

Peter Schuck

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237
papers

16,980
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61
h-index

124
g-index

324
ext. papers

18,716
ext. citations

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avg, IF

7.12
L-index

#	Paper	IF	Citations
237	Size-distribution analysis of macromolecules by sedimentation velocity ultracentrifugation and lamm equation modeling. <i>Biophysical Journal</i> , 2000 , 78, 1606-19	2.9	3035
236	Size-distribution analysis of proteins by analytical ultracentrifugation: strategies and application to model systems. <i>Biophysical Journal</i> , 2002 , 82, 1096-111	2.9	588
235	Modern analytical ultracentrifugation in protein science: look forward, not back. <i>Protein Science</i> , 2003 , 12, 2647-9; discussion 2649-50	6.3	558
234	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, 541-66		532
233	On the analysis of protein self-association by sedimentation velocity analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2003 , 320, 104-24	3.1	513
232	Macromolecular size-and-shape distributions by sedimentation velocity analytical ultracentrifugation. <i>Biophysical Journal</i> , 2006 , 90, 4651-61	2.9	426
231	Crystal structure of an NK cell immunoglobulin-like receptor in complex with its class I MHC ligand. <i>Nature</i> , 2000 , 405, 537-43	50.4	339
230	High-precision isothermal titration calorimetry with automated peak-shape analysis. <i>Analytical Chemistry</i> , 2012 , 84, 5066-73	7.8	329
229	Sedimentation equilibrium analysis of protein interactions with global implicit mass conservation constraints and systematic noise decomposition. <i>Analytical Biochemistry</i> , 2004 , 326, 234-56	3.1	312
228	Sedimentation analysis of noninteracting and self-associating solutes using numerical solutions to the Lamm equation. <i>Biophysical Journal</i> , 1998 , 75, 1503-12	2.9	308
227	On the distribution of protein refractive index increments. <i>Biophysical Journal</i> , 2011 , 100, 2309-17	2.9	300
226	Determination of the sedimentation coefficient distribution by least-squares boundary modeling. <i>Biopolymers</i> , 2000 , 54, 328-41	2.2	278
225	Modern analytical ultracentrifugation in protein science: a tutorial review. <i>Protein Science</i> , 2002 , 11, 2067-79	6.3	265
224	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	6.3	248
223	Calculating sedimentation coefficient distributions by direct modeling of sedimentation velocity concentration profiles. <i>Methods in Enzymology</i> , 2004 , 384, 185-212	1.7	232
222	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, 1230-49	2.9	206
221	Analysis of mass transport-limited binding kinetics in evanescent wave biosensors. <i>Analytical Biochemistry</i> , 1996 , 240, 262-72	3.1	204

220	SEDPHAT--a platform for global ITC analysis and global multi-method analysis of molecular interactions. <i>Methods</i> , 2015 , 76, 137-148	4.6	173
219	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	17.6	164
218	Reliable determination of binding affinity and kinetics using surface plasmon resonance biosensors. <i>Current Opinion in Biotechnology</i> , 1997 , 8, 498-502	11.4	154
217	Direct sedimentation analysis of interference optical data in analytical ultracentrifugation. <i>Biophysical Journal</i> , 1999 , 76, 2288-96	2.9	153
216	Sedimentation velocity analysis of heterogeneous protein-protein interactions: Lamm equation modeling and sedimentation coefficient distributions c(s). <i>Biophysical Journal</i> , 2005 , 89, 619-34	2.9	149
215	Integration and global analysis of isothermal titration calorimetry data for studying macromolecular interactions. <i>Nature Protocols</i> , 2016 , 11, 882-94	18.8	135
214	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	1.4	125
213	Kinetic analysis of biosensor data: elementary tests for self-consistency. <i>Trends in Biochemical Sciences</i> , 1996 , 21, 458-60	10.3	124
212	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, 81-6	11.5	119
211	Crystal structure of a superantigen bound to the high-affinity, zinc-dependent site on MHC class II. <i>Immunity</i> , 2001 , 14, 93-104	32.3	119
210	Overview of current methods in sedimentation velocity and sedimentation equilibrium analytical ultracentrifugation. <i>Current Protocols in Protein Science</i> , 2013 , Chapter 20, Unit20.12	3.1	118
209	Variable MHC class I engagement by Ly49 natural killer cell receptors demonstrated by the crystal structure of Ly49C bound to H-2K(b). <i>Nature Immunology</i> , 2003 , 4, 1213-22	19.1	118
208	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, 30936-44	5.4	114
207	Higher-order oligomerization promotes localization of SPOP to liquid nuclear speckles. <i>EMBO Journal</i> , 2016 , 35, 1254-75	13	113
206	A conformational switch in HP1 releases auto-inhibition to drive heterochromatin assembly. <i>Nature</i> , 2013 , 496, 377-81	50.4	107
205	Combined affinity and rate constant distributions of ligand populations from experimental surface binding kinetics and equilibria. <i>Biophysical Journal</i> , 2003 , 84, 4062-77	2.9	105
204	Self-association of human apolipoprotein E3 and E4 in the presence and absence of phospholipid. <i>Journal of Biological Chemistry</i> , 2000 , 275, 36758-65	5.4	101
203	Structure and assembly mechanism for heteromeric kainate receptors. <i>Neuron</i> , 2011 , 71, 319-31	13.9	96

