Curriculum Vitae
Christopher J. Roberts, Ph.D

Professor, Chemical and Biomolecular Engineering
University of Delaware, Newark, DE 19716
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Positions / Appointments

2018 -	Associate Institute Director, National Institute for Innovation in Manufacturing Biopharmaceuticals, USA
2017 - 2018	Associate Chair for Undergraduate Studies, Chemical & Biomolecular Engineering, University of Delaware
2016 - 2017	Visiting Professor, School of Chemical Engineering and Analytical Sciences, University of Manchester
2015 -	Director, Center for Biomanufacturing Science and Technology, University of Delaware
2015 -	Professor, Department of Chemical and Biomolecular Engineering, University of Delaware
2014 -	Director, Biomolecular Interaction Technologies Center, University of Delaware
2010 -	Guest Researcher, National Institute of Standards and Technology, NIST Center for Neutron Research
2009 -	Faculty Member, Center for Molecular and Engineering Thermodynamics, University of Delaware
2003 -	Faculty Member, UD Chemistry-Biology Interface Program, University of Delaware
2010	Visiting Investigator, GlaxoSmithKline
2010 - 2014	Associate Professor (affiliated), Biomedical Engineering, University of Delaware
2009 - 2015	Associate Professor, Department of Chemical and Biomolecular Engineering, University of Delaware
2008 - 2014	Graduate Program Co-Director, Department of Chemical and Biomolecular Engineering, University of Delaware
2006 - 2008	Faculty Member, University of Delaware IGERT Biotechnology Program
2002 - 2009	Assistant Professor, Department of Chemical Engineering, University of Delaware
2000 - 2002	Senior Research Scientist, Department of Pharmaceutical R&D, Pfizer Global Research and Development
1999 - 2000	Research Scientist, Department of Pharmaceutical R&D, Pfizer Central Research
1994 - 1999	Graduate Research Associate, Department of Chemical Engineering, Princeton University
1995	Visiting Research Associate, Pafra Biopreservation, Ltd., Cambridge UK

Education

Princeton University	Chemical Engineering, Ph.D.	1999
University of Delaware	Chemical Engineering, BChE *summa cum laude*	1994

Selected Honors

Research & Scholarship

- Inaugural John Finlayson Lecture, US Food & Drug Administration (2016)
- AAPS Chapter Pharmaceutics Lecturer, University of Kansas (2006)
- AAPS New Investigator Award (Pharmaceutics and Pharmaceutical Technology) (2005)
- Merck Faculty Fellow, University of Delaware (2004-2007)
- Ebert Prize, American Pharmaceutical Association & American Pharmaceutical Research Society (2004)
- Wallace Memorial Fellowship, Princeton University (1998)
- National Science Foundation Graduate Fellowship (1994-1998)
- Barry M. Goldwater Scholarship (1992-1994)

Teaching and Service

- Co-Chair, inaugural Gordon Research Conference on *Biotherapeutics and Vaccines Development* (2019)
- Editorial Advisory Board, *J. Pharm. Sci.* (2017-present)
- Industrial & Academic Advisory Board, PIPPI consortium (2016-2018)
- College of Engineering, Excellence-in-Teaching Award, University of Delaware (2008)
- Nominated, University Excellence-in-Teaching Award, University of Delaware (2004, 2006, 2009)
- *Journal of Pharmaceutical Sciences* Service Award (2007, 2008, 2012, 2015), *Biophysical Chemistry* Service Award (2014)

Peer-Reviewed Publications

1. Roberts CJ, Franks F* Crystalline and amorphous phases in the binary system water – β,β trehalose. *J. Chem. Soc. Faraday Trans*. 92:1337-1343 (1996).
2. Roberts CJ, Debenedetti PG* Polyamorphism and density anomalies in network-forming fluids: Zeroth- and first-order approximations. *J. Chem. Phys.* 105:658-672(1996).
3. Roberts CJ, Panagiotopoulos AZ, Debenedetti PG* Liquid-liquid immiscibility in pure fluids: Polyamorphism in simulations of a network-forming fluid. *Phys. Rev. Lett.* 77:4386-4389 (1996).
4. Roberts CJ, Karayiannakis GA, Debenedetti PG* Pure-fluid liquid-liquid equilibrium in a model of network-