List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Size-Distribution Analysis of Macromolecules by Sedimentation Velocity Ultracentrifugation and Lamm Equation Modeling. Biophysical Journal, 2000, 78, 1606-1619.	0.5	3,484
2	Modern analytical ultracentrifugation in protein science: A tutorial review. Protein Science, 2009, 11, 2067-2079.	7.6	642
3	Size-Distribution Analysis of Proteins by Analytical Ultracentrifugation: Strategies and Application to Model Systems. Biophysical Journal, 2002, 82, 1096-1111.	0.5	639
4	USE OF SURFACE PLASMON RESONANCE TO PROBE THE EQUILIBRIUM AND DYNAMIC ASPECTS OF INTERACTIONS BETWEEN BIOLOGICAL MACROMOLECULES. Annual Review of Biophysics and Biomolecular Structure, 1997, 26, 541-566.	18.3	589
5	On the analysis of protein self-association by sedimentation velocity analytical ultracentrifugation. Analytical Biochemistry, 2003, 320, 104-124.	2.4	578
6	Macromolecular Size-and-Shape Distributions by Sedimentation Velocity Analytical Ultracentrifugation. Biophysical Journal, 2006, 90, 4651-4661.	0.5	494
7	High-Precision Isothermal Titration Calorimetry with Automated Peak-Shape Analysis. Analytical Chemistry, 2012, 84, 5066-5073.	6.5	440
8	On the Distribution of Protein Refractive Index Increments. Biophysical Journal, 2011, 100, 2309-2317.	0.5	410
9	Crystal structure of an NK cell immunoglobulin-like receptor in complex with its class I MHC ligand. Nature, 2000, 405, 537-543.	27.8	386
10	Sedimentation equilibrium analysis of protein interactions with global implicit mass conservation constraints and systematic noise decomposition. Analytical Biochemistry, 2004, 326, 234-256.	2.4	333
11	Sedimentation Analysis of Noninteracting and Self-Associating Solutes Using Numerical Solutions to the Lamm Equation. Biophysical Journal, 1998, 75, 1503-1512.	0.5	331
12	Determination of the sedimentation coefficient distribution by least-squares boundary modeling. Biopolymers, 2000, 54, 328-341.	2.4	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. Protein Science, 2007, 16, 30-42.	7.6	295
14	Modern analytical ultracentrifugation in protein science: a tutorial review. Protein Science, 2002, 11, 2067-79.	7.6	286
15	Calculating Sedimentation Coefficient Distributions by Direct Modeling of Sedimentation Velocity Concentration Profiles. Methods in Enzymology, 2004, 384, 185-212.	1.0	264
16	SEDPHAT – A platform for global ITC analysis and global multi-method analysis of molecular interactions. Methods, 2015, 76, 137-148.	3.8	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. Biophysical Journal, 1996, 70, 1230-1249.	0.5	226
18	Integration and global analysis of isothermal titration calorimetry data for studying macromolecular interactions. Nature Protocols, 2016, 11, 882-894.	12.0	225

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19	Analysis of Mass Transport-Limited Binding Kinetics in Evanescent Wave Biosensors. Analytical Biochemistry, 1996, 240, 262-272.	2.4	217
20	Oligomerization of signaling complexes by the multipoint binding of GRB2 to both LAT and SOS1. Nature Structural and Molecular Biology, 2006, 13, 798-805.	8.2	195
21	Higherâ€order oligomerization promotes localization of <scp>SPOP</scp> to liquid nuclear speckles. EMBO Journal, 2016, 35, 1254-1275.	7.8	172
22	Direct Sedimentation Analysis of Interference Optical Data in Analytical Ultracentrifugation. Biophysical Journal, 1999, 76, 2288-2296.	0.5	168
23	Sedimentation Velocity Analysis of Heterogeneous Protein-Protein Interactions: Lamm Equation Modeling and Sedimentation Coefficient Distributions c(s). Biophysical Journal, 2005, 89, 619-634.	0.5	168