202	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, 651-66	2.9	94
201	Bacteriorhodopsin/amphipol complexes: structural and functional properties. <i>Biophysical Journal</i> , 2008 , 94, 3523-37	2.9	93
200	Binding specificity of multiprotein signaling complexes is determined by both cooperative interactions and affinity preferences. <i>Biochemistry</i> , 2004 , 43, 4170-8	3.2	93
199	Conformational restriction blocks glutamate receptor desensitization. <i>Nature Structural and Molecular Biology</i> , 2006 , 13, 1120-7	17.6	92
198	The N-terminal domain of GluR6-subtype glutamate receptor ion channels. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 631-8	17.6	90
197	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		88
196	Cooperative interactions at the SLP-76 complex are critical for actin polymerization. <i>EMBO Journal</i> , 2010 , 29, 2315-28	13	85
195	Exposure of acidic residues as a danger signal for recognition of fibrinogen and other macromolecules by integrin α X β 2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 1614-9	11.5	85
194	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, 1895-900	11.5	84
193	Rotavirus nonstructural protein NSP2 self-assembles into octamers that undergo ligand-induced conformational changes. <i>Journal of Biological Chemistry</i> , 2001 , 276, 9679-87	5.4	81
192	Non-ideality by sedimentation velocity of halophilic malate dehydrogenase in complex solvents. <i>Biophysical Journal</i> , 2001 , 81, 1868-80	2.9	81
191	Recorded scan times can limit the accuracy of sedimentation coefficients in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2013 , 437, 104-8	3.1	79
190	Characterizing protein-protein interactions by sedimentation velocity analytical ultracentrifugation. <i>Current Protocols in Immunology</i> , 2008 , Chapter 18, Unit 18.15	4	75
189	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, 4611-7	5.4	74
188	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, 4589-98	6.6	74
187	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, 1742-58	2.9	73
186	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. <i>Journal of Molecular Biology</i> , 1999 , 290, 685-98	6.5	73
185	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	4.2	71

184	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, 1882-7	11.5	71
183	Determination of sedimentation coefficients for small peptides. <i>Biophysical Journal</i> , 1998 , 74, 466-74	2.9	71
182	Determination of binding constants by equilibrium titration with circulating sample in a surface plasmon resonance biosensor. <i>Analytical Biochemistry</i> , 1998 , 265, 79-91	3.1	70
181	A model for sedimentation in inhomogeneous media. I. Dynamic density gradients from sedimenting co-solutes. <i>Biophysical Chemistry</i> , 2004 , 108, 187-200	3.5	69
180	SEDFIT-MSTAR: molecular weight and molecular weight distribution analysis of polymers by sedimentation equilibrium in the ultracentrifuge. <i>Analyst, The</i> , 2014 , 139, 79-92	5	68
179	Humanized monoclonal antibodies derived from chimpanzee Fabs protect against Japanese encephalitis virus in vitro and in vivo. <i>Journal of Virology</i> , 2008 , 82, 7009-21	6.6	62
178	Apolipoprotein C-II amyloid fibrils assemble via a reversible pathway that includes fibril breaking and rejoining. <i>Journal of Molecular Biology</i> , 2008 , 376, 1116-29	6.5	61
177	Efficient neutralization of anthrax toxin by chimpanzee monoclonal antibodies against protective antigen. <i>Journal of Infectious Diseases</i> , 2006 , 193, 625-33	7	61
176	Biochemical and biological characterization of a dodecameric CD4-Ig fusion protein: implications for therapeutic and vaccine strategies. <i>Journal of Biological Chemistry</i> , 2002 , 277, 11456-64	5.4	61
175	Analytical Ultracentrifugation as a Tool for Studying Protein Interactions. <i>Biophysical Reviews</i> , 2013 , 5, 159-171	3.7	60
174	The human immunodeficiency virus type 1 gp120 V2 domain mediates gp41-independent intersubunit contacts. <i>Journal of Virology</i> , 2000 , 74, 4448-55	6.6	60
173	Sedimentation patterns of rapidly reversible protein interactions. <i>Biophysical Journal</i> , 2010 , 98, 2005-13	2.9	56
172	The molecular refractive function of lens β Crystallins. <i>Journal of Molecular Biology</i> , 2011 , 411, 680-99	6.5	55
171	Autoinhibition of Arf GTPase-activating protein activity by the BAR domain in ASAP1. <i>Journal of Biological Chemistry</i> , 2009 , 284, 1652-63	5.4	55
170	Using prior knowledge in the determination of macromolecular size-distributions by analytical ultracentrifugation. <i>Biomacromolecules</i> , 2007 , 8, 2011-24	6.9	55
169	Mass spectrometry after capture and small-volume elution of analyte from a surface plasmon resonance biosensor. <i>Analytical Chemistry</i> , 2002 , 74, 2041-7	7.8	55
168	A multilaboratory comparison of calibration accuracy and the performance of external references in analytical ultracentrifugation. <i>PLoS ONE</i> , 2015 , 10, e0126420	3.7	55
167	Biointeractions of ultrasmall glutathione-coated gold nanoparticles: effect of small size variations. <i>Nanoscale</i> , 2016 , 8, 6577-88	7.7	54

