Hue Sun Chan

List of Publications by Year
in descending order

133 papers	12,369 citations	31902 53 h-index	28224 105 g-index
147 all docs	147 docs citations	147 times ranked	6252 citing authors

#	Article	IF	Citations
1	From Levinthal to pathways to funnels. Nature Structural and Molecular Biology, 1997, 4, 10-19.	3.6	2,125
2	Principles of protein folding â€" A perspective from simple exact models. Protein Science, 1995, 4, 561-602.	3.1	1,321
3	Protein folding in the landscape perspective: Chevron plots and non-arrhenius kinetics. , 1998, 30, 2-33.		397
4	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.	3.3	381
5	Transition states and folding dynamics of proteins and heteropolymers. Journal of Chemical Physics, 1994, 100, 9238-9257.	1.2	274
6	Compact polymers. Macromolecules, 1989, 22, 4559-4573.	2.2	233
7	Sequence-Specific Polyampholyte Phase Separation in Membraneless Organelles. Physical Review Letters, 2016, 117, 178101.	2.9	224
8	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, 9650-9655.	3.3	207
9	Biophysics of protein evolution and evolutionary protein biophysics. Journal of the Royal Society Interface, 2014, 11, 20140419.	1.5	202
10	The effects of internal constraints on the configurations of chain molecules. Journal of Chemical Physics, 1990, 92, 3118-3135.	1.2	199
11	Intrachain loops in polymers: Effects of excluded volume. Journal of Chemical Physics, 1989, 90, 492-509.	1.2	195
12	Phase Separation and Single-Chain Compactness of Charged Disordered Proteins Are Strongly Correlated. Biophysical Journal, 2017, 112, 2043-2046.	0.2	192
13	Cooperativity, Local-Nonlocal Coupling, and Nonnative Interactions: Principles of Protein Folding from Coarse-Grained Models. Annual Review of Physical Chemistry, 2011, 62, 301-326.	4.8	187
14	Theories for Sequence-Dependent Phase Behaviors of Biomolecular Condensates. Biochemistry, 2018, 57, 2499-2508.	1.2	184
15	â€˜â€˜Sequence space soupâ€™â€™ of proteins and copolymers. Journal of Chemical Physics, 1991, 95, 3775-3787.	2.2	176
16	Solvation Effects and Driving Forces for Protein Thermodynamic and Kinetic Cooperativity: How Adequate is Native-centric Topological Modeling?. Journal of Molecular Biology, 2003, 326, 911-931.	2.0	167
17	The why and how of DNA unlinking. Nucleic Acids Research, 2009, 37, 661-671.	6.5	164
18	Cooperativity Principles in Protein Folding. Methods in Enzymology, 2004, 380, 350-379.	0.4	160

#	Article	IF	Citations
19	Comparative roles of charge, Ï€ , 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.	3.3	159
20	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.	1.2	156
21	Polymer principles of protein calorimetric two-state cooperativity. Proteins: Structure, Function and Bioinformatics, 2000, 40, 637-661.	1.5	151
22	Modeling protein density of states: Additive hydrophobic effects are insufficient for calorimetric two-state cooperativity. Proteins: Structure, Function and Bioinformatics, 2000, 40, 543-571.	1.5	127
23	Energy landscapes and the collapse dynamics of homopolymers. Journal of Chemical Physics, 1993, 99, 2116-2127.	1.2	120
24	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.	3.3	120
25	Modeling the effects of mutations on the denatured states of proteins. Protein Science, 1992, 1, 201-215.	3.1	119
26	Folding kinetics of proteins and copolymers. Journal of Chemical Physics, 1992, 96, 768-780.	1.2	118
27	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.	2.3	103
28	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.	1.3	98
29	Charge pattern matching as a â€˜fuzzyâ€™ mode of molecular recognition for the functional phase separations of intrinsically disordered proteins. New Journal of Physics, 2017, 19, 115003.	1.2	96
30	Temperature, Hydrostatic Pressure, and Osmolyte Effects on Liquidâ€“Liquid Phase Separation in Protein Condensates: Physical Chemistry and Biological Implications. Chemistry - A European Journal, 2019, 25, 13049-13069.	1.7	96
31	Energetic Components of Cooperative Protein Folding. Physical Review Letters, 2000, 85, 4823-4826.	2.9	91
32	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, 2920-2925.	3.3	91
33	A Lattice Model of Charge-Pattern-Dependent Polyampholyte Phase Separation. Journal of Physical Chemistry B, 2018, 122, 5418-5431.	1.2	89
34	Towards a consistent modeling of protein thermodynamic and kinetic cooperativity: how applicable is the transition state picture to folding and unfolding? 1 1Edited by C. R. Matthews. Journal of Molecular Biology, 2002, 315, 899-909.	2.0	87
35	Comparing folding codes for proteins and polymers. , 1996, 24, 335-344.		86
36	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, 809-814.	3.3	85