24	Reliable determination of binding affinity and kinetics using surface plasmon resonance biosensors. Current Opinion in Biotechnology, 1997, 8, 498-502.	6.6	160
25	The Role of Mass Transport Limitation and Surface Heterogeneity in the Biophysical Characterization of Macromolecular Binding Processes by SPR Biosensing. Methods in Molecular Biology, 2010, 627, 15-54.	0.9	160
26	Overview of Current Methods in Sedimentation Velocity and Sedimentation Equilibrium Analytical Ultracentrifugation. Current Protocols in Protein Science, 2013, 71, Unit20.12.	2.8	154
27	A conformational switch in HP1 releases auto-inhibition to drive heterochromatin assembly. Nature, 2013, 496, 377-381.	27.8	141
28	Combining biophysical methods for the analysis of protein complex stoichiometry and affinity in <i>SEDPHAT</i> . Acta Crystallographica Section D: Biological Crystallography, 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. Immunity, 2001, 14, 93-104.	14.3	134
30	Studying multiprotein complexes by multisignal sedimentation velocity analytical ultracentrifugation. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 81-86.	7.1	132
31	Kinetic analysis of biosensor data: elementary tests for self-consistency. Trends in Biochemical Sciences, 1996, 21, 458-460.	7.5	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. Journal of Biological Chemistry, 2003, 278, 30936-30944.	3.4	130
33	Variable MHC class I engagement by Ly49 natural killer cell receptors demonstrated by the crystal structure of Ly49C bound to H-2Kb. Nature Immunology, 2003, 4, 1213-1222.	14.5	127
34	Combined Affinity and Rate Constant Distributions of Ligand Populations from Experimental Surface Binding Kinetics and Equilibria. Biophysical Journal, 2003, 84, 4062-4077.	0.5	118
35	Sedimentation Velocity Analysis of Heterogeneous Protein-Protein Interactions: Sedimentation Coefficient Distributions c(s) and Asymptotic Boundary Profiles from Gilbert-Jenkins Theory. Biophysical Journal, 2005, 89, 651-666.	0.5	109
36	Self-association of Human Apolipoprotein E3 and E4 in the Presence and Absence of Phospholipid. Journal of Biological Chemistry, 2000, 275, 36758-36765.	3.4	108

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37	Conformational restriction blocks glutamate receptor desensitization. Nature Structural and Molecular Biology, 2006, 13, 1120-1127.	8.2	106
38	Binding Specificity of Multiprotein Signaling Complexes Is Determined by Both Cooperative Interactions and Affinity Preferences. Biochemistry, 2004, 43, 4170-4178.	2.5	105
39	Structure and Assembly Mechanism for Heteromeric Kainate Receptors. Neuron, 2011, 71, 319-331.	8.1	102
40	Recorded scan times can limit the accuracy of sedimentation coefficients in analytical ultracentrifugation. Analytical Biochemistry, 2013, 437, 104-108.	2.4	102
41	Cooperative interactions at the SLP-76 complex are critical for actin polymerization. EMBO Journal, 2010, 29, 2315-2328.	7.8	98
42	Bacteriorhodopsin/Amphipol Complexes: Structural and Functional Properties. Biophysical Journal, 2008, 94, 3523-3537.	0.5	97
43	The N-terminal domain of GluR6-subtype glutamate receptor ion channels. Nature Structural and Molecular Biology, 2009, 16, 631-638.	8.2	97
44	Chimpanzee/human mAbs to vaccinia virus B5 protein neutralize vaccinia and smallpox viruses and protect mice against vaccinia virus. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 1882-1887.	7.1	94
45	Exposure of acidic residues as a danger signal for recognition of fibrinogen and other macromolecules by integrin ÂXÂ2. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1614-1619.	7.1	91