166	Improving the thermal, radial, and temporal accuracy of the analytical ultracentrifuge through external references. <i>Analytical Biochemistry</i> , 2013 , 440, 81-95	3.1	54
165	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, 2828-35	7.8	53
164	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> , 2016 , 113, E1006-15	11.5	52
163	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, 14877-82	11.5	50
162	Interaction of the NK cell inhibitory receptor Ly49A with H-2Dd: identification of a site distinct from the TCR site. <i>Immunity</i> , 1999 , 11, 591-601	32.3	49
161	Stability of ligand-binding domain dimer assembly controls kainate receptor desensitization. <i>EMBO Journal</i> , 2009 , 28, 1518-30	13	48
160	Basic Principles of Analytical Ultracentrifugation		47
159	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, 3902-8	3.7	46
158	On the analysis of sedimentation velocity in the study of protein complexes. <i>European Biophysics Journal</i> , 2009 , 38, 1079-99	1.9	46
157	Simultaneous radial and wavelength analysis with the Optima XL-A analytical ultracentrifuge 1994 , 1-13		46
156	SDR grafting of a murine antibody using multiple human germline templates to minimize its immunogenicity. <i>Molecular Immunology</i> , 2004 , 41, 863-72	4.3	45
155	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	2.5	43
154	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, 11296-306	3.2	43
153	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, 12329-34	11.5	42
152	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, 8989-95	6.6	42
151	Crystal structure of the C-terminal peptidoglycan-binding domain of human peptidoglycan recognition protein Ialpha. <i>Journal of Biological Chemistry</i> , 2004 , 279, 31873-82	5.4	42
150	Calcium-sensitive interaction between calmodulin and modified forms of rat brain neurogranin/RC3. <i>Biochemistry</i> , 2000 , 39, 7291-9	3.2	42
149	Eukaryotic RNases H1 act processively by interactions through the duplex RNA-binding domain. <i>Nucleic Acids Research</i> , 2005 , 33, 2166-75	20.1	41

