Allen P Minton

List of Publications by Citations

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133	12,401	50	110
papers	citations	h-index	g-index
141	13,326	4.2	7.05
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
133	Macromolecular crowding and confinement: biochemical, biophysical, and potential physiological consequences. *Annual Review of Biophysics*, **2008**, 37, 375-97	21.1	1553
132	The influence of macromolecular crowding and macromolecular confinement on biochemical reactions in physiological media. *Journal of Biological Chemistry*, **2001**, 276, 10577-80	5.4	1089
131	Implications of macromolecular crowding for protein assembly. *Current Opinion in Structural Biology* , **2000**, 10, 34-9	8.1	543
130	Excluded volume as a determinant of macromolecular structure and reactivity. *Biopolymers*, **1981**, 20, 2093-2120	2.2	490
129	The effect of volume occupancy upon the thermodynamic activity of proteins: some biochemical consequences. *Molecular and Cellular Biochemistry*, **1983**, 55, 119-40	4.2	449
128	Macromolecular crowding: qualitative and semiquantitative successes, quantitative challenges. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2003**, 1649, 127-39	4	384
127	How can biochemical reactions within cells differ from those in test tubes?. *Journal of Cell Science*, **2006**, 119, 2863-9	5.3	342
126	Protein aggregation in crowded environments. *Biological Chemistry*, **2006**, 387, 485-97	4.5	281
125	Models for excluded volume interaction between an unfolded protein and rigid macromolecular cosolutes: macromolecular crowding and protein stability revisited. *Biophysical Journal*, **2005**, 88, 971-85	2.9	274
124	Effect of dextran on protein stability and conformation attributed to macromolecular crowding. *Journal of Molecular Biology*, **2003**, 326, 1227-37	6.5	256
123	Analysis of non-ideal behavior in concentrated hemoglobin solutions. *Journal of Molecular Biology*, **1977**, 112, 437-52	6.5	255
122	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, 127-49	1.7	250
121	Macromolecular Crowding In Vitro, In Vivo, and In Between. *Trends in Biochemical Sciences*, **2016**, 41, 970-981	10.3	241
120	Influence of macromolecular crowding upon the stability and state of association of proteins: predictions and observations. *Journal of Pharmaceutical Sciences*, **2005**, 94, 1668-75	3.9	214
119	Macromolecular crowding accelerates amyloid formation by human apolipoprotein C-II. *Journal of Biological Chemistry*, **2002**, 277, 7824-30	5.4	212
118	Analysis of mass transport-limited binding kinetics in evanescent wave biosensors. *Analytical Biochemistry*, **1996**, 240, 262-72	3.1	204
117	Effect of a concentrated "inert" 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, 101-9	2.9	189

116	Influence of excluded volume upon macromolecular structure and associations in RcrowdedRmedia. *Current Opinion in Biotechnology*, **1997**, 8, 65-9	11.4	175
115	Analytical ultracentrifugation for the study of protein association and assembly. *Current Opinion in Chemical Biology*, **2006**, 10, 430-6	9.7	153
114	Magnesium-induced linear self-association of the FtsZ bacterial cell division protein monomer. The primary steps for FtsZ assembly. *Journal of Biological Chemistry*, **2000**, 275, 11740-9	5.4	150
113	Direct observation of the self-association of dilute proteins in the presence of inert macromolecules at high concentration via tracer sedimentation equilibrium: theory, experiment, and biological significance. *Biochemistry*, **1999**, 38, 9379-88	3.2	146
112	Hard quasispherical model for the viscosity of hemoglobin solutions. *Biochemical and Biophysical Research Communications*, **1977**, 76, 971-6	3.4	116
111	Attractive protein-polymer interactions markedly alter the effect of macromolecular crowding on protein association equilibria. *Biophysical Journal*, **2010**, 99, 914-23	2.9	111
110	Prion domains: sequences, structures and interactions. *Nature Cell Biology*, **2005**, 7, 1039-44	23.4	110
109	Intermolecular interactions of IgG1 monoclonal antibodies at high concentrations characterized by light scattering. *Journal of Physical Chemistry B*, **2010**, 114, 12948-57	3.4	104
108	Quantitative assessment of the relative contributions of steric repulsion and chemical interactions to macromolecular crowding. *Biopolymers*, **2013**, 99, 239-44	2.2	103
107	Macromolecular crowding. *Current Biology*, **2006**, 16, R269-71	6.3	92
106	Effects of excluded surface area and adsorbate clustering on surface adsorption of proteins. II. Kinetic models. *Biophysical Journal*, **2001**, 80, 1641-8	2.9	89
105	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, 176-87	2.9	89
104	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, 1895-900	11.5	84
103	Non-ideality and the thermodynamics of sickle-cell hemoglobin gelation. *Journal of Molecular Biology*, **1977**, 110, 89-103	6.5	76
102	Characterization of heterologous protein-protein interactions using analytical ultracentrifugation. *Methods*, **1999**, 19, 194-212	4.6	75
101	Light scattering of bovine serum albumin solutions: Extension of the hard particle model to allow for electrostatic repulsion. *Biopolymers*, **1982**, 21, 451-458	2.2	75
100	A thermodynamic model for gelation of sickle-cell hemoglobin. *Journal of Molecular Biology*, **1974**, 82, 483-98	6.5	75
99	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, 103-10	3.1	74

