

# Peter Schuck

## List of Publications by Year in descending order

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272  
papers

20,098  
citations

18887

64  
h-index

14779

131  
g-index

324  
all docs

324  
docs citations

324  
times ranked

20290  
citing authors

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | Best Practices for Aggregate Quantitation of Antibody Therapeutics by Sedimentation Velocity Analytical Ultracentrifugation. <i>Journal of Pharmaceutical Sciences</i> , 2022, 111, 2121-2133.   | 1.6 | 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.  | 1.6 | 7         |
| 4  | A multi-laboratory benchmark study of isothermal titration calorimetry (ITC) using Ca <sup>2+</sup> and Mg <sup>2+</sup> binding to EDTA. <i>European Biophysics Journal</i> , 2021, 50, 429-451.  | 1.2 | 12        |
| 5  | Determining the Stoichiometry of a Proteinâ€“Polymer Conjugate Using Multisignal Sedimentation Velocity Analytical Ultracentrifugation. <i>Bioconjugate Chemistry</i> , 2021, 32, 942-949.   | 1.8 | 5         |
| 6  | Energetic and structural features of SARS-CoV-2 N-protein co-assemblies with nucleic acids. <i>IScience</i> , 2021, 24, 102523.  | 1.9 | 34        |
| 7  | A multi-step nucleation process determines the kinetics of prion-like domain phase separation. <i>Nature Communications</i> , 2021, 12, 4513.  | 5.8 | 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, . | 3.3 | 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, .                 | 3.3 | 11        |
| 10 | Calibrating analytical ultracentrifuges. <i>European Biophysics Journal</i> , 2021, 50, 353-362.   | 1.2 | 4         |
| 11 | Biomolecular interactions of ultrasmall metallic nanoparticles and nanoclusters. <i>Nanoscale Advances</i> , 2021, 3, 2995-3027.   | 2.2 | 27        |
| 12 | The intrinsic kinase activity of BRD4 spans its BD2-B-BID domains. <i>Journal of Biological Chemistry</i> , 2021, 297, 101326.   | 1.6 | 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.                | 3.3 | 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.   | 2.1 | 4         |
| 15 | Measuring aggregates, self-association, and weak interactions in concentrated therapeutic antibody solutions. <i>MAbs</i> , 2020, 12, 1810488.   | 2.6 | 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.  | 1.6 | 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.                            | 1.2 | 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.  | 1.5 | 18        |
| 20 | Nucleic acid-induced dimerization of HIV-1 Gag protein. <i>Journal of Biological Chemistry</i> , 2019, 294, 16480-16493.   | 1.6 | 15        |
| 21 | Efficient data acquisition with three-channel centerpieces in sedimentation velocity. <i>Analytical Biochemistry</i> , 2019, 586, 113414.  | 1.1 | 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.   | 6.6 | 22        |
| 23 | All tubulins are not alike: Heterodimer dissociation differs among different biological sources. <i>Journal of Biological Chemistry</i> , 2019, 294, 10315-10324.  | 1.6 | 13        |
| 24 | A Reappraisal of Sedimentation Nonideality Coefficients for the Analysis of Weak Interactions of Therapeutic Proteins. <i>AAPS Journal</i> , 2019, 21, 35.   | 2.2 | 11        |
| 25 | Enhanced Sample Handling for Analytical Ultracentrifugation with 3D-Printed Centerpieces. <i>Analytical Chemistry</i> , 2019, 91, 5866-5873.   | 3.2 | 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.         | 0.2 | 1         |
| 27 | Measuring Macromolecular Size-Distributions and Interactions at High Concentrations by Sedimentation Velocity. <i>Biophysical Journal</i> , 2019, 116, 158a.   | 0.2 | 0         |
| 28 | Allosteric inhibition of $\hat{\pm}$ -thrombin enzymatic activity with ultrasmall gold nanoparticles. <i>Nanoscale Advances</i> , 2019, 1, 378-388.  | 2.2 | 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.  | 2.4 | 23        |
| 30 | Binding kinetics of ultrasmall gold nanoparticles with proteins. <i>Nanoscale</i> , 2018, 10, 3235-3244.   | 2.8 | 39        |
| 31 | Congratulations to Dr. Fumio Arisaka on his 70th birthday. <i>Biophysical Reviews</i> , 2018, 10, 137-137.   | 1.5 | 1         |
| 32 | Assembly of Kainate and AMPA Receptors. <i>Biophysical Journal</i> , 2018, 114, 126a.  | 0.2 | 0         |
| 33 | Sedimentation Boundary Structure of Multi-Component Solutions with Rapidly Reversible Interactions. <i>Biophysical Journal</i> , 2018, 114, 172a-173a.   | 0.2 | 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. | 3.3 | 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.   | 3.3 | 24        |
| 36 | Measuring macromolecular size distributions and interactions at high concentrations by sedimentation velocity. <i>Nature Communications</i> , 2018, 9, 4415.   | 5.8 | 48        |