148	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	11.5	41
147	A comparison of binding surfaces for SPR biosensing using an antibody-antigen system and affinity distribution analysis. <i>Methods</i> , 2013 , 59, 328-35	4.6	40
146	Global multi-method analysis of affinities and cooperativity in complex systems of macromolecular interactions. <i>Analytical Chemistry</i> , 2012 , 84, 9513-9	7.8	40
145	Extended Fujita approach to the molecular weight distribution of polysaccharides and other polymeric systems. <i>Methods</i> , 2011 , 54, 136-44	4.6	40
144	Analysis of high-affinity assembly for AMPA receptor amino-terminal domains. <i>Journal of General Physiology</i> , 2012 , 139, 371-88	3.4	40
143	Amino acid residues that influence Fc epsilon RI-mediated effector functions of human immunoglobulin E. <i>Biochemistry</i> , 1998 , 37, 16152-64	3.2	40
142	An allosteric site in the T-cell receptor CD domain plays a critical signalling role. <i>Nature Communications</i> , 2017 , 8, 15260	17.4	39
141	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, 7082-93	6.6	39
140	Density contrast sedimentation velocity for the determination of protein partial-specific volumes. <i>PLoS ONE</i> , 2011 , 6, e26221	3.7	39
139	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, 37236-45	5.4	37
138	Analysis of protein interactions with picomolar binding affinity by fluorescence-detected sedimentation velocity. <i>Analytical Chemistry</i> , 2014 , 86, 3181-7	7.8	36
137	Analysis of transport experiments using pseudo-absorbance data. <i>Analytical Biochemistry</i> , 2000 , 285, 135-42	3.1	36
136	Characterizing the Solution Properties of Supramolecular Systems by Analytical Ultracentrifugation. <i>Chemistry - A European Journal</i> , 1999 , 5, 1377-1383	4.8	36
135	Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5. <i>ELife</i> , 2018 , 7,	8.9	36
134	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, 4140-51	4.8	35
133	Biophysical characterization of DNA and RNA aptamer interactions with hen egg lysozyme. <i>International Journal of Biological Macromolecules</i> , 2011 , 48, 392-7	7.9	35
132	Sedimentation equilibrium analysis of recombinant mouse FcRn with murine IgG1. <i>Molecular Immunology</i> , 1999 , 36, 1117-25	4.3	35
131	Bayesian analysis of heterogeneity in the distribution of binding properties of immobilized surface sites. <i>Langmuir</i> , 2008 , 24, 11577-86	4	34

130	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, 3076-84	5.3	33
129	Measuring macromolecular size distributions and interactions at high concentrations by sedimentation velocity. <i>Nature Communications</i> , 2018 , 9, 4415	17.4	33
128	Regulation of ASAP1 by phospholipids is dependent on the interface between the PH and Arf GAP domains. <i>Cellular Signalling</i> , 2005 , 17, 1276-88	4.9	32
127	The boundary structure in the analysis of reversibly interacting systems by sedimentation velocity. <i>Methods</i> , 2011 , 54, 16-30	4.6	31
126	A bayesian approach for quantifying trace amounts of antibody aggregates by sedimentation velocity analytical ultracentrifugation. <i>AAPS Journal</i> , 2008 , 10, 481-93	3.7	31
125	A model for sedimentation in inhomogeneous media. II. Compressibility of aqueous and organic solvents. <i>Biophysical Chemistry</i> , 2004 , 108, 201-14	3.5	31
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, 491-7	3.6	31
123	Use of fluorescence-detected sedimentation velocity to study high-affinity protein interactions. <i>Nature Protocols</i> , 2017 , 12, 1777-1791	18.8	30
122	Diffusion of the reaction boundary of rapidly interacting macromolecules in sedimentation velocity. <i>Biophysical Journal</i> , 2010 , 98, 2741-51	2.9	30
121	Measuring protein-protein interactions by equilibrium sedimentation. <i>Current Protocols in Immunology</i> , 2007 , Chapter 18, Unit 18.8	4	30
120	Quantifying the energetics of cooperativity in a ternary protein complex. <i>Biochemistry</i> , 2002 , 41, 5177-84.2		29
119	Sedimentation Velocity Analytical Ultracentrifugation		29
118	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	3.7	28
117	Differences in the binding capacity of human apolipoprotein E3 and E4 to size-fractionated lipid emulsions. <i>FEBS Journal</i> , 2002 , 269, 5939-49		28
116	Reversible and fast association equilibria of a molecular chaperone, gp57A, of bacteriophage T4. <i>Biophysical Journal</i> , 2003 , 85, 2606-18	2.9	28
115	Analytical ultracentrifugation as a tool for studying membrane proteins 1991 , 12-22		28
114	Binding kinetics of ultrasmall gold nanoparticles with proteins. <i>Nanoscale</i> , 2018 , 10, 3235-3244	7.7	27
113	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, 102-13	6.5	27

