Allen P Minton

List of Publications by Year
in descending order

137 papers	14,306 citations	51 h-index (41627)	117 g-index (22488)
141 all docs	141 docs citations	141 times ranked	9412 citing authors

#	Article	IF	Citations
1	Influence of Nonspecific Interactions on Protein Associations: Implications for Biochemistry In Vivo. Annual Review of Biochemistry, 2022, 91, 321-351.	5.0	25
2	Water Loss in Aging Erythrocytes Provides a Clue to a General Mechanism of Cellular Senescence. Biophysical Journal, 2020, 119, 2039-2044.	0.2	14
3	Implications of excluded volume for chemical inhibition of protein fibrillation. Biochimica Et Biophysica Acta - General Subjects, 2020, 1864, 129704.	1.1	0
4	Simple Calculation of Phase Diagrams for Liquidâ€“Liquid Phase Separation in Solutions of Two Macromolecular Solute Species. Journal of Physical Chemistry B, 2020, 124, 2363-2370.	1.2	21
5	Comparison of composition-gradient sedimentation equilibrium and composition-gradient static light scattering as techniques for quantitative characterization of biomolecular interactions: A case study. Analytical Biochemistry, 2019, 583, 113339.	1.1	0
6	The Cumulative Effect of Surface Adsorption and Excluded Volume in 2D and 3D on Protein Fibrillation. Biophysical Journal, 2019, 117, 1666-1673.	0.2	7
7	Quantitative characterization of the concentrationâ€dependent interaction between molecules of Dextran 70 in aqueous solution: Measurement and analysis in the context of thermodynamic and compressible sphere models. Biopolymers, 2019, 110, e23284.	1.2	2
8	Non-specific Interactions Between Macromolecular Solutes in Concentrated Solution: Physico-Chemical Manifestations and Biochemical Consequences. Frontiers in Molecular Biosciences, 2019, 6, 10.	1.6	7
9	Editorial: Biochemical Reactions in Cytomimetic Media. Frontiers in Molecular Biosciences, 2019, 6, 145.	1.6	4
10	Comparison of the thermal stabilization of proteins by oligosaccharides and monosaccharide mixtures: Measurement and analysis in the context of excluded volume theory. Biophysical Chemistry, 2018, 237, 31-37.	1.5	23
11	Toward an understanding of biochemical equilibria within living cells. Biophysical Reviews, 2018, 10, 241-253.	1.5	81
12	Explicit Incorporation of Hard and Soft Proteinâ€“Protein Interactions into Models for Crowding Effects in Protein Mixtures. 2. Effects of Varying Hard and Soft Interactions upon Prototypical Chemical Equilibria. Journal of Physical Chemistry B, 2017, 121, 5515-5522.	1.2	20
13	The pH Dependence of Saccharides' Influence on Thermal Denaturation of Two Model Proteins Supports an Excluded Volume Model for Stabilization Generalized to Allow for Intramolecular Electrostatic Interactions. Journal of Biological Chemistry, 2017, 292, 505-511.	1.6	33
14	Nucleotide and receptor density modulate binding of bacterial division FtsZ protein to ZipA containing lipid-coated microbeads. Scientific Reports, 2017, 7, 13707.	1.6	11
15	Big ideas from â€œsmall scienceâ€. Biophysical Reviews, 2016, 8, 285-286.	1.5	3
16	Modulation of Conformational Equilibria in the <i>S</i>-Adenosylmethionine (SAM) II Riboswitch by SAM, Mg²⁺, and Trimethylamine <i>N</i>-Oxide. Biochemistry, 2016, 55, 5010-5020.	1.2	10
17	Macromolecular Crowding In Vitro , In Vivo , and In Between. Trends in Biochemical Sciences, 2016, 41, 970-981.	3.7	359
18	Incorporation of Hard and Soft Proteinâ€“Protein Interactions into Models for Crowding Effects in Binary and Ternary Protein Mixtures. Comparison of Approximate Analytical Solutions with Numerical Simulation. Journal of Physical Chemistry B, 2016, 120, 11866-11872.	1.2	23

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19	Recent applications of light scattering measurement in the biological and biopharmaceutical sciences. Analytical Biochemistry, 2016, 501, 4-22.	1.1	95
20	Detection and Quantitative Characterization of Macromolecular Heteroassociations via Composition Gradient Sedimentation Equilibrium. , 2016, , 523-532.		1
