Ernesto Freire

List of Publications by Year in Descending Order

163 papers	14,244 citations	69 h-index	116 g-index
169 ext. papers	15,280 ext. citations	5.8 avg, IF	6.51 L-index

#	Paper	IF	Citations
163	Development of High affinity Nanobodies Specific for Na1.4 and Na1.5 Voltage-Gated Sodium Channel Isoforms.. *Journal of Biological Chemistry*, **2022**, 101763	5.4	
162	Reversibility and irreversibility in the temperature denaturation of monoclonal antibodies. *Analytical Biochemistry*, **2021**, 626, 114240	3.1	6
161	Binding Thermodynamics to Intrinsically Disordered Protein Domains. *Methods in Molecular Biology*, **2020**, 2141, 449-462	1.4	1
160	Bioinspired supramolecular engineering of self-assembling immunofibers for high affinity binding of immunoglobulin G. *Biomaterials*, **2018**, 178, 448-457	15.6	8
159	A human monoclonal antibody prevents malaria infection by targeting a new site of vulnerability on the parasite. *Nature Medicine*, **2018**, 24, 408-416	50.5	136
158	SOSIP Changes Affect Human Immunodeficiency Virus Type 1 Envelope Glycoprotein Conformation and CD4 Engagement. *Journal of Virology*, **2018**, 92,	6.6	18
157	Long term stability of a HIV-1 neutralizing monoclonal antibody using isothermal calorimetry. *Analytical Biochemistry*, **2018**, 554, 61-69	3.1	7
156	Isothermal calorimetry of a monoclonal antibody using a conventional differential scanning calorimeter. *Analytical Biochemistry*, **2018**, 558, 50-52	3.1	0
155	The 20-21 of gp120 is a regulatory switch for HIV-1 Env conformational transitions. *Nature Communications*, **2017**, 8, 1049	17.4	54
154	Crystal structures of trimeric HIV envelope with entry inhibitors BMS-378806 and BMS-626529. *Nature Chemical Biology*, **2017**, 13, 1115-1122	11.7	73
153	A novel lipoate attachment enzyme is shared by Plasmodium and Chlamydia species. *Molecular Microbiology*, **2017**, 106, 439-451	4.1	7
152	Temperature stability of proteins: Analysis of irreversible denaturation using isothermal calorimetry. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 2009-2016	4.2	37
151	Enthalpy screen of drug candidates. *Analytical Biochemistry*, **2016**, 513, 1-6	3.1	14
150	Small-Molecule CD4-Mimics: Structure-Based Optimization of HIV-1 Entry Inhibition. *ACS Medicinal Chemistry Letters*, **2016**, 7, 330-4	4.3	60
149	Three easy pieces. *Biochimica Et Biophysica Acta - General Subjects*, **2016**, 1860, 975-980	4	5
148	Conformational stability and self-association equilibrium in biologics. *Drug Discovery Today*, **2016**, 21, 342-7	8.8	18
147	Crystal structure, conformational fixation and entry-related interactions of mature ligand-free HIV-1 Env. *Nature Structural and Molecular Biology*, **2015**, 22, 522-31	17.6	254

146	CD4 mimetics sensitize HIV-1-infected cells to ADCC. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, E2687-94	11.5	89
145	Synthetic, structural mimetics of the β-hairpin flap of HIV-1 protease inhibit enzyme function. *Bioorganic and Medicinal Chemistry*, **2015**, 23, 7095-109	3.4	2
144	Impact of Surface Polyethylene Glycol (PEG) Density on Biodegradable Nanoparticle Transport in Mucus ex Vivo and Distribution in Vivo. *ACS Nano*, **2015**, 9, 9217-27	16.7	322
143	Denatured state aggregation parameters derived from concentration dependence of protein stability. *Analytical Biochemistry*, **2015**, 488, 45-50	3.1	22
142	The Binding Thermodynamics of Drug Candidates. *Methods and Principles in Medicinal Chemistry*, **2015**, 1-13	0.4	6
141	Single-Chain Soluble BG505.SOSIP gp140 Trimers as Structural and Antigenic Mimics of Mature Closed HIV-1 Env. *Journal of Virology*, **2015**, 89, 5318-29	6.6	86