46	Non-Ideality by Sedimentation Velocity of Halophilic Malate Dehydrogenase in Complex Solvents. Biophysical Journal, 2001, 81, 1868-1880.	0.5	90
47	Cooperative behavior of <i>Escherichia coli</i> 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.	7.1	90
48	Rotavirus Nonstructural Protein NSP2 Self-assembles into Octamers That Undergo Ligand-induced Conformational Changes. Journal of Biological Chemistry, 2001, 276, 9679-9687.	3.4	88
49	A new adaptive grid-size algorithm for the simulation of sedimentation velocity profiles in analytical ultracentrifugation. Computer Physics Communications, 2008, 178, 105-120.	7.5	84
50	Characterizing Proteinâ€Protein Interactions by Sedimentation Velocity Analytical Ultracentrifugation. Current Protocols in Immunology, 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. Journal of Virology, 2005, 79, 4589-4598.	3.4	83
52	Probing the Functional Heterogeneity of Surface Binding Sites by Analysis of Experimental Binding Traces and the Effect of Mass Transport Limitation. Biophysical Journal, 2007, 92, 1742-1758.	0.5	83
53	SEDFIT–MSTAR: molecular weight and molecular weight distribution analysis of polymers by sedimentation equilibrium in the ultracentrifuge. Analyst, The, 2014, 139, 79-92.	3.5	83
54	Inhibition of Hemostasis by a High Affinity Biogenic Amine-binding Protein from the Saliva of a Blood-feeding Insect. Journal of Biological Chemistry, 2003, 278, 4611-4617.	3.4	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 1Edited by I. A. Wilson. Journal of Molecular Biology, 1999, 290, 685-698.	4.2	79
56	A model for sedimentation in inhomogeneous media. I. Dynamic density gradients from sedimenting co-solutes. Biophysical Chemistry, 2004, 108, 187-200.	2.8	77
57	Determination of Sedimentation Coefficients for Small Peptides. Biophysical Journal, 1998, 74, 466-474.	0.5	74
58	Determination of Binding Constants by Equilibrium Titration with Circulating Sample in a Surface Plasmon Resonance Biosensor. Analytical Biochemistry, 1998, 265, 79-91.	2.4	73
59	Efficient Neutralization of Anthrax Toxin by Chimpanzee Monoclonal Antibodies against Protective Antigen. Journal of Infectious Diseases, 2006, 193, 625-633.	4.0	73
60	Analytical ultracentrifugation as a tool for studying protein interactions. Biophysical Reviews, 2013, 5, 159-171.	3.2	73
61	Interaction of TAPBPR, a tapasin homolog, with MHC-I molecules promotes peptide editing. Proceedings of the United States of America, 2016, 113, E1006-15.	7.1	73
62	A multi-step nucleation process determines the kinetics of prion-like domain phase separation. Nature Communications, 2021, 12, 4513.	12.8	73
63	Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5. ELife, 2018, 7, .	6.0	73
64	Biochemical and Biological Characterization of a Dodecameric CD4-Ig Fusion Protein. Journal of Biological Chemistry, 2002, 277, 11456-11464.	3.4	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.	3.4	71
66	A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. PLoS ONE, 2015, 10, e0126420.	2.5	71
67	Biointeractions of ultrasmall glutathione-coated gold nanoparticles: effect of small size variations. Nanoscale, 2016, 8, 6577-6588.	5.6	69
68	Basic Principles of Analytical Ultracentrifugation. , 0, , .		69
69	The Molecular Refractive Function of Lens γ-Crystallins. Journal of Molecular Biology, 2011, 411, 680-699.	4.2	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.	4.2	66
71	Using Prior Knowledge in the Determination of Macromolecular Size-Distributions by Analytical Ultracentrifugation. Biomacromolecules, 2007, 8, 2011-2024.	5.4	65
