Vincent J Hilser

List of Publications by Year
in descending order

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Version: 2024-02-01

90 papers	6,086 citations	101535 36 h-index	79691 73 g-index
110 all docs	110 docs citations	110 times ranked	5663 citing authors

#	Article	IF	Citations
1	The ensemble nature of allostery. Nature, 2014, 508, 331-339.	27.8	1,026
2	The heat capacity of proteins. Proteins: Structure, Function and Bioinformatics, 1995, 22, 404-412.	2.6	421
3	Intrinsic disorder as a mechanism to optimize allosteric coupling in proteins. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 8311-8315.	7.1	376
4	Allostery in Its Many Disguises: From Theory to Applications. Structure, 2019, 27, 566-578.	3.3	285
5	Structural and Energetic Basis of Allostery. Annual Review of Biophysics, 2012, 41, 585-609.	10.0	265
6	Structure-based Calculation of the Equilibrium Folding Pathway of Proteins. Correlation with Hydrogen Exchange Protection Factors. Journal of Molecular Biology, 1996, 262, 756-772.	4.2	241
7	The magnitude of the backbone conformational entropy change in protein folding. Proteins: Structure, Function and Bioinformatics, 1996, 25, 143-156.	2.6	222
8	A Statistical Thermodynamic Model of the Protein Ensemble. Chemical Reviews, 2006, 106, 1545-1558.	47.7	175
9	Rational modulation of conformational fluctuations in adenylate kinase reveals a local unfolding mechanism for allostery and functional adaptation in proteins. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16984-16989.	7.1	161
10	Local conformational fluctuations can modulate the coupling between proton binding and global structural transitions in proteins. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4282-4287.	7.1	156
11	Dynamic allostery can drive cold adaptation in enzymes. Nature, 2018, 558, 324-328.	27.8	154
12	Direct access to the cooperative substructure of proteins and the protein ensemble via cold denaturation. Nature Structural and Molecular Biology, 2004, 11, 352-357.	8.2	134
13	The enthalpy change in protein folding and binding: Refinement of parameters for structure-based calculations. , 1996, 26, 123-133.		127
14	The magnitude of the backbone conformational entropy change in protein folding. , 1996, 25, 143-156.		116
15	An Ensemble View of Allostery. Science, 2010, 327, 653-654.	12.6	112
16	Coupled Motion in Proteins Revealed by Pressure Perturbation. Journal of the American Chemical Society, 2012, 134, 8543-8550.	13.7	99
17	The role of protein conformational fluctuations in allostery, function, and evolution. Biophysical Chemistry, 2011, 159, 129-141.	2.8	97
18	Agonism/antagonism switching in allosteric ensembles. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4134-4139.	7.1	94

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19	Predicting the equilibrium protein folding pathway: Structure-based analysis of staphylococcal nuclease. , 1997, 27, 171-183.		85
20	Genetically tunable frustration controls allostery in an intrinsically disordered transcription factor. ELife, 2017, 6, .	6.0	81
21	The effect of the polyproline II (PPII) conformation on the denatured state entropy. Protein Science, 2003, 12, 447-457.	7.6	73
22	Structural Dynamics, Intrinsic Disorder, and Allostery in Nuclear Receptors as Transcription Factors. Journal of Biological Chemistry, 2011, 286, 39675-39682.	3.4	69
23	Functional residues serve a dominant role in mediating the cooperativity of the protein ensemble. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 4347-4352.	7.1	66
24	Design of protein switches based on an ensemble model of allostery. Nature Communications, 2015, 6, 6968.	12.8	62
25	Quantitative Assessment of Protein Structural Models by Comparison of H/D Exchange MS Data with Exchange Behavior Accurately Predicted by DXCOREX. Journal of the American Society for Mass Spectrometry, 2012, 23, 43-56.	2.8	60
26	Structure-based statistical thermodynamic analysis of T4 lysozyme mutants: structural mapping of cooperative interactions. Biophysical Chemistry, 1997, 64, 69-79.	2.8	56
27	Interplay between allostery and intrinsic disorder in an ensemble. Biochemical Society Transactions, 2012, 40, 975-980.	3.4	55
28	Thermodynamics of Binding to SH3 Domains:â€‰ The Energetic Impact of Polyproline II (PII) Helix Formation. Biochemistry, 2004, 43, 7787-7797.	2.5	53
29	Evolutionary conservation of the polyproline II conformation surrounding intrinsically disordered phosphorylation sites. Protein Science, 2013, 22, 405-417.	7.6	50
30	The origin of pH-dependent changes in m-values for the denaturant-induced unfolding of proteins. Journal of Molecular Biology, 2001, 309, 1165-1175.	4.2	47
31	Thermodynamic Dissection of the Intrinsically Disordered N-terminal Domain of Human Glucocorticoid Receptor. Journal of Biological Chemistry, 2012, 287, 26777-26787.	3.4	47
32	Ligand-induced changes in dynamics in the RT loop of the C-terminal SH3 domain of Sem-5 indicate cooperative conformational coupling. Protein Science, 2003, 12, 982-996.	7.6	46
33	Ensemble-based signatures of energy propagation in proteins: A new view of an old phenomenon. Proteins: Structure, Function and Bioinformatics, 2005, 62, 728-738.	2.6	44
34	COREX/BEST server: a web browser-based program that calculates regional stability variations within protein structures. Bioinformatics, 2005, 21, 3318-3319.	4.1	43
35	Ribosome A and P sites revealed by length analysis of ribosome profiling data. Nucleic Acids Research, 2015, 43, 3680-3687.	14.5	43
36	Thermodynamic Mechanism and Consequences of the Polyproline II (PII) Structural Bias in the Denatured States of Proteinsâ€. Biochemistry, 2004, 43, 9790-9799.	2.5	41

