Hue Sun Chan

List of Publications by Year in Descending Order

127 papers	10,666 citations	54 h-index	102 g-index
147 ext. papers	11,538 ext. citations	5.9 avg, IF	6.58 L-index

#	Paper	IF	Citations
127	Assembly of model postsynaptic densities involves interactions auxiliary to stoichiometric binding. *Biophysical Journal*, **2021**,	2.9	3
126	A Simple Explicit-Solvent Model of Polyampholyte Phase Behaviors and Its Ramifications for Dielectric Effects in Biomolecular Condensates. *Journal of Physical Chemistry B*, **2021**, 125, 4337-4358	3.4	12
125	Subcompartmentalization of polyampholyte species in organelle-like condensates is promoted by charge-pattern mismatch and strong excluded-volume interaction. *Physical Review E*, **2021**, 103, 042406	2.4	11
124	Small-Angle X-ray Scattering Signatures of Conformational Heterogeneity and Homogeneity of Disordered Protein Ensembles. *Journal of Physical Chemistry B*, **2021**, 125, 6451-6478	3.4	4
123	Comparative roles of charge, , and hydrophobic interactions in sequence-dependent phase separation of intrinsically disordered proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 28795-28805	11.5	56
122	Analytical Theory for Sequence-Specific Binary Fuzzy Complexes of Charged Intrinsically Disordered Proteins. *Journal of Physical Chemistry B*, **2020**, 124, 6709-6720	3.4	21
121	A unified analytical theory of heteropolymers for sequence-specific phase behaviors of polyelectrolytes and polyampholytes. *Journal of Chemical Physics*, **2020**, 152, 045102	3.9	27
120	Pressure Sensitivity of SynGAP/PSD-95 Condensates as a Model for Postsynaptic Densities and Its Biophysical and Neurological Ramifications. *Chemistry - A European Journal*, **2020**, 26, 11024-11031	4.8	10
119	Temperature, Hydrostatic Pressure, and Osmolyte Effects on Liquid-Liquid Phase Separation in Protein Condensates: Physical Chemistry and Biological Implications. *Chemistry - A European Journal* , **2019**, 25, 13049-13069	4.8	56
118	Pressure-Sensitive and Osmolyte-Modulated Liquid-Liquid Phase Separation of Eye-Lens Crystallins. *Journal of the American Chemical Society*, **2019**, 141, 7347-7354	16.4	33
117	Theories for Sequence-Dependent Phase Behaviors of Biomolecular Condensates. *Biochemistry*, **2018**, 57, 2499-2508	3.2	115
116	A Lattice Model of Charge-Pattern-Dependent Polyampholyte Phase Separation. *Journal of Physical Chemistry B*, **2018**, 122, 5418-5431	3.4	62
115	Pressure-Induced Dissolution and Reentrant Formation of Condensed, Liquid-Liquid Phase-Separated Elastomeric Elastin. *Chemistry - A European Journal*, **2018**, 24, 8286-8291	4.8	25
114	Coarse-grained residue-based models of disordered protein condensates: utility and limitations of simple charge pattern parameters. *Physical Chemistry Chemical Physics*, **2018**, 20, 28558-28574	3.6	63
113	A critical comparison of coarse-grained structure-based approaches and atomic models of protein folding. *Physical Chemistry Chemical Physics*, **2017**, 19, 13629-13639	3.6	20
112	Phase Separation and Single-Chain Compactness of Charged Disordered Proteins Are Strongly Correlated. *Biophysical Journal*, **2017**, 112, 2043-2046	2.9	117
111	An allosteric conduit facilitates dynamic multisite substrate recognition by the SCF ubiquitin ligase. *Nature Communications*, **2017**, 8, 13943	17.4	28