98	Quantitative characterization of heparin binding to Tau protein: implication for inducer-mediated Tau filament formation. *Journal of Biological Chemistry*, **2010**, 285, 3592-3599	5.4	72
97	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, 316-22		72
96	Recent applications of light scattering measurement in the biological and biopharmaceutical sciences. *Analytical Biochemistry*, **2016**, 501, 4-22	3.1	71
95	Static light scattering from concentrated protein solutions, I: General theory for protein mixtures and application to self-associating proteins. *Biophysical Journal*, **2007**, 93, 1321-8	2.9	70
94	Temperature dependence of nonideality in concentrated solutions of hemoglobin. *Biopolymers*, **1978**, 17, 2285-8	2.2	69
93	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, 132-8	3.1	59
92	Sedimentation equilibrium in macromolecular solutions of arbitrary concentration. I. Self-associating proteins. *Biopolymers*, **1987**, 26, 507-24	2.2	58
91	Static light scattering from concentrated protein solutions II: experimental test of theory for protein mixtures and weakly self-associating proteins. *Biophysical Journal*, **2009**, 96, 1992-8	2.9	56
90	Effects of excluded surface area and adsorbate clustering on surface adsorption of proteins I. Equilibrium models. *Biophysical Chemistry*, **2000**, 86, 239-47	3.5	56
89	Protein folding: Thickening the broth. *Current Biology*, **2000**, 10, R97-9	6.3	53
88	A molecular model for the dependence of the osmotic pressure of bovine serum albumin upon concentration and pH. *Biophysical Chemistry*, **1995**, 57, 65-70	3.5	52
87	Toward an understanding of biochemical equilibria within living cells. *Biophysical Reviews*, **2018**, 10, 241-253	3.7	51
86	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, 3466-9	3.9	51
85	Holobiochemistry: the effect of local environment upon the equilibria and rates of biochemical reactions. *International Journal of Biochemistry & Cell Biology*, **1990**, 22, 1063-7		50
84	Quantitative characterization of weak self-association in concentrated solutions of immunoglobulin G via the measurement of sedimentation equilibrium and osmotic pressure. *Biochemistry*, **2007**, 46, 8373-8	3.2	48
83	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	6.5	45
82	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	3.5	45
81	pH-dependent self-association of zinc-free insulin characterized by concentration-gradient static light scattering. *Biophysical Chemistry*, **2010**, 148, 28-33	3.5	44

