

Peter Schuck

List of Publications by Year in descending order

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272
papers

20,098
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16411

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12910

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324
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docs citations

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times ranked

18225
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 1 | Size-Distribution Analysis of Macromolecules by Sedimentation Velocity Ultracentrifugation and Lamm Equation Modeling. <i>Biophysical Journal</i> , 2000, 78, 1606-1619. | 0.2 | 3,484 |
| 2 | Modern analytical ultracentrifugation in protein science: A tutorial review. <i>Protein Science</i> , 2009, 11, 2067-2079. | 3.1 | 642 |
| 3 | Size-Distribution Analysis of Proteins by Analytical Ultracentrifugation: Strategies and Application to Model Systems. <i>Biophysical Journal</i> , 2002, 82, 1096-1111. | 0.2 | 639 |
| 4 | 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, 541-566. | 18.3 | 589 |
| 5 | On the analysis of protein self-association by sedimentation velocity analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2003, 320, 104-124. | 1.1 | 578 |
| 6 | Macromolecular Size-and-Shape Distributions by Sedimentation Velocity Analytical Ultracentrifugation. <i>Biophysical Journal</i> , 2006, 90, 4651-4661. | 0.2 | 494 |
| 7 | High-Precision Isothermal Titration Calorimetry with Automated Peak-Shape Analysis. <i>Analytical Chemistry</i> , 2012, 84, 5066-5073. | 3.2 | 440 |
| 8 | On the Distribution of Protein Refractive Index Increments. <i>Biophysical Journal</i> , 2011, 100, 2309-2317. | 0.2 | 410 |
| 9 | Crystal structure of an NK cell immunoglobulin-like receptor in complex with its class I MHC ligand. <i>Nature</i> , 2000, 405, 537-543. | 13.7 | 386 |
| 10 | Sedimentation equilibrium analysis of protein interactions with global implicit mass conservation constraints and systematic noise decomposition. <i>Analytical Biochemistry</i> , 2004, 326, 234-256. | 1.1 | 333 |
| 11 | Sedimentation Analysis of Noninteracting and Self-Associating Solutes Using Numerical Solutions to the Lamm Equation. <i>Biophysical Journal</i> , 1998, 75, 1503-1512. | 0.2 | 331 |
| 12 | Determination of the sedimentation coefficient distribution by least-squares boundary modeling. <i>Biopolymers</i> , 2000, 54, 328-341. | 1.2 | 306 |
| 13 | Studying multisite binary and ternary protein interactions by global analysis of isothermal titration calorimetry data in SEDPHAT: Application to adaptor protein complexes in cell signaling. <i>Protein Science</i> , 2007, 16, 30-42. | 3.1 | 295 |
| 14 | Modern analytical ultracentrifugation in protein science: a tutorial review. <i>Protein Science</i> , 2002, 11, 2067-79. | 3.1 | 286 |
| 15 | Calculating Sedimentation Coefficient Distributions by Direct Modeling of Sedimentation Velocity Concentration Profiles. <i>Methods in Enzymology</i> , 2004, 384, 185-212. | 0.4 | 264 |
| 16 | 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 |
| 17 | Kinetics of ligand binding to receptor immobilized in a polymer matrix, as detected with an evanescent wave biosensor. I. A computer simulation of the influence of mass transport. <i>Biophysical Journal</i> , 1996, 70, 1230-1249. | 0.2 | 226 |
| 18 | Integration and global analysis of isothermal titration calorimetry data for studying macromolecular interactions. <i>Nature Protocols</i> , 2016, 11, 882-894. | 5.5 | 225 |