110	Molecular recognition and packing frustration in a helical protein. *PLoS Computational Biology*, **2017**, 13, e1005909	5	4
109	Structural and hydrodynamic properties of an intrinsically disordered region of a germ cell-specific protein on phase separation. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E8194-E8203	11.5	227
108	Conformational Heterogeneity and FRET Data Interpretation for Dimensions of Unfolded Proteins. *Biophysical Journal*, **2017**, 113, 1012-1024	2.9	45
107	Random-phase-approximation theory for sequence-dependent, biologically functional liquid-liquid phase separation of intrinsically disordered proteins. *Journal of Molecular Liquids*, **2017**, 228, 176-193	6	73
106	Charge pattern matching as a 'fuzzy' mode of molecular recognition for the functional phase separations of intrinsically disordered proteins. *New Journal of Physics*, **2017**, 19, 115003	2.9	61
105	Sequence-Specific Polyampholyte Phase Separation in Membraneless Organelles. *Physical Review Letters*, **2016**, 117, 178101	7.4	149
104	Volumetric Physics of Polypeptide Coil-Helix Transitions. *Biochemistry*, **2016**, 55, 6269-6281	3.2	10
103	Theoretical Insights into the Biophysics of Protein Bi-stability and Evolutionary Switches. *PLoS Computational Biology*, **2016**, 12, e1004960	5	16
102	Conformations of a Metastable SH3 Domain Characterized by smFRET and an Excluded-Volume Polymer Model. *Biophysical Journal*, **2016**, 110, 1510-1522	2.9	15
101	Thermodynamics and kinetics of TopoII action: A consensus on T-segment curvature selection? Comment on "Disentangling DNA Molecules" by Alexander Vologodskii. *Physics of Life Reviews*, **2016**, 18, 135-138	2.1	1
100	Native contact density and nonnative hydrophobic effects in the folding of bacterial immunity proteins. *PLoS Computational Biology*, **2015**, 11, e1004260	5	32
99	Consistent rationalization of type-2 topoisomerases' unknotting, decatenating, supercoil-relaxing actions and their scaling relation. *Journal of Physics Condensed Matter*, **2015**, 27, 354103	1.8	4
98	An Adequate Account of Excluded Volume Is Necessary To Infer Compactness and Asphericity of Disordered Proteins by Förster Resonance Energy Transfer. *Journal of Physical Chemistry B*, **2015**, 119, 15191-202	3.4	39
97	Theoretical perspectives on nonnative interactions and intrinsic disorder in protein folding and binding. *Current Opinion in Structural Biology*, **2015**, 30, 32-42	8.1	60
96	Effects of desolvation barriers and sidechains on local-nonlocal coupling and chevron behaviors in coarse-grained models of protein folding. *Physical Chemistry Chemical Physics*, **2014**, 16, 6460-79	3.6	26
95	Pressure-Dependent Properties of Elementary Hydrophobic Interactions: Ramifications for Activation Properties of Protein Folding. *Journal of Physical Chemistry B*, **2014**, 118, 7488-7509	3.4	44
94	Biophysics of protein evolution and evolutionary protein biophysics. *Journal of the Royal Society Interface*, **2014**, 11, 20140419	4.1	144
93	Spatial ranges of driving forces are a key determinant of protein folding cooperativity and rate diversity. *Physical Review E*, **2013**, 88, 044701	2.4	14

92	Polycation-π interactions are a driving force for molecular recognition by an intrinsically disordered oncoprotein family. *PLoS Computational Biology*, **2013**, 9, e1003239	5	50
91	Transition paths, diffusive processes, and preequilibria of protein folding. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 20919-24	11.5	32
90	Quantitative analysis of the effects of photoswitchable distance constraints on the structure of a globular protein. *Biochemistry*, **2012**, 51, 6421-31	3.2	21
89	Kinetic consequences of native state optimization of surface-exposed electrostatic interactions in the Fyn SH3 domain. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 858-70	4.2	40
88	Evolutionary dynamics on protein bi-stability landscapes can potentially resolve adaptive conflicts. *PLoS Computational Biology*, **2012**, 8, e1002659	5	22
87	Escape from Adaptive Conflict follows from weak functional trade-offs and mutational robustness. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 14888-93	11.5	46
86	Cooperativity, local-nonlocal coupling, and nonnative interactions: principles of protein folding from coarse-grained models. *Annual Review of Physical Chemistry*, **2011**, 62, 301-26	15.7	163
85	Short-range contact preferences and long-range indifference: is protein folding stoichiometry driven?. *Journal of Biomolecular Structure and Dynamics*, **2011**, 28, 603-5; discussion 669-674	3.6	2
84	Hydrophobic interactions in the formation of secondary structures in small peptides. *Physical Review E*, **2011**, 84, 041931	2.4	18
83	Local site preference rationalizes disentangling by DNA topoisomerases. *Physical Review E*, **2010**, 81, 031902	2.4	13
82	Competition between native topology and nonnative interactions in simple and complex folding kinetics of natural and designed proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 2920-5	11.5	80
81	Evolvability and single-genotype fluctuation in phenotypic properties: a simple heteropolymer model. *Biophysical Journal*, **2010**, 98, 2487-96	2.9	8
80	Action at hooked or twisted-hooked DNA juxtapositions rationalizes unlinking preference of type-2 topoisomerases. *Journal of Molecular Biology*, **2010**, 400, 963-82	6.5	23
79	The why and how of DNA unlinking. *Nucleic Acids Research*, **2009**, 37, 661-71	20.1	127
78	Interplaying roles of native topology and chain length in marginally cooperative and noncooperative folding of small protein fragments. *International Journal of Quantum Chemistry*, **2009**, 109, 3482-3499	2.1	8
77	Liaison amid disorder: non-native interactions may underpin long-range coupling in proteins. *Journal of Biology*, **2009**, 8, 27		5
76	Desolvation barrier effects are a likely contributor to the remarkable diversity in the folding rates of small proteins. *Journal of Molecular Biology*, **2009**, 389, 619-36	6.5	44
75	Native topology of the designed protein Top7 is not conducive to cooperative folding. *Biophysical Journal*, **2009**, 96, L25-7	2.9	27

