

Peter Schuck

List of Publications by Year in descending order

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272
papers

20,098
citations

16451

64
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12946

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324
times ranked

18225
citing authors

#	ARTICLE	IF	CITATIONS
1	Best Practices for Aggregate Quantitation of Antibody Therapeutics by Sedimentation Velocity Analytical Ultracentrifugation. <i>Journal of Pharmaceutical Sciences</i> , 2022, 111, 2121-2133.	3.3	9
2	Plasticity in structure and assembly of SARS-CoV-2 nucleocapsid protein. , 2022, 1, .		36
3	Global multi-method analysis of interaction parameters for reversibly self-associating macromolecules at high concentrations. <i>Scientific Reports</i> , 2021, 11, 5741.	3.3	7
4	A multi-laboratory benchmark study of isothermal titration calorimetry (ITC) using Ca ²⁺ and Mg ²⁺ binding to EDTA. <i>European Biophysics Journal</i> , 2021, 50, 429-451.	2.2	12
5	Determining the Stoichiometry of a Proteinâ€“Polymer Conjugate Using Multisignal Sedimentation Velocity Analytical Ultracentrifugation. <i>Bioconjugate Chemistry</i> , 2021, 32, 942-949.	3.6	5
6	Energetic and structural features of SARS-CoV-2 N-protein co-assemblies with nucleic acids. <i>IScience</i> , 2021, 24, 102523.	4.1	34
7	A multi-step nucleation process determines the kinetics of prion-like domain phase separation. <i>Nature Communications</i> , 2021, 12, 4513.	12.8	73
8	Characterization of DNAâ€“protein complexes by nanoparticle tracking analysis and their association with systemic lupus erythematosus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	7
9	Competing stress-dependent oligomerization pathways regulate self-assembly of the periplasmic protease-chaperone DegP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	11
10	Calibrating analytical ultracentrifuges. <i>European Biophysics Journal</i> , 2021, 50, 353-362.	2.2	4
11	Biomolecular interactions of ultrasmall metallic nanoparticles and nanoclusters. <i>Nanoscale Advances</i> , 2021, 3, 2995-3027.	4.6	27
12	The intrinsic kinase activity of BRD4 spans its BD2-B-BID domains. <i>Journal of Biological Chemistry</i> , 2021, 297, 101326.	3.4	10
13	An intrinsically disordered motif regulates the interaction between the p47 adaptor and the p97 AAA+ ATPase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 26226-26236.	7.1	19
14	Distinct disease features in chimpanzees infected with a precore HBV mutant associated with acute liver failure in humans. <i>PLoS Pathogens</i> , 2020, 16, e1008793.	4.7	4
15	Measuring aggregates, self-association, and weak interactions in concentrated therapeutic antibody solutions. <i>MAbs</i> , 2020, 12, 1810488.	5.2	14
16	Quantitative Analysis of Protein Selfâ€“Association by Sedimentation Velocity. <i>Current Protocols in Protein Science</i> , 2020, 101, e109.	2.8	8
17	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.	3.4	36
18	Ultrasmall Gold Nanoparticles Coated with Zwitterionic Glutathione Monoethyl Ester: A Model Platform for the Incorporation of Functional Peptides. <i>Journal of Physical Chemistry B</i> , 2020, 124, 3892-3902.	2.6	12