72	Sedimentation Patterns of Rapidly Reversible Protein Interactions. Biophysical Journal, 2010, 98, 2005-2013.	0.5	65

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73	SDR grafting of a murine antibody using multiple human germline templates to minimize its immunogenicity. Molecular Immunology, 2004, 41, 863-872.	2.2	64
74	An allosteric site in the T-cell receptor $\hat{Cl^2}$ domain plays a critical signalling role. Nature Communications, 2017, 8, 15260.	12.8	64
75	Autoinhibition of Arf GTPase-activating Protein Activity by the BAR Domain in ASAP1. Journal of Biological Chemistry, 2009, 284, 1652-1663.	3.4	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. Journal of Virology, 2007, 81, 8989-8995.	3.4	61
77	The Human Immunodeficiency Virus Type 1 gp120 V2 Domain Mediates gp41-Independent Intersubunit Contacts. Journal of Virology, 2000, 74, 4448-4455.	3.4	60
78	Adaptation of a Surface Plasmon Resonance Biosensor with Microfluidics for Use with Small Sample Volumes and Long Contact Times. Analytical Chemistry, 2001, 73, 2828-2835.	6.5	60
79	Improving the thermal, radial, and temporal accuracy of the analytical ultracentrifuge through external references. Analytical Biochemistry, 2013, 440, 81-95.	2.4	60
80	Role of humoral immunity against hepatitis B virus core antigen in the pathogenesis of acute liver failure. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11369-E11378.	7.1	59
81	Mass Spectrometry after Capture and Small-Volume Elution of Analyte from a Surface Plasmon Resonance Biosensor. Analytical Chemistry, 2002, 74, 2041-2047.	6.5	58
82	Stability of ligand-binding domain dimer assembly controls kainate receptor desensitization. EMBO Journal, 2009, 28, 1518-1530.	7.8	54
83	Oligomeric structure of virion-associated and soluble forms of the simian immunodeficiency virus envelope protein in the prefusion activated conformation. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 14877-14882.	7.1	52
84	A comparison of binding surfaces for SPR biosensing using an antibody–antigen system and affinity distribution analysis. Methods, 2013, 59, 328-335.	3.8	52
85	Crystal Structure of the C-terminal Peptidoglycan-binding Domain of Human Peptidoglycan Recognition Protein Iα. Journal of Biological Chemistry, 2004, 279, 31873-31882.	3.4	51
86	Novel Chimpanzee/Human Monoclonal Antibodies That Neutralize Anthrax Lethal Factor, and Evidence for Possible Synergy with Anti-Protective Antigen Antibody. Infection and Immunity, 2009, 77, 3902-3908.	2.2	51
87	On the analysis of sedimentation velocity in the study of protein complexes. European Biophysics Journal, 2009, 38, 1079-1099.	2.2	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. Immunity, 1999, 11, 591-601.	14.3	50
90	Density Contrast Sedimentation Velocity for the Determination of Protein Partial-Specific Volumes. PLoS ONE, 2011, 6, e26221.	2.5	49

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91	Surface plasmon resonance-based competition assay to assess the sera reactivity of variants of humanized antibodies. Journal of Immunological Methods, 2002, 268, 197-210.	1.4	48
92	Global Multi-Method Analysis of Affinities and Cooperativity in Complex Systems of Macromolecular Interactions. Analytical Chemistry, 2012, 84, 9513-9519.	6.5	48
93	Measuring macromolecular size distributions and interactions at high concentrations by sedimentation velocity. Nature Communications, 2018, 9, 4415.	12.8	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. Biochemistry, 1994, 33, 11296-11306.	2.5	46