80	A simple semiempirical model for the effect of molecular confinement upon the rate of protein folding. *Biochemistry*, **2006**, 45, 13356-60	3.2	44
79	Physicochemical characterization of generation 5 polyamidoamine dendrimers. *Biopolymers*, **2000**, 53, 316-28	2.2	41
78	The effect of self-association on the interaction of the Escherichia coli regulatory protein TyrR with DNA. *Journal of Molecular Biology*, **1996**, 263, 671-84	6.5	41
77	Hidden self-association of proteins. *Journal of Molecular Recognition*, **1989**, 1, 166-71	2.6	40
76	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, 1308-14	3.4	40
75	Dynamic interaction of the Escherichia coli cell division ZipA and FtsZ proteins evidenced in nanodiscs. *Journal of Biological Chemistry*, **2012**, 287, 30097-104	5.4	39
74	Macromolecular crowding and molecular recognition. *Journal of Molecular Recognition*, **1993**, 6, 211-4	2.6	39
73	Rapid quantitative characterization of protein interactions by composition gradient static light scattering. *Biophysical Journal*, **2006**, 90, 2164-9	2.9	38
72	Acceleration of fibrin gel formation by unrelated proteins. *Thrombosis Research*, **1985**, 37, 681-8	8.2	37
71	Analytical centrifugation with preparative ultracentrifuges. *Analytical Biochemistry*, **1989**, 176, 209-16	3.1	36
70	Quantitative characterization of reversible molecular associations via analytical centrifugation. *Analytical Biochemistry*, **1990**, 190, 1-6	3.1	36
69	Self-association in highly concentrated solutions of myoglobin: a novel analysis of sedimentation equilibrium of highly nonideal solutions. *Biophysical Chemistry*, **1981**, 14, 317-24	3.5	36
68	Turbidity as a probe of tubulin polymerization kinetics: a theoretical and experimental re-examination. *Analytical Biochemistry*, **2005**, 345, 198-213	3.1	35
67	An automated method for rapid determination of diffusion coefficients via measurements of boundary spreading. *Analytical Biochemistry*, **1988**, 168, 345-51	3.1	35
66	Structure within eukaryotic cytoplasm and its relationship to glycolytic metabolism. *Cell Biochemistry and Function*, **1996**, 14, 237-48	4.2	34
65	Effects of inert volume-excluding macromolecules on protein fiber formation. I. Equilibrium models. *Biophysical Chemistry*, **2002**, 98, 93-104	3.5	33
64	Characterization of self-association and heteroassociation of bacterial cell division proteins FtsZ and ZipA in solution by composition gradient-static light scattering. *Biochemistry*, **2010**, 49, 10780-7	3.2	32
63	Effective hard particle model for the osmotic pressure of highly concentrated binary protein solutions. *Biophysical Journal*, **2008**, 94, L57-9	2.9	32

62	An automated method for determination of the molecular weight of macromolecules via sedimentation equilibrium in a preparative ultracentrifuge. *Analytical Biochemistry*, **1983**, 133, 142-52	3.1	30
61	Relations between oxygen saturation and aggregation of sickle-cell hemoglobin. *Journal of Molecular Biology*, **1976**, 100, 519-42	6.5	30
60	Concentration dependence of the diffusion coefficient of hemoglobin. *The Journal of Physical Chemistry*, **1978**, 82, 1934-1938		30
59	Thermodynamic analysis of the chemical inhibition of sickle-cell hemoglobin gelation. *Journal of Molecular Biology*, **1975**, 95, 289-307	6.5	29
58	Automated measurement of the static light scattering of macromolecular solutions over a broad range of concentrations. *Analytical Biochemistry*, **2008**, 381, 254-7	3.1	28
57	Excluded volume as a determinant of protein structure and stability. *Biophysical Journal*, **1980**, 32, 77-9	2.9	28
56	Thermal Stabilization of Proteins by Mono- and Oligosaccharides: Measurement and Analysis in the Context of an Excluded Volume Model. *Biochemistry*, **2015**, 54, 3594-603	3.2	27
55	Quantitative characterization of polymer-polymer, protein-protein, and polymer-protein interaction via tracer sedimentation equilibrium. *Journal of Physical Chemistry B*, **2010**, 114, 10876-80	3.4	27
54	Effects of inert volume-excluding macromolecules on protein fiber formation. II. Kinetic models for nucleated fiber growth. *Biophysical Chemistry*, **2004**, 107, 299-316	3.5	27
53	Sedimentation equilibrium in macromolecular solutions of arbitrary concentration. II. Two protein components. *Biopolymers*, **1987**, 26, 1097-113	2.2	27
52	Modulation of functionally significant conformational equilibria in adenylate kinase by high concentrations of trimethylamine oxide attributed to volume exclusion. *Biophysical Journal*, **2011**, 100, 2991-9	2.9	25
51	Technique and apparatus for automated fractionation of the contents of small centrifuge tubes: application to analytical ultracentrifugation. *Analytical Biochemistry*, **1986**, 152, 319-28	3.1	25
50	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	3.5	22
49	Calcium-linked self-association of human complement C1s. *Biochemistry*, **1992**, 31, 11707-12	3.2	22
48	The pH Dependence of SaccharidesRInfluence 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	5.4	21
47	Mg(2+)-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, 4541-50	3.2	21
46	Self-association of Zn-insulin at neutral pH: investigation by concentration gradient--static and dynamic light scattering. *Biophysical Chemistry*, **2010**, 148, 23-7	3.5	21
45	Hard quasispherical particle models for the viscosity of solutions of protein mixtures. *Journal of Physical Chemistry B*, **2012**, 116, 9310-5	3.4	20