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37	Revealing the Nature of the Native State Ensemble through Cold Denaturationâ€. Biochemistry, 2006, 45, 10163-10174.	2.5	41
38	Sequence-Based Analysis of Protein Energy Landscapes Reveals Nonuniform Thermal Adaptation within the Proteome. Molecular Biology and Evolution, 2009, 26, 2217-2227.	8.9	41
39	The Disordered C-Terminal Domain of Human DNA Glycosylase NEIL1 Contributes to Its Stability via Intramolecular Interactions. Journal of Molecular Biology, 2013, 425, 2359-2371.	4.2	41
40	Ensemble modulation as an origin of denaturant-independent hydrogen exchange in proteins 1 1Edited by I. Wilson. Journal of Molecular Biology, 2000, 301, 247-256.	4.2	39
41	Phosphorylation Increases Persistence Length and End-to-End Distance of a Segment of Tau Protein. Biophysical Journal, 2016, 110, 362-371.	0.5	39
42	Protein and peptide mobility in capillary zone electrophoresis. Journal of Chromatography A, 1993, 630, 329-336.	3.7	35
43	Molecular mechanisms of pH-driven conformational transitions of proteins: Insights from continuum electrostatics calculations of acid unfolding. Proteins: Structure, Function and Bioinformatics, 2006, 63, 113-126.	2.6	35
44	Thermodynamic propensities of amino acids in the native state ensemble: Implications for fold recognition. Protein Science, 2001, 10, 1032-1045.	7.6	28
45	Ensemble allosteric model: energetic frustration within the intrinsically disordered glucocorticoid receptor. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20170175.	4.0	28
46	Denatured-State Energy Landscapes of a Protein Structural Database Reveal the Energetic Determinants of a Framework Model for Folding. Journal of Molecular Biology, 2008, 381, 1184-1201.	4.2	25
47	Finding the wet spots. Nature, 2011, 469, 166-167.	27.8	24
48	Allostery vs. â€œallokairyâ€• Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11430-11431.	7.1	24
49	Modeling the Native State Ensemble. , 2001, 168, 093-116.		21
50	Exploring the impact of polyproline II (P_{II}) conformational bias on the binding of peptides to the SEMâ€5 SH3 domain. Protein Science, 2008, 17, 1200-1211.	7.6	21
51	Predicting the Energetics of Conformational Fluctuations in Proteins from Sequence: A Strategy for Profiling the Proteome. Structure, 2008, 16, 1627-1637.	3.3	20
52	Temperature and Urea Have Opposing Impacts on Polyproline II Conformational Bias. Biochemistry, 2013, 52, 949-958.	2.5	20
53	Thermodynamic environments in proteins: Fundamental determinants of fold specificity. Protein Science, 2002, 11, 1945-1957.	7.6	19
54	Single-Molecule Chemo-Mechanical Spectroscopy Provides Structural Identity of Folding Intermediates. Biophysical Journal, 2016, 110, 1280-1290.	0.5	19