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|----|--|-----|-----------|
| 37 | All Tubulins are Not Alike: Dimer Dissociation and Monomer Exchange Differ Depending on the Biological Source of Tubulin. <i>Biophysical Journal</i> , 2018, 114, 504a.  | 0.2 | 2         |
| 38 | A radial calibration window for analytical ultracentrifugation. <i>PLoS ONE</i> , 2018, 13, e0201529.  | 1.1 | 8         |
| 39 | Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5. <i>ELife</i> , 2018, 7, .  | 2.8 | 73        |
| 40 | Sedimentation Velocity Analytical Ultracentrifugation. , 2018, , 1-14.   |     | 0         |
| 41 | Sedimentation of Reversibly Interacting Macromolecules with Changes in Fluorescence Quantum Yield. <i>Biophysical Journal</i> , 2017, 112, 1374-1382.  | 0.2 | 8         |
| 42 | An allosteric site in the T-cell receptor C $\beta$ domain plays a critical signalling role. <i>Nature Communications</i> , 2017, 8, 15260.  | 5.8 | 64        |
| 43 | Measuring Protein Interactions by Optical Biosensors. <i>Current Protocols in Protein Science</i> , 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. <i>Biophysical Journal</i> , 2017, 112, 192a.  | 0.2 | 0         |
| 45 | A General Framework for the Boundary Structure in Multi-Component Sedimentation Velocity with Reversible Interactions. <i>Biophysical Journal</i> , 2017, 112, 199a.   | 0.2 | 0         |
| 46 | Fluorescence Detected Sedimentation Velocity Analytical Ultracentrifugation for Investigating Affinity and Stoichiometry of Protein Interactions. <i>Biophysical Journal</i> , 2017, 112, 199a.                            | 0.2 | 0         |
| 47 | All Tubulins are Not the Same: Reversible Dissociation of AB-Tubulin Dimers Differ Depending on the Source of Tubulin. <i>Biophysical Journal</i> , 2017, 112, 360a.   | 0.2 | 0         |
| 48 | Use of fluorescence-detected sedimentation velocity to study high-affinity protein interactions. <i>Nature Protocols</i> , 2017, 12, 1777-1791.  | 5.5 | 37        |
| 49 | Crystal Structure of Chicken $\beta$ 3-Crystallin Reveals Lattice Contacts with Implications for Function in the Lens and the Evolution of the $\beta$ 2 $\beta$ 3-Crystallins. <i>Structure</i> , 2017, 25, 1068-1078.e2. | 1.6 | 15        |
| 50 | Preferential assembly of heteromeric kainate and AMPA receptor amino terminal domains. <i>ELife</i> , 2017, 6, .   | 2.8 | 25        |
| 51 | Higher-order oligomerization promotes localization of SPOP to liquid nuclear speckles. <i>EMBO Journal</i> , 2016, 35, 1254-1275.  | 3.5 | 172       |
| 52 | Sedimentation coefficient distributions of large particles. <i>Analyst, The</i> , 2016, 141, 4400-4409.  | 1.7 | 17        |
| 53 | Biointeractions of Ultrasmall Gold Nanoparticles: Influence of Nanoparticle Size and Surface Chemistry. <i>Biophysical Journal</i> , 2016, 110, 530a.  | 0.2 | 0         |
| 54 | Study Molecular Interactions in whole Cell Extracts by Fluorescence-Detected Analytical Ultracentrifugation. <i>Biophysical Journal</i> , 2016, 110, 384a.   | 0.2 | 0         |