| # | ARTICLE | IF | CITATIONS |
|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 19 | Analysis of Mass Transport-Limited Binding Kinetics in Evanescent Wave Biosensors. <i>Analytical Biochemistry</i> , 1996, 240, 262-272. | 1.1 | 217 |
| 20 | 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. | 3.6 | 195 |
| 21 | Higher-order oligomerization promotes localization of SPOP to liquid nuclear speckles. <i>EMBO Journal</i> , 2016, 35, 1254-1275. | 3.5 | 172 |
| 22 | Direct Sedimentation Analysis of Interference Optical Data in Analytical Ultracentrifugation. <i>Biophysical Journal</i> , 1999, 76, 2288-2296. | 0.2 | 168 |
| 23 | Sedimentation Velocity Analysis of Heterogeneous Protein-Protein Interactions: Lamm Equation Modeling and Sedimentation Coefficient Distributions $c(s)$. <i>Biophysical Journal</i> , 2005, 89, 619-634. | 0.2 | 168 |
| 24 | Reliable determination of binding affinity and kinetics using surface plasmon resonance biosensors. <i>Current Opinion in Biotechnology</i> , 1997, 8, 498-502. | 3.3 | 160 |
| 25 | 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. | 0.4 | 160 |
| 26 | 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 |
| 27 | A conformational switch in HPI releases auto-inhibition to drive heterochromatin assembly. <i>Nature</i> , 2013, 496, 377-381. | 13.7 | 141 |
| 28 | 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 |
| 29 | Crystal Structure of a Superantigen Bound to the High-Affinity, Zinc-Dependent Site on MHC Class II. <i>Immunity</i> , 2001, 14, 93-104. | 6.6 | 134 |
| 30 | 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, 81-86. | 3.3 | 132 |
| 31 | Kinetic analysis of biosensor data: elementary tests for self-consistency. <i>Trends in Biochemical Sciences</i> , 1996, 21, 458-460. | 3.7 | 131 |
| 32 | Alanine-scanning Mutations in Domain 4 of Anthrax Toxin Protective Antigen Reveal Residues Important for Binding to the Cellular Receptor and to a Neutralizing Monoclonal Antibody. <i>Journal of Biological Chemistry</i> , 2003, 278, 30936-30944. | 1.6 | 130 |
| 33 | Variable MHC class I engagement by Ly49 natural killer cell receptors demonstrated by the crystal structure of Ly49C bound to H-2Kb. <i>Nature Immunology</i> , 2003, 4, 1213-1222. | 7.0 | 127 |
| 34 | Combined Affinity and Rate Constant Distributions of Ligand Populations from Experimental Surface Binding Kinetics and Equilibria. <i>Biophysical Journal</i> , 2003, 84, 4062-4077. | 0.2 | 118 |
| 35 | 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, 651-666. | 0.2 | 109 |
| 36 | Self-association of Human Apolipoprotein E3 and E4 in the Presence and Absence of Phospholipid. <i>Journal of Biological Chemistry</i> , 2000, 275, 36758-36765. | 1.6 | 108 |

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| 37 | Conformational restriction blocks glutamate receptor desensitization. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 1120-1127. | 3.6 | 106 |
| 38 | Binding Specificity of Multiprotein Signaling Complexes Is Determined by Both Cooperative Interactions and Affinity Preferences. <i>Biochemistry</i> , 2004, 43, 4170-4178. | 1.2 | 105 |
| 39 | Structure and Assembly Mechanism for Heteromeric Kainate Receptors. <i>Neuron</i> , 2011, 71, 319-331. | 3.8 | 102 |
| 40 | Recorded scan times can limit the accuracy of sedimentation coefficients in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2013, 437, 104-108. | 1.1 | 102 |
| 41 | Cooperative interactions at the SLP-76 complex are critical for actin polymerization. <i>EMBO Journal</i> , 2010, 29, 2315-2328. | 3.5 | 98 |
| 42 | Bacteriorhodopsin/Amphipol Complexes: Structural and Functional Properties. <i>Biophysical Journal</i> , 2008, 94, 3523-3537. | 0.2 | 97 |
| 43 | The N-terminal domain of GluR6-subtype glutamate receptor ion channels. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 631-638. | 3.6 | 97 |
| 44 | 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, 1882-1887. | 3.3 | 94 |
| 45 | Exposure of acidic residues as a danger signal for recognition of fibrinogen and other macromolecules by integrin $\alpha 2$. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1614-1619. | 3.3 | 91 |
| 46 | Non-Ideality by Sedimentation Velocity of Halophilic Malate Dehydrogenase in Complex Solvents. <i>Biophysical Journal</i> , 2001, 81, 1868-1880. | 0.2 | 90 |
| 47 | 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, 1895-1900. | 3.3 | 90 |
| 48 | Rotavirus Nonstructural Protein NSP2 Self-assembles into Octamers That Undergo Ligand-induced Conformational Changes. <i>Journal of Biological Chemistry</i> , 2001, 276, 9679-9687. | 1.6 | 88 |
| 49 | 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. | 3.0 | 84 |
| 50 | Characterizing Protein-Protein Interactions by Sedimentation Velocity Analytical Ultracentrifugation. <i>Current Protocols in Immunology</i> , 2008, 81, Unit 18.15. | 3.6 | 84 |
| 51 | Characterization of DC-SIGN/R Interaction with Human Immunodeficiency Virus Type 1 gp120 and ICAM Molecules Favors the Receptor's Role as an Antigen-Capturing Rather than an Adhesion Receptor. <i>Journal of Virology</i> , 2005, 79, 4589-4598. | 1.5 | 83 |
| 52 | 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. | 0.2 | 83 |
| 53 | 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 |
| 54 | 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, 4611-4617. | 1.6 | 80 |