95	Eukaryotic RNases H1 act processively by interactions through the duplex RNA-binding domain. Nucleic Acids Research, 2005, 33, 2166-2175.	14.5	46
96	Energetics of glutamate receptor ligand binding domain dimer assembly are modulated by allosteric ions. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12329-12334.	7.1	46
97	Analysis of Transport Experiments Using Pseudo-Absorbance Data. Analytical Biochemistry, 2000, 285, 135-142.	2.4	45
98	Biophysical characterization of DNA and RNA aptamer interactions with hen egg lysozyme. International Journal of Biological Macromolecules, 2011, 48, 392-397.	7.5	45
99	Extended Fujita approach to the molecular weight distribution of polysaccharides and other polymeric systems. Methods, 2011, 54, 136-144.	3.8	45
100	Analysis of high-affinity assembly for AMPA receptor amino-terminal domains. Journal of General Physiology, 2012, 139, 371-388.	1.9	45
101	Amino Acid Residues That Influence FcεRI-Mediated Effector Functions of Human Immunoglobulin Eâ€. Biochemistry, 1998, 37, 16152-16164.	2.5	44
102	Calcium-Sensitive Interaction between Calmodulin and Modified Forms of Rat Brain Neurogranin/RC3. Biochemistry, 2000, 39, 7291-7299.	2.5	43
103	Grafting of "Abbreviated―Complementarity-Determining Regions Containing Specificity-Determining Residues Essential for Ligand Contact to Engineer a Less Immunogenic Humanized Monoclonal Antibody. Journal of Immunology, 2002, 169, 3076-3084.	0.8	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. Molecular and Cellular Biology, 2013, 33, 4140-4151.	2.3	43
105	Sedimentation Velocity Analytical Ultracentrifugation. , 0, , .		42
106	Bayesian Analysis of Heterogeneity in the Distribution of Binding Properties of Immobilized Surface Sites. Langmuir, 2008, 24, 11577-11586.	3.5	41
107	Analysis of Protein Interactions with Picomolar Binding Affinity by Fluorescence-Detected Sedimentation Velocity. Analytical Chemistry, 2014, 86, 3181-3187.	6.5	41
108	Analysis of a Temperature-Sensitive Mutant Rotavirus Indicates that NSP2 Octamers Are the Functional Form of the Protein. Journal of Virology, 2002, 76, 7082-7093.	3.4	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. Journal of Biological Chemistry, 2005, 280, 37236-37245.	3.4	40
110	Characterizing the Solution Properties of Supramolecular Systems by Analytical Ultracentrifugation. Chemistry - A European Journal, 1999, 5, 1377-1383.	3.3	39
111	Binding kinetics of ultrasmall gold nanoparticles with proteins. Nanoscale, 2018, 10, 3235-3244.	5.6	39
112	Sedimentation equilibrium analysis of recombinant mouse FcRn with murine IgG1. Molecular Immunology, 1999, 36, 1117-1125.	2.2	37
113	Regulation of ASAP1 by phospholipids is dependent on the interface between the PH and Arf GAP domains. Cellular Signalling, 2005, 17, 1276-1288.	3.6	37
114	Use of fluorescence-detected sedimentation velocity to study high-affinity protein interactions. Nature Protocols, 2017, 12, 1777-1791.	12.0	37
115	A Bayesian Approach for Quantifying Trace Amounts of Antibody Aggregates by Sedimentation Velocity Analytical Ultracentrifugation. AAPS Journal, 2008, 10, 481-93.	4.4	36
116	The biofilm adhesion protein Aap from Staphylococcus epidermidis forms zinc-dependent amyloid fibers. Journal of Biological Chemistry, 2020, 295, 4411-4427.	3.4	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. Biophysical Chemistry, 2004, 108, 201-214.	2.8	35
119	The boundary structure in the analysis of reversibly interacting systems by sedimentation velocity. Methods, 2011, 54, 16-30.	3.8	35
120	Diffusion of the Reaction Boundary of Rapidly Interacting Macromolecules in Sedimentation Velocity. Biophysical Journal, 2010, 98, 2741-2751.	0.5	34