21	Thermal Stabilization of Proteins by Mono- and Oligosaccharides: Measurement and Analysis in the Context of an Excluded Volume Model. Biochemistry, 2015, 54, 3594-3603.	1.2	35
22	An Equilibrium Model for the Combined Effect of Macromolecular Crowding and Surface Adsorption on the Formation of Linear Protein Fibrils. Biophysical Journal, 2015, 108, 957-966.	0.2	21
23	Quantitative Characterization of Nonspecific Self- and Hetero-Interactions of Proteins in Nonideal Solutions via Static Light Scattering. Journal of Physical Chemistry B, 2015, 119, 1891-1898.	1.2	17
24	The effect of time-dependent macromolecular crowding on the kinetics of protein aggregation: a simple model for the onset of age-related neurodegenerative disease. Frontiers in Physics, 2014, 2, .	1.0	14
25	Concentration-Dependent Viscosity of Binary and Ternary Mixtures of Nonassociating Proteins: Measurement and Analysis. Journal of Physical Chemistry B, 2013, 117, 13861-13865.	1.2	4
26	Quantitative assessment of the relative contributions of steric repulsion and chemical interactions to macromolecular crowding. Biopolymers, 2013, 99, 239-244.	1.2	115
27	Quantitative Characterization of the Interaction between Sucrose and Native Proteins via Static Light Scattering. Biophysical Journal, 2013, 104, 565a-566a.	0.2	1
28	Quantitative Characterization of the Interaction Between Sucrose and Native Proteins via Static Light Scattering. Journal of Physical Chemistry B, 2013, 117, 111-117.	1.2	16
29	Quantitative Characterization of the Compensating Effects of Trimethylamine-N-oxide and Guanidine Hydrochloride on the Dissociation of Human Cyanmethmoglobin. Journal of Physical Chemistry B, 2013, 117, 9395-9399.	1.2	8
30	Compensating Effects of Urea and Trimethylamine-N-Oxide on the Heteroassociation of Î±-Chymotrypsin and Soybean Trypsin Inhibitor. Journal of Physical Chemistry B, 2013, 117, 3554-3559.	1.2	7
31	Dynamic Interaction of the Escherichia coli Cell Division ZipA and FtsZ Proteins Evidenced in Nanodiscs. Journal of Biological Chemistry, 2012, 287, 30097-30104.	1.6	45
32	Hard Quasispherical Particle Models for the Viscosity of Solutions of Protein Mixtures. Journal of Physical Chemistry B, 2012, 116, 9310-9315.	1.2	21
33	An Equilibrium Model for the Mg²⁺-Linked Self-Assembly of FtsZ in the Presence of GTP or a GTP Analogue. Biochemistry, 2012, 51, 6108-6113.	1.2	11
34	Capillary Viscometer for Fully Automated Measurement of the Concentration and Shear Dependence of the Viscosity of Macromolecular Solutions. Analytical Chemistry, 2012, 84, 10732-10736.	3.2	19
35	Mg²⁺-Linked Self-Assembly of FtsZ in the Presence of GTP or a GTP Analogue Involves the Concerted Formation of a Narrow Size Distribution of Oligomeric Species. Biochemistry, 2012, 51, 4541-4550.	1.2	21
36	Quantitative Characterization of Temperature-Independent and Temperature-Dependent Proteinâ€“Protein Interactions in Highly Nonideal Solutions. Journal of Physical Chemistry B, 2011, 115, 11261-11268.	1.2	16

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37	Effect of Nonadditive Repulsive Intermolecular Interactions on the Light Scattering of Concentrated Proteinâ^'Osmolyte Mixtures. Journal of Physical Chemistry B, 2011, 115, 1289-1293.	1.2	17
38	Modulation of Functionally Significant Conformational Equilibria in Adenylate Kinase by High Concentrations of Trimethylamine Oxide Attributed to Volume Exclusion. Biophysical Journal, 2011, 100, 2991-2999.	0.2	27
39	Beyond the second virial coefficient: Sedimentation equilibrium in highly non-ideal solutions. Methods, 2011, 54, 167-174.	1.9	22
40	Biochemical Reactions in the Crowded and Confined Physiological Environment: Physical Chemistry Meets Synthetic Biology. , 2011, , 73-89.		3
41	Characterization of Self-Association and Heteroassociation of Bacterial Cell Division Proteins FtsZ and ZipA in Solution by Composition Gradientâ^'Static Light Scattering. Biochemistry, 2010, 49, 10780-10787.	1.2	38