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|----|--|-----|-----------|
| 55 | Zwitterionic glutathione monoethyl ester as a new capping ligand for ultrasmall gold nanoparticles. <i>RSC Advances</i> , 2016, 6, 46350-46355.  | 1.7 | 20        |
| 56 | Gravitational Sweep Sedimentation Velocity. <i>Biophysical Journal</i> , 2016, 110, 384a.  | 0.2 | 0         |
| 57 | Integration and global analysis of isothermal titration calorimetry data for studying macromolecular interactions. <i>Nature Protocols</i> , 2016, 11, 882-894.  | 5.5 | 225       |
| 58 | Tubulin Dimer Reversible Dissociation. <i>Journal of Biological Chemistry</i> , 2016, 291, 9281-9294.  | 1.6 | 13        |
| 59 | A New Dimension of Detection in Analytical Ultracentrifugation with Fluorescence Detection using Photoswitchable FPs as Time Domain Probes. <i>Biophysical Journal</i> , 2016, 110, 347a.                      | 0.2 | 0         |
| 60 | Tubulin Monomer-Monomer Association is Less Influenced by the Solvent than Dimer-Dimer Association: Structure and Function of Tubulin Interaction Interfaces. <i>Biophysical Journal</i> , 2016, 110, 26a-27a. | 0.2 | 1         |
| 61 | 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.         | 3.3 | 73        |
| 62 | Biointeractions of ultrasmall glutathione-coated gold nanoparticles: effect of small size variations. <i>Nanoscale</i> , 2016, 8, 6577-6588.   | 2.8 | 69        |
| 63 | Variable Field Analytical Ultracentrifugation: II. Gravitational Sweep Sedimentation Velocity. <i>Biophysical Journal</i> , 2016, 110, 103-112.  | 0.2 | 25        |
| 64 | 3D-Printing for Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2016, 11, e0155201.  | 1.1 | 27        |
| 65 | Monochromatic multicomponent fluorescence sedimentation velocity for the study of high-affinity protein interactions. <i>ELife</i> , 2016, 5, .  | 2.8 | 11        |
| 66 | Sedimentation in a Time-Varying Centrifugal Field for Rapid Attainment of Sedimentation Equilibrium. <i>Biophysical Journal</i> , 2015, 108, 222a.   | 0.2 | 0         |
| 67 | Sedimentation Velocity Analysis of the EGFPs in <i>E. coli</i> Whole Cell Extracts using Fluorescence Detection System. <i>Biophysical Journal</i> , 2015, 108, 624a.  | 0.2 | 0         |
| 68 | The Role of Higher-Order SPOP Oligomers for Localization to Cellular "Bodies" and Ubiquitination Activity. <i>Biophysical Journal</i> , 2015, 108, 390a.   | 0.2 | 0         |
| 69 | Accounting for Photophysical Processes and Specific Signal Intensity Change in Fluorescence-Detected Sedimentation Velocity Analytical Ultracentrifugation. <i>Biophysical Journal</i> , 2015, 108, 624a.      | 0.2 | 0         |
| 70 | AUC and Small-Angle Scattering for Membrane Proteins. <i>Methods in Enzymology</i> , 2015, 562, 257-286.   | 0.4 | 34        |
| 71 | A histogram approach to the quality of fit in sedimentation velocity analyses. <i>Analytical Biochemistry</i> , 2015, 483, 1-3.  | 1.1 | 14        |
| 72 | Combining biophysical methods for the analysis of protein complex stoichiometry and affinity in SEDPHAT. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 3-14.                 | 2.5 | 139       |