121	AUC and Small-Angle Scattering for Membrane Proteins. Methods in Enzymology, 2015, 562, 257-286.	1.0	34
122	Energetic and structural features of SARS-CoV-2 N-protein co-assemblies with nucleic acids. IScience, 2021, 24, 102523.	4.1	34
123	Differences in the binding capacity of human apolipoprotein E3 and E4 to size-fractionated lipid emulsions. FEBS Journal, 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. Virology, 2005, 332, 491-497.	2.4	33
125	Reversible and Fast Association Equilibria of a Molecular Chaperone, gp57A, of Bacteriophage T4. Biophysical Journal, 2003, 85, 2606-2618.	0.5	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. Biochemical Society Transactions, 1998, 26, 745-749.	3.4	31
128	Quantifying the Energetics of Cooperativity in a Ternary Protein Complexâ€. Biochemistry, 2002, 41, 5177-5184.	2.5	31
129	Measuring Proteinâ€Protein Interactions by Equilibrium Sedimentation. Current Protocols in Immunology, 2007, 79, Unit 18.8.	3.6	31
130	Direct Interaction of the Mouse Cytomegalovirus m152/gp40 Immunoevasin with RAE-1 Isoforms. Biochemistry, 2010, 49, 2443-2453.	2.5	31
131	The role of macromolecular crowding in the evolution of lens crystallins with high molecular refractive index. Physical Biology, 2011, 8, 046004.	1.8	31
132	Analysis of High Affinity Self-Association by Fluorescence Optical Sedimentation Velocity Analytical Ultracentrifugation of Labeled Proteins: Opportunities and Limitations. PLoS ONE, 2013, 8, e83439.	2.5	31
133	Structural, Bioinformatic, and In Vivo Analyses of Two Treponema pallidum Lipoproteins Reveal a Unique TRAP Transporter. Journal of Molecular Biology, 2012, 416, 678-696.	4.2	30
134	Solution properties of γâ€crystallins: Hydration of fish and mammal γâ€crystallins. Protein Science, 2014, 23, 88-99.	7.6	30
135	On computational approaches for size-and-shape distributions from sedimentation velocity analytical ultracentrifugation. European Biophysics Journal, 2010, 39, 1261-1275.	2.2	29
136	Band 3-hemoglobin associations The band 3 tetramer is the oxyhemoglobin binding site. FEBS Letters, 1991, 293, 81-84.	2.8	28
137	Minimizing immunogenicity of the SDR-grafted humanized antibody CC49 by genetic manipulation of the framework residues. Molecular Immunology, 2003, 40, 337-349.	2.2	28
138	Variable Dimerization of the Ly49A Natural Killer Cell Receptor Results in Differential Engagement of its MHC Class I Ligand. Journal of Molecular Biology, 2006, 362, 102-113.	4.2	27
139	Crystal Structure of Group A Streptococcus Mac-1: Insight into Dimer-Mediated Specificity for Recognition of Human IgG. Structure, 2006, 14, 225-235.	3.3	27
140	Structural and Thermodynamic Characterization of the Interaction between Two Periplasmic Treponema pallidum Lipoproteins that are Components of a TPR-Protein-Associated TRAP Transporter (TPAT). Journal of Molecular Biology, 2012, 420, 70-86.	4.2	27
141	Allosteric inhibition of α-thrombin enzymatic activity with ultrasmall gold nanoparticles. Nanoscale Advances, 2019, 1, 378-388.	4.6	27
142	Biomolecular interactions of ultrasmall metallic nanoparticles and nanoclusters. Nanoscale Advances, 2021, 3, 2995-3027.	4.6	27
143	Tools for the Quantitative Analysis of Sedimentation Boundaries Detected by Fluorescence Optical Analytical Ultracentrifugation. PLoS ONE, 2013, 8, e77245.	2.5	27
144	3D-Printing for Analytical Ultracentrifugation. PLoS ONE, 2016, 11, e0155201.	2.5	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. Macromolecular Bioscience, 2010, 10, 736-745.	4.1	26