74	Efficient chain moves for Monte Carlo simulations of a wormlike DNA model: excluded volume, supercoils, site juxtapositions, knots, and comparisons with random-flight and lattice models. *Journal of Chemical Physics*, **2008**, 128, 145104	3.9	23
73	Probing possible downhill folding: native contact topology likely places a significant constraint on the folding cooperativity of proteins with approximately 40 residues. *Journal of Molecular Biology*, **2008**, 384, 512-30	6.5	35
72	Theoretical and experimental demonstration of the importance of specific nonnative interactions in protein folding. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 9999-10004	11.5	109
71	Hydrophobic association of alpha-helices, steric dewetting, and enthalpic barriers to protein folding. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 6206-10	11.5	74
70	Pressure and temperature dependence of hydrophobic hydration: volumetric, compressibility, and thermodynamic signatures. *Journal of Chemical Physics*, **2007**, 126, 114507	3.9	43
69	A structural model of latent evolutionary potentials underlying neutral networks in proteins. *HFSP Journal*, **2007**, 1, 79-87		55
68	Polyelectrostatic interactions of disordered ligands suggest a physical basis for ultrasensitivity. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 9650-5	11.5	186
67	A structural model of latent evolutionary potentials underlying neutral networks in proteins **2007**, 1, 79-87		33
66	Selective adsorption of block copolymers on patterned surfaces. *Journal of Chemical Physics*, **2006**, 125, 164909	3.9	7
65	Conformational entropic barriers in topology-dependent protein folding: perspectives from a simple native-centric polymer model. *Journal of Physics Condensed Matter*, **2006**, 18, S307-S328	1.8	34
64	Inferring global topology from local juxtaposition geometry: interlinking polymer rings and ramifications for topoisomerase action. *Biophysical Journal*, **2006**, 90, 2344-55	2.9	34
63	Topological information embodied in local juxtaposition geometry provides a statistical mechanical basis for unknotting by type-2 DNA topoisomerases. *Journal of Molecular Biology*, **2006**, 361, 268-85	6.5	53
62	Criteria for downhill protein folding: calorimetry, chevron plot, kinetic relaxation, and single-molecule radius of gyration in chain models with subdued degrees of cooperativity. *Proteins: Structure, Function and Bioinformatics*, **2006**, 65, 373-91	4.2	63
61	A critical assessment of the topomer search model of protein folding using a continuum explicit-chain model with extensive conformational sampling. *Protein Science*, **2005**, 14, 1643-60	6.3	35
60	Desolvation is a likely origin of robust enthalpic barriers to protein folding. *Journal of Molecular Biology*, **2005**, 349, 872-89	6.5	73
59	Comparing folding codes in simple heteropolymer models of protein evolutionary landscape: robustness of the superfunnel paradigm. *Biophysical Journal*, **2005**, 88, 118-31	2.9	35
58	Chevron behavior and isostable enthalpic barriers in protein folding: successes and limitations of simple G□like modeling. *Biophysical Journal*, **2005**, 89, 520-35	2.9	30
57	Solvation and desolvation effects in protein folding: native flexibility, kinetic cooperativity and enthalpic barriers under isostability conditions. *Physical Biology*, **2005**, 2, S75-85	3	49