44	Beyond the second virial coefficient: Sedimentation equilibrium in highly non-ideal solutions. *Methods*, **2011**, 54, 167-74	4.6	20
43	Non-ideal tracer sedimentation equilibrium: a powerful tool for the characterization of macromolecular interactions in crowded solutions. *Journal of Molecular Recognition*, **2004**, 17, 362-7	2.6	20
42	Ca(2+)-linked association of human complement C1s and C1r. *Biochemistry*, **1994**, 33, 2341-8	3.2	20
41	Capillary viscometer for fully automated measurement of the concentration and shear dependence of the viscosity of macromolecular solutions. *Analytical Chemistry*, **2012**, 84, 10732-6	7.8	18
40	A didactic model of macromolecular crowding effects on protein folding. *PLoS ONE*, **2010**, 5, e11936	3.7	18
39	Models for the gelling behavior of binary mixtures of hemoglobin variants. *Journal of Molecular Biology*, **1973**, 75, 559-74	6.5	18
38	Effect of nonadditive repulsive intermolecular interactions on the light scattering of concentrated protein-osmolyte mixtures. *Journal of Physical Chemistry B*, **2011**, 115, 1289-93	3.4	17
37	Effect of high concentration of inert cosolutes on the refolding of an enzyme: carbonic anhydrase B in sucrose and ficoll 70. *Journal of Biological Chemistry*, **2007**, 282, 33452-33458	5.4	17
36	New developments in the study of biomolecular associations via sedimentation equilibrium. *Trends in Biochemical Sciences*, **1993**, 18, 284-7	10.3	17
35	A strategy for efficient characterization of macromolecular heteroassociations via measurement of sedimentation equilibrium. *Journal of Molecular Recognition*, **1991**, 4, 93-104	2.6	17
34	Explicit Incorporation of Hard and Soft Protein-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	3.4	16
33	Incorporation of Hard and Soft Protein-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	3.4	16
32	Solubility relationships in binary mixtures of hemoglobin variants Application to the "gelationrd of sickle-cell hemoglobin. *Biophysical Chemistry*, **1974**, 1, 387-95	3.5	16
31	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	2.9	14
30	Quantitative characterization of the interaction between sucrose and native proteins via static light scattering. *Journal of Physical Chemistry B*, **2013**, 117, 111-7	3.4	14
29	Quantitative characterization of temperature-independent and temperature-dependent protein-protein interactions in highly nonideal solutions. *Journal of Physical Chemistry B*, **2011**, 115, 11261-8	3.4	14
28	An automated method for determination of the sedimentation coefficient of macromolecules using a preparative centrifuge. *Analytical Biochemistry*, **1984**, 136, 407-15	3.1	14
27	Quantitative characterization of nonspecific self- and hetero-interactions of proteins in nonideal solutions via static light scattering. *Journal of Physical Chemistry B*, **2015**, 119, 1891-8	3.4	13