42	Analysis of membrane binding equilibria of peripheral proteins: Allowance for excluded area of bound protein. Analytical Biochemistry, 2010, 397, 247-249.	1.1	6
43	Self-association of Zn-insulin at neutral pH: Investigation by concentration gradient-static and dynamic light scattering. Biophysical Chemistry, 2010, 148, 23-27.	1.5	30
44	pH-dependent self-association of zinc-free insulin characterized by concentration-gradient static light scattering. Biophysical Chemistry, 2010, 148, 28-33.	1.5	55
45	A Didactic Model of Macromolecular Crowding Effects on Protein Folding. PLoS ONE, 2010, 5, e11936.	1.1	19
46	Quantitative Characterization of Heparin Binding to Tau Protein. Journal of Biological Chemistry, 2010, 285, 3592-3599.	1.6	96
47	Attractive Protein-Polymer Interactions Markedly Alter the Effect of Macromolecular Crowding on Protein Association Equilibria. Biophysical Journal, 2010, 99, 914-923.	0.2	127
48	Quantitative Characterization of Polymerâ^'Polymer, Proteinâ^'Protein, and Polymerâ^'Protein Interaction via Tracer Sedimentation Equilibrium. Journal of Physical Chemistry B, 2010, 114, 10876-10880.	1.2	35
49	Intermolecular Interactions of IgG1 Monoclonal Antibodies at High Concentrations Characterized by Light Scattering. Journal of Physical Chemistry B, 2010, 114, 12948-12957.	1.2	122
50	Analytical Ultracentrifugation Studies of Phage Ï•29 Protein p6 Binding to DNA. Journal of Molecular Biology, 2009, 385, 1616-1629.	2.0	11
51	Static Light Scattering From Concentrated Protein Solutions II: Experimental Test of Theory for Protein Mixtures and Weakly Self-Associating Proteins. Biophysical Journal, 2009, 96, 1992-1998.	0.2	69
52	Automated measurement of the static light scattering of macromolecular solutions over a broad range of concentrations. Analytical Biochemistry, 2008, 381, 254-257.	1.1	31
53	Macromolecular Crowding and Confinement: Biochemical, Biophysical, and Potential Physiological Consequences. Annual Review of Biophysics, 2008, 37, 375-397.	4.5	1,826
54	Effective Hard Particle Model for the Osmotic Pressure of Highly Concentrated Binary Protein Solutions. Biophysical Journal, 2008, 94, L57-L59.	0.2	35

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55	Effect of High Concentration of Inert Cosolutes on the Refolding of an Enzyme. Journal of Biological Chemistry, 2007, 282, 33452-33458.	1.6	18
56	Static Light Scattering from Concentrated Protein Solutions, I: General Theory for Protein Mixtures and Application to Self-Associating Proteins. Biophysical Journal, 2007, 93, 1321-1328.	0.2	78
57	Quantitative Characterization of Weak Self-Association in Concentrated Solutions of Immunoglobulin G via the Measurement of Sedimentation Equilibrium and Osmotic Pressure. Biochemistry, 2007, 46, 8373-8378.	1.2	49
58	The effective hard particle model provides a simple, robust, and broadly applicable description of nonideal behavior in concentrated solutions of bovine serum albumin and other nonassociating proteins. Journal of Pharmaceutical Sciences, 2007, 96, 3466-3469.	1.6	55
59	Rapid Quantitative Characterization of Protein Interactions by Composition Gradient Static Light Scattering. Biophysical Journal, 2006, 90, 2164-2169.	0.2	44
60	A Simple Semiempirical Model for the Effect of Molecular Confinement upon the Rate of Protein Folding. Biochemistry, 2006, 45, 13356-13360.	1.2	48
61	Macromolecular Crowding Stabilizes the Molten Globule Form of Apomyoglobin with Respect to Both Cold and Heat Unfolding. Journal of Molecular Biology, 2006, 361, 7-10.	2.0	48
62	Analytical ultracentrifugation for the study of protein association and assembly. Current Opinion in Chemical Biology, 2006, 10, 430-436.	2.8	165
63	Macromolecular crowding. Current Biology, 2006, 16, R269-R271.	1.8	103
64	How can biochemical reactions within cells differ from those in test tubes?. Journal of Cell Science, 2006, 119, 2863-2869.	1.2	391
65	Protein aggregation in crowded environments. Biological Chemistry, 2006, 387, 485-97.	1.2	338