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|----|--|-----|-----------|
| 73 | Biocalorimetry. <i>Methods</i> , 2015, 76, 1-2.  | 1.9 | 9         |
| 74 | SEDPHAT – A platform for global ITC analysis and global multi-method analysis of molecular interactions. <i>Methods</i> , 2015, 76, 137-148.   | 1.9 | 264       |
| 75 | Variable-Field Analytical Ultracentrifugation: I. Time-Optimized Sedimentation Equilibrium. <i>Biophysical Journal</i> , 2015, 109, 827-837.   | 0.2 | 12        |
| 76 | A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2015, 10, e0126420.                     | 1.1 | 71        |
| 77 | 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> , 2014, 9, e87921.       | 1.1 | 13        |
| 78 | Solution properties of $\beta$ -crystallins: Hydration of fish and mammal $\beta$ -crystallins. <i>Protein Science</i> , 2014, 23, 88-99.  | 3.1 | 30        |
| 79 | Human Herpesvirus 7 U21 Tetramerizes To Associate with Class I Major Histocompatibility Complex Molecules. <i>Journal of Virology</i> , 2014, 88, 3298-3308.                                 | 1.5 | 17        |
| 80 | Analysis of High-Affinity Protein Interactions by Fluorescence Optical Analytical Ultracentrifugation. <i>Biophysical Journal</i> , 2014, 106, 236a.   | 0.2 | 0         |
| 81 | Tubulin Heterodimers Reversibly Dissociate with Moderate Kinetics as Demonstrated using Sedimentation Velocity Analytical Ultracentrifugation. <i>Biophysical Journal</i> , 2014, 106, 351a. | 0.2 | 0         |
| 82 | SEDFIT – MSTAR: molecular weight and molecular weight distribution analysis of polymers by sedimentation equilibrium in the ultracentrifuge. <i>Analyst</i> , 2014, 139, 79-92.              | 1.7 | 83        |
| 83 | Solution properties of $\beta$ -crystallins: Compact structure and low frictional ratio are conserved properties of diverse $\beta$ -crystallins. <i>Protein Science</i> , 2014, 23, 76-87.  | 3.1 | 23        |
| 84 | Accounting for Photophysical Processes and Specific Signal Intensity Changes in Fluorescence-Detected Sedimentation Velocity. <i>Analytical Chemistry</i> , 2014, 86, 9286-9292.             | 3.2 | 11        |
| 85 | Analysis of Protein Interactions with Picomolar Binding Affinity by Fluorescence-Detected Sedimentation Velocity. <i>Analytical Chemistry</i> , 2014, 86, 3181-3187.                         | 3.2 | 41        |
| 86 | Role of Amino-Terminal Domain in the Assembly Mechanism of Kainate-Subtype Glutamate Receptor Ion Channels. <i>Biophysical Journal</i> , 2014, 106, 151a.                                    | 0.2 | 0         |
| 87 | Improved measurement of the rotor temperature in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2014, 451, 69-75.  | 1.1 | 20        |
| 88 | Measurement of the temperature of the resting rotor in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2014, 458, 37-39.  | 1.1 | 14        |
| 89 | Investigating High Affinity Protein Self-Association by Fluorescence Optical Sedimentation Velocity Analytical Ultracentrifugation. <i>Biophysical Journal</i> , 2014, 106, 151a.            | 0.2 | 0         |
| 90 | Analytical ultracentrifugation as a tool for studying protein interactions. <i>Biophysical Reviews</i> , 2013, 5, 159-171.   | 1.5 | 73        |