112	Direct interaction of the mouse cytomegalovirus m152/gp40 immunoevasin with RAE-1 isoforms. <i>Biochemistry</i> , 2010 , 49, 2443-53	3.2	26
111	Solution properties of β -crystallins: hydration of fish and mammal β -crystallins. <i>Protein Science</i> , 2014 , 23, 88-99	6.3	25
110	Analytical band centrifugation of proteins and protein complexes. <i>Biochemical Society Transactions</i> , 1998 , 26, 745-9	5.1	25
109	Band 3-hemoglobin associations. The band 3 tetramer is the oxyhemoglobin binding site. <i>FEBS Letters</i> , 1991 , 293, 81-4	3.8	25
108	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, 806-12		25
107	Tools for the quantitative analysis of sedimentation boundaries detected by fluorescence optical analytical ultracentrifugation. <i>PLoS ONE</i> , 2013 , 8, e77245	3.7	25
106	The role of macromolecular crowding in the evolution of lens crystallins with high molecular refractive index. <i>Physical Biology</i> , 2011 , 8, 046004	3	24
105	AUC and Small-Angle Scattering for Membrane Proteins. <i>Methods in Enzymology</i> , 2015 , 562, 257-86	1.7	23
104	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, 678-96	6.5	23
103	Self-association and ligand-induced conformational changes of iron regulatory proteins 1 and 2. <i>Biochemistry</i> , 2005 , 44, 8470-8	3.2	23
102	Sedimentation equilibrium analysis of interference optical data by systematic noise decomposition. <i>Analytical Biochemistry</i> , 1999 , 272, 199-208	3.1	23
101	Malaria vaccine candidate: design of a multivalent subunit helical coiled coil poly-epitope. <i>Vaccine</i> , 2011 , 29, 7090-9	4.1	22
100	Crystal structure of group A streptococcus Mac-1: insight into dimer-mediated specificity for recognition of human IgG. <i>Structure</i> , 2006 , 14, 225-35	5.2	22
99	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, 35247-58	5.4	22
98	On computational approaches for size-and-shape distributions from sedimentation velocity analytical ultracentrifugation. <i>European Biophysics Journal</i> , 2010 , 39, 1261-75	1.9	21
97	Rapid determination of molar mass in modified Archibald experiments using direct fitting of the Lamm equation. <i>Analytical Biochemistry</i> , 1998 , 259, 48-53	3.1	21
96	Minimizing immunogenicity of the SDR-grafted humanized antibody CC49 by genetic manipulation of the framework residues. <i>Molecular Immunology</i> , 2003 , 40, 337-49	4.3	21
95	A mechanism for assembly of complexes of vitronectin and plasminogen activator inhibitor-1 from sedimentation velocity analysis. <i>Journal of Biological Chemistry</i> , 2005 , 280, 28711-20	5.4	21

94	Characterization of serum albumin nanoparticles by sedimentation velocity analysis and electron microscopy 2002 , 31-36		21
93	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	6.5	20
92	Accounting for solvent signal offsets in the analysis of interferometric sedimentation velocity data. <i>Macromolecular Bioscience</i> , 2010 , 10, 736-45	5.5	20
91	Extended polypeptide linkers establish the spatial architecture of a pyruvate dehydrogenase multienzyme complex. <i>Structure</i> , 2008 , 16, 93-103	5.2	20
90	3D-Printing for Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2016 , 11, e0155201	3.7	20
89	Allosteric inhibition of β thrombin enzymatic activity with ultrasmall gold nanoparticles. <i>Nanoscale Advances</i> , 2019 , 1, 378-388	5.1	20
88	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> , 2007 , 68, 389-402	4.2	19
87	Hydrodynamics of nanoscopic tubulin rings in dilute solutions. <i>Physical Review Letters</i> , 2004 , 93, 098106	7.4	19
86	Preferential assembly of heteromeric kainate and AMPA receptor amino terminal domains. <i>ELife</i> , 2017 , 6,	8.9	18
85	Variable Field Analytical Ultracentrifugation: II. Gravitational Sweep Sedimentation Velocity. <i>Biophysical Journal</i> , 2016 , 110, 103-12	2.9	18
84	Solution properties of β crystallins: compact structure and low frictional ratio are conserved properties of diverse β crystallins. <i>Protein Science</i> , 2014 , 23, 76-87	6.3	18
83	In vitro affinity maturation of a specificity-determining region-grafted humanized anticarcinoma antibody: isolation and characterization of minimally immunogenic high-affinity variants. <i>Clinical Cancer Research</i> , 2003 , 9, 5521-31	12.9	18
82	An equilibrium model for linear and closed-loop amyloid fibril formation. <i>Journal of Molecular Biology</i> , 2012 , 421, 364-77	6.5	17
81	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	5.6	16
80	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	3.7	16
79	The C-terminal domain of <i>Plasmodium falciparum</i> merozoite surface protein 3 self-assembles into alpha-helical coiled coil tetramer. <i>Molecular and Biochemical Parasitology</i> , 2009 , 165, 153-61	1.9	16
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