

# Peter Schuck

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

237  
papers

16,980  
citations

61  
h-index

124  
g-index

324  
ext. papers

18,716  
ext. citations

5.4  
avg, IF

7.12  
L-index

#	Paper	IF	Citations
237	The intrinsic kinase activity of BRD4 spans its BD2-B-BID domains. <i>Journal of Biological Chemistry</i> , <b>2021</b> , 297, 101326	5.4	3
236	Global multi-method analysis of interaction parameters for reversibly self-associating macromolecules at high concentrations. <i>Scientific Reports</i> , <b>2021</b> , 11, 5741	4.9	2
235	A multi-laboratory benchmark study of isothermal titration calorimetry (ITC) using Ca and Mg binding to EDTA. <i>European Biophysics Journal</i> , <b>2021</b> , 50, 429-451	1.9	2
234	Determining the Stoichiometry of a Protein-Polymer Conjugate Using Multisignal Sedimentation Velocity Analytical Ultracentrifugation. <i>Bioconjugate Chemistry</i> , <b>2021</b> , 32, 942-949	6.3	0
233	Energetic and structural features of SARS-CoV-2 N-protein co-assemblies with nucleic acids. <i>IScience</i> , <b>2021</b> , 24, 102523	6.1	8
232	A multi-step nucleation process determines the kinetics of prion-like domain phase separation. <i>Nature Communications</i> , <b>2021</b> , 12, 4513	17.4	13
231	Characterization of DNA-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> , <b>2021</b> , 118,	11.5	1
230	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> , <b>2021</b> , 118,	11.5	5
229	Calibrating analytical ultracentrifuges. <i>European Biophysics Journal</i> , <b>2021</b> , 50, 353-362	1.9	2
228	Biomolecular interactions of ultrasmall metallic nanoparticles and nanoclusters. <i>Nanoscale Advances</i> , <b>2021</b> , 3, 2995-3027	5.1	9
227	Quantitative Analysis of Protein Self-Association by Sedimentation Velocity. <i>Current Protocols in Protein Science</i> , <b>2020</b> , 101, e109	3.1	4
226	The biofilm adhesion protein Aap from forms zinc-dependent amyloid fibers. <i>Journal of Biological Chemistry</i> , <b>2020</b> , 295, 4411-4427	5.4	15
225	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> , <b>2020</b> , 124, 3892-3902	3.4	8
224	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> , <b>2020</b> , 117, 26226-26236	11.5	6
223	Distinct disease features in chimpanzees infected with a precore HBV mutant associated with acute liver failure in humans. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008793	7.6	4
222	Measuring aggregates, self-association, and weak interactions in concentrated therapeutic antibody solutions. <i>MAbs</i> , <b>2020</b> , 12, 1810488	6.6	5
221	Nucleic acid-induced dimerization of HIV-1 Gag protein. <i>Journal of Biological Chemistry</i> , <b>2019</b> , 294, 16480-16493	5.1	3