140	Isothermal chemical denaturation to determine binding affinity of small molecules to G-protein coupled receptors. *Analytical Biochemistry*, **2015**, 473, 41-5	3.1	11
139	Characterization of protein-protein interactions by isothermal titration calorimetry. *Methods in Molecular Biology*, **2015**, 1278, 183-204	1.4	41
138	Structure-based design, synthesis and validation of CD4-mimetic small molecule inhibitors of HIV-1 entry: conversion of a viral entry agonist to an antagonist. *Accounts of Chemical Research*, **2014**, 47, 1228-37	24.3	67
137	CD4-mimetic small molecules sensitize human immunodeficiency virus to vaccine-elicited antibodies. *Journal of Virology*, **2014**, 88, 6542-55	6.6	40
136	Optimization of plasmepsin inhibitor by focusing on similar structural feature with chloroquine to avoid drug-resistant mechanism of Plasmodium falciparum. *Bioorganic and Medicinal Chemistry Letters*, **2014**, 24, 1698-701	2.9	4
135	Design, synthesis, and biological evaluation of novel dipeptide-type SARS-CoV 3CL protease inhibitors: structure-activity relationship study. *European Journal of Medicinal Chemistry*, **2013**, 65, 436-47	6.8	36
134	Development of potent dipeptide-type SARS-CoV 3CL protease inhibitors with novel P3 scaffolds: design, synthesis, biological evaluation, and docking studies. *European Journal of Medicinal Chemistry*, **2013**, 68, 372-84	6.8	42
133	Design and synthesis of new tripeptide-type SARS-CoV 3CL protease inhibitors containing an electrophilic arylketone moiety. *Bioorganic and Medicinal Chemistry*, **2013**, 21, 412-24	3.4	40
132	Chemical denaturation as a tool in the formulation optimization of biologics. *Drug Discovery Today*, **2013**, 18, 1007-13	8.8	41
131	Ligand binding analysis and screening by chemical denaturation shift. *Analytical Biochemistry*, **2013**, 443, 52-7	3.1	27
130	Optimization of CD4/gp120 inhibitors by thermodynamic-guided alanine-scanning mutagenesis. *Chemical Biology and Drug Design*, **2013**, 81, 72-8	2.9	19
129	Structure-Based Design and Synthesis of an HIV-1 Entry Inhibitor Exploiting X-Ray and Thermodynamic Characterization. *ACS Medicinal Chemistry Letters*, **2013**, 4, 338-343	4.3	50

128	Some Practical Rules for the Thermodynamic Optimization of Drug Candidates **2012**, 23-31		1
127	Structure-based design, synthesis, and characterization of dual hotspot small-molecule HIV-1 entry inhibitors. *Journal of Medicinal Chemistry*, **2012**, 55, 4382-96	8.3	78
126	Inhibiting early-stage events in HIV-1 replication by small-molecule targeting of the HIV-1 capsid. *Journal of Virology*, **2012**, 86, 8472-81	6.6	59
125	The Plasmepsin Family as Antimalarial Drug Targets. *Methods and Principles in Medicinal Chemistry*, **2011**, 511-547	0.4	
124	Conformational and structural features of HIV-1 gp120 underlying the dual receptor antagonism by cross-reactive neutralizing antibody m18. *Biochemistry*, **2011**, 50, 2756-68	3.2	5
123	ITC: More Than Just Binding Affinities **2011**, 303-312		
122	Some binding-related drug properties are dependent on thermodynamic signature. *Chemical Biology and Drug Design*, **2011**, 77, 161-5	2.9	30
121	Finding a better path to drug selectivity. *Drug Discovery Today*, **2011**, 16, 985-90	8.8	100
120	Synthesis and biochemical evaluation of triazole/tetrazole-containing sulfonamides against thrombin and related serine proteases. *Bioorganic and Medicinal Chemistry Letters*, **2011**, 21, 5305-9	2.9	19
119	Design, synthesis and biological evaluation of small molecule inhibitors of CD4-gp120 binding based on virtual screening. *Bioorganic and Medicinal Chemistry*, **2011**, 19, 91-101	3.4	65
