

Peter Schuck

List of Publications by Year in descending order

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272
papers

20,098
citations

18887

64
h-index

14779

131
g-index

324
all docs

324
docs citations

324
times ranked

20290
citing authors

#	ARTICLE	IF	CITATIONS
1	Size-Distribution Analysis of Macromolecules by Sedimentation Velocity Ultracentrifugation and Lamm Equation Modeling. <i>Biophysical Journal</i> , 2000, 78, 1606-1619.	0.2	3,484
2	Modern analytical ultracentrifugation in protein science: A tutorial review. <i>Protein Science</i> , 2009, 11, 2067-2079.	3.1	642
3	Size-Distribution Analysis of Proteins by Analytical Ultracentrifugation: Strategies and Application to Model Systems. <i>Biophysical Journal</i> , 2002, 82, 1096-1111.	0.2	639
4	USE OF SURFACE PLASMON RESONANCE TO PROBE THE EQUILIBRIUM AND DYNAMIC ASPECTS OF INTERACTIONS BETWEEN BIOLOGICAL MACROMOLECULES. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1997, 26, 541-566.	18.3	589
5	On the analysis of protein self-association by sedimentation velocity analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2003, 320, 104-124.	1.1	578
6	Macromolecular Size-and-Shape Distributions by Sedimentation Velocity Analytical Ultracentrifugation. <i>Biophysical Journal</i> , 2006, 90, 4651-4661.	0.2	494
7	High-Precision Isothermal Titration Calorimetry with Automated Peak-Shape Analysis. <i>Analytical Chemistry</i> , 2012, 84, 5066-5073.	3.2	440
8	On the Distribution of Protein Refractive Index Increments. <i>Biophysical Journal</i> , 2011, 100, 2309-2317.	0.2	410
9	Crystal structure of an NK cell immunoglobulin-like receptor in complex with its class I MHC ligand. <i>Nature</i> , 2000, 405, 537-543.	13.7	386
10	Sedimentation equilibrium analysis of protein interactions with global implicit mass conservation constraints and systematic noise decomposition. <i>Analytical Biochemistry</i> , 2004, 326, 234-256.	1.1	333
11	Sedimentation Analysis of Noninteracting and Self-Associating Solutes Using Numerical Solutions to the Lamm Equation. <i>Biophysical Journal</i> , 1998, 75, 1503-1512.	0.2	331
12	Determination of the sedimentation coefficient distribution by least-squares boundary modeling. <i>Biopolymers</i> , 2000, 54, 328-341.	1.2	306
13	Studying multisite binary and ternary protein interactions by global analysis of isothermal titration calorimetry data in SEDPHAT: Application to adaptor protein complexes in cell signaling. <i>Protein Science</i> , 2007, 16, 30-42.	3.1	295
14	Modern analytical ultracentrifugation in protein science: a tutorial review. <i>Protein Science</i> , 2002, 11, 2067-79.	3.1	286
15	Calculating Sedimentation Coefficient Distributions by Direct Modeling of Sedimentation Velocity Concentration Profiles. <i>Methods in Enzymology</i> , 2004, 384, 185-212.	0.4	264
16	SEDPHAT – A platform for global ITC analysis and global multi-method analysis of molecular interactions. <i>Methods</i> , 2015, 76, 137-148.	1.9	264
17	Kinetics of ligand binding to receptor immobilized in a polymer matrix, as detected with an evanescent wave biosensor. I. A computer simulation of the influence of mass transport. <i>Biophysical Journal</i> , 1996, 70, 1230-1249.	0.2	226
18	Integration and global analysis of isothermal titration calorimetry data for studying macromolecular interactions. <i>Nature Protocols</i> , 2016, 11, 882-894.	5.5	225