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| 55 | An antibody single-domain phage display library of a native heavy chain variable region: isolation of functional single-domain VH molecules with a unique interface 1 Edited by I. A. Wilson. Journal of Molecular Biology, 1999, 290, 685-698. | 2.0 | 79 |
| 56 | A model for sedimentation in inhomogeneous media. I. Dynamic density gradients from sedimenting co-solutes. Biophysical Chemistry, 2004, 108, 187-200. | 1.5 | 77 |
| 57 | Determination of Sedimentation Coefficients for Small Peptides. Biophysical Journal, 1998, 74, 466-474. | 0.2 | 74 |
| 58 | Determination of Binding Constants by Equilibrium Titration with Circulating Sample in a Surface Plasmon Resonance Biosensor. Analytical Biochemistry, 1998, 265, 79-91. | 1.1 | 73 |
| 59 | Efficient Neutralization of Anthrax Toxin by Chimpanzee Monoclonal Antibodies against Protective Antigen. Journal of Infectious Diseases, 2006, 193, 625-633. | 1.9 | 73 |
| 60 | Analytical ultracentrifugation as a tool for studying protein interactions. Biophysical Reviews, 2013, 5, 159-171. | 1.5 | 73 |
| 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. | 3.3 | 73 |
| 62 | A multi-step nucleation process determines the kinetics of prion-like domain phase separation. Nature Communications, 2021, 12, 4513. | 5.8 | 73 |
| 63 | Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5. ELife, 2018, 7, . | 2.8 | 73 |
| 64 | Biochemical and Biological Characterization of a Dodecameric CD4-Ig Fusion Protein. Journal of Biological Chemistry, 2002, 277, 11456-11464. | 1.6 | 71 |
| 65 | Humanized Monoclonal Antibodies Derived from Chimpanzee Fabs Protect against Japanese Encephalitis Virus In Vitro and In Vivo. Journal of Virology, 2008, 82, 7009-7021. | 1.5 | 71 |
| 66 | A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. PLoS ONE, 2015, 10, e0126420. | 1.1 | 71 |
| 67 | Biointeractions of ultrasmall glutathione-coated gold nanoparticles: effect of small size variations. Nanoscale, 2016, 8, 6577-6588. | 2.8 | 69 |
| 68 | Basic Principles of Analytical Ultracentrifugation. , 0, , . | | 69 |
| 69 | The Molecular Refractive Function of Lens $\hat{1}^3$ -Crystallins. Journal of Molecular Biology, 2011, 411, 680-699. | 2.0 | 68 |
| 70 | Apolipoprotein C-II Amyloid Fibrils Assemble via a Reversible Pathway that Includes Fibril Breaking and Rejoining. Journal of Molecular Biology, 2008, 376, 1116-1129. | 2.0 | 66 |
| 71 | Using Prior Knowledge in the Determination of Macromolecular Size-Distributions by Analytical Ultracentrifugation. Biomacromolecules, 2007, 8, 2011-2024. | 2.6 | 65 |
| 72 | Sedimentation Patterns of Rapidly Reversible Protein Interactions. Biophysical Journal, 2010, 98, 2005-2013. | 0.2 | 65 |

