Hue Sun Chan

List of Publications by Year
in descending order

133	12,369	31976 53	28297 105
papers	citations	h-index	g-index

147	147	147	6252
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Assembly of model postsynaptic densities involves interactions auxiliary to stoichiometric binding. Biophysical Journal, 2022, 121, 157-171.	0.5	24
2	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.	2.6	9
3	Field theory description of ion association in re-entrant phase separation of polyampholytes. Journal of Chemical Physics, 2022, 156, .	3.0	2
4	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.	2.6	24
5	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.	2.1	24
6	Small-Angle X-ray Scattering Signatures of Conformational Heterogeneity and Homogeneity of Disordered Protein Ensembles. Journal of Physical Chemistry B, 2021, 125, 6451-6478.	2.6	19
7	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.	7.1	159
8	SAXS Signatures of Conformational Heterogeneity and Homogeneity of Disordered Protein Ensembles. Biophysical Journal, 2020, 118, 503a.	0.5	1
9	Analytical Theory for Sequence-Specific Binary Fuzzy Complexes of Charged Intrinsically Disordered Proteins. Journal of Physical Chemistry B, 2020, 124, 6709-6720.	2.6	38
10	A unified analytical theory of heteropolymers for sequence-specific phase behaviors of polyelectrolytes and polyampholytes. Journal of Chemical Physics, 2020, 152, 045102.	3.0	45
11	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.	3.3	13
12	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.	3.3	96
13	Theoretical Saxs Signatures of Conformational Heterogeneity and Homogeneity of Disordered Protein Ensembles. Biophysical Journal, 2019, 116, 199a.	0.5	1
14	Pressure-Sensitive and Osmolyte-Modulated Liquidâ€“Liquid Phase Separation of Eye-Lens Î³-Crystallins. Journal of the American Chemical Society, 2019, 141, 7347-7354.	13.7	59
15	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, .	3.3	0
16	Theories for Sequence-Dependent Phase Behaviors of Biomolecular Condensates. Biochemistry, 2018, 57, 2499-2508.	2.5	184
17	A Lattice Model of Charge-Pattern-Dependent Polyampholyte Phase Separation. Journal of Physical Chemistry B, 2018, 122, 5418-5431.	2.6	89
18	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.	2.8	98

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19	Pressureâ€Induced Dissolution and Reentrant Formation of Condensed, Liquidâ€“Liquid Phaseâ€Separated Elastomeric Î±â€Elastin. Chemistry - A European Journal, 2018, 24, 8286-8291.	3.3	36
20	A critical comparison of coarse-grained structure-based approaches and atomic models of protein folding. Physical Chemistry Chemical Physics, 2017, 19, 13629-13639.	2.8	24
21	Phase Separation and Single-Chain Compactness of Charged Disordered Proteins Are Strongly Correlated. Biophysical Journal, 2017, 112, 2043-2046.	0.5	192
22	An allosteric conduit facilitates dynamic multisite substrate recognition by the SCFCdc4 ubiquitin ligase. Nature Communications, 2017, 8, 13943.	12.8	33
23	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.	7.1	381
24	Conformational Heterogeneity and FRET Data Interpretation for Dimensions of Unfolded Proteins. Biophysical Journal, 2017, 113, 1012-1024.	0.5	61
25	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.	4.9	103
26	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.	2.9	96
27	Molecular recognition and packing frustration in a helical protein. PLoS Computational Biology, 2017, 13, e1005909.	3.2	5
28	Conformations of a Metastable SH3 Domain Characterized by smFRET and an Excluded-Volume Polymer Model. Biophysical Journal, 2016, 110, 1510-1522.	0.5	23
29	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.	2.8	1
30	Sequence-Specific Polyampholyte Phase Separation in Membraneless Organelles. Physical Review Letters, 2016, 117, 178101.	7.8	224
31	Volumetric Physics of Polypeptide Coilâ€“Helix Transitions. Biochemistry, 2016, 55, 6269-6281.	2.5	11
32	Theoretical Insights into the Biophysics of Protein Bi-stability and Evolutionary Switches. PLoS Computational Biology, 2016, 12, e1004960.	3.2	24
33	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	7
34	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.	2.6	44
35	Theoretical perspectives on nonnative interactions and intrinsic disorder in protein folding and binding. Current Opinion in Structural Biology, 2015, 30, 32-42.	5.7	70
36	Native Contact Density and Nonnative Hydrophobic Effects in the Folding of Bacterial Immunity Proteins. PLoS Computational Biology, 2015, 11, e1004260.	3.2	34