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19	Analysis of Mass Transport-Limited Binding Kinetics in Evanescent Wave Biosensors. <i>Analytical Biochemistry</i> , 1996, 240, 262-272.	1.1	217
20	Oligomerization of signaling complexes by the multipoint binding of GRB2 to both LAT and SOS1. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 798-805.	3.6	195
21	Higher-order oligomerization promotes localization of SPOP to liquid nuclear speckles. <i>EMBO Journal</i> , 2016, 35, 1254-1275.	3.5	172
22	Direct Sedimentation Analysis of Interference Optical Data in Analytical Ultracentrifugation. <i>Biophysical Journal</i> , 1999, 76, 2288-2296.	0.2	168
23	Sedimentation Velocity Analysis of Heterogeneous Protein-Protein Interactions: Lamm Equation Modeling and Sedimentation Coefficient Distributions $c(s)$. <i>Biophysical Journal</i> , 2005, 89, 619-634.	0.2	168
24	Reliable determination of binding affinity and kinetics using surface plasmon resonance biosensors. <i>Current Opinion in Biotechnology</i> , 1997, 8, 498-502.	3.3	160
25	The Role of Mass Transport Limitation and Surface Heterogeneity in the Biophysical Characterization of Macromolecular Binding Processes by SPR Biosensing. <i>Methods in Molecular Biology</i> , 2010, 627, 15-54.	0.4	160
26	Overview of Current Methods in Sedimentation Velocity and Sedimentation Equilibrium Analytical Ultracentrifugation. <i>Current Protocols in Protein Science</i> , 2013, 71, Unit20.12.	2.8	154
27	A conformational switch in HPI releases auto-inhibition to drive heterochromatin assembly. <i>Nature</i> , 2013, 496, 377-381.	13.7	141
28	Combining biophysical methods for the analysis of protein complex stoichiometry and affinity in SEDPHAT. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 3-14.	2.5	139
29	Crystal Structure of a Superantigen Bound to the High-Affinity, Zinc-Dependent Site on MHC Class II. <i>Immunity</i> , 2001, 14, 93-104.	6.6	134
30	Studying multiprotein complexes by multisignal sedimentation velocity analytical ultracentrifugation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 81-86.	3.3	132
31	Kinetic analysis of biosensor data: elementary tests for self-consistency. <i>Trends in Biochemical Sciences</i> , 1996, 21, 458-460.	3.7	131
32	Alanine-scanning Mutations in Domain 4 of Anthrax Toxin Protective Antigen Reveal Residues Important for Binding to the Cellular Receptor and to a Neutralizing Monoclonal Antibody. <i>Journal of Biological Chemistry</i> , 2003, 278, 30936-30944.	1.6	130
33	Variable MHC class I engagement by Ly49 natural killer cell receptors demonstrated by the crystal structure of Ly49C bound to H-2Kb. <i>Nature Immunology</i> , 2003, 4, 1213-1222.	7.0	127
34	Combined Affinity and Rate Constant Distributions of Ligand Populations from Experimental Surface Binding Kinetics and Equilibria. <i>Biophysical Journal</i> , 2003, 84, 4062-4077.	0.2	118
35	Sedimentation Velocity Analysis of Heterogeneous Protein-Protein Interactions: Sedimentation Coefficient Distributions $c(s)$ and Asymptotic Boundary Profiles from Gilbert-Jenkins Theory. <i>Biophysical Journal</i> , 2005, 89, 651-666.	0.2	109
36	Self-association of Human Apolipoprotein E3 and E4 in the Presence and Absence of Phospholipid. <i>Journal of Biological Chemistry</i> , 2000, 275, 36758-36765.	1.6	108