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| 73 | SDR grafting of a murine antibody using multiple human germline templates to minimize its immunogenicity. <i>Molecular Immunology</i> , 2004, 41, 863-872. | 1.0 | 64 |
| 74 | An allosteric site in the T-cell receptor C β 2 domain plays a critical signalling role. <i>Nature Communications</i> , 2017, 8, 15260. | 5.8 | 64 |
| 75 | Autoinhibition of Arf GTPase-activating Protein Activity by the BAR Domain in ASAP1. <i>Journal of Biological Chemistry</i> , 2009, 284, 1652-1663. | 1.6 | 63 |
| 76 | Characterization of Chimpanzee/Human Monoclonal Antibodies to Vaccinia Virus A33 Glycoprotein and Its Variola Virus Homolog In Vitro and in a Vaccinia Virus Mouse Protection Model. <i>Journal of Virology</i> , 2007, 81, 8989-8995. | 1.5 | 61 |
| 77 | The Human Immunodeficiency Virus Type 1 gp120 V2 Domain Mediates gp41-Independent Intersubunit Contacts. <i>Journal of Virology</i> , 2000, 74, 4448-4455. | 1.5 | 60 |
| 78 | 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, 2828-2835. | 3.2 | 60 |
| 79 | 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 |
| 80 | 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 |
| 81 | Mass Spectrometry after Capture and Small-Volume Elution of Analyte from a Surface Plasmon Resonance Biosensor. <i>Analytical Chemistry</i> , 2002, 74, 2041-2047. | 3.2 | 58 |
| 82 | Stability of ligand-binding domain dimer assembly controls kainate receptor desensitization. <i>EMBO Journal</i> , 2009, 28, 1518-1530. | 3.5 | 54 |
| 83 | 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, 14877-14882. | 3.3 | 52 |
| 84 | 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 |
| 85 | Crystal Structure of the C-terminal Peptidoglycan-binding Domain of Human Peptidoglycan Recognition Protein I β . <i>Journal of Biological Chemistry</i> , 2004, 279, 31873-31882. | 1.6 | 51 |
| 86 | 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, 3902-3908. | 1.0 | 51 |
| 87 | On the analysis of sedimentation velocity in the study of protein complexes. <i>European Biophysics Journal</i> , 2009, 38, 1079-1099. | 1.2 | 51 |
| 88 | Simultaneous radial and wavelength analysis with the Optima XL-A analytical ultracentrifuge. , 1994, , 1-13. | | 50 |
| 89 | Interaction of the NK Cell Inhibitory Receptor Ly49A with H-2Dd. <i>Immunity</i> , 1999, 11, 591-601. | 6.6 | 50 |
| 90 | Density Contrast Sedimentation Velocity for the Determination of Protein Partial-Specific Volumes. <i>PLoS ONE</i> , 2011, 6, e26221. | 1.1 | 49 |