118	Thermodynamics-based drug design: strategies for inhibiting protein-protein interactions. *Future Medicinal Chemistry*, **2011**, 3, 1129-37	4.1	44
117	How much binding affinity can be gained by filling a cavity?. *Chemical Biology and Drug Design*, **2010** , 75, 143-51	2.9	42
116	Adding calorimetric data to decision making in lead discovery: a hot tip. *Nature Reviews Drug Discovery*, **2010**, 9, 23-7	64.1	315
115	Naturally occurring variability in the envelope glycoprotein of HIV-1 and development of cell entry inhibitors. *Biochemistry*, **2010**, 49, 2359-67	3.2	16
114	Mutation of Asn28 disrupts the dimerization and enzymatic activity of SARS 3CL(pro). *Biochemistry*, **2010**, 49, 4308-17	3.2	33
113	Use of the quartz crystal microbalance to monitor ligand-induced conformational rearrangements in HIV-1 envelope protein gp120. *Analytical and Bioanalytical Chemistry*, **2010**, 396, 1143-52	4.4	23
112	The active core in a triazole peptide dual-site antagonist of HIV-1 gp120. *ChemMedChem*, **2010**, 5, 1871-9	3.7	31
111	A thermodynamic approach to the affinity optimization of drug candidates. *Chemical Biology and Drug Design*, **2009**, 74, 468-72	2.9	104

110	New developments for the design, synthesis and biological evaluation of potent SARS-CoV 3CL(pro) inhibitors. *Bioorganic and Medicinal Chemistry Letters*, **2009**, 19, 2722-7	2.9	41
109	Binding thermodynamics of the N-terminal peptide of the CCR5 coreceptor to HIV-1 envelope glycoprotein gp120. *Biochemistry*, **2009**, 48, 779-85	3.2	21
108	Isothermal titration calorimetry: general formalism using binding polynomials. *Methods in Enzymology*, **2009**, 455, 127-55	1.7	111
107	Do enthalpy and entropy distinguish first in class from best in class?. *Drug Discovery Today*, **2008**, 13, 869-74	8.8	388
106	Small-molecule CD4 mimics interact with a highly conserved pocket on HIV-1 gp120. *Structure*, **2008** , 16, 1689-701	5.2	143
105	The flavodoxin from Helicobacter pylori: structural determinants of thermostability and FMN cofactor binding. *Biochemistry*, **2008**, 47, 627-39	3.2	28
104	Antimalarial activity enhancement in hydroxymethylcarbonyl (HMC) isostere-based dipeptidomimetics targeting malarial aspartic protease plasmepsin. *Bioorganic and Medicinal Chemistry*, **2008**, 16, 10049-60	3.4	25
103	Structural determinants for affinity enhancement of a dual antagonist peptide entry inhibitor of human immunodeficiency virus type-1. *Journal of Medicinal Chemistry*, **2008**, 51, 2638-47	8.3	36
102	Inhibition of HIV-2 protease by HIV-1 protease inhibitors in clinical use. *Chemical Biology and Drug Design*, **2008**, 71, 298-305	2.9	79
101	Development of broad-spectrum halomethyl ketone inhibitors against coronavirus main protease 3CL(pro). *Chemical Biology and Drug Design*, **2008**, 72, 34-49	2.9	38
100	Characterization of intramolecular interactions of HIV-1 accessory protein Nef by differential scanning calorimetry. *Biophysical Chemistry*, **2007**, 126, 36-42	3.5	5
99	Compensating enthalpic and entropic changes hinder binding affinity optimization. *Chemical Biology and Drug Design*, **2007**, 69, 413-22	2.9	148
98	Strategies for targeting HIV-1 envelope glycoprotein gp120 in the development of new antivirals. *Future HIV Therapy*, **2007**, 1, 223-229		2
97	The native-state ensemble of proteins provides clues for folding, misfolding and function. *Trends in Biochemical Sciences*, **2006**, 31, 494-6	10.3	29
96	Overcoming HIV-1 resistance to protease inhibitors. *Drug Discovery Today Disease Mechanisms*, **2006**, 3, 281-286		15
95	Thermodynamics of binding of a low-molecular-weight CD4 mimetic to HIV-1 gp120. *Biochemistry*, **2006**, 45, 10973-80	3.2	134
94	Long-range cooperative interactions modulate dimerization in SARS 3CLpro. *Biochemistry*, **2006**, 45, 14908-16	3.2	58