56	Explicit-chain model of native-state hydrogen exchange: implications for event ordering and cooperativity in protein folding. *Proteins: Structure, Function and Bioinformatics*, **2005**, 58, 31-44	4.2	22
55	Temperature dependence of three-body hydrophobic interactions: potential of mean force, enthalpy, entropy, heat capacity, and nonadditivity. *Journal of the American Chemical Society*, **2005**, 127, 303-16	16.4	58
54	Simplified Models of Protein Folding **2005**, 1823-1836		0
53	Simplified Models of Protein Folding **2005**, 1823-1836		
52	Sparsely populated folding intermediates of the Fyn SH3 domain: matching native-centric essential dynamics and experiment. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 14748-53	11.5	28
51	Energetics of protein thermodynamic cooperativity: contributions of local and nonlocal interactions. *Polymer*, **2004**, 45, 623-632	3.9	20
50	Exploring the effects of hydrogen bonding and hydrophobic interactions on the foldability and cooperativity of helical proteins using a simplified atomic model. *Chemical Physics*, **2004**, 307, 187-199	2.3	20
49	Cooperativity principles in protein folding. *Methods in Enzymology*, **2004**, 380, 350-79	1.7	157
48	Contact order dependent protein folding rates: kinetic consequences of a cooperative interplay between favorable nonlocal interactions and local conformational preferences. *Proteins: Structure, Function and Bioinformatics*, **2003**, 52, 524-33	4.2	68
47	Simple two-state protein folding kinetics requires near-levinthal thermodynamic cooperativity. *Proteins: Structure, Function and Bioinformatics*, **2003**, 52, 510-23	4.2	61
46	Solvation effects and driving forces for protein thermodynamic and kinetic cooperativity: how adequate is native-centric topological modeling?. *Journal of Molecular Biology*, **2003**, 326, 911-31	6.5	161
45	Origins of chevron rollovers in non-two-state protein folding kinetics. *Physical Review Letters*, **2003**, 90, 258104	7.4	52
44	Anti-cooperativity and cooperativity in hydrophobic interactions: Three-body free energy landscapes and comparison with implicit-solvent potential functions for proteins. *Proteins: Structure, Function and Bioinformatics*, **2002**, 48, 15-30	4.2	77
43	Origins of protein denatured state compactness and hydrophobic clustering in aqueous urea: inferences from nonpolar potentials of mean force. *Proteins: Structure, Function and Bioinformatics*, **2002**, 49, 560-6	4.2	82
42	Recombinatoric exploration of novel folded structures: a heteropolymer-based model of protein evolutionary landscapes. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 809-14	11.5	80
41	Reply to Comment on Anti-cooperativity in hydrophobic interactions: A simulation study of spatial dependence of three-body effects and beyond [J. Chem. Phys. 116, 2665 (2002)]. *Journal of Chemical Physics*, **2002**, 116, 2668-2669	3.9	11
40	Towards a consistent modeling of protein thermodynamic and kinetic cooperativity: how applicable is the transition state picture to folding and unfolding?. *Journal of Molecular Biology*, **2002**, 315, 899-909	6.5	85
39	Amino Acid Side-chain Hydrophobicity **2002**,		6