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19	Mechanistic Insights into Ultrasmall Gold Nanoparticle-Protein Interactions through Measurement of Binding Kinetics. <i>Journal of Physical Chemistry C</i> , 2019, 123, 28450-28459.	3.1	18
20	Nucleic acid-induced dimerization of HIV-1 Gag protein. <i>Journal of Biological Chemistry</i> , 2019, 294, 16480-16493.	3.4	15
21	Efficient data acquisition with three-channel centerpieces in sedimentation velocity. <i>Analytical Biochemistry</i> , 2019, 586, 113414.	2.4	5
22	Measuring Ultra-Weak Protein Self-Association by Non-ideal Sedimentation Velocity. <i>Journal of the American Chemical Society</i> , 2019, 141, 2990-2996.	13.7	22
23	All tubulins are not alike: Heterodimer dissociation differs among different biological sources. <i>Journal of Biological Chemistry</i> , 2019, 294, 10315-10324.	3.4	13
24	A Reappraisal of Sedimentation Nonideality Coefficients for the Analysis of Weak Interactions of Therapeutic Proteins. <i>AAPS Journal</i> , 2019, 21, 35.	4.4	11
25	Enhanced Sample Handling for Analytical Ultracentrifugation with 3D-Printed Centerpieces. <i>Analytical Chemistry</i> , 2019, 91, 5866-5873.	6.5	16
26	Studying Multi-Protein Interactions by Fluorescence Detected Sedimentation Velocity Combining Hydrodynamic Separation of Complexes with Fluorescence Quenching Analysis. <i>Biophysical Journal</i> , 2019, 116, 194a.	0.5	1
27	Measuring Macromolecular Size-Distributions and Interactions at High Concentrations by Sedimentation Velocity. <i>Biophysical Journal</i> , 2019, 116, 158a.	0.5	0
28	Allosteric inhibition of α -thrombin enzymatic activity with ultrasmall gold nanoparticles. <i>Nanoscale Advances</i> , 2019, 1, 378-388.	4.6	27
29	Identification of nanomaterials: A validation report of two laboratories using analytical ultracentrifugation with fixed and ramped speed options. <i>NanoImpact</i> , 2018, 10, 87-96.	4.5	23
30	Binding kinetics of ultrasmall gold nanoparticles with proteins. <i>Nanoscale</i> , 2018, 10, 3235-3244.	5.6	39
31	Congratulations to Dr. Fumio Arisaka on his 70th birthday. <i>Biophysical Reviews</i> , 2018, 10, 137-137.	3.2	1
32	Assembly of Kainate and AMPA Receptors. <i>Biophysical Journal</i> , 2018, 114, 126a.	0.5	0
33	Sedimentation Boundary Structure of Multi-Component Solutions with Rapidly Reversible Interactions. <i>Biophysical Journal</i> , 2018, 114, 172a-173a.	0.5	0
34	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.	7.1	59
35	Cooperative assembly of a four-molecule signaling complex formed upon T cell antigen receptor activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11914-E11923.	7.1	24
36	Measuring macromolecular size distributions and interactions at high concentrations by sedimentation velocity. <i>Nature Communications</i> , 2018, 9, 4415.	12.8	48

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37	All Tubulins are Not Alike: Dimer Dissociation and Monomer Exchange Differ Depending on the Biological Source of Tubulin. Biophysical Journal, 2018, 114, 504a.	0.5	2
38	A radial calibration window for analytical ultracentrifugation. PLoS ONE, 2018, 13, e0201529.	2.5	8
39	Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5. ELife, 2018, 7, .	6.0	73
40	Sedimentation Velocity Analytical Ultracentrifugation. , 2018, , 1-14.		0
41	Sedimentation of Reversibly Interacting Macromolecules with Changes in Fluorescence Quantum Yield. Biophysical Journal, 2017, 112, 1374-1382.	0.5	8
42	An allosteric site in the T-cell receptor C β domain plays a critical signalling role. Nature Communications, 2017, 8, 15260.	12.8	64
43	Measuring Protein Interactions by Optical Biosensors. Current Protocols in Protein Science, 2017, 88, 20.2.1-20.2.25.	2.8	13
44	A New Temporal Dimension for Multisignal Sedimentation Velocity as a Tool to Analyze Multicomponent Interactions. Biophysical Journal, 2017, 112, 192a.	0.5	0
45	A General Framework for the Boundary Structure in Multi-Component Sedimentation Velocity with Reversible Interactions. Biophysical Journal, 2017, 112, 199a.	0.5	0
46	Fluorescence Detected Sedimentation Velocity Analytical Ultracentrifugation for Investigating Affinity and Stoichiometry of Protein Interactions. Biophysical Journal, 2017, 112, 199a.	0.5	0
47	All Tubulins are Not the Same: Reversible Dissociation of AB-Tubulin Dimers Differ Depending on the Source of Tubulin. Biophysical Journal, 2017, 112, 360a.	0.5	0
48	Use of fluorescence-detected sedimentation velocity to study high-affinity protein interactions. Nature Protocols, 2017, 12, 1777-1791.	12.0	37
49	Crystal Structure of Chicken β 3-Crystallin Reveals Lattice Contacts with Implications for Function in the Lens and the Evolution of the β 2 β 3-Crystallins. Structure, 2017, 25, 1068-1078.e2.	3.3	15
50	Preferential assembly of heteromeric kainate and AMPA receptor amino terminal domains. ELife, 2017, 6, .	6.0	25
51	Higher-order oligomerization promotes localization of SPOP to liquid nuclear speckles. EMBO Journal, 2016, 35, 1254-1275.	7.8	172
52	Sedimentation coefficient distributions of large particles. Analyst, The, 2016, 141, 4400-4409.	3.5	17
53	Biointeractions of Ultrasmall Gold Nanoparticles: Influence of Nanoparticle Size and Surface Chemistry. Biophysical Journal, 2016, 110, 530a.	0.5	0
54	Study Molecular Interactions in whole Cell Extracts by Fluorescence-Detected Analytical Ultracentrifugation. Biophysical Journal, 2016, 110, 384a.	0.5	0