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55	Signalling from disordered proteins. Nature, 2013, 498, 308-310.	27.8	18
56	Directed discovery of bivalent peptide ligands to an SH3 domain. Protein Science, 2004, 13, 626-632.	7.6	17
57	Conformational Heterogeneity Within the LID Domain Mediates Substrate Binding to Escherichia coli Adenylate Kinase: Function Follows Fluctuations. Topics in Current Chemistry, 2013, 337, 95-121.	4.0	17
58	Using biochemistry and biophysics to extinguish androgen receptor signaling in prostate cancer. Journal of Biological Chemistry, 2021, 296, 100240.	3.4	17
59	Analysis of the â€œthermodynamic information contentâ€•of aHomo sapiensstructural database reveals hierarchical thermodynamic organization. Protein Science, 2004, 13, 1787-1801.	7.6	16
60	Exploring allosteric coupling in the Î±-subunit of Heterotrimeric G proteins using evolutionary and ensemble-based approaches. BMC Structural Biology, 2008, 8, 23.	2.3	16
61	Characterizing the Role of Ensemble Modulation in Mutation-Induced Changes in Binding Affinity. Journal of the American Chemical Society, 2009, 131, 6785-6793.	13.7	14
62	Strategies for the Thermodynamic Characterization of Linked Binding/Local Folding Reactions Within the Native State. Methods in Enzymology, 2011, 492, 253-282.	1.0	14
63	The role of negative selection in protein evolution revealed through the energetics of the native state ensemble. Proteins: Structure, Function and Bioinformatics, 2016, 84, 435-447.	2.6	13
64	Ligand Effects on the Protein Ensemble: Unifying the Descriptions of Ligand Binding, Local Conformational Fluctuations, and Protein Stability. Methods in Cell Biology, 2008, 84, 871-891.	1.1	12
65	Chapter 11 Energetic Profiling of Protein Folds. Methods in Enzymology, 2009, 455, 299-327.	1.0	11
66	Investigating Homology between Proteins using Energetic Profiles. PLoS Computational Biology, 2010, 6, e1000722.	3.2	11
67	Structural Stability of the Coiled-Coil Domain of Tumor Susceptibility Gene (TSG)-101. Biochemistry, 2017, 56, 4646-4655.	2.5	10
68	Using the COREX/BEST Server to Model the Native-State Ensemble. Methods in Molecular Biology, 2014, 1084, 255-269.	0.9	10
69	Comparison of the utility of capillary zone electrophoresis and high-performance liquid chromatography in peptide mapping and separation. Journal of Chromatography A, 1994, 672, 219-229.	3.7	9
70	Thermodynamic Mechanism for the Evasion of Antibody Neutralization in Flaviviruses. Journal of the American Chemical Society, 2014, 136, 10315-10324.	13.7	9
71	Hidden dynamic signatures drive substrate selectivity in the disordered phosphoproteome. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23606-23616.	7.1	9
72	Tumor Susceptibility Gene 101 Regulates the Glucocorticoid Receptor through Disorder-Mediated Allostery. Biochemistry, 2021, 60, 1647-1657.	2.5	8

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73	Assessing Allostery in Intrinsically Disordered Proteins With Ensemble Allosteric Model. Methods in Enzymology, 2018, 611, 531-557.	1.0	7
74	An Experimental Strategy to Evaluate the Thermodynamic Stability of Highly Dynamic Binding Sites in Proteins Using Hydrogen Exchange. Journal of the American Chemical Society, 2004, 126, 12774-12775.	13.7	6
75	Disordered allostery: lessons from glucocorticoid receptor. Biophysical Reviews, 2015, 7, 257-265.	3.2	6
76	An Energetic Representation of Protein Architecture that Is Independent of Primary and Secondary Structure. Biophysical Journal, 2009, 97, 1461-1470.	0.5	5
77	Effect of Diffusion on Resonance Energy Transfer Rate Distributions: Implications for Distance Measurements. Journal of Physical Chemistry B, 2015, 119, 12603-12622.	2.6	5
78	A Unique BSL-3 Cryo-Electron Microscopy Laboratory at UTMB. Applied Biosafety, 2010, 15, 130-136.	0.5	4
79	Conserved allosteric ensembles in disordered proteins using TROSY/anti-TROSY R2-filtered spectroscopy. Biophysical Journal, 2021, 120, 2498-2510.	0.5	4
80	Phylogenetic convergence of phase separation and mitotic function in the disordered protein <scp>BuGZ</scp>. Protein Science, 2022, 31, 822-834.	7.6	4
81	Intrinsically Disordered Protein: A Thermodynamic Perspective. Biophysical Journal, 2015, 108, 228a.	0.5	2
82	Allosteric Regulation and Intrinsic Disorder in Nuclear Hormone Receptors. , 2015, , 73-91.		2
83	The equilibrium ensemble of conformational states in staphylococcal nuclease. Techniques in Protein Chemistry, 1997, 8, 767-781.	0.3	1
84	A Horizontal Alignment Tool for Numerical Trend Discovery in Sequence Data: Application to Protein Hydropathy. PLoS Computational Biology, 2013, 9, e1003247.	3.2	1
85	The Disordered Protein Bugz Conserves Mitotic Function and Liquid-Liquid Phase Separation across 1.6 Billion Years of Evolution. Biophysical Journal, 2019, 116, 179a-180a.	0.5	1
86	Direct Calorimetric Determination of a Complete Polyproline II (pII) Propensity Scale Reveals PII Enhancement in Intrinsically Disordered Proteins. Biophysical Journal, 2011, 100, 229a.	0.5	0
87	Catching Excited States in the Act: Functional Unfolding in E. Coli Adenylate Kinase. Biophysical Journal, 2016, 110, 207a-208a.	0.5	0
88	Whatâ€™s in an Average? An Ensemble View of Phosphorylation Effects. Structure, 2017, 25, 573-575.	3.3	0
89	Design Implications for an Ensembleâ€based View of Proteins. FASEB Journal, 2008, 22, 407.2.	0.5	0
90	A Thermodynamic Atlas of Proteomes Reveals Energetic Innovation across the Tree of Life. Molecular Biology and Evolution, 2022, 39, .	8.9	0