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| 91 | 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. | 0.6 | 48 |
| 92 | 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 |
| 93 | Measuring macromolecular size distributions and interactions at high concentrations by sedimentation velocity. <i>Nature Communications</i> , 2018, 9, 4415. | 5.8 | 48 |
| 94 | The dimerization stability of the HLH-LZ transcription protein family is modulated by the leucine zippers: A CD and NMR study of TFEB and c-Myc. <i>Biochemistry</i> , 1994, 33, 11296-11306. | 1.2 | 46 |
| 95 | Eukaryotic RNases H1 act processively by interactions through the duplex RNA-binding domain. <i>Nucleic Acids Research</i> , 2005, 33, 2166-2175. | 6.5 | 46 |
| 96 | 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, 12329-12334. | 3.3 | 46 |
| 97 | Analysis of Transport Experiments Using Pseudo-Absorbance Data. <i>Analytical Biochemistry</i> , 2000, 285, 135-142. | 1.1 | 45 |
| 98 | 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 |
| 99 | Extended Fujita approach to the molecular weight distribution of polysaccharides and other polymeric systems. <i>Methods</i> , 2011, 54, 136-144. | 1.9 | 45 |
| 100 | Analysis of high-affinity assembly for AMPA receptor amino-terminal domains. <i>Journal of General Physiology</i> , 2012, 139, 371-388. | 0.9 | 45 |
| 101 | Amino Acid Residues That Influence FcγRI-Mediated Effector Functions of Human Immunoglobulin E. <i>Biochemistry</i> , 1998, 37, 16152-16164. | 1.2 | 44 |
| 102 | Calcium-Sensitive Interaction between Calmodulin and Modified Forms of Rat Brain Neurogranin/RC3. <i>Biochemistry</i> , 2000, 39, 7291-7299. | 1.2 | 43 |
| 103 | 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, 3076-3084. | 0.4 | 43 |
| 104 | Multipoint Binding of the SLP-76 SH2 Domain to ADAP Is Critical for Oligomerization of SLP-76 Signaling Complexes in Stimulated T Cells. <i>Molecular and Cellular Biology</i> , 2013, 33, 4140-4151. | 1.1 | 43 |
| 105 | Sedimentation Velocity Analytical Ultracentrifugation. , 0, , . | | 42 |
| 106 | Bayesian Analysis of Heterogeneity in the Distribution of Binding Properties of Immobilized Surface Sites. <i>Langmuir</i> , 2008, 24, 11577-11586. | 1.6 | 41 |
| 107 | Analysis of Protein Interactions with Picomolar Binding Affinity by Fluorescence-Detected Sedimentation Velocity. <i>Analytical Chemistry</i> , 2014, 86, 3181-3187. | 3.2 | 41 |
| 108 | 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, 7082-7093. | 1.5 | 40 |

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| 109 | Dissection of Merozoite Surface Protein 3, a Representative of a Family of Plasmodium falciparum Surface Proteins, Reveals an Oligomeric and Highly Elongated Molecule. <i>Journal of Biological Chemistry</i> , 2005, 280, 37236-37245. | 1.6 | 40 |
| 110 | Characterizing the Solution Properties of Supramolecular Systems by Analytical Ultracentrifugation. <i>Chemistry - A European Journal</i> , 1999, 5, 1377-1383. | 1.7 | 39 |
| 111 | Binding kinetics of ultrasmall gold nanoparticles with proteins. <i>Nanoscale</i> , 2018, 10, 3235-3244. | 2.8 | 39 |
| 112 | Sedimentation equilibrium analysis of recombinant mouse FcRn with murine IgG1. <i>Molecular Immunology</i> , 1999, 36, 1117-1125. | 1.0 | 37 |
| 113 | Regulation of ASAP1 by phospholipids is dependent on the interface between the PH and Arf GAP domains. <i>Cellular Signalling</i> , 2005, 17, 1276-1288. | 1.7 | 37 |
| 114 | Use of fluorescence-detected sedimentation velocity to study high-affinity protein interactions. <i>Nature Protocols</i> , 2017, 12, 1777-1791. | 5.5 | 37 |
| 115 | A Bayesian Approach for Quantifying Trace Amounts of Antibody Aggregates by Sedimentation Velocity Analytical Ultracentrifugation. <i>AAPS Journal</i> , 2008, 10, 481-93. | 2.2 | 36 |
| 116 | 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 |
| 117 | Plasticity in structure and assembly of SARS-CoV-2 nucleocapsid protein. , 2022, 1, . | | 36 |
| 118 | A model for sedimentation in inhomogeneous media. II. Compressibility of aqueous and organic solvents. <i>Biophysical Chemistry</i> , 2004, 108, 201-214. | 1.5 | 35 |
| 119 | The boundary structure in the analysis of reversibly interacting systems by sedimentation velocity. <i>Methods</i> , 2011, 54, 16-30. | 1.9 | 35 |
| 120 | Diffusion of the Reaction Boundary of Rapidly Interacting Macromolecules in Sedimentation Velocity. <i>Biophysical Journal</i> , 2010, 98, 2741-2751. | 0.2 | 34 |
| 121 | AUC and Small-Angle Scattering for Membrane Proteins. <i>Methods in Enzymology</i> , 2015, 562, 257-286. | 0.4 | 34 |
| 122 | Energetic and structural features of SARS-CoV-2 N-protein co-assemblies with nucleic acids. <i>IScience</i> , 2021, 24, 102523. | 1.9 | 34 |
| 123 | Differences in the binding capacity of human apolipoprotein E3 and E4 to size-fractionated lipid emulsions. <i>FEBS Journal</i> , 2002, 269, 5939-5949. | 0.2 | 33 |
| 124 | Targeted lysis of HIV-infected cells by natural killer cells armed and triggered by a recombinant immunoglobulin fusion protein: implications for immunotherapy. <i>Virology</i> , 2005, 332, 491-497. | 1.1 | 33 |
| 125 | Reversible and Fast Association Equilibria of a Molecular Chaperone, gp57A, of Bacteriophage T4. <i>Biophysical Journal</i> , 2003, 85, 2606-2618. | 0.2 | 32 |
| 126 | Analytical ultracentrifugation as a tool for studying membrane proteins. , 1991, , 12-22. | | 31 |