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37	Conformational restriction blocks glutamate receptor desensitization. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 1120-1127.	3.6	106
38	Binding Specificity of Multiprotein Signaling Complexes Is Determined by Both Cooperative Interactions and Affinity Preferences. <i>Biochemistry</i> , 2004, 43, 4170-4178.	1.2	105
39	Structure and Assembly Mechanism for Heteromeric Kainate Receptors. <i>Neuron</i> , 2011, 71, 319-331.	3.8	102
40	Recorded scan times can limit the accuracy of sedimentation coefficients in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2013, 437, 104-108.	1.1	102
41	Cooperative interactions at the SLP-76 complex are critical for actin polymerization. <i>EMBO Journal</i> , 2010, 29, 2315-2328.	3.5	98
42	Bacteriorhodopsin/Amphipol Complexes: Structural and Functional Properties. <i>Biophysical Journal</i> , 2008, 94, 3523-3537.	0.2	97
43	The N-terminal domain of GluR6-subtype glutamate receptor ion channels. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 631-638.	3.6	97
44	Chimpanzee/human mAbs to vaccinia virus B5 protein neutralize vaccinia and smallpox viruses and protect mice against vaccinia virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 1882-1887.	3.3	94
45	Exposure of acidic residues as a danger signal for recognition of fibrinogen and other macromolecules by integrin $\alpha 2$. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1614-1619.	3.3	91
46	Non-Ideality by Sedimentation Velocity of Halophilic Malate Dehydrogenase in Complex Solvents. <i>Biophysical Journal</i> , 2001, 81, 1868-1880.	0.2	90
47	Cooperative behavior of Escherichia coli cell-division protein FtsZ assembly involves the preferential cyclization of long single-stranded fibrils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1895-1900.	3.3	90
48	Rotavirus Nonstructural Protein NSP2 Self-assembles into Octamers That Undergo Ligand-induced Conformational Changes. <i>Journal of Biological Chemistry</i> , 2001, 276, 9679-9687.	1.6	88
49	A new adaptive grid-size algorithm for the simulation of sedimentation velocity profiles in analytical ultracentrifugation. <i>Computer Physics Communications</i> , 2008, 178, 105-120.	3.0	84
50	Characterizing Protein-Protein Interactions by Sedimentation Velocity Analytical Ultracentrifugation. <i>Current Protocols in Immunology</i> , 2008, 81, Unit 18.15.	3.6	84
51	Characterization of DC-SIGN/R Interaction with Human Immunodeficiency Virus Type 1 gp120 and ICAM Molecules Favors the Receptor's Role as an Antigen-Capturing Rather than an Adhesion Receptor. <i>Journal of Virology</i> , 2005, 79, 4589-4598.	1.5	83
52	Probing the Functional Heterogeneity of Surface Binding Sites by Analysis of Experimental Binding Traces and the Effect of Mass Transport Limitation. <i>Biophysical Journal</i> , 2007, 92, 1742-1758.	0.2	83
53	SEDFIT-MSTAR: molecular weight and molecular weight distribution analysis of polymers by sedimentation equilibrium in the ultracentrifuge. <i>Analyst</i> , 2014, 139, 79-92.	1.7	83
54	Inhibition of Hemostasis by a High Affinity Biogenic Amine-binding Protein from the Saliva of a Blood-feeding Insect. <i>Journal of Biological Chemistry</i> , 2003, 278, 4611-4617.	1.6	80

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55	An antibody single-domain phage display library of a native heavy chain variable region: isolation of functional single-domain VH molecules with a unique interface 1 Edited by I. A. Wilson. Journal of Molecular Biology, 1999, 290, 685-698.	2.0	79
56	A model for sedimentation in inhomogeneous media. I. Dynamic density gradients from sedimenting co-solutes. Biophysical Chemistry, 2004, 108, 187-200.	1.5	77
57	Determination of Sedimentation Coefficients for Small Peptides. Biophysical Journal, 1998, 74, 466-474.	0.2	74
58	Determination of Binding Constants by Equilibrium Titration with Circulating Sample in a Surface Plasmon Resonance Biosensor. Analytical Biochemistry, 1998, 265, 79-91.	1.1	73
59	Efficient Neutralization of Anthrax Toxin by Chimpanzee Monoclonal Antibodies against Protective Antigen. Journal of Infectious Diseases, 2006, 193, 625-633.	1.9	73
60	Analytical ultracentrifugation as a tool for studying protein interactions. Biophysical Reviews, 2013, 5, 159-171.	1.5	73
61	Interaction of TAPBPR, a tapasin homolog, with MHC-I molecules promotes peptide editing. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1006-15.	3.3	73
62	A multi-step nucleation process determines the kinetics of prion-like domain phase separation. Nature Communications, 2021, 12, 4513.	5.8	73
63	Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5. ELife, 2018, 7, .	2.8	73
64	Biochemical and Biological Characterization of a Dodecameric CD4-Ig Fusion Protein. Journal of Biological Chemistry, 2002, 277, 11456-11464.	1.6	71
65	Humanized Monoclonal Antibodies Derived from Chimpanzee Fabs Protect against Japanese Encephalitis Virus In Vitro and In Vivo. Journal of Virology, 2008, 82, 7009-7021.	1.5	71
66	A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. PLoS ONE, 2015, 10, e0126420.	1.1	71
67	Biointeractions of ultrasmall glutathione-coated gold nanoparticles: effect of small size variations. Nanoscale, 2016, 8, 6577-6588.	2.8	69
68	Basic Principles of Analytical Ultracentrifugation. , 0, , .		69
69	The Molecular Refractive Function of Lens $\hat{1}^3$ -Crystallins. Journal of Molecular Biology, 2011, 411, 680-699.	2.0	68
70	Apolipoprotein C-II Amyloid Fibrils Assemble via a Reversible Pathway that Includes Fibril Breaking and Rejoining. Journal of Molecular Biology, 2008, 376, 1116-1129.	2.0	66
71	Using Prior Knowledge in the Determination of Macromolecular Size-Distributions by Analytical Ultracentrifugation. Biomacromolecules, 2007, 8, 2011-2024.	2.6	65
72	Sedimentation Patterns of Rapidly Reversible Protein Interactions. Biophysical Journal, 2010, 98, 2005-2013.	0.2	65