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55	Zwitterionic glutathione monoethyl ester as a new capping ligand for ultrasmall gold nanoparticles. RSC Advances, 2016, 6, 46350-46355.	3.6	20
56	Gravitational Sweep Sedimentation Velocity. Biophysical Journal, 2016, 110, 384a.	0.5	0
57	Integration and global analysis of isothermal titration calorimetry data for studying macromolecular interactions. Nature Protocols, 2016, 11, 882-894.	12.0	225
58	Tubulin Dimer Reversible Dissociation. Journal of Biological Chemistry, 2016, 291, 9281-9294.	3.4	13
59	A New Dimension of Detection in Analytical Ultracentrifugation with Fluorescence Detection using Photoswitchable FPs as Time Domain Probes. Biophysical Journal, 2016, 110, 347a.	0.5	0
60	Tubulin Monomer-Monomer Association is Less Influenced by the Solvent than Dimer-Dimer Association: Structure and Function of Tubulin Interaction Interfaces. Biophysical Journal, 2016, 110, 26a-27a.	0.5	1
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.	7.1	73
62	Biointeractions of ultrasmall glutathione-coated gold nanoparticles: effect of small size variations. Nanoscale, 2016, 8, 6577-6588.	5.6	69
63	Variable Field Analytical Ultracentrifugation: II. Gravitational Sweep Sedimentation Velocity. Biophysical Journal, 2016, 110, 103-112.	0.5	25
64	3D-Printing for Analytical Ultracentrifugation. PLoS ONE, 2016, 11, e0155201.	2.5	27
65	Monochromatic multicomponent fluorescence sedimentation velocity for the study of high-affinity protein interactions. ELife, 2016, 5, .	6.0	11
66	Sedimentation in a Time-Varying Centrifugal Field for Rapid Attainment of Sedimentation Equilibrium. Biophysical Journal, 2015, 108, 222a.	0.5	0
67	Sedimentation Velocity Analysis of the EGFPs in E. coli Whole Cell Extracts using Fluorescence Detection System. Biophysical Journal, 2015, 108, 624a.	0.5	0
68	The Role of Higher-Order SPOP Oligomers for Localization to Cellular "Bodies" and Ubiquitination Activity. Biophysical Journal, 2015, 108, 390a.	0.5	0
69	Accounting for Photophysical Processes and Specific Signal Intensity Change in Fluorescence-Detected Sedimentation Velocity Analytical Ultracentrifugation. Biophysical Journal, 2015, 108, 624a.	0.5	0
70	AUC and Small-Angle Scattering for Membrane Proteins. Methods in Enzymology, 2015, 562, 257-286.	1.0	34
71	A histogram approach to the quality of fit in sedimentation velocity analyses. Analytical Biochemistry, 2015, 483, 1-3.	2.4	14
72	Combining biophysical methods for the analysis of protein complex stoichiometry and affinity in SEDPHAT. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 3-14.	2.5	139