220	Efficient data acquisition with three-channel centerpieces in sedimentation velocity. <i>Analytical Biochemistry</i> , <b>2019</b> , 586, 113414	3.1	4
219	Measuring Ultra-Weak Protein Self-Association by Non-ideal Sedimentation Velocity. <i>Journal of the American Chemical Society</i> , <b>2019</b> , 141, 2990-2996	16.4	15
218	All tubulins are not alike: Heterodimer dissociation differs among different biological sources. <i>Journal of Biological Chemistry</i> , <b>2019</b> , 294, 10315-10324	5.4	7
217	A Reappraisal of Sedimentation Nonideality Coefficients for the Analysis of Weak Interactions of Therapeutic Proteins. <i>AAPS Journal</i> , <b>2019</b> , 21, 35	3.7	10
216	Enhanced Sample Handling for Analytical Ultracentrifugation with 3D-Printed Centerpieces. <i>Analytical Chemistry</i> , <b>2019</b> , 91, 5866-5873	7.8	10
215	Mechanistic Insights into Ultrasmall Gold Nanoparticle-Protein Interactions through Measurement of Binding Kinetics. <i>Journal of Physical Chemistry C</i> , <b>2019</b> , 123, 28450-28459	3.8	10
214	Allosteric inhibition of $\alpha$ -thrombin enzymatic activity with ultrasmall gold nanoparticles. <i>Nanoscale Advances</i> , <b>2019</b> , 1, 378-388	5.1	20
213	Identification of nanomaterials: A validation report of two laboratories using analytical ultracentrifugation with fixed and ramped speed options. <i>NanoImpact</i> , <b>2018</b> , 10, 87-96	5.6	16
212	Binding kinetics of ultrasmall gold nanoparticles with proteins. <i>Nanoscale</i> , <b>2018</b> , 10, 3235-3244	7.7	27
211	Congratulations to Dr. Fumio Arisaka on his 70th birthday. <i>Biophysical Reviews</i> , <b>2018</b> , 10, 137	3.7	0
210	Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5. <i>ELife</i> , <b>2018</b> , 7,	8.9	36
209	Author response: Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5 <b>2018</b> ,		2
208	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> , <b>2018</b> , 115, E11369-E11378	11.5	41
207	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> , <b>2018</b> , 115, E11914-E11923	11.5	13
206	Measuring macromolecular size distributions and interactions at high concentrations by sedimentation velocity. <i>Nature Communications</i> , <b>2018</b> , 9, 4415	17.4	33
205	A radial calibration window for analytical ultracentrifugation. <i>PLoS ONE</i> , <b>2018</b> , 13, e0201529	3.7	7
204	Sedimentation of Reversibly Interacting Macromolecules with Changes in Fluorescence Quantum Yield. <i>Biophysical Journal</i> , <b>2017</b> , 112, 1374-1382	2.9	6
203	An allosteric site in the T-cell receptor CD $\alpha$ domain plays a critical signalling role. <i>Nature Communications</i> , <b>2017</b> , 8, 15260	17.4	39

202	Measuring Protein Interactions by Optical Biosensors. <i>Current Protocols in Protein Science</i> , <b>2017</b> , 88, 20.231-20.2125		
201	Preferential assembly of heteromeric kainate and AMPA receptor amino terminal domains. <i>ELife</i> , <b>2017</b> , 6,	8.9	18
200	Use of fluorescence-detected sedimentation velocity to study high-affinity protein interactions. <i>Nature Protocols</i> , <b>2017</b> , 12, 1777-1791	18.8	30
199	Crystal Structure of Chicken $\beta$ -Crystallin Reveals Lattice Contacts with Implications for Function in the Lens and the Evolution of the $\beta$ Crystallins. <i>Structure</i> , <b>2017</b> , 25, 1068-1078.e2	5.2	13
198	Sedimentation Velocity Analytical Ultracentrifugation <b>2017</b> ,		11
197	Interaction of TAPBPR, a tapasin homolog, with MHC-I molecules promotes peptide editing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E1006-15	11.5	52
196	Biointeractions of ultrasmall glutathione-coated gold nanoparticles: effect of small size variations. <i>Nanoscale</i> , <b>2016</b> , 8, 6577-88	7.7	54
195	Variable Field Analytical Ultracentrifugation: II. Gravitational Sweep Sedimentation Velocity. <i>Biophysical Journal</i> , <b>2016</b> , 110, 103-12	2.9	18
194	3D-Printing for Analytical Ultracentrifugation. <i>PLoS ONE</i> , <b>2016</b> , 11, e0155201	3.7	20
193	Monochromatic multicomponent fluorescence sedimentation velocity for the study of high-affinity protein interactions. <i>ELife</i> , <b>2016</b> , 5,	8.9	10
192	Higher-order oligomerization promotes localization of SPOP to liquid nuclear speckles. <i>EMBO Journal</i> , <b>2016</b> , 35, 1254-75	13	113
191	Sedimentation coefficient distributions of large particles. <i>Analyst, The</i> , <b>2016</b> , 141, 4400-9	5	12
190	Zwitterionic glutathione monoethyl ester as a new capping ligand for ultrasmall gold nanoparticles. <i>RSC Advances</i> , <b>2016</b> , 6, 46350-46355	3.7	15
189	Integration and global analysis of isothermal titration calorimetry data for studying macromolecular interactions. <i>Nature Protocols</i> , <b>2016</b> , 11, 882-94	18.8	135
188	Tubulin Dimer Reversible Dissociation: AFFINITY, KINETICS, AND DEMONSTRATION OF A STABLE MONOMER. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 9281-94	5.4	11
187	Combining biophysical methods for the analysis of protein complex stoichiometry and affinity in SEDPHAT. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 3-14		88
186	SEDPHAT--a platform for global ITC analysis and global multi-method analysis of molecular interactions. <i>Methods</i> , <b>2015</b> , 76, 137-148	4.6	173
185	Variable-Field Analytical Ultracentrifugation: I. Time-Optimized Sedimentation Equilibrium. <i>Biophysical Journal</i> , <b>2015</b> , 109, 827-37	2.9	9