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73	SDR grafting of a murine antibody using multiple human germline templates to minimize its immunogenicity. <i>Molecular Immunology</i> , 2004, 41, 863-872.	1.0	64
74	An allosteric site in the T-cell receptor C β 2 domain plays a critical signalling role. <i>Nature Communications</i> , 2017, 8, 15260.	5.8	64
75	Autoinhibition of Arf GTPase-activating Protein Activity by the BAR Domain in ASAP1. <i>Journal of Biological Chemistry</i> , 2009, 284, 1652-1663.	1.6	63
76	Characterization of Chimpanzee/Human Monoclonal Antibodies to Vaccinia Virus A33 Glycoprotein and Its Variola Virus Homolog In Vitro and in a Vaccinia Virus Mouse Protection Model. <i>Journal of Virology</i> , 2007, 81, 8989-8995.	1.5	61
77	The Human Immunodeficiency Virus Type 1 gp120 V2 Domain Mediates gp41-Independent Intersubunit Contacts. <i>Journal of Virology</i> , 2000, 74, 4448-4455.	1.5	60
78	Adaptation of a Surface Plasmon Resonance Biosensor with Microfluidics for Use with Small Sample Volumes and Long Contact Times. <i>Analytical Chemistry</i> , 2001, 73, 2828-2835.	3.2	60
79	Improving the thermal, radial, and temporal accuracy of the analytical ultracentrifuge through external references. <i>Analytical Biochemistry</i> , 2013, 440, 81-95.	1.1	60
80	Role of humoral immunity against hepatitis B virus core antigen in the pathogenesis of acute liver failure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11369-E11378.	3.3	59
81	Mass Spectrometry after Capture and Small-Volume Elution of Analyte from a Surface Plasmon Resonance Biosensor. <i>Analytical Chemistry</i> , 2002, 74, 2041-2047.	3.2	58
82	Stability of ligand-binding domain dimer assembly controls kainate receptor desensitization. <i>EMBO Journal</i> , 2009, 28, 1518-1530.	3.5	54
83	Oligomeric structure of virion-associated and soluble forms of the simian immunodeficiency virus envelope protein in the prefusion activated conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 14877-14882.	3.3	52
84	A comparison of binding surfaces for SPR biosensing using an antibody-antigen system and affinity distribution analysis. <i>Methods</i> , 2013, 59, 328-335.	1.9	52
85	Crystal Structure of the C-terminal Peptidoglycan-binding Domain of Human Peptidoglycan Recognition Protein I β . <i>Journal of Biological Chemistry</i> , 2004, 279, 31873-31882.	1.6	51
86	Novel Chimpanzee/Human Monoclonal Antibodies That Neutralize Anthrax Lethal Factor, and Evidence for Possible Synergy with Anti-Protective Antigen Antibody. <i>Infection and Immunity</i> , 2009, 77, 3902-3908.	1.0	51
87	On the analysis of sedimentation velocity in the study of protein complexes. <i>European Biophysics Journal</i> , 2009, 38, 1079-1099.	1.2	51
88	Simultaneous radial and wavelength analysis with the Optima XL-A analytical ultracentrifuge. , 1994, , 1-13.		50
89	Interaction of the NK Cell Inhibitory Receptor Ly49A with H-2Dd. <i>Immunity</i> , 1999, 11, 591-601.	6.6	50
90	Density Contrast Sedimentation Velocity for the Determination of Protein Partial-Specific Volumes. <i>PLoS ONE</i> , 2011, 6, e26221.	1.1	49