147	Malaria vaccine candidate: Design of a multivalent subunit α-helical coiled coil poly-epitope. Vaccine, 2011, 29, 7090-7099.	3.8	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. FEBS Journal, 1995, 230, 806-812.	0.2	26
149	Variable Field Analytical Ultracentrifugation: II. Gravitational Sweep Sedimentation Velocity. Biophysical Journal, 2016, 110, 103-112.	0.5	25
150	Preferential assembly of heteromeric kainate and AMPA receptor amino terminal domains. ELife, 2017, 6,	6.0	25
151	Rapid Determination of Molar Mass in Modified Archibald Experiments Using Direct Fitting of the Lamm Equation. Analytical Biochemistry, 1998, 259, 48-53.	2.4	24
152	Self-Association and Ligand-Induced Conformational Changes of Iron Regulatory Proteins 1 and 2. Biochemistry, 2005, 44, 8470-8478.	2.5	24
153	Cooperative assembly of a four-molecule signaling complex formed upon T cell antigen receptor activation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11914-E11923.	7.1	24
154	Sedimentation Equilibrium Analysis of Interference Optical Data by Systematic Noise Decomposition. Analytical Biochemistry, 1999, 272, 199-208.	2.4	23
155	Solution properties of γâ€crystallins: Compact structure and low frictional ratio are conserved properties of diverse γâ€crystallins. Protein Science, 2014, 23, 76-87.	7.6	23
156	Identification of nanomaterials: A validation report of two laboratories using analytical ultracentrifugation with fixed and ramped speed options. NanoImpact, 2018, 10, 87-96.	4.5	23
157	Cellular Expression and Crystal Structure of the Murine Cytomegalovirus Major Histocompatibility Complex Class I-like Glycoprotein, m153. Journal of Biological Chemistry, 2007, 282, 35247-35258.	3.4	22
158	Superantigen natural affinity maturation revealed by the crystal structure of staphylococcal enterotoxin G and its binding to T-cell receptor VÎ28.2. Proteins: Structure, Function and Bioinformatics, 2007, 68, 389-402.	2.6	22
159	Extended Polypeptide Linkers Establish the Spatial Architecture of a Pyruvate Dehydrogenase Multienzyme Complex. Structure, 2008, 16, 93-103.	3.3	22
160	Measuring Ultra-Weak Protein Self-Association by Non-ideal Sedimentation Velocity. Journal of the American Chemical Society, 2019, 141, 2990-2996.	13.7	22
161	A Mechanism for Assembly of Complexes of Vitronectin and Plasminogen Activator Inhibitor-1 from Sedimentation Velocity Analysis. Journal of Biological Chemistry, 2005, 280, 28711-28720.	3.4	21
162	The C-terminal domain of Plasmodium falciparum merozoite surface protein 3 self-assembles into α-helical coiled coil tetramer. Molecular and Biochemical Parasitology, 2009, 165, 153-161.	1.1	20

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163	Improved measurement of the rotor temperature in analytical ultracentrifugation. Analytical Biochemistry, 2014, 451, 69-75.	2.4	20
164	Zwitterionic glutathione monoethyl ester as a new capping ligand for ultrasmall gold nanoparticles. RSC Advances, 2016, 6, 46350-46355.	3.6	20
165	In vitro affinity maturation of a specificity-determining region-grafted humanized anticarcinoma antibody: isolation and characterization of minimally immunogenic high-affinity variants. Clinical Cancer Research, 2003, 9, 5521-31.	7.0	20
166	Hydrodynamics of Nanoscopic Tubulin Rings in Dilute Solutions. Physical Review Letters, 2004, 93, 098106.	7.8	19
167	Influence of Temperature on the Conformation of Canine Plasminogen:  An Analytical Ultracentrifugation and Dynamic Light Scattering Study. Biochemistry, 2005, 44, 13122-13131.	2.5	19
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