93	Overcoming roadblocks in lead optimization: a thermodynamic perspective. *Chemical Biology and Drug Design*, **2006**, 67, 2-4	2.9	107

92	Isothermal titration calorimetry to determine association constants for high-affinity ligands. *Nature Protocols*, **2006**, 1, 186-91	18.8	223
91	Synthesis of glutamic acid and glutamine peptides possessing a trifluoromethyl ketone group as SARS-CoV 3CL protease inhibitors. *Tetrahedron*, **2006**, 62, 8601-8609	2.4	35
90	ITC in the post-genomic era...? Priceless. *Biophysical Chemistry*, **2005**, 115, 115-24	3.5	172
89	Binding thermodynamics of statins to HMG-CoA reductase. *Biochemistry*, **2005**, 44, 11741-8	3.2	82
88	Adaptive inhibitors of the HIV-1 protease. *Progress in Biophysics and Molecular Biology*, **2005**, 88, 193-208	4.7	106
87	Soluble mimetics of human immunodeficiency virus type 1 viral spikes produced by replacement of the native trimerization domain with a heterologous trimerization motif: characterization and ligand binding analysis. *Journal of Virology*, **2005**, 79, 9954-69	6.6	65
86	A Thermodynamic Guide to Affinity Optimization of Drug Candidates **2005**, 291-307		6
85	Interactions of HIV-1 proteins gp120 and Nef with cellular partners define a novel allosteric paradigm. *Current Protein and Peptide Science*, **2004**, 5, 1-8	2.8	32
84	Design of inhibitors against HIV, HTLV-I, and Plasmodium falciparum aspartic proteases. *Biological Chemistry*, **2004**, 385, 1035-9	4.5	25
83	Characterization of protein-protein interactions by isothermal titration calorimetry. *Methods in Molecular Biology*, **2004**, 261, 35-54	1.4	134
82	A structural and thermodynamic escape mechanism from a drug resistant mutation of the HIV-1 protease. *Proteins: Structure, Function and Bioinformatics*, **2004**, 55, 594-602	4.2	49
81	Search for substrate-based inhibitors fitting the S2Tspace of malarial aspartic protease plasmepsin II. *Journal of Peptide Science*, **2004**, 10, 641-7	2.1	36
80	Identification of novel inhibitors of the SARS coronavirus main protease 3CLpro. *Biochemistry*, **2004** , 43, 4906-12	3.2	180
79	Isothermal titration calorimetry. *Current Protocols in Cell Biology*, **2004**, Chapter 17, Unit 17.8	2.3	97
78	Thermodynamic rules for the design of high affinity HIV-1 protease inhibitors with adaptability to mutations and high selectivity towards unwanted targets. *International Journal of Biochemistry and Cell Biology*, **2004**, 36, 1787-99	5.6	63
77	Isothermal titration calorimetry: controlling binding forces in lead optimization. *Drug Discovery Today: Technologies*, **2004**, 1, 295-9	7.1	54
76	Multidrug resistance to HIV-1 protease inhibition requires cooperative coupling between distal mutations. *Biochemistry*, **2003**, 42, 13659-66	3.2	120
75	The binding of HIV-1 protease inhibitors to human serum proteins. *Biophysical Chemistry*, **2003**, 105, 221-30	3.3	54

74	A major role for a set of non-active site mutations in the development of HIV-1 protease drug resistance. *Biochemistry*, **2003**, 42, 631-8	3.2	120
73	High-affinity inhibition of a family of Plasmodium falciparum proteases by a designed adaptive inhibitor. *Biochemistry*, **2003**, 42, 8459-64	3.2	109
72	Structural and thermodynamic basis of resistance to HIV-1 protease inhibition: implications for inhibitor design. *Current Drug Targets Infectious Disorders*, **2003**, 3, 311-28		48
71	Protease inhibition in African subtypes of HIV-1. *AIDS Reviews*, **2003**, 5, 165-71	1.5	32
70	The integration of genomic and structural information in the development of high affinity plasmepsin inhibitors. *International Journal for Parasitology*, **2002**, 32, 1669-76	4.3	29