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91	Surface plasmon resonance-based competition assay to assess the sera reactivity of variants of humanized antibodies. <i>Journal of Immunological Methods</i> , 2002, 268, 197-210.	0.6	48
92	Global Multi-Method Analysis of Affinities and Cooperativity in Complex Systems of Macromolecular Interactions. <i>Analytical Chemistry</i> , 2012, 84, 9513-9519.	3.2	48
93	Measuring macromolecular size distributions and interactions at high concentrations by sedimentation velocity. <i>Nature Communications</i> , 2018, 9, 4415.	5.8	48
94	The dimerization stability of the HLH-LZ transcription protein family is modulated by the leucine zippers: A CD and NMR study of TFEB and c-Myc. <i>Biochemistry</i> , 1994, 33, 11296-11306.	1.2	46
95	Eukaryotic RNases H1 act processively by interactions through the duplex RNA-binding domain. <i>Nucleic Acids Research</i> , 2005, 33, 2166-2175.	6.5	46
96	Energetics of glutamate receptor ligand binding domain dimer assembly are modulated by allosteric ions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12329-12334.	3.3	46
97	Analysis of Transport Experiments Using Pseudo-Absorbance Data. <i>Analytical Biochemistry</i> , 2000, 285, 135-142.	1.1	45
98	Biophysical characterization of DNA and RNA aptamer interactions with hen egg lysozyme. <i>International Journal of Biological Macromolecules</i> , 2011, 48, 392-397.	3.6	45
99	Extended Fujita approach to the molecular weight distribution of polysaccharides and other polymeric systems. <i>Methods</i> , 2011, 54, 136-144.	1.9	45
100	Analysis of high-affinity assembly for AMPA receptor amino-terminal domains. <i>Journal of General Physiology</i> , 2012, 139, 371-388.	0.9	45
101	Amino Acid Residues That Influence FcγRI-Mediated Effector Functions of Human Immunoglobulin E. <i>Biochemistry</i> , 1998, 37, 16152-16164.	1.2	44
102	Calcium-Sensitive Interaction between Calmodulin and Modified Forms of Rat Brain Neurogranin/RC3. <i>Biochemistry</i> , 2000, 39, 7291-7299.	1.2	43
103	Grafting of Abbreviated-Complementarity-Determining Regions Containing Specificity-Determining Residues Essential for Ligand Contact to Engineer a Less Immunogenic Humanized Monoclonal Antibody. <i>Journal of Immunology</i> , 2002, 169, 3076-3084.	0.4	43
104	Multipoint Binding of the SLP-76 SH2 Domain to ADAP Is Critical for Oligomerization of SLP-76 Signaling Complexes in Stimulated T Cells. <i>Molecular and Cellular Biology</i> , 2013, 33, 4140-4151.	1.1	43
105	Sedimentation Velocity Analytical Ultracentrifugation. , 0, , .		42
106	Bayesian Analysis of Heterogeneity in the Distribution of Binding Properties of Immobilized Surface Sites. <i>Langmuir</i> , 2008, 24, 11577-11586.	1.6	41
107	Analysis of Protein Interactions with Picomolar Binding Affinity by Fluorescence-Detected Sedimentation Velocity. <i>Analytical Chemistry</i> , 2014, 86, 3181-3187.	3.2	41
108	Analysis of a Temperature-Sensitive Mutant Rotavirus Indicates that NSP2 Octamers Are the Functional Form of the Protein. <i>Journal of Virology</i> , 2002, 76, 7082-7093.	1.5	40