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73	Biocalorimetry. Methods, 2015, 76, 1-2.	3.8	9
74	SEDPHAT – A platform for global ITC analysis and global multi-method analysis of molecular interactions. Methods, 2015, 76, 137-148.	3.8	264
75	Variable-Field Analytical Ultracentrifugation: I. Time-Optimized Sedimentation Equilibrium. Biophysical Journal, 2015, 109, 827-837.	0.5	12
76	A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. PLoS ONE, 2015, 10, e0126420.	2.5	71
77	A Structural Framework for a Near-Minimal Form of Life: Mass and Compositional Analysis of the Helical Mollicute Spiroplasma melliferum BC3. PLoS ONE, 2014, 9, e87921.	2.5	13
78	Solution properties of β -crystallins: Hydration of fish and mammal β -crystallins. Protein Science, 2014, 23, 88-99.	7.6	30
79	Human Herpesvirus 7 U21 Tetramerizes To Associate with Class I Major Histocompatibility Complex Molecules. Journal of Virology, 2014, 88, 3298-3308.	3.4	17
80	Analysis of High-Affinity Protein Interactions by Fluorescence Optical Analytical Ultracentrifugation. Biophysical Journal, 2014, 106, 236a.	0.5	0
81	Tubulin Heterodimers Reversibly Dissociate with Moderate Kinetics as Demonstrated using Sedimentation Velocity Analytical Ultracentrifugation. Biophysical Journal, 2014, 106, 351a.	0.5	0
82	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
83	Solution properties of β -crystallins: Compact structure and low frictional ratio are conserved properties of diverse β -crystallins. Protein Science, 2014, 23, 76-87.	7.6	23
84	Accounting for Photophysical Processes and Specific Signal Intensity Changes in Fluorescence-Detected Sedimentation Velocity. Analytical Chemistry, 2014, 86, 9286-9292.	6.5	11
85	Analysis of Protein Interactions with Picomolar Binding Affinity by Fluorescence-Detected Sedimentation Velocity. Analytical Chemistry, 2014, 86, 3181-3187.	6.5	41
86	Role of Amino-Terminal Domain in the Assembly Mechanism of Kainate-Subtype Glutamate Receptor Ion Channels. Biophysical Journal, 2014, 106, 151a.	0.5	0
87	Improved measurement of the rotor temperature in analytical ultracentrifugation. Analytical Biochemistry, 2014, 451, 69-75.	2.4	20
88	Measurement of the temperature of the resting rotor in analytical ultracentrifugation. Analytical Biochemistry, 2014, 458, 37-39.	2.4	14
89	Investigating High Affinity Protein Self-Association by Fluorescence Optical Sedimentation Velocity Analytical Ultracentrifugation. Biophysical Journal, 2014, 106, 151a.	0.5	0
90	Analytical ultracentrifugation as a tool for studying protein interactions. Biophysical Reviews, 2013, 5, 159-171.	3.2	73

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91	Biophysical methods for the study of protein interactions. <i>Methods</i> , 2013, 59, 259-260.	3.8	2
92	A comparison of binding surfaces for SPR biosensing using an antibody-antigen system and affinity distribution analysis. <i>Methods</i> , 2013, 59, 328-335.	3.8	52
93	Improving the thermal, radial, and temporal accuracy of the analytical ultracentrifuge through external references. <i>Analytical Biochemistry</i> , 2013, 440, 81-95.	2.4	60
94	A conformational switch in HP1 releases auto-inhibition to drive heterochromatin assembly. <i>Nature</i> , 2013, 496, 377-381.	27.8	141
95	Recorded scan times can limit the accuracy of sedimentation coefficients in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2013, 437, 104-108.	2.4	102
96	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
97	Multi-Signal Sedimentation Velocity Analysis with Mass Conservation for Determining the Stoichiometry of Protein Complexes. <i>PLoS ONE</i> , 2013, 8, e62694.	2.5	18
98	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.	2.3	43
99	Complexes of Neutralizing and Non-Neutralizing Affinity Matured Fabs with a Mimetic of the Internal Trimeric Coiled-Coil of HIV-1 gp41. <i>PLoS ONE</i> , 2013, 8, e78187.	2.5	17
100	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.	2.5	31
101	Tools for the Quantitative Analysis of Sedimentation Boundaries Detected by Fluorescence Optical Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2013, 8, e77245.	2.5	27
102	Abstract IA23: Functional and structural studies of HP1 heterochromatin. , 2013, , .		0
103	Analysis of high-affinity assembly for AMPA receptor amino-terminal domains. <i>Journal of General Physiology</i> , 2012, 139, 371-388.	1.9	45
104	Global Multi-Method Analysis of Affinities and Cooperativity in Complex Systems of Macromolecular Interactions. <i>Analytical Chemistry</i> , 2012, 84, 9513-9519.	6.5	48
105	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.	4.2	30
106	An Equilibrium Model for Linear and Closed-Loop Amyloid Fibril Formation. <i>Journal of Molecular Biology</i> , 2012, 421, 364-377.	4.2	19
107	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.	4.2	27
108	The Molecular Refractive Function of Lens Gamma Crystallins. <i>Biophysical Journal</i> , 2012, 102, 185a.	0.5	0