#	Article	IF	Citations
37	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, 560-566.	1.5	85
38	Conformational propagation with prion-like characteristics in a simple model of protein folding. Protein Science, 2001, 10, 819-835.	3.1	84
39	A simple model of chaperonin-mediated protein folding. Proteins: Structure, Function and Bioinformatics, 1996, 24, 345-351.	1.5	81
40	SOLVATION: HOW TO OBTAIN MICROSCOPIC ENERGIES FROM PARTITIONING AND SOLVATION EXPERIMENTS. Annual Review of Biophysics and Biomolecular Structure, 1997, 26, 425-459.	18.3	81
41	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.	1.5	81
42	Hydrophobic association of Â-helices, steric dewetting, and enthalpic barriers to protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6206-6210.	3.3	78
43	Folding alphabets. , 1999, 6, 994-996.		76
44	Desolvation is a Likely Origin of Robust Enthalpic Barriers to Protein Folding. Journal of Molecular Biology, 2005, 349, 872-889.	2.0	75
45	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, 524-533.	1.5	71
46	Solvation: Effects of molecular size and shape. Journal of Chemical Physics, 1994, 101, 7007-7026.	1.2	70
47	Does Compactness Induce Secondary Structure in Proteins?. Journal of Molecular Biology, 1994, 241, 557-573.	2.0	70
48	Theoretical perspectives on nonnative interactions and intrinsic disorder in protein folding and binding. Current Opinion in Structural Biology, 2015, 30, 32-42.	2.6	70
49	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, 373-391.	1.5	66
50	Matching speed and locality. Nature, 1998, 392, 761-763.	13.7	65
51	Simple two-state protein folding kinetics requires near-levinthal thermodynamic cooperativity. Proteins: Structure, Function and Bioinformatics, 2003, 52, 510-523.	1.5	63
52	Temperature Dependence of Three-Body Hydrophobic Interactions:Â Potential of Mean Force, Enthalpy, Entropy, Heat Capacity, and Nonadditivity. Journal of the American Chemical Society, 2005, 127, 303-316.	6.6	63
53	A structural model of latent evolutionary potentials underlying neutral networks in proteins. HFSP Journal, 2007, 1, 79-87.	2.5	61
54	Conformational Heterogeneity and FRET Data Interpretation for Dimensions of Unfolded Proteins. Biophysical Journal, 2017, 113, 1012-1024.	0.2	61