69	Structural parameterization of the binding enthalpy of small ligands. *Proteins: Structure, Function and Bioinformatics*, **2002**, 49, 181-90	4.2	110
68	HIV-1 evades antibody-mediated neutralization through conformational masking of receptor-binding sites. *Nature*, **2002**, 420, 678-82	50.4	731
67	Designing drugs against heterogeneous targets. *Nature Biotechnology*, **2002**, 20, 15-6	44.5	39
66	Identification and characterization of allophenylnorstatine-based inhibitors of plasmepsin II, an antimalarial target. *Biochemistry*, **2002**, 41, 2273-80	3.2	85
65	The linkage between protein folding and functional cooperativity: two sides of the same coin?. *Annual Review of Biophysics and Biomolecular Structure*, **2002**, 31, 235-56		145
64	Overcoming drug resistance in HIV-1 chemotherapy: the binding thermodynamics of Amprenavir and TMC-126 to wild-type and drug-resistant mutants of the HIV-1 protease. *Protein Science*, **2002**, 11, 1908-16	6.3	85
63	Amplification of the effects of drug resistance mutations by background polymorphisms in HIV-1 protease from African subtypes. *Biochemistry*, **2002**, 41, 8613-9	3.2	84
62	The application of thermodynamic methods in drug design. *Thermochimica Acta*, **2001**, 380, 217-227	2.9	42
61	Incorporating target heterogeneity in drug design. *Journal of Cellular Biochemistry*, **2001**, Suppl 37, 82-8	4.7	27
60	Direct measurement of protein binding energetics by isothermal titration calorimetry. *Current Opinion in Structural Biology*, **2001**, 11, 560-6	8.1	557
59	The thermodynamic linkage between protein structure, stability, and function. *Methods in Molecular Biology*, **2001**, 168, 37-68	1.4	24
58	The binding energetics of first- and second-generation HIV-1 protease inhibitors: implications for drug design. *Archives of Biochemistry and Biophysics*, **2001**, 390, 169-75	4.1	135
57	Thermodynamic studies of the core histones: stability of the octamer subunits is not altered by removal of their terminal domains. *Biochemistry*, **2001**, 40, 13114-23	3.2	23

56	Structural stability of binding sites: Consequences for binding affinity and allosteric effects. *Proteins: Structure, Function and Bioinformatics*, **2000**, 41, 63-71	4.2	135
55	Binding of small organic molecules to macromolecular targets: Evaluation of conformational entropy changes. *Proteins: Structure, Function and Bioinformatics*, **2000**, 41, 93-107	4.2	23
54	Thermodynamic dissection of the binding energetics of KNI-272, a potent HIV-1 protease inhibitor. *Protein Science*, **2000**, 9, 1801-9	6.3	85
53	Thermodynamic basis of resistance to HIV-1 protease inhibition: calorimetric analysis of the V82F/I84V active site resistant mutant. *Biochemistry*, **2000**, 39, 11876-83	3.2	111
52	HIV-1 protease inhibitors: enthalpic versus entropic optimization of the binding affinity. *Biochemistry*, **2000**, 39, 2201-7	3.2	131
51	Structural stability of binding sites: Consequences for binding affinity and allosteric effects. *Proteins: Structure, Function and Bioinformatics*, **2000**, 41, 63-71	4.2	17
50	Structural stability of binding sites: consequences for binding affinity and allosteric effects. *Proteins: Structure, Function and Bioinformatics*, **2000**, Suppl 4, 63-71	4.2	51
49	Binding of small organic molecules to macromolecular targets: evaluation of conformational entropy changes. *Proteins: Structure, Function and Bioinformatics*, **2000**, Suppl 4, 93-107	4.2	3
48	The propagation of binding interactions to remote sites in proteins: analysis of the binding of the monoclonal antibody D1.3 to lysozyme. *Proceedings of the National Academy of Sciences of the United States of America*, **1999**, 96, 10118-22	11.5	169