184	AUC and Small-Angle Scattering for Membrane Proteins. <i>Methods in Enzymology</i> , <b>2015</b> , 562, 257-86	1.7	23
183	A histogram approach to the quality of fit in sedimentation velocity analyses. <i>Analytical Biochemistry</i> , <b>2015</b> , 483, 1-3	3.1	9
182	A multilaboratory comparison of calibration accuracy and the performance of external references in analytical ultracentrifugation. <i>PLoS ONE</i> , <b>2015</b> , 10, e0126420	3.7	55
181	SEDFIT-MSTAR: molecular weight and molecular weight distribution analysis of polymers by sedimentation equilibrium in the ultracentrifuge. <i>Analyst, The</i> , <b>2014</b> , 139, 79-92	5	68
180	Solution properties of $\beta$ -crystallins: compact structure and low frictional ratio are conserved properties of diverse $\beta$ -crystallins. <i>Protein Science</i> , <b>2014</b> , 23, 76-87	6.3	18
179	Accounting for photophysical processes and specific signal intensity changes in fluorescence-detected sedimentation velocity. <i>Analytical Chemistry</i> , <b>2014</b> , 86, 9286-92	7.8	10
178	Analysis of protein interactions with picomolar binding affinity by fluorescence-detected sedimentation velocity. <i>Analytical Chemistry</i> , <b>2014</b> , 86, 3181-7	7.8	36
177	Improved measurement of the rotor temperature in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , <b>2014</b> , 451, 69-75	3.1	15
176	Measurement of the temperature of the resting rotor in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , <b>2014</b> , 458, 37-9	3.1	9
175	A structural framework for a near-minimal form of life: mass and compositional analysis of the helical mollicute <i>Spiroplasma melliferum</i> BC3. <i>PLoS ONE</i> , <b>2014</b> , 9, e87921	3.7	8
174	Solution properties of $\beta$ -crystallins: hydration of fish and mammal $\beta$ -crystallins. <i>Protein Science</i> , <b>2014</b> , 23, 88-99	6.3	25
173	Human herpesvirus 7 U21 tetramerizes to associate with class I major histocompatibility complex molecules. <i>Journal of Virology</i> , <b>2014</b> , 88, 3298-308	6.6	13
172	Analytical Ultracentrifugation as a Tool for Studying Protein Interactions. <i>Biophysical Reviews</i> , <b>2013</b> , 5, 159-171	3.7	60
171	A comparison of binding surfaces for SPR biosensing using an antibody-antigen system and affinity distribution analysis. <i>Methods</i> , <b>2013</b> , 59, 328-35	4.6	40
170	Improving the thermal, radial, and temporal accuracy of the analytical ultracentrifuge through external references. <i>Analytical Biochemistry</i> , <b>2013</b> , 440, 81-95	3.1	54
169	A conformational switch in HP1 releases auto-inhibition to drive heterochromatin assembly. <i>Nature</i> , <b>2013</b> , 496, 377-81	50.4	107
168	Recorded scan times can limit the accuracy of sedimentation coefficients in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , <b>2013</b> , 437, 104-8	3.1	79
167	Overview of current methods in sedimentation velocity and sedimentation equilibrium analytical ultracentrifugation. <i>Current Protocols in Protein Science</i> , <b>2013</b> , Chapter 20, Unit20.12	3.1	118