66	Turbidity as a probe of tubulin polymerization kinetics: A theoretical and experimental re-examination. Analytical Biochemistry, 2005, 345, 198-213.	1.1	39
67	Composition gradient static light scattering: A new technique for rapid detection and quantitative characterization of reversible macromolecular hetero-associations in solution. Analytical Biochemistry, 2005, 346, 132-138.	1.1	64
68	Prion domains: sequences, structures and interactions. Nature Cell Biology, 2005, 7, 1039-1044.	4.6	120
69	Influence of macromolecular crowding upon the stability and state of association of proteins: Predictions and observations. Journal of Pharmaceutical Sciences, 2005, 94, 1668-1675.	1.6	251
70	New methods for measuring macromolecular interactions in solution via static light scattering: basic methodology and application to nonassociating and self-associating proteins. Analytical Biochemistry, 2005, 337, 103-110.	1.1	82
71	Cooperative behavior of Escherichia coli cell-division protein FtsZ assembly involves the preferential cyclization of long single-stranded fibrils. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1895-1900.	3.3	90
72	Models for Excluded Volume Interaction between an Unfolded Protein and Rigid Macromolecular Cosolutes: Macromolecular Crowding and Protein Stability Revisited. Biophysical Journal, 2005, 88, 971-985.	0.2	312

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73	Non-ideal tracer sedimentation equilibrium: a powerful tool for the characterization of macromolecular interactions in crowded solutions. Journal of Molecular Recognition, 2004, 17, 362-367.	1.1	22
74	Effects of inert volume-excluding macromolecules on protein fiber formation. II. Kinetic models for nucleated fiber growth. Biophysical Chemistry, 2004, 107, 299-316.	1.5	34
75	Sedimentation equilibrium in a solution containing an arbitrary number of solute species at arbitrary concentrations: theory and application to concentrated solutions of ribonuclease. Biophysical Chemistry, 2004, 108, 89-100.	1.5	45
76	Effect of large refractive index gradients on the performance of absorption optics in the Beckman XL-A/I analytical ultracentrifuge: an experimental study. Analytical Biochemistry, 2003, 313, 133-136.	1.1	13
77	Macromolecular crowding: qualitative and semiquantitative successes, quantitative challenges. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2003, 1649, 127-139.	1.1	431
78	Effect of Dextran on Protein Stability and Conformation Attributed to Macromolecular Crowding. Journal of Molecular Biology, 2003, 326, 1227-1237.	2.0	296
79	Macromolecular Crowding Accelerates Amyloid Formation by Human Apolipoprotein C-II. Journal of Biological Chemistry, 2002, 277, 7824-7830.	1.6	243
80	Effects of inert volume-excluding macromolecules on protein fiber formation. I. Equilibrium models. Biophysical Chemistry, 2002, 98, 93-104.	1.5	41
81	Effects of Excluded Surface Area and Adsorbate Clustering on Surface Adsorption of Proteins. II. Kinetic Models. Biophysical Journal, 2001, 80, 1641-1648.	0.2	101
82	The Influence of Macromolecular Crowding and Macromolecular Confinement on Biochemical Reactions in Physiological Media. Journal of Biological Chemistry, 2001, 276, 10577-10580.	1.6	1,263
83	Physicochemical characterization of generation 5 polyamidoamine dendrimers. Biopolymers, 2000, 53, 316-328.	1.2	45
84	Effects of excluded surface area and adsorbate clustering on surface adsorption of proteins. Biophysical Chemistry, 2000, 86, 239-247.	1.5	61
85	Implications of macromolecular crowding for protein assembly. Current Opinion in Structural Biology, 2000, 10, 34-39.	2.6	605
86	Protein folding: Thickening the broth. Current Biology, 2000, 10, R97-R99.	1.8	58
87	Magnesium-induced Linear Self-association of the FtsZ Bacterial Cell Division Protein Monomer. Journal of Biological Chemistry, 2000, 275, 11740-11749.	1.6	173
88	Quantitative characterization of reversible macromolecular associations via sedimentation equilibrium: an introduction. Experimental and Molecular Medicine, 2000, 32, 1-5.	3.2	15