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37	Biophysics of protein evolution and evolutionary protein biophysics. Journal of the Royal Society Interface, 2014, 11, 20140419.	3.4	202
38	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.	2.8	31
39	Pressure-Dependent Properties of Elementary Hydrophobic Interactions: Ramifications for Activation Properties of Protein Folding. Journal of Physical Chemistry B, 2014, 118, 7488-7509.	2.6	49
40	Spatial ranges of driving forces are a key determinant of protein folding cooperativity and rate diversity. Physical Review E, 2013, 88, 044701.	2.1	14
41	Polycation-Ï€ Interactions Are a Driving Force for Molecular Recognition by an Intrinsically Disordered Oncoprotein Family. PLoS Computational Biology, 2013, 9, e1003239.	3.2	57
42	Evolutionary Dynamics on Protein Bi-stability Landscapes can Potentially Resolve Adaptive Conflicts. PLoS Computational Biology, 2012, 8, e1002659.	3.2	26
43	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.	7.1	59
44	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.	7.1	38
45	Quantitative Analysis of the Effects of Photoswitchable Distance Constraints on the Structure of a Globular Protein. Biochemistry, 2012, 51, 6421-6431.	2.5	23
46	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.	2.6	42
47	Short-Range Contact Preferences and Long-Range Indifference: Is Protein Folding Stoichiometry Driven?. Journal of Biomolecular Structure and Dynamics, 2011, 28, 603-605.	3.5	3
48	Cooperativity, Local-Nonlocal Coupling, and Nonnative Interactions: Principles of Protein Folding from Coarse-Grained Models. Annual Review of Physical Chemistry, 2011, 62, 301-326.	10.8	187
49	Hydrophobic interactions in the formation of secondary structures in small peptides. Physical Review E, 2011, 84, 041931.	2.1	20
50	Local site preference rationalizes disentangling by DNA topoisomerases. Physical Review E, 2010, 81, 031902.	2.1	14
51	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.	7.1	91
52	Evolvability and Single-Genotype Fluctuation in Phenotypic Properties: AÂSimple Heteropolymer Model. Biophysical Journal, 2010, 98, 2487-2496.	0.5	9
53	Action at Hooked or Twistedâ€“Hooked DNA Juxtapositions Rationalizes Unlinking Preference of Type-2 Topoisomerases. Journal of Molecular Biology, 2010, 400, 963-982.	4.2	27
54	The why and how of DNA unlinking. Nucleic Acids Research, 2009, 37, 661-671.	14.5	164

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55	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.	2.0	8
56	Liaison amid disorder: non-native interactions may underpin long-range coupling in proteins. Journal of Biology, 2009, 8, 27.	2.7	5
57	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.	4.2	47
58	Native Topology of the Designed Protein Top7 is Not Conducive to Cooperative Folding. Biophysical Journal, 2009, 96, L25-L27.	0.5	31
59	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.	7.6	36
60	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.	3.0	28
61	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.	4.2	38
62	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.	7.1	120
63	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.	7.1	78
64	Pressure and temperature dependence of hydrophobic hydration: Volumetric, compressibility, and thermodynamic signatures. Journal of Chemical Physics, 2007, 126, 114507.	3.0	46
65	A structural model of latent evolutionary potentials underlying neutral networks in proteins. HFSP Journal, 2007, 1, 79-87.	2.5	61
66	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.	7.1	207
67	A structural model of latent evolutionary potentials underlying neutral networks in proteins. HFSP Journal, 2007, 1, 79.	2.5	34
68	Inferring Global Topology from Local Juxtaposition Geometry: Interlinking Polymer Rings and Ramifications for Topoisomerase Action. Biophysical Journal, 2006, 90, 2344-2355.	0.5	35
69	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.	4.2	56
70	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.	2.6	66
71	Selective adsorption of block copolymers on patterned surfaces. Journal of Chemical Physics, 2006, 125, 164909.	3.0	10
72	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	41

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73	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.	13.7	63
74	Desolvation is a Likely Origin of Robust Enthalpic Barriers to Protein Folding. Journal of Molecular Biology, 2005, 349, 872-889.	4.2	75
75	Comparing Folding Codes in Simple Heteropolymer Models of Protein Evolutionary Landscape: Robustness of the Superfunnel Paradigm. Biophysical Journal, 2005, 88, 118-131.	0.5	36
76	Chevron Behavior and Isostable Enthalpic Barriers in Protein Folding: Successes and Limitations of Simple GÅ•like Modeling. Biophysical Journal, 2005, 89, 520-535.	0.5	31
77	Solvation and desolvation effects in protein folding: native flexibility, kinetic cooperativity and enthalpic barriers under isostability conditions. Physical Biology, 2005, 2, S75-S85.	1.8	52
78	Simplified Models of Protein Folding. , 2005, , 1823-1836.		1
79	Simplified Models of Protein Folding. , 2005, , 1823-1836.		0
80	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.	7.1	31
81	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.	2.6	23
82	Energetics of protein thermodynamic cooperativity: contributions of local and nonlocal interactions. Polymer, 2004, 45, 623-632.	3.8	20
83	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.	1.9	21
84	Cooperativity Principles in Protein Folding. Methods in Enzymology, 2004, 380, 350-379.	1.0	160
85	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.	2.6	71
86	Simple two-state protein folding kinetics requires near-levinthal thermodynamic cooperativity. Proteins: Structure, Function and Bioinformatics, 2003, 52, 510-523.	2.6	63
87	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.	4.2	167
88	Origins of Chevron Rollovers in Non-Two-State Protein Folding Kinetics. Physical Review Letters, 2003, 90, 258104.	7.8	54
89	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.	7.1	85
90	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.	3.0	11