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109	Dissection of Merozoite Surface Protein 3, a Representative of a Family of Plasmodium falciparum Surface Proteins, Reveals an Oligomeric and Highly Elongated Molecule. <i>Journal of Biological Chemistry</i> , 2005, 280, 37236-37245.	1.6	40
110	Characterizing the Solution Properties of Supramolecular Systems by Analytical Ultracentrifugation. <i>Chemistry - A European Journal</i> , 1999, 5, 1377-1383.	1.7	39
111	Binding kinetics of ultrasmall gold nanoparticles with proteins. <i>Nanoscale</i> , 2018, 10, 3235-3244.	2.8	39
112	Sedimentation equilibrium analysis of recombinant mouse FcRn with murine IgG1. <i>Molecular Immunology</i> , 1999, 36, 1117-1125.	1.0	37
113	Regulation of ASAP1 by phospholipids is dependent on the interface between the PH and Arf GAP domains. <i>Cellular Signalling</i> , 2005, 17, 1276-1288.	1.7	37
114	Use of fluorescence-detected sedimentation velocity to study high-affinity protein interactions. <i>Nature Protocols</i> , 2017, 12, 1777-1791.	5.5	37
115	A Bayesian Approach for Quantifying Trace Amounts of Antibody Aggregates by Sedimentation Velocity Analytical Ultracentrifugation. <i>AAPS Journal</i> , 2008, 10, 481-93.	2.2	36
116	The biofilm adhesion protein Aap from <i>Staphylococcus epidermidis</i> forms zinc-dependent amyloid fibers. <i>Journal of Biological Chemistry</i> , 2020, 295, 4411-4427.	1.6	36
117	Plasticity in structure and assembly of SARS-CoV-2 nucleocapsid protein. , 2022, 1, .		36
118	A model for sedimentation in inhomogeneous media. II. Compressibility of aqueous and organic solvents. <i>Biophysical Chemistry</i> , 2004, 108, 201-214.	1.5	35
119	The boundary structure in the analysis of reversibly interacting systems by sedimentation velocity. <i>Methods</i> , 2011, 54, 16-30.	1.9	35
120	Diffusion of the Reaction Boundary of Rapidly Interacting Macromolecules in Sedimentation Velocity. <i>Biophysical Journal</i> , 2010, 98, 2741-2751.	0.2	34
121	AUC and Small-Angle Scattering for Membrane Proteins. <i>Methods in Enzymology</i> , 2015, 562, 257-286.	0.4	34
122	Energetic and structural features of SARS-CoV-2 N-protein co-assemblies with nucleic acids. <i>IScience</i> , 2021, 24, 102523.	1.9	34
123	Differences in the binding capacity of human apolipoprotein E3 and E4 to size-fractionated lipid emulsions. <i>FEBS Journal</i> , 2002, 269, 5939-5949.	0.2	33
124	Targeted lysis of HIV-infected cells by natural killer cells armed and triggered by a recombinant immunoglobulin fusion protein: implications for immunotherapy. <i>Virology</i> , 2005, 332, 491-497.	1.1	33
125	Reversible and Fast Association Equilibria of a Molecular Chaperone, gp57A, of Bacteriophage T4. <i>Biophysical Journal</i> , 2003, 85, 2606-2618.	0.2	32
126	Analytical ultracentrifugation as a tool for studying membrane proteins. , 1991, , 12-22.		31