89	Effect of a Concentrated â€œInertâ€•Macromolecular Cosolute on the Stability of a Globular Protein with Respect to Denaturation by Heat and by Chaotropes: A Statistical-Thermodynamic Model. Biophysical Journal, 2000, 78, 101-109.	0.2	207
90	Direct Observation of the Self-Association of Dilute Proteins in the Presence of Inert Macromolecules at High Concentration via Tracer Sedimentation Equilibrium:Â Theory, Experiment, and Biological Significance. Biochemistry, 1999, 38, 9379-9388.	1.2	160

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91	Adsorption of Globular Proteins on Locally Planar Surfaces. II. Models for the Effect of Multiple Adsorbate Conformations on Adsorption Equilibria and Kinetics. Biophysical Journal, 1999, 76, 176-187.	0.2	98
92	Characterization of Heterologous Proteinâ€"Protein Interactions Using Analytical Ultracentrifugation. Methods, 1999, 19, 194-212.	1.9	81
93	[7] Molecular crowding: Analysis of effects of high concentrations of inert cosolutes on biochemical equilibria and rates in terms of volume exclusion. Methods in Enzymology, 1998, 295, 127-149.	0.4	291
94	Influence of excluded volume upon macromolecular structure and associations in â€˜crowdedâ€•media. Current Opinion in Biotechnology, 1997, 8, 65-69.	3.3	188
95	The Effect of Self-association on the Interaction of theEscherichia coliRegulatory Protein TyrR with DNA. Journal of Molecular Biology, 1996, 263, 671-684.	2.0	44
96	Binding of fibrinogen to platelet integrin Î±IIbÎ²3 in solution as monitored by tracer sedimentation equilibrium. , 1996, 9, 31-38.		11
97	Analysis of Mass Transport-Limited Binding Kinetics in Evanescent Wave Biosensors. Analytical Biochemistry, 1996, 240, 262-272.	1.1	217
98	Structure within eukaryotic cytoplasm and its relationship to glycolytic metabolism. Cell Biochemistry and Function, 1996, 14, 237-248.	1.4	39
99	Structure Within Eukaryotic Cytoplasm and its Relationship to Glycolytic Metabolism. Cell Biochemistry and Function, 1996, 14, 237-248.	1.4	0
100	A molecular model for the dependence of the osmotic pressure of bovine serum albumin upon concentration and pH. Biophysical Chemistry, 1995, 57, 65-70.	1.5	56
101	Ca2+-Linked Association of Human Complement C1s.hivin. and C1r.hivin.. Biochemistry, 1994, 33, 2341-2348.	1.2	23
102	Macromolecular crowding and molecular recognition. Journal of Molecular Recognition, 1993, 6, 211-214.	1.1	47
103	New developments in the study of biomolecular associations via sedimentation equilibrium. Trends in Biochemical Sciences, 1993, 18, 284-287.	3.7	19
104	Calcium ion induced self-association of human complement C1.lovin.s. Biochemistry, 1992, 31, 11707-11712.	1.2	26
105	A strategy for efficient characterization of macromolecular heteroassociations via measurement of sedimentation equilibrium. Journal of Molecular Recognition, 1991, 4, 93-104.	1.1	20
106	Holobiochemistry: The effect of local environment upon the equilibria and rates of biochemical reactions. International Journal of Biochemistry & Cell Biology, 1990, 22, 1063-1067.	0.8	57
107	Quantitative characterization of reversible molecular associations via analytical centrifugation. Analytical Biochemistry, 1990, 190, 1-6.	1.1	36
108	Hidden self-association of proteins. Journal of Molecular Recognition, 1989, 1, 166-171.	1.1	44

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109	Analytical centrifugation with preparative ultracentrifuges. Analytical Biochemistry, 1989, 176, 209-216.	1.1	37
110	An automated method for rapid determination of diffusion coefficients via measurements of boundary spreading. Analytical Biochemistry, 1988, 168, 345-351.	1.1	37
111	Simultaneous determination of the individual concentration gradients of two solute species in a centrifuged mixture: Application to analytical ultracentrifugation. Analytical Biochemistry, 1987, 162, 409-419.	1.1	16
