scientific Reports, 2020, 10, 21191.	3.3	0
39	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
40	Mutation effects on FAS1 domain 4 based on structure and solubility. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2022, 1870, 140746.	2.3	0
41	Effect of linker on the binding free energy of stapled p53/HDM2 complex. , 2020, 15, e0232613.		0
42	Effect of linker on the binding free energy of stapled p53/HDM2 complex. , 2020, 15, e0232613.		0
43	Effect of linker on the binding free energy of stapled p53/HDM2 complex. , 2020, 15, e0232613.		0
44	Effect of linker on the binding free energy of stapled p53/HDM2 complex. , 2020, 15, e0232613.		0
45	Effect of linker on the binding free energy of stapled p53/HDM2 complex. , 2020, 15, e0232613.		0
46	Effect of linker on the binding free energy of stapled p53/HDM2 complex. , 2020, 15, e0232613.		0