47	The effect of inhibitor binding on the structural stability and cooperativity of the HIV-1 protease. *Proteins: Structure, Function and Bioinformatics*, **1999**, 36, 147-56	4.2	51
46	The native state conformational ensemble of the SH3 domain from alpha-spectrin. *Biochemistry*, **1999**, 38, 8899-906	3.2	73
45	Structure-based thermodynamic design of peptide ligands: Application to peptide inhibitors of the aspartic protease endothiapepsin. *Proteins: Structure, Function and Bioinformatics*, **1998**, 30, 74-85	4.2	37
44	Molecular basis of resistance to HIV-1 protease inhibition: a plausible hypothesis. *Biochemistry*, **1998**, 37, 5791-7	3.2	77
43	The conformational equilibrium of human growth hormone. *Journal of Molecular Biology*, **1998**, 277, 409-18	6.5	25
42	The structural stability of the HIV-1 protease. *Journal of Molecular Biology*, **1998**, 283, 475-88	6.5	162
41	Statistical thermodynamic linkage between conformational and binding equilibria. *Advances in Protein Chemistry*, **1998**, 51, 255-79		53
40	Structure-based prediction of binding affinities and molecular design of peptide ligands. *Methods in Enzymology*, **1998**, 295, 100-27	1.7	86
39	Structure-based thermodynamic analysis of HIV-1 protease inhibitors. *Biochemistry*, **1997**, 36, 6588-96	3.2	73

38	The structural stability of the co-chaperonin GroES. *Journal of Molecular Biology*, **1997**, 272, 770-9	6.5	67
37	Structure-based statistical thermodynamic analysis of T4 lysozyme mutants: structural mapping of cooperative interactions. *Biophysical Chemistry*, **1997**, 64, 69-79	3.5	48
36	Predicting the equilibrium protein folding pathway: structure-based analysis of staphylococcal nuclease. *Proteins: Structure, Function and Bioinformatics*, **1997**, 27, 171-83	4.2	71
35	Structure-based thermodynamic scale of alpha-helix propensities in amino acids. *Biochemistry*, **1996** , 35, 13681-8	3.2	110
34	Thermodynamic studies of the core histones: pH and ionic strength effects on the stability of the (H3-H4)/(H3-H4)2 system. *Biochemistry*, **1996**, 35, 2037-46	3.2	52
33	Structure-based calculation of the equilibrium folding pathway of proteins. Correlation with hydrogen exchange protection factors. *Journal of Molecular Biology*, **1996**, 262, 756-72	6.5	220
32	Structural stability of small oligomeric proteins. *Techniques in Protein Chemistry*, **1996**, 459-467		6
31	The magnitude of the backbone conformational entropy change in protein folding. *Proteins: Structure, Function and Bioinformatics*, **1996**, 25, 143-56	4.2	98
30	The enthalpy change in protein folding and binding: refinement of parameters for structure-based calculations. *Proteins: Structure, Function and Bioinformatics*, **1996**, 26, 123-33	4.2	115
29	Docking enzyme-inhibitor complexes using a preference-based free-energy surface. *Proteins: Structure, Function and Bioinformatics*, **1996**, 25, 403-19	4.2	209
28	Configurational effects in antibody-antigen interactions studied by microcalorimetry. *Proteins: Structure, Function and Bioinformatics*, **1995**, 21, 83-90	4.2	69
27	The heat capacity of proteins. *Proteins: Structure, Function and Bioinformatics*, **1995**, 22, 404-12	4.2	371
26	A calorimetric characterization of the salt dependence of the stability of the GCN4 leucine zipper. *Protein Science*, **1995**, 4, 1934-8	6.3	51
25	Differential scanning calorimetry. *Methods in Molecular Biology*, **1995**, 40, 191-218	1.4	89
24	Thermal denaturation methods in the study of protein folding. *Methods in Enzymology*, **1995**, 259, 144-68	1.7	77
23	Thermodynamic mapping of the inhibitor site of the aspartic protease endothiapepsin. *Journal of Molecular Biology*, **1995**, 252, 337-50	6.5	226