#	Article	IF	Citations
55	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, 14888-14893.	3.3	59
56	Pressure-Sensitive and Osmolyte-Modulated Liquidâ€“Liquid Phase Separation of Eye-Lens Î³-Crystallins. Journal of the American Chemical Society, 2019, 141, 7347-7354.	6.6	59
57	Configuration-Dependent Heat Capacity of Pairwise Hydrophobic Interactions. Journal of the American Chemical Society, 2001, 123, 2083-2084.	6.6	57
58	Polycation-Ï€ Interactions Are a Driving Force for Molecular Recognition by an Intrinsically Disordered Oncoprotein Family. PLoS Computational Biology, 2013, 9, e1003239.	1.5	57
59	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, 268-285.	2.0	56
60	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.	1.2	55
61	Origins of Chevron Rollovers in Non-Two-State Protein Folding Kinetics. Physical Review Letters, 2003, 90, 258104.	2.9	54
62	Solvation and desolvation effects in protein folding: native flexibility, kinetic cooperativity and enthalpic barriers under isostability conditions. Physical Biology, 2005, 2, S75-S85.	0.8	52
63	Pressure-Dependent Properties of Elementary Hydrophobic Interactions: Ramifications for Activation Properties of Protein Folding. Journal of Physical Chemistry B, 2014, 118, 7488-7509.	1.2	49
64	Desolvation Barrier Effects Are a Likely Contributor to the Remarkable Diversity in the Folding Rates of Small Proteins. Journal of Molecular Biology, 2009, 389, 619-636.	2.0	47
65	Pressure and temperature dependence of hydrophobic hydration: Volumetric, compressibility, and thermodynamic signatures. Journal of Chemical Physics, 2007, 126, 114507.	1.2	46
66	New ghost-free infrared-soft gauges. Physical Review D, 1986, 33, 540-547.	1.6	45
67	A unified analytical theory of heteropolymers for sequence-specific phase behaviors of polyelectrolytes and polyampholytes. Journal of Chemical Physics, 2020, 152, 045102.	1.2	45
68	An Adequate Account of Excluded Volume Is Necessary To Infer Compactness and Asphericity of Disordered Proteins by FÃ¶rster Resonance Energy Transfer. Journal of Physical Chemistry B, 2015, 119, 15191-15202.	1.2	44
69	Kinetics of protein folding. Nature, 1995, 373, 664-665.	13.7	43
70	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.	1.2	42
71	Kinetic consequences of native state optimization of surfaceâ€exposed electrostatic interactions in the Fyn SH3 domain. Proteins: Structure, Function and Bioinformatics, 2012, 80, 858-870.	1.5	42
72	Perspectives on protein evolution from simple exact models. Applied Bioinformatics, 2002, 1, 121-44.	1.7	42

#	Article	IF	Citations
73	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.	0.7	41
74	Enhanced structure in polymers at interfaces. Journal of Chemical Physics, 1991, 94, 8542-8557.	1.2	39
75	Probing Possible Downhill Folding: Native Contact Topology Likely Places a Significant Constraint on the Folding Cooperativity of Proteins with â^¼40 Residues. Journal of Molecular Biology, 2008, 384, 512-530.	2.0	38
76	Transition paths, diffusive processes, and preequilibria of protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20919-20924.	3.3	38
77	Analytical Theory for Sequence-Specific Binary Fuzzy Complexes of Charged Intrinsically Disordered Proteins. Journal of Physical Chemistry B, 2020, 124, 6709-6720.	1.2	38
78	Comparing Folding Codes in Simple Heteropolymer Models of Protein Evolutionary Landscape: Robustness of the Superfunnel Paradigm. Biophysical Journal, 2005, 88, 118-131.	0.2	36
79	A critical assessment of the topomer search model of protein folding using a continuum explicit-chain model with extensive conformational sampling. Protein Science, 2009, 14, 1643-1660.	3.1	36
80	Pressureâ€Induced Dissolution and Reentrant Formation of Condensed, Liquidâ€“Liquid Phaseâ€Separated Elastomeric Î±â€Elastin. Chemistry - A European Journal, 2018, 24, 8286-8291.	1.7	36
81	Inferring Global Topology from Local Juxtaposition Geometry: Interlinking Polymer Rings and Ramifications for Topoisomerase Action. Biophysical Journal, 2006, 90, 2344-2355.	0.2	35
82	Native Contact Density and Nonnative Hydrophobic Effects in the Folding of Bacterial Immunity Proteins. PLoS Computational Biology, 2015, 11, e1004260.	1.5	34
83	A structural model of latent evolutionary potentials underlying neutral networks in proteins. , 2007, 1, 79-87.		34
84	An allosteric conduit facilitates dynamic multisite substrate recognition by the SCFCdc4 ubiquitin ligase. Nature Communications, 2017, 8, 13943.	5.8	33
85	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, 14748-14753.	3.3	31
86	Chevron Behavior and Isostable Enthalpic Barriers in Protein Folding: Successes and Limitations of Simple GÅ•like Modeling. Biophysical Journal, 2005, 89, 520-535.	0.2	31
87	Native Topology of the Designed Protein Top7 is Not Conducive to Cooperative Folding. Biophysical Journal, 2009, 96, L25-L27.	0.2	31
88	Effects of desolvation barriers and sidechains on localâ€“nonlocal coupling and chevron behaviors in coarse-grained models of protein folding. Physical Chemistry Chemical Physics, 2014, 16, 6460-6479.	1.3	31
89	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.	1.2	28
90	Action at Hooked or Twistedâ€“Hooked DNA Juxtapositions Rationalizes Unlinking Preference of Type-2 Topoisomerases. Journal of Molecular Biology, 2010, 400, 963-982.	2.0	27