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| 127 | Analytical band centrifugation of proteins and protein complexes. <i>Biochemical Society Transactions</i> , 1998, 26, 745-749. | 1.6 | 31 |
| 128 | Quantifying the Energetics of Cooperativity in a Ternary Protein Complex. <i>Biochemistry</i> , 2002, 41, 5177-5184. | 1.2 | 31 |
| 129 | Measuring Protein-Protein Interactions by Equilibrium Sedimentation. <i>Current Protocols in Immunology</i> , 2007, 79, Unit 18.8. | 3.6 | 31 |
| 130 | Direct Interaction of the Mouse Cytomegalovirus m152/gp40 Immuno-evasin with RAE-1 Isoforms. <i>Biochemistry</i> , 2010, 49, 2443-2453. | 1.2 | 31 |
| 131 | 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 |
| 132 | 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 |
| 133 | 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 |
| 134 | Solution properties of β -crystallins: Hydration of fish and mammal β -crystallins. <i>Protein Science</i> , 2014, 23, 88-99. | 3.1 | 30 |
| 135 | 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 |
| 136 | Band 3-hemoglobin associations The band 3 tetramer is the oxyhemoglobin binding site. <i>FEBS Letters</i> , 1991, 293, 81-84. | 1.3 | 28 |
| 137 | Minimizing immunogenicity of the SDR-grafted humanized antibody CC49 by genetic manipulation of the framework residues. <i>Molecular Immunology</i> , 2003, 40, 337-349. | 1.0 | 28 |
| 138 | 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, 102-113. | 2.0 | 27 |
| 139 | Crystal Structure of Group A Streptococcus Mac-1: Insight into Dimer-Mediated Specificity for Recognition of Human IgG. <i>Structure</i> , 2006, 14, 225-235. | 1.6 | 27 |
| 140 | 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 |
| 141 | Allosteric inhibition of β -thrombin enzymatic activity with ultrasmall gold nanoparticles. <i>Nanoscale Advances</i> , 2019, 1, 378-388. | 2.2 | 27 |
| 142 | Biomolecular interactions of ultrasmall metallic nanoparticles and nanoclusters. <i>Nanoscale Advances</i> , 2021, 3, 2995-3027. | 2.2 | 27 |
| 143 | Tools for the Quantitative Analysis of Sedimentation Boundaries Detected by Fluorescence Optical Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2013, 8, e77245. | 1.1 | 27 |
| 144 | 3D-Printing for Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2016, 11, e0155201. | 1.1 | 27 |

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