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|-----|--|------|-----------|
| 91  | Biophysical methods for the study of protein interactions. <i>Methods</i> , 2013, 59, 259-260.   | 1.9  | 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.   | 1.9  | 52        |
| 93  | Improving the thermal, radial, and temporal accuracy of the analytical ultracentrifuge through external references. <i>Analytical Biochemistry</i> , 2013, 440, 81-95.   | 1.1  | 60        |
| 94  | A conformational switch in HP1 releases auto-inhibition to drive heterochromatin assembly. <i>Nature</i> , 2013, 496, 377-381.   | 13.7 | 141       |
| 95  | Recorded scan times can limit the accuracy of sedimentation coefficients in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2013, 437, 104-108.   | 1.1  | 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.   | 1.1  | 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.  | 1.1  | 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.   | 1.1  | 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.  | 1.1  | 31        |
| 101 | Tools for the Quantitative Analysis of Sedimentation Boundaries Detected by Fluorescence Optical Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2013, 8, e77245.  | 1.1  | 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.  | 0.9  | 45        |
| 104 | Global Multi-Method Analysis of Affinities and Cooperativity in Complex Systems of Macromolecular Interactions. <i>Analytical Chemistry</i> , 2012, 84, 9513-9519.   | 3.2  | 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.  | 2.0  | 30        |
| 106 | An Equilibrium Model for Linear and Closed-Loop Amyloid Fibril Formation. <i>Journal of Molecular Biology</i> , 2012, 421, 364-377.  | 2.0  | 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. | 2.0  | 27        |
| 108 | The Molecular Refractive Function of Lens Gamma Crystallins. <i>Biophysical Journal</i> , 2012, 102, 185a.   | 0.2  | 0         |

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|-----|--|-----|-----------|
| 109 | Analysis of Oligomer Assembly for the GluA2 Amino Terminal Domain. <i>Biophysical Journal</i> , 2012, 102, 335a-336a.  | 0.2 | 0         |
| 110 | High-Precision Isothermal Titration Calorimetry with Automated Peak-Shape Analysis. <i>Analytical Chemistry</i> , 2012, 84, 5066-5073.   | 3.2 | 440       |
| 111 | Strategies for assessing proton linkage to bimolecular interactions by global analysis of isothermal titration calorimetry data. <i>Journal of Chemical Thermodynamics</i> , 2012, 52, 95-107. | 1.0 | 14        |
| 112 | Dimeric States of Neural- and Epithelial-Cadherins are Distinguished by the Rate of Disassembly. <i>Biochemistry</i> , 2011, 50, 2951-2961.  | 1.2 | 13        |
| 113 | The role of macromolecular crowding in the evolution of lens crystallins with high molecular refractive index. <i>Physical Biology</i> , 2011, 8, 046004.                                      | 0.8 | 31        |
| 114 | NBD-Labeled Phospholipid Accelerates Apolipoprotein C-II Amyloid Fibril Formation but Is Not Incorporated into Mature Fibrils. <i>Biochemistry</i> , 2011, 50, 9579-9586.                      | 1.2 | 13        |
| 115 | Studying Rapidly Reversible Protein-Protein Interactions by Sedimentation Velocity Analytical Ultracentrifugation. <i>Biophysical Journal</i> , 2011, 100, 387a.                               | 0.2 | 0         |
| 116 | Biophysical characterization of DNA and RNA aptamer interactions with hen egg lysozyme. <i>International Journal of Biological Macromolecules</i> , 2011, 48, 392-397.                         | 3.6 | 45        |
| 117 | The Molecular Refractive Function of Lens $\hat{I}^3$ -Crystallins. <i>Journal of Molecular Biology</i> , 2011, 411, 680-699.  | 2.0 | 68        |
| 118 | Malaria vaccine candidate: Design of a multivalent subunit $\hat{I}^{\pm}$ -helical coiled coil poly-epitope. <i>Vaccine</i> , 2011, 29, 7090-7099.  | 1.7 | 26        |
| 119 | Extended Fujita approach to the molecular weight distribution of polysaccharides and other polymeric systems. <i>Methods</i> , 2011, 54, 136-144.  | 1.9 | 45        |
| 120 | The boundary structure in the analysis of reversibly interacting systems by sedimentation velocity. <i>Methods</i> , 2011, 54, 16-30.  | 1.9 | 35        |
| 121 | Editorial for the special issue of methods $\hat{I}^{\pm}$ Modern Analytical Ultracentrifugation $\hat{I}^{\pm}$ . <i>Methods</i> , 2011, 54, 1-3.   | 1.9 | 14        |
| 122 | Structure and Assembly Mechanism for Heteromeric Kainate Receptors. <i>Neuron</i> , 2011, 71, 319-331.   | 3.8 | 102       |
| 123 | On the Distribution of Protein Refractive Index Increments. <i>Biophysical Journal</i> , 2011, 100, 2309-2317.   | 0.2 | 410       |
| 124 | Density Contrast Sedimentation Velocity for the Determination of Protein Partial-Specific Volumes. <i>PLoS ONE</i> , 2011, 6, e26221.  | 1.1 | 49        |
| 125 | On computational approaches for size-and-shape distributions from sedimentation velocity analytical ultracentrifugation. <i>European Biophysics Journal</i> , 2010, 39, 1261-1275.             | 1.2 | 29        |
| 126 | Accounting for Solvent Signal Offsets in the Analysis of Interferometric Sedimentation Velocity Data. <i>Macromolecular Bioscience</i> , 2010, 10, 736-745.                                    | 2.1 | 26        |