38	Perspectives on protein evolution from simple exact models. *Applied Bioinformatics*, **2002**, 1, 121-44		40
37	Statistical mechanics of solvophobic aggregation: Additive and cooperative effects. *Journal of Chemical Physics*, **2001**, 115, 3424-3431	3.9	16
36	Anti-cooperativity in hydrophobic interactions: A simulation study of spatial dependence of three-body effects and beyond. *Journal of Chemical Physics*, **2001**, 115, 1414-1421	3.9	42
35	Conformational propagation with prion-like characteristics in a simple model of protein folding. *Protein Science*, **2001**, 10, 819-35	6.3	79
34	Configuration-dependent heat capacity of pairwise hydrophobic interactions. *Journal of the American Chemical Society*, **2001**, 123, 2083-4	16.4	55
33	Modeling protein density of states: additive hydrophobic effects are insufficient for calorimetric two-state cooperativity. *Proteins: Structure, Function and Bioinformatics*, **2000**, 40, 543-71	4.2	123
32	Polymer principles of protein calorimetric two-state cooperativity. *Proteins: Structure, Function and Bioinformatics*, **2000**, 40, 637-61	4.2	147
31	Energetic components of cooperative protein folding. *Physical Review Letters*, **2000**, 85, 4823-6	7.4	89
30	Temperature dependence of hydrophobic interactions: A mean force perspective, effects of water density, and nonadditivity of thermodynamic signatures. *Journal of Chemical Physics*, **2000**, 113, 4683-4700	3.9	152
29	Extracting Microscopic Energies from Oil-Phase Solvation Experiments. *Journal of Physical Chemistry B*, **2000**, 104, 7471-7482	3.4	10
28	Polymer principles of protein calorimetric two-state cooperativity **2000**, 40, 637		2
27	Polymer principles of protein calorimetric two-state cooperativity **2000**, 40, 637		2
26	Protein folding in the landscape perspective: chevron plots and non-Arrhenius kinetics. *Proteins: Structure, Function and Bioinformatics*, **1998**, 30, 2-33	4.2	364
25	Oil/Water Partitioning Has a Different Thermodynamic Signature When the Oil Solvent Chains Are Aligned Than When They Are Amorphous. *Journal of Physical Chemistry B*, **1998**, 102, 7272-7279	3.4	52
24	Solvation: how to obtain microscopic energies from partitioning and solvation experiments. *Annual Review of Biophysics and Biomolecular Structure*, **1997**, 26, 425-59		79
23	From Levinthal to pathways to funnels. *Nature Structural and Molecular Biology*, **1997**, 4, 10-9	17.6	1924
22	Comparing folding codes for proteins and polymers. *Proteins: Structure, Function and Bioinformatics* , **1996**, 24, 335-44	4.2	79
21	A simple model of chaperonin-mediated protein folding. *Proteins: Structure, Function and Bioinformatics*, **1996**, 24, 345-51	4.2	76

20	A simple model of chaperonin-mediated protein folding **1996**, 24, 345		2
19	Principles of protein folding--a perspective from simple exact models. *Protein Science*, **1995**, 4, 561-602	6.3	1159
18	Kinetics of protein folding. *Nature*, **1995**, 373, 664-5	50.4	39
17	An exact lattice model of complex solutions: Chemical potentials depend on solute and solvent shape. *Journal of Chemical Physics*, **1995**, 103, 10675-10688	3.9	19
16	Solvation: Effects of molecular size and shape. *Journal of Chemical Physics*, **1994**, 101, 7007-7026	3.9	65
15	Transition states and folding dynamics of proteins and heteropolymers. *Journal of Chemical Physics*, **1994**, 100, 9238-9257	3.9	263
14	Does compactness induce secondary structure in proteins? A study of poly-alanine chains computed by distance geometry. *Journal of Molecular Biology*, **1994**, 241, 557-73	6.5	65
13	Energy landscapes and the collapse dynamics of homopolymers. *Journal of Chemical Physics*, **1993**, 99, 2116-2127	3.9	111
12	Coordinate-space formulation of polymer lattice cluster theory. *Journal of Chemical Physics*, **1993**, 98, 9951-9962	3.9	16
11	Folding kinetics of proteins and copolymers. *Journal of Chemical Physics*, **1992**, 96, 768-780	3.9	113
10	Modeling the effects of mutations on the denatured states of proteins. *Protein Science*, **1992**, 1, 201-15	6.3	114
9	Enhanced structure in polymers at interfaces. *Journal of Chemical Physics*, **1991**, 94, 8542-8557	3.9	34
8	Sequence space soup of proteins and copolymers. *Journal of Chemical Physics*, **1991**, 95, 3775-3787	3.9	168
7	The effects of internal constraints on the configurations of chain molecules. *Journal of Chemical Physics*, **1990**, 92, 3118-3135	3.9	189
6	Compact polymers. *Macromolecules*, **1989**, 22, 4559-4573	5.5	225
5	Intrachain loops in polymers: Effects of excluded volume. *Journal of Chemical Physics*, **1989**, 90, 492-509	3.9	185
4	Non-Grassmann formulation of regularized gauge theory with fermions. *Zeitschrift Für Physik C-Particles and Fields*, **1987**, 34, 267-276		7
3	Continuum-regularized quantum gravity. *Zeitschrift Für Physik C-Particles and Fields*, **1987**, 36, 669-693		10

2	Continuum regularization of gauge theory with fermions. *Zeitschrift F□ Physik C-Particles and Fields* , **1986**, 33, 77-88		20
1	New ghost-free infrared-soft gauges. *Physical Review D*, **1986**, 33, 540-547	4.9	42