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109	Analysis of Oligomer Assembly for the GluA2 Amino Terminal Domain. Biophysical Journal, 2012, 102, 335a-336a.	0.5	0
110	High-Precision Isothermal Titration Calorimetry with Automated Peak-Shape Analysis. Analytical Chemistry, 2012, 84, 5066-5073.	6.5	440
111	Strategies for assessing proton linkage to bimolecular interactions by global analysis of isothermal titration calorimetry data. Journal of Chemical Thermodynamics, 2012, 52, 95-107.	2.0	14
112	Dimeric States of Neural- and Epithelial-Cadherins are Distinguished by the Rate of Disassembly. Biochemistry, 2011, 50, 2951-2961.	2.5	13
113	The role of macromolecular crowding in the evolution of lens crystallins with high molecular refractive index. Physical Biology, 2011, 8, 046004.	1.8	31
114	NBD-Labeled Phospholipid Accelerates Apolipoprotein C-II Amyloid Fibril Formation but Is Not Incorporated into Mature Fibrils. Biochemistry, 2011, 50, 9579-9586.	2.5	13
115	Studying Rapidly Reversible Protein-Protein Interactions by Sedimentation Velocity Analytical Ultracentrifugation. Biophysical Journal, 2011, 100, 387a.	0.5	0
116	Biophysical characterization of DNA and RNA aptamer interactions with hen egg lysozyme. International Journal of Biological Macromolecules, 2011, 48, 392-397.	7.5	45
117	The Molecular Refractive Function of Lens γ -Crystallins. Journal of Molecular Biology, 2011, 411, 680-699.	4.2	68
118	Malaria vaccine candidate: Design of a multivalent subunit α -helical coiled coil poly-epitope. Vaccine, 2011, 29, 7090-7099.	3.8	26
119	Extended Fujita approach to the molecular weight distribution of polysaccharides and other polymeric systems. Methods, 2011, 54, 136-144.	3.8	45
120	The boundary structure in the analysis of reversibly interacting systems by sedimentation velocity. Methods, 2011, 54, 16-30.	3.8	35
121	Editorial for the special issue of methods "Modern Analytical Ultracentrifugation", Methods, 2011, 54, 1-3.	3.8	14
122	Structure and Assembly Mechanism for Heteromeric Kainate Receptors. Neuron, 2011, 71, 319-331.	8.1	102
123	On the Distribution of Protein Refractive Index Increments. Biophysical Journal, 2011, 100, 2309-2317.	0.5	410
124	Density Contrast Sedimentation Velocity for the Determination of Protein Partial-Specific Volumes. PLoS ONE, 2011, 6, e26221.	2.5	49
125	On computational approaches for size-and-shape distributions from sedimentation velocity analytical ultracentrifugation. European Biophysics Journal, 2010, 39, 1261-1275.	2.2	29
126	Accounting for Solvent Signal Offsets in the Analysis of Interferometric Sedimentation Velocity Data. Macromolecular Bioscience, 2010, 10, 736-745.	4.1	26

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127	Macromol. Biosci. 7/2010. Macromolecular Bioscience, 2010, 10, .	4.1	0
128	Some statistical properties of differencing schemes for baseline correction of sedimentation velocity data. Analytical Biochemistry, 2010, 401, 280-287.	2.4	19
129	Cooperative interactions at the SLP-76 complex are critical for actin polymerization. EMBO Journal, 2010, 29, 2315-2328.	7.8	98
130	Energetics of Allosteric ion Binding to a Ligand-Gated ion Channel. Biophysical Journal, 2010, 98, 610a.	0.5	0
131	Fredholm Integral Equations in Biophysical Data Analysis. IFMBE Proceedings, 2010, , 340-343.	0.3	1
132	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
133	Determining Thermodynamic Parameters of Protein Interactions By Global Analysis of Data From Multiple Techniques. Biophysical Journal, 2010, 98, 61a.	0.5	0
134	Sedimentation Patterns of Rapidly Reversible Protein Interactions. Biophysical Journal, 2010, 98, 2005-2013.	0.5	65
135	Diffusion of the Reaction Boundary of Rapidly Interacting Macromolecules in Sedimentation Velocity. Biophysical Journal, 2010, 98, 2741-2751.	0.5	34
136	Direct Interaction of the Mouse Cytomegalovirus m152/gp40 Immuno-evasin with RAE-1 Isoforms. Biochemistry, 2010, 49, 2443-2453.	2.5	31
137	Phospholipids Enhance Nucleation but Not Elongation of Apolipoprotein C-II Amyloid Fibrils. Journal of Molecular Biology, 2010, 399, 731-740.	4.2	15
138	Autoinhibition of Arf GTPase-activating Protein Activity by the BAR Domain in ASAP1. Journal of Biological Chemistry, 2009, 284, 1652-1663.	3.4	63
139	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
140	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
141	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
142	On the analysis of sedimentation velocity in the study of protein complexes. European Biophysics Journal, 2009, 38, 1079-1099.	2.2	51
143	Stability of ligand-binding domain dimer assembly controls kainate receptor desensitization. EMBO Journal, 2009, 28, 1518-1530.	7.8	54
144	The N-terminal domain of GluR6-subtype glutamate receptor ion channels. Nature Structural and Molecular Biology, 2009, 16, 631-638.	8.2	97