22	GroES and the chaperonin-assisted protein folding cycle: GroES has no affinity for nucleotides. *FEBS Letters*, **1995**, 359, 123-5	3.8	15
21	Precise scanning calorimeter for studying thermal properties of biological macromolecules in dilute solution. *Analytical Biochemistry*, **1995**, 232, 79-85	3.1	181

20	Entropy in biological binding processes: estimation of translational entropy loss. *Proteins: Structure, Function and Bioinformatics*, **1994**, 18, 63-7	4.2	162
19	Molecular basis of cooperativity in protein folding. V. Thermodynamic and structural conditions for the stabilization of compact denatured states. *Proteins: Structure, Function and Bioinformatics*, **1994** , 19, 291-301	4.2	116
18	Estimation of changes in side chain configurational entropy in binding and folding: general methods and application to helix formation. *Proteins: Structure, Function and Bioinformatics*, **1994**, 20, 68-84	4.2	204
17	Thermodynamic strategies for stabilizing intermediate states of proteins. *Biopolymers*, **1994**, 34, 261-72	2.2	5
16	Thermodynamic characterization of an equilibrium folding intermediate of staphylococcal nuclease. *Protein Science*, **1994**, 3, 2175-84	6.3	39
15	Thermodynamic characterization of the structural stability of the coiled-coil region of the bZIP transcription factor GCN4. *Biochemistry*, **1993**, 32, 5491-6	3.2	186
14	Structural energetics of peptide recognition: angiotensin II/antibody binding. *Proteins: Structure, Function and Bioinformatics*, **1993**, 15, 113-20	4.2	161
13	Structural energetics of the molten globule state. *Proteins: Structure, Function and Bioinformatics*, **1993**, 16, 115-40	4.2	134
12	Molecular basis of cooperativity in protein folding. IV. CORE: a general cooperative folding model. *Proteins: Structure, Function and Bioinformatics*, **1993**, 17, 111-23	4.2	26
11	Thermodynamics of structural stability and cooperative folding behavior in proteins. *Advances in Protein Chemistry*, **1992**, 43, 313-61		474
10	Temperature and guanidine hydrochloride dependence of the structural stability of ribonuclease T1. *Biochemistry*, **1992**, 31, 11196-202	3.2	33
9	Molecular basis of co-operativity in protein folding. III. Structural identification of cooperative folding units and folding intermediates. *Journal of Molecular Biology*, **1992**, 227, 293-306	6.5	172
8	Thermodynamic Strategies for Protein Design. *ACS Symposium Series*, **1992**, 122-135	0.4	3
7	Two-dimensional differential scanning calorimetry: simultaneous resolution of intrinsic protein structural energetics and ligand binding interactions by global linkage analysis. *Analytical Biochemistry*, **1992**, 203, 259-68	3.1	101
6	Direct calorimetric analysis of the enzymatic activity of yeast cytochrome c oxidase. *Biochemistry*, **1991**, 30, 8494-500	3.2	101
5	Isothermal titration calorimetry. *Analytical Chemistry*, **1990**, 62, 950A-959A	7.8	428
4	Statistical mechanical deconvolution of thermal transitions in macromolecules. I. Theory and application to homogeneous systems. *Biopolymers*, **1978**, 17, 463-479	2.2	364
3	Statistical mechanical deconvolution of thermal transitions in macromolecules. II. General treatment of cooperative phenomena. *Biopolymers*, **1978**, 17, 481-496	2.2	59

2	Statistical mechanical deconvolution of thermal transitions in macromolecules. III. Application to double-stranded to single-stranded transitions of nucleic acids. *Biopolymers*, **1978**, 17, 497-510	2.2	31
1	Thermodynamics of transfer ribonucleic acids: the effect of sodium on the thermal unfolding of yeast tRNAPhe. *Biopolymers*, **1978**, 17, 1257-72	2.2	30