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|-----|--|-----|-----------|
| 127 | Macromol. Biosci. 7/2010. Macromolecular Bioscience, 2010, 10, .   | 2.1 | 0         |
| 128 | Some statistical properties of differencing schemes for baseline correction of sedimentation velocity data. Analytical Biochemistry, 2010, 401, 280-287.   | 1.1 | 19        |
| 129 | Cooperative interactions at the SLP-76 complex are critical for actin polymerization. EMBO Journal, 2010, 29, 2315-2328.   | 3.5 | 98        |
| 130 | Energetics of Allosteric ion Binding to a Ligand-Gated ion Channel. Biophysical Journal, 2010, 98, 610a.   | 0.2 | 0         |
| 131 | Fredholm Integral Equations in Biophysical Data Analysis. IFMBE Proceedings, 2010, , 340-343.  | 0.2 | 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.       | 0.4 | 160       |
| 133 | Determining Thermodynamic Parameters of Protein Interactions By Global Analysis of Data From Multiple Techniques. Biophysical Journal, 2010, 98, 61a.  | 0.2 | 0         |
| 134 | Sedimentation Patterns of Rapidly Reversible Protein Interactions. Biophysical Journal, 2010, 98, 2005-2013.   | 0.2 | 65        |
| 135 | Diffusion of the Reaction Boundary of Rapidly Interacting Macromolecules in Sedimentation Velocity. Biophysical Journal, 2010, 98, 2741-2751.  | 0.2 | 34        |
| 136 | Direct Interaction of the Mouse Cytomegalovirus m152/gp40 Immuno-evasin with RAE-1 Isoforms. Biochemistry, 2010, 49, 2443-2453.  | 1.2 | 31        |
| 137 | Phospholipids Enhance Nucleation but Not Elongation of Apolipoprotein C-II Amyloid Fibrils. Journal of Molecular Biology, 2010, 399, 731-740.  | 2.0 | 15        |
| 138 | Autoinhibition of Arf GTPase-activating Protein Activity by the BAR Domain in ASAP1. Journal of Biological Chemistry, 2009, 284, 1652-1663.  | 1.6 | 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.        | 1.0 | 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. | 3.3 | 46        |
| 141 | The C-terminal domain of Plasmodium falciparum merozoite surface protein 3 self-assembles into $\pm$ -helical coiled coil tetramer. Molecular and Biochemical Parasitology, 2009, 165, 153-161.                  | 0.5 | 20        |
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