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127	Analytical band centrifugation of proteins and protein complexes. <i>Biochemical Society Transactions</i> , 1998, 26, 745-749.	1.6	31
128	Quantifying the Energetics of Cooperativity in a Ternary Protein Complex. <i>Biochemistry</i> , 2002, 41, 5177-5184.	1.2	31
129	Measuring Protein-Protein Interactions by Equilibrium Sedimentation. <i>Current Protocols in Immunology</i> , 2007, 79, Unit 18.8.	3.6	31
130	Direct Interaction of the Mouse Cytomegalovirus m152/gp40 Immuno-evasin with RAE-1 Isoforms. <i>Biochemistry</i> , 2010, 49, 2443-2453.	1.2	31
131	The role of macromolecular crowding in the evolution of lens crystallins with high molecular refractive index. <i>Physical Biology</i> , 2011, 8, 046004.	0.8	31
132	Analysis of High Affinity Self-Association by Fluorescence Optical Sedimentation Velocity Analytical Ultracentrifugation of Labeled Proteins: Opportunities and Limitations. <i>PLoS ONE</i> , 2013, 8, e83439.	1.1	31
133	Structural, Bioinformatic, and In Vivo Analyses of Two <i>Treponema pallidum</i> Lipoproteins Reveal a Unique TRAP Transporter. <i>Journal of Molecular Biology</i> , 2012, 416, 678-696.	2.0	30
134	Solution properties of β -crystallins: Hydration of fish and mammal β -crystallins. <i>Protein Science</i> , 2014, 23, 88-99.	3.1	30
135	On computational approaches for size-and-shape distributions from sedimentation velocity analytical ultracentrifugation. <i>European Biophysics Journal</i> , 2010, 39, 1261-1275.	1.2	29
136	Band 3-hemoglobin associations The band 3 tetramer is the oxyhemoglobin binding site. <i>FEBS Letters</i> , 1991, 293, 81-84.	1.3	28
137	Minimizing immunogenicity of the SDR-grafted humanized antibody CC49 by genetic manipulation of the framework residues. <i>Molecular Immunology</i> , 2003, 40, 337-349.	1.0	28
138	Variable Dimerization of the Ly49A Natural Killer Cell Receptor Results in Differential Engagement of its MHC Class I Ligand. <i>Journal of Molecular Biology</i> , 2006, 362, 102-113.	2.0	27
139	Crystal Structure of Group A Streptococcus Mac-1: Insight into Dimer-Mediated Specificity for Recognition of Human IgG. <i>Structure</i> , 2006, 14, 225-235.	1.6	27
140	Structural and Thermodynamic Characterization of the Interaction between Two Periplasmic <i>Treponema pallidum</i> Lipoproteins that are Components of a TPR-Protein-Associated TRAP Transporter (TPAT). <i>Journal of Molecular Biology</i> , 2012, 420, 70-86.	2.0	27
141	Allosteric inhibition of β -thrombin enzymatic activity with ultrasmall gold nanoparticles. <i>Nanoscale Advances</i> , 2019, 1, 378-388.	2.2	27
142	Biomolecular interactions of ultrasmall metallic nanoparticles and nanoclusters. <i>Nanoscale Advances</i> , 2021, 3, 2995-3027.	2.2	27
143	Tools for the Quantitative Analysis of Sedimentation Boundaries Detected by Fluorescence Optical Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2013, 8, e77245.	1.1	27
144	3D-Printing for Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2016, 11, e0155201.	1.1	27

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145	Characterization of serum albumin nanoparticles by sedimentation velocity analysis and electron microscopy. , 2002, , 31-36.		26
146	Accounting for Solvent Signal Offsets in the Analysis of Interferometric Sedimentation Velocity Data. <i>Macromolecular Bioscience</i> , 2010, 10, 736-745.	2.1	26
147	Malaria vaccine candidate: Design of a multivalent subunit α -helical coiled coil poly-epitope. <i>Vaccine</i> , 2011, 29, 7090-7099.	1.7	26
148	The Influence of Two Anion-transport Inhibitors, 4,4'-Diisothiocyanatodihydrostilbene-2,2'-Disulfonate and 4,4'-Dibenzoylstilbene-2,2'-Disulfonate, on the Self-association of Erythrocyte Band 3 Protein. <i>FEBS Journal</i> , 1995, 230, 806-812.	0.2	26
149	Variable Field Analytical Ultracentrifugation: II. Gravitational Sweep Sedimentation Velocity. <i>Biophysical Journal</i> , 2016, 110, 103-112.	0.2	25
150	Preferential assembly of heteromeric kainate and AMPA receptor amino terminal domains. <i>ELife</i> , 2017, 6, .	2.8	25
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