#	Article	IF	Citations
91	Evolutionary Dynamics on Protein Bi-stability Landscapes can Potentially Resolve Adaptive Conflicts. PLoS Computational Biology, 2012, 8, e1002659.	1.5	26
92	A critical comparison of coarse-grained structure-based approaches and atomic models of protein folding. Physical Chemistry Chemical Physics, 2017, 19, 13629-13639.	1.3	24
93	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.	1.2	24
94	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.	0.8	24
95	Theoretical Insights into the Biophysics of Protein Bi-stability and Evolutionary Switches. PLoS Computational Biology, 2016, 12, e1004960.	1.5	24
96	Assembly of model postsynaptic densities involves interactions auxiliary to stoichiometric binding. Biophysical Journal, 2022, 121, 157-171.	0.2	24
97	Explicit-chain model of native-state hydrogen exchange: Implications for event ordering and cooperativity in protein folding. Proteins: Structure, Function and Bioinformatics, 2004, 58, 31-44.	1.5	23
98	Quantitative Analysis of the Effects of Photoswitchable Distance Constraints on the Structure of a Globular Protein. Biochemistry, 2012, 51, 6421-6431.	1.2	23
99	Conformations of a Metastable SH3 Domain Characterized by smFRET and an Excluded-Volume Polymer Model. Biophysical Journal, 2016, 110, 1510-1522.	0.2	23
100	An exact lattice model of complex solutions: Chemical potentials depend on solute and solvent shape. Journal of Chemical Physics, 1995, 103, 10675-10688.	1.2	21
101	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.	0.9	21
102	Continuum regularization of gauge theory with fermions. Zeitschrift FÃ¼r Physik C-Particles and Fields, 1986, 33, 77-88.	1.5	20
103	Energetics of protein thermodynamic cooperativity: contributions of local and nonlocal interactions. Polymer, 2004, 45, 623-632.	1.8	20
104	Hydrophobic interactions in the formation of secondary structures in small peptides. Physical Review E, 2011, 84, 041931.	0.8	20
105	Small-Angle X-ray Scattering Signatures of Conformational Heterogeneity and Homogeneity of Disordered Protein Ensembles. Journal of Physical Chemistry B, 2021, 125, 6451-6478.	1.2	19
106	Coordinateâ€space formulation of polymer lattice cluster theory. Journal of Chemical Physics, 1993, 98, 9951-9962.	1.2	17
107	Statistical mechanics of solvophobic aggregation: Additive and cooperative effects. Journal of Chemical Physics, 2001, 115, 3424-3431.	1.2	17
108	Local site preference rationalizes disentangling by DNA topoisomerases. Physical Review E, 2010, 81, 031902.	0.8	14