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145	Probing the Heterogeneity in the Distribution of Binding Properties of Immobilized Surface Sites through Bayesian Analysis. <i>Biophysical Journal</i> , 2009, 96, 74a-75a.	0.5	0
146	Modern analytical ultracentrifugation in protein science: A tutorial review. <i>Protein Science</i> , 2009, 11, 2067-2079.	7.6	642
147	Structure And Stability Of Ligand Binding Core Dimer Assembly Controls Desensitization In A Kainate Receptor. <i>Biophysical Journal</i> , 2009, 96, 491a.	0.5	0
148	Assembly, Loading, and Alignment of an Analytical Ultracentrifuge Sample Cell. <i>Journal of Visualized Experiments</i> , 2009, , .	0.3	16
149	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.	7.5	84
150	A Bayesian Approach for Quantifying Trace Amounts of Antibody Aggregates by Sedimentation Velocity Analytical Ultracentrifugation. <i>AAPS Journal</i> , 2008, 10, 481-93.	4.4	36
151	Extended Polypeptide Linkers Establish the Spatial Architecture of a Pyruvate Dehydrogenase Multienzyme Complex. <i>Structure</i> , 2008, 16, 93-103.	3.3	22
152	Bacteriorhodopsin/Amphipol Complexes: Structural and Functional Properties. <i>Biophysical Journal</i> , 2008, 94, 3523-3537.	0.5	97
153	Apolipoprotein C-II Amyloid Fibrils Assemble via a Reversible Pathway that Includes Fibril Breaking and Rejoining. <i>Journal of Molecular Biology</i> , 2008, 376, 1116-1129.	4.2	66
154	Bayesian Analysis of Heterogeneity in the Distribution of Binding Properties of Immobilized Surface Sites. <i>Langmuir</i> , 2008, 24, 11577-11586.	3.5	41
155	Characterizing Protein-Protein Interactions by Sedimentation Velocity Analytical Ultracentrifugation. <i>Current Protocols in Immunology</i> , 2008, 81, Unit 18.15.	3.6	84
156	Humanized Monoclonal Antibodies Derived from Chimpanzee Fabs Protect against Japanese Encephalitis Virus In Vitro and In Vivo. <i>Journal of Virology</i> , 2008, 82, 7009-7021.	3.4	71
157	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.	3.4	61
158	Cellular Expression and Crystal Structure of the Murine Cytomegalovirus Major Histocompatibility Complex Class I-like Glycoprotein, m153. <i>Journal of Biological Chemistry</i> , 2007, 282, 35247-35258.	3.4	22
159	Measuring Protein-Protein Interactions by Equilibrium Sedimentation. <i>Current Protocols in Immunology</i> , 2007, 79, Unit 18.8.	3.6	31
160	Using Prior Knowledge in the Determination of Macromolecular Size-Distributions by Analytical Ultracentrifugation. <i>Biomacromolecules</i> , 2007, 8, 2011-2024.	5.4	65
161	Two Interferons Alpha Influence Each Other during Their Interaction with the Extracellular Domain of Human Type I Interferon Receptor Subunit 2. <i>Biochemistry</i> , 2007, 46, 14638-14649.	2.5	9
162	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.	0.5	83

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163	Sedimentation Equilibrium Analytical Ultracentrifugation for Multicomponent Protein Interactions. , 2007, , 289-316.		8
164	Single-walled tubulin ring polymers. Biopolymers, 2007, 86, 424-436.	2.4	11
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