166	Multi-signal sedimentation velocity analysis with mass conservation for determining the stoichiometry of protein complexes. <i>PLoS ONE</i> , <b>2013</b> , 8, e62694	3.7	11
165	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> , <b>2013</b> , 33, 4140-51	4.8	35
164	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> , <b>2013</b> , 8, e78187	3.7	16
163	Analysis of high affinity self-association by fluorescence optical sedimentation velocity analytical ultracentrifugation of labeled proteins: opportunities and limitations. <i>PLoS ONE</i> , <b>2013</b> , 8, e83439	3.7	28
162	Tools for the quantitative analysis of sedimentation boundaries detected by fluorescence optical analytical ultracentrifugation. <i>PLoS ONE</i> , <b>2013</b> , 8, e77245	3.7	25
161	Strategies for assessing proton linkage to bimolecular interactions by global analysis of isothermal titration calorimetry data. <i>Journal of Chemical Thermodynamics</i> , <b>2012</b> , 52, 95-107	2.9	12
160	Global multi-method analysis of affinities and cooperativity in complex systems of macromolecular interactions. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 9513-9	7.8	40
159	Structural, bioinformatic, and in vivo analyses of two <i>Treponema pallidum</i> lipoproteins reveal a unique TRAP transporter. <i>Journal of Molecular Biology</i> , <b>2012</b> , 416, 678-96	6.5	23
158	An equilibrium model for linear and closed-loop amyloid fibril formation. <i>Journal of Molecular Biology</i> , <b>2012</b> , 421, 364-77	6.5	17
157	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> , <b>2012</b> , 420, 70-86	6.5	20
156	High-precision isothermal titration calorimetry with automated peak-shape analysis. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 5066-73	7.8	329
155	Analysis of high-affinity assembly for AMPA receptor amino-terminal domains. <i>Journal of General Physiology</i> , <b>2012</b> , 139, 371-88	3.4	40
154	Biophysical characterization of DNA and RNA aptamer interactions with hen egg lysozyme. <i>International Journal of Biological Macromolecules</i> , <b>2011</b> , 48, 392-7	7.9	35
153	The molecular refractive function of lens $\beta$ Crystallins. <i>Journal of Molecular Biology</i> , <b>2011</b> , 411, 680-99	6.5	55
152	Malaria vaccine candidate: design of a multivalent subunit $\beta$ helical coiled coil poly-epitope. <i>Vaccine</i> , <b>2011</b> , 29, 7090-9	4.1	22
151	Extended Fujita approach to the molecular weight distribution of polysaccharides and other polymeric systems. <i>Methods</i> , <b>2011</b> , 54, 136-44	4.6	40
150	The boundary structure in the analysis of reversibly interacting systems by sedimentation velocity. <i>Methods</i> , <b>2011</b> , 54, 16-30	4.6	31
149	Structure and assembly mechanism for heteromeric kainate receptors. <i>Neuron</i> , <b>2011</b> , 71, 319-31	13.9	96