26	Quantitative characterization of reversible macromolecular associations via sedimentation equilibrium: an introduction. *Experimental and Molecular Medicine*, **2000**, 32, 1-5	12.8	13
25	Simultaneous determination of the individual concentration gradients of two solute species in a centrifuged mixture: application to analytical ultracentrifugation. *Analytical Biochemistry*, **1987**, 162, 409-19	3.1	13
24	Thermodynamic nonideality and the dependence of partition coefficient upon solute concentration in exclusion chromatography. II. An improved theory of equilibrium partitioning of concentrated protein solutions. Application to hemoglobin. *Biophysical Chemistry*, **1983**, 18, 139-43	3.5	12
23	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,	3.9	11
22	An equilibrium model for the Mg(2+)-linked self-assembly of FtsZ in the presence of GTP or a GTP analogue. *Biochemistry*, **2012**, 51, 6108-13	3.2	10
21	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, 133-6	3.1	10
20	Binding of fibrinogen to platelet integrin □b□ in solution as monitored by tracer sedimentation equilibrium **1996**, 9, 31-38		10
19	Analytical ultracentrifugation studies of phage phi29 protein p6 binding to DNA. *Journal of Molecular Biology*, **2009**, 385, 1616-29	6.5	9
18	Simple Calculation of Phase Diagrams for Liquid-Liquid Phase Separation in Solutions of Two Macromolecular Solute Species. *Journal of Physical Chemistry B*, **2020**, 124, 2363-2370	3.4	8
17	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, 9395-9	3.4	8
16	Nucleotide and receptor density modulate binding of bacterial division FtsZ protein to ZipA containing lipid-coated microbeads. *Scientific Reports*, **2017**, 7, 13707	4.9	7
15	Compensating effects of urea and trimethylamine-N-oxide on the heteroassociation of □-chymotrypsin and soybean trypsin inhibitor. *Journal of Physical Chemistry B*, **2013**, 117, 3554-9	3.4	7
14	Comments on extensions of the allosteric model for haemoglobin. *Nature: New Biology*, **1971**, 232, 145-7		7
13	Analysis of membrane binding equilibria of peripheral proteins: allowance for excluded area of bound protein. *Analytical Biochemistry*, **2010**, 397, 247-9	3.1	5
12	Water Loss in Aging Erythrocytes Provides a Clue to a General Mechanism of Cellular Senescence. *Biophysical Journal*, **2020**, 119, 2039-2044	2.9	4
11	Structural Model for the Dielectric Relaxation of Liquid Water. *Nature: Physical Science*, **1971**, 234, 165-168		3
10	Biochemical Reactions in the Crowded and Confined Physiological Environment: Physical Chemistry Meets Synthetic Biology **2011**, 73-89		3
9	Modulation of Conformational Equilibria in the S-Adenosylmethionine (SAM) II Riboswitch by SAM, Mg(2+), and Trimethylamine N-Oxide. *Biochemistry*, **2016**, 55, 5010-20	3.2	3

8	The Cumulative Effect of Surface Adsorption and Excluded Volume in 2D and 3D on Protein Fibrillation. *Biophysical Journal*, **2019**, 117, 1666-1673	2.9	2
7	Concentration-dependent viscosity of binary and ternary mixtures of nonassociating proteins: measurement and analysis. *Journal of Physical Chemistry B*, **2013**, 117, 13861-5	3.4	2
6	Non-specific Interactions Between Macromolecular Solutes in Concentrated Solution: Physico-Chemical Manifestations and Biochemical Consequences. *Frontiers in Molecular Biosciences*, **2019**, 6, 10	5.6	2
5	Quantitative characterization of the concentration-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	2.2	1
4	Big ideas from "small science". *Biophysical Reviews*, **2016**, 8, 285-286	3.7	1
3	Implications of excluded volume for chemical inhibition of protein fibrillation. *Biochimica Et Biophysica Acta - General Subjects*, **2020**, 1864, 129704	4	
2	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	3.1	
1	Detection and Quantitative Characterization of Macromolecular Heteroassociations via Composition Gradient Sedimentation Equilibrium **2016**, 523-532		