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91	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.	4.2	87
92	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.	2.6	81
93	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.	2.6	85
94	Perspectives on protein evolution from simple exact models. Applied Bioinformatics, 2002, 1, 121-44.	1.6	42
95	Conformational propagation with prion-like characteristics in a simple model of protein folding. Protein Science, 2001, 10, 819-835.	7.6	84
96	Configuration-Dependent Heat Capacity of Pairwise Hydrophobic Interactions. Journal of the American Chemical Society, 2001, 123, 2083-2084.	13.7	57
97	Statistical mechanics of solvophobic aggregation: Additive and cooperative effects. Journal of Chemical Physics, 2001, 115, 3424-3431.	3.0	17
98	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.	3.0	42
99	Modeling protein density of states: Additive hydrophobic effects are insufficient for calorimetric two-state cooperativity. Proteins: Structure, Function and Bioinformatics, 2000, 40, 543-571.	2.6	127
100	Polymer principles of protein calorimetric two-state cooperativity. Proteins: Structure, Function and Bioinformatics, 2000, 40, 637-661.	2.6	151
101	Energetic Components of Cooperative Protein Folding. Physical Review Letters, 2000, 85, 4823-4826.	7.8	91
102	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.	3.0	156
103	Extracting Microscopic Energies from Oil-Phase Solvation Experiments. Journal of Physical Chemistry B, 2000, 104, 7471-7482.	2.6	10
104	Polymer principles of protein calorimetric two-state cooperativity. , 2000, 40, 637.		2
105	Polymer principles of protein calorimetric twoâ€state cooperativity. Proteins: Structure, Function and Bioinformatics, 2000, 40, 637-661.	2.6	2
106	Folding alphabets. , 1999, 6, 994-996.		76
107	Matching speed and locality. Nature, 1998, 392, 761-763.	27.8	65
108	Protein folding in the landscape perspective: Chevron plots and non-arrhenius kinetics. , 1998, 30, 2-33.		397

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109	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.	2.6	55
110	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
111	From Levinthal to pathways to funnels. Nature Structural and Molecular Biology, 1997, 4, 10-19.	8.2	2,125
112	Comparing folding codes for proteins and polymers. , 1996, 24, 335-344.		86
113	A simple model of chaperonin-mediated protein folding. Proteins: Structure, Function and Bioinformatics, 1996, 24, 345-351.	2.6	81
114	A simple model of chaperoninâ€mediated protein folding. Proteins: Structure, Function and Bioinformatics, 1996, 24, 345-351.	2.6	2
115	Kinetics of protein folding. Nature, 1995, 373, 664-665.	27.8	43
116	An exact lattice model of complex solutions: Chemical potentials depend on solute and solvent shape. Journal of Chemical Physics, 1995, 103, 10675-10688.	3.0	21
117	Principles of protein folding â€" A perspective from simple exact models. Protein Science, 1995, 4, 561-602.	7.6	1,321
118	Solvation: Effects of molecular size and shape. Journal of Chemical Physics, 1994, 101, 7007-7026.	3.0	70
119	Transition states and folding dynamics of proteins and heteropolymers. Journal of Chemical Physics, 1994, 100, 9238-9257.	3.0	274
120	Does Compactness Induce Secondary Structure in Proteins?. Journal of Molecular Biology, 1994, 241, 557-573.	4.2	70
121	Energy landscapes and the collapse dynamics of homopolymers. Journal of Chemical Physics, 1993, 99, 2116-2127.	3.0	120
122	Coordinateâ€space formulation of polymer lattice cluster theory. Journal of Chemical Physics, 1993, 98, 9951-9962.	3.0	17
123	Folding kinetics of proteins and copolymers. Journal of Chemical Physics, 1992, 96, 768-780.	3.0	118
124	Modeling the effects of mutations on the denatured states of proteins. Protein Science, 1992, 1, 201-215.	7.6	119
125	â€˜â€˜Sequence space soupâ€™â€™ of proteins and copolymers. Journal of Chemical Physics, 1991, 95, 3775-3787.	3.0	176
126	Enhanced structure in polymers at interfaces. Journal of Chemical Physics, 1991, 94, 8542-8557.	3.0	39

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127	The effects of internal constraints on the configurations of chain molecules. Journal of Chemical Physics, 1990, 92, 3118-3135.	3.0	199
128	Compact polymers. Macromolecules, 1989, 22, 4559-4573.	4.8	233
129	Intrachain loops in polymers: Effects of excluded volume. Journal of Chemical Physics, 1989, 90, 492-509.	3.0	195
130	Non-Grassmann formulation of regularized gauge theory with fermions. Zeitschrift FÃ¼r Physik C-Particles and Fields, 1987, 34, 267-276.	1.5	7
131	Continuum-regularized quantum gravity. Zeitschrift FÃ¼r Physik C-Particles and Fields, 1987, 36, 669-693.	1.5	10
132	Continuum regularization of gauge theory with fermions. Zeitschrift FÃ¼r Physik C-Particles and Fields, 1986, 33, 77-88.	1.5	20
133	New ghost-free infrared-soft gauges. Physical Review D, 1986, 33, 540-547.	4.7	45