148	On the distribution of protein refractive index increments. <i>Biophysical Journal</i> , <b>2011</b> , 100, 2309-17	2.9	300
147	Dimeric states of neural- and epithelial-cadherins are distinguished by the rate of disassembly. <i>Biochemistry</i> , <b>2011</b> , 50, 2951-61	3.2	12
146	The role of macromolecular crowding in the evolution of lens crystallins with high molecular refractive index. <i>Physical Biology</i> , <b>2011</b> , 8, 046004	3	24
145	NBD-labeled phospholipid accelerates apolipoprotein C-II amyloid fibril formation but is not incorporated into mature fibrils. <i>Biochemistry</i> , <b>2011</b> , 50, 9579-86	3.2	10
144	Density contrast sedimentation velocity for the determination of protein partial-specific volumes. <i>PLoS ONE</i> , <b>2011</b> , 6, e26221	3.7	39
143	Cooperative interactions at the SLP-76 complex are critical for actin polymerization. <i>EMBO Journal</i> , <b>2010</b> , 29, 2315-28	13	85
142	Fredholm Integral Equations in Biophysical Data Analysis. <i>IFMBE Proceedings</i> , <b>2010</b> , 340-343	0.2	1
141	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> , <b>2010</b> , 627, 15-54	1.4	125
140	Sedimentation patterns of rapidly reversible protein interactions. <i>Biophysical Journal</i> , <b>2010</b> , 98, 2005-13	2.9	56
139	Diffusion of the reaction boundary of rapidly interacting macromolecules in sedimentation velocity. <i>Biophysical Journal</i> , <b>2010</b> , 98, 2741-51	2.9	30
138	Direct interaction of the mouse cytomegalovirus m152/gp40 immunoevasin with RAE-1 isoforms. <i>Biochemistry</i> , <b>2010</b> , 49, 2443-53	3.2	26
137	Phospholipids enhance nucleation but not elongation of apolipoprotein C-II amyloid fibrils. <i>Journal of Molecular Biology</i> , <b>2010</b> , 399, 731-40	6.5	15
136	Analytical Ultracentrifugation <b>2010</b> ,		3
135	On computational approaches for size-and-shape distributions from sedimentation velocity analytical ultracentrifugation. <i>European Biophysics Journal</i> , <b>2010</b> , 39, 1261-75	1.9	21
134	Accounting for solvent signal offsets in the analysis of interferometric sedimentation velocity data. <i>Macromolecular Bioscience</i> , <b>2010</b> , 10, 736-45	5.5	20
133	Some statistical properties of differencing schemes for baseline correction of sedimentation velocity data. <i>Analytical Biochemistry</i> , <b>2010</b> , 401, 280-7	3.1	16
132	Autoinhibition of Arf GTPase-activating protein activity by the BAR domain in ASAP1. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 1652-63	5.4	55
131	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> , <b>2009</b> , 77, 3902-8	3.7	46

130	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> , <b>2009</b> , 106, 12329-34	11.5	42
129	The C-terminal domain of Plasmodium falciparum merozoite surface protein 3 self-assembles into alpha-helical coiled coil tetramer. <i>Molecular and Biochemical Parasitology</i> , <b>2009</b> , 165, 153-61	1.9	16
128	On the analysis of sedimentation velocity in the study of protein complexes. <i>European Biophysics Journal</i> , <b>2009</b> , 38, 1079-99	1.9	46
127	Stability of ligand-binding domain dimer assembly controls kainate receptor desensitization. <i>EMBO Journal</i> , <b>2009</b> , 28, 1518-30	13	48
126	The N-terminal domain of GluR6-subtype glutamate receptor ion channels. <i>Nature Structural and Molecular Biology</i> , <b>2009</b> , 16, 631-8	17.6	90
125	Assembly, loading, and alignment of an analytical ultracentrifuge sample cell. <i>Journal of Visualized Experiments</i> , <b>2009</b> ,	1.6	16
124	Extended polypeptide linkers establish the spatial architecture of a pyruvate dehydrogenase multienzyme complex. <i>Structure</i> , <b>2008</b> , 16, 93-103	5.2	20
123	Bacteriorhodopsin/amphipol complexes: structural and functional properties. <i>Biophysical Journal</i> , <b>2008</b> , 94, 3523-37	2.9	93
122	Apolipoprotein C-II amyloid fibrils assemble via a reversible pathway that includes fibril breaking and rejoining. <i>Journal of Molecular Biology</i> , <b>2008</b> , 376, 1116-29	6.5	61
121	Bayesian analysis of heterogeneity in the distribution of binding properties of immobilized surface sites. <i>Langmuir</i> , <b>2008</b> , 24, 11577-86	4	34
120	Characterizing protein-protein interactions by sedimentation velocity analytical ultracentrifugation. <i>Current Protocols in Immunology</i> , <b>2008</b> , Chapter 18, Unit 18.15	4	75
119	Humanized monoclonal antibodies derived from chimpanzee Fabs protect against Japanese encephalitis virus in vitro and in vivo. <i>Journal of Virology</i> , <b>2008</b> , 82, 7009-21	6.6	62
118	A new adaptive grid-size algorithm for the simulation of sedimentation velocity profiles in analytical ultracentrifugation. <i>Computer Physics Communications</i> , <b>2008</b> , 178, 105-120	4.2	71
117	A bayesian approach for quantifying trace amounts of antibody aggregates by sedimentation velocity analytical ultracentrifugation. <i>AAPS Journal</i> , <b>2008</b> , 10, 481-93	3.7	31
116	Using prior knowledge in the determination of macromolecular size-distributions by analytical ultracentrifugation. <i>Biomacromolecules</i> , <b>2007</b> , 8, 2011-24	6.9	55
115	Two interferons alpha influence each other during their interaction with the extracellular domain of human type interferon receptor subunit 2. <i>Biochemistry</i> , <b>2007</b> , 46, 14638-49	3.2	9
114	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> , <b>2007</b> , 92, 1742-58	2.9	73
113	Sedimentation Equilibrium Analytical Ultracentrifugation for Multicomponent Protein Interactions <b>2007</b> , 289-316		7