112	Sedimentation equilibrium in macromolecular solutions of arbitrary concentration. I. Self-associating proteins. Biopolymers, 1987, 26, 507-524.	1.2	61
113	Sedimentation equilibrium in macromolecular solutions of arbitrary concentration. II. Two protein components. Biopolymers, 1987, 26, 1097-1113.	1.2	27
114	Technique and apparatus for automated fractionation of the contents of small centrifuge tubes: Application to analytical ultracentrifugation. Analytical Biochemistry, 1986, 152, 319-328.	1.1	26
115	Acceleration of fibrin gel formation by unrelated proteins. Thrombosis Research, 1985, 37, 681-688.	0.8	44
116	An automated method for determination of the sedimentation coefficient of macromolecules using a preparative centrifuge. Analytical Biochemistry, 1984, 136, 407-415.	1.1	16
117	The effect of volume occupancy upon the thermodynamic activity of proteins: some biochemical consequences. Molecular and Cellular Biochemistry, 1983, 55, 119-140.	1.4	496
118	An automated method for determination of the molecular weight of macromolecules via sedimentation equilibrium in a preparative ultracentrifuge. Analytical Biochemistry, 1983, 133, 142-152.	1.1	32
119	Thermodynamic nonideality and the dependence of partition coefficient upon solute concentration in exclusion chromatography II. An improved theory of e. Biophysical Chemistry, 1983, 18, 139-143.	1.5	15
120	Light scattering of bovine serum albumin solutions: Extension of the hard particle model to allow for electrostatic repulsion. Biopolymers, 1982, 21, 451-458.	1.2	84
121	Excluded volume as a determinant of macromolecular structure and reactivity. Biopolymers, 1981, 20, 2093-2120.	1.2	557
122	Self-association in highly concentrated solutions of myoglobin: a novel analysis of sedimentation equilibrium of highly nonideal solutions. Biophysical Chemistry, 1981, 14, 317-324.	1.5	39
123	Evidence for protein self-association induced by excluded volume Myoglobin in the presence of globular proteins. Biochimica Et Biophysica Acta (BBA) - Protein Structure, 1981, 670, 316-322.	1.7	76
124	Excluded volume as a determinant of protein structure and stability. Biophysical Journal, 1980, 32, 77-79.	0.2	37
125	The effect of non-aggregating proteins upon the gelation of sickle cell hemoglobin: Model calculations and data analysis. Biochemical and Biophysical Research Communications, 1979, 88, 1308-1314.	1.0	44
126	Temperature dependence of nonideality in concentrated solutions of hemoglobin. Biopolymers, 1978, 17, 2285-2288.	1.2	76

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127	Concentration dependence of the diffusion coefficient of hemoglobin. The Journal of Physical Chemistry, 1978, 82, 1934-1938.	2.9	34
128	Hard quasispherical model for the viscosity of hemoglobin solutions. Biochemical and Biophysical Research Communications, 1977, 76, 971-976.	1.0	138
129	Non-ideality and the thermodynamics of sickle-cell hemoglobin gelation. Journal of Molecular Biology, 1977, 110, 89-103.	2.0	89
130	Analysis of non-ideal behavior in concentrated hemoglobin solutions. Journal of Molecular Biology, 1977, 112, 437-452.	2.0	270
131	Relations between oxygen saturation and aggregation of sickle-cell hemoglobin. Journal of Molecular Biology, 1976, 100, 519-542.	2.0	33
132	Thermodynamic analysis of the chemical inhibition of Sickle-Cell hemoglobin gelation. Journal of Molecular Biology, 1975, 95, 289-307.	2.0	32
133	Solubility relationships in binary mixtures of hemoglobin variants. Biophysical Chemistry, 1974, 1, 387-395.	1.5	16
134	A thermodynamic model for gelation of sickle-cell hemoglobin. Journal of Molecular Biology, 1974, 82, 483-498.	2.0	80
135	Models for the gelling behavior of binary mixtures of hemoglobin variants. Journal of Molecular Biology, 1973, 75, 559-574.	2.0	19
136	Structural Model for the Dielectric Relaxation of Liquid Water. Nature: Physical Science, 1971, 234, 165-168.	0.8	3
137	Comments on Extensions of the Allosteric Model for Haemoglobin. Nature: New Biology, 1971, 232, 145-147.	4.5	8