#	Article	IF	Citations
109	Spatial ranges of driving forces are a key determinant of protein folding cooperativity and rate diversity. Physical Review E, 2013, 88, 044701.	0.8	14
110	Pressure Sensitivity of SynGAP/PSDâ€95 Condensates as a Model for Postsynaptic Densities and Its Biophysical and Neurological Ramifications. Chemistry - A European Journal, 2020, 26, 11024-11031.	1.7	13
111	Reply to â€œComment on â€˜Anti-cooperativity in hydrophobic interactions: A simulation study of spatial dependence of three-body effects and beyondâ€™â€Šâ€•[J. Chem. Phys. 116, 2665 (2002)]. Journal of Chemical Physics, 2002, 116, 2668-2669.	1.2	11
112	Volumetric Physics of Polypeptide Coilâ€“Helix Transitions. Biochemistry, 2016, 55, 6269-6281.	1.2	11
113	Continuum-regularized quantum gravity. Zeitschrift FÃ¼r Physik C-Particles and Fields, 1987, 36, 669-693.	1.5	10
114	Extracting Microscopic Energies from Oil-Phase Solvation Experiments. Journal of Physical Chemistry B, 2000, 104, 7471-7482.	1.2	10
115	Selective adsorption of block copolymers on patterned surfaces. Journal of Chemical Physics, 2006, 125, 164909.	1.2	10
116	Evolvability and Single-Genotype Fluctuation in Phenotypic Properties: AÂSimple Heteropolymer Model. Biophysical Journal, 2010, 98, 2487-2496.	0.2	9
117	Effects of Cosolvents and Crowding Agents on the Stability and Phase Transition Kinetics of the SynGAP/PSD-95 Condensate Model of Postsynaptic Densities. Journal of Physical Chemistry B, 2022, 126, 1734-1741.	1.2	9
118	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.	1.0	8
119	Non-Grassmann formulation of regularized gauge theory with fermions. Zeitschrift FÃ¼r Physik C-Particles and Fields, 1987, 34, 267-276.	1.5	7
120	Consistent rationalization of type-2 topoisomerases' unknotting, decatenating, supercoil-relaxing actions and their scaling relation. Journal of Physics Condensed Matter, 2015, 27, 354103.	0.7	7
121	Liaison amid disorder: non-native interactions may underpin long-range coupling in proteins. Journal of Biology, 2009, 8, 27.	2.7	5
122	Molecular recognition and packing frustration in a helical protein. PLoS Computational Biology, 2017, 13, e1005909.	1.5	5
123	Short-Range Contact Preferences and Long-Range Indifference: Is Protein Folding Stoichiometry Driven?. Journal of Biomolecular Structure and Dynamics, 2011, 28, 603-605.	2.0	3
124	A simple model of chaperoninâ€mediated protein folding. Proteins: Structure, Function and Bioinformatics, 1996, 24, 345-351.	1.5	2
125	Polymer principles of protein calorimetric two-state cooperativity. , 2000, 40, 637.		2
126	Polymer principles of protein calorimetric two-state cooperativity. , 2000, 40, 637.		2

#	Article	IF	Citations
127	Field theory description of ion association in re-entrant phase separation of polyampholytes. Journal of Chemical Physics, 2022, 156, .	1.2	2
128	Thermodynamics and kinetics of TopoII action: A consensus on T-segment curvature selection? Comment on â€œDisentangling DNA Moleculesâ€•by Alexander Vologodskii. Physics of Life Reviews, 2016, 18, 135-138.	1.5	1
129	Theoretical Saxs Signatures of Conformational Heterogeneity and Homogeneity of Disordered Protein Ensembles. Biophysical Journal, 2019, 116, 199a.	0.2	1
130	SAXS Signatures of Conformational Heterogeneity and Homogeneity of Disordered Protein Ensembles. Biophysical Journal, 2020, 118, 503a.	0.2	1
131	Simplified Models of Protein Folding. , 2005, , 1823-1836.		1
132	Frontispiece: Temperature, Hydrostatic Pressure, and Osmolyte Effects on Liquidâ€“Liquid Phase Separation in Protein Condensates: Physical Chemistry and Biological Implications. Chemistry - A European Journal, 2019, 25, .	1.7	0
133	Simplified Models of Protein Folding. , 2005, , 1823-1836.		0