112	Single-walled tubulin ring polymers. <i>Biopolymers</i> , <b>2007</b> , 86, 424-36	2.2	11
111	Superantigen natural affinity maturation revealed by the crystal structure of staphylococcal enterotoxin G and its binding to T-cell receptor Vbeta8.2. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 68, 389-402	4.2	19
110	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> , <b>2007</b> , 16, 30-42	6.3	248
109	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> , <b>2007</b> , 81, 8989-95	6.6	42
108	Cellular expression and crystal structure of the murine cytomegalovirus major histocompatibility complex class I-like glycoprotein, m153. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 35247-58	5.4	22
107	Measuring protein-protein interactions by equilibrium sedimentation. <i>Current Protocols in Immunology</i> , <b>2007</b> , Chapter 18, Unit 18.8	4	30
106	Sedimentation Velocity in the Study of Reversible Multiprotein Complexes <b>2007</b> , 469-518		5
105	Surface Plasmon Resonance Biosensing in the Study of Ternary Systems of Interacting Proteins <b>2007</b> , 97-141		4
104	Crystal structure of group A streptococcus Mac-1: insight into dimer-mediated specificity for recognition of human IgG. <i>Structure</i> , <b>2006</b> , 14, 225-35	5.2	22
103	Efficient neutralization of anthrax toxin by chimpanzee monoclonal antibodies against protective antigen. <i>Journal of Infectious Diseases</i> , <b>2006</b> , 193, 625-33	7	61
102	Quaternary structure and cleavage specificity of a poxvirus holliday junction resolvase. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 11618-26	5.4	14
101	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> , <b>2006</b> , 103, 1882-7	11.5	71
100	Macromolecular size-and-shape distributions by sedimentation velocity analytical ultracentrifugation. <i>Biophysical Journal</i> , <b>2006</b> , 90, 4651-61	2.9	426
99	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> , <b>2006</b> , 362, 102-13	6.5	27
98	Protein S multimers and monomers each have direct anticoagulant activity. <i>Journal of Thrombosis and Haemostasis</i> , <b>2006</b> , 4, 385-91	15.4	15
97	Oligomerization of signaling complexes by the multipoint binding of GRB2 to both LAT and SOS1. <i>Nature Structural and Molecular Biology</i> , <b>2006</b> , 13, 798-805	17.6	164
96	Conformational restriction blocks glutamate receptor desensitization. <i>Nature Structural and Molecular Biology</i> , <b>2006</b> , 13, 1120-7	17.6	92
95	Eukaryotic RNases H1 act processively by interactions through the duplex RNA-binding domain. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 2166-75	20.1	41

94	Self-association and ligand-induced conformational changes of iron regulatory proteins 1 and 2. <i>Biochemistry</i> , <b>2005</b> , 44, 8470-8	3.2	23
93	Influence of temperature on the conformation of canine plasminogen: an analytical ultracentrifugation and dynamic light scattering study. <i>Biochemistry</i> , <b>2005</b> , 44, 13122-31	3.2	15
92	Sedimentation velocity analysis of heterogeneous protein-protein interactions: Lamm equation modeling and sedimentation coefficient distributions c(s). <i>Biophysical Journal</i> , <b>2005</b> , 89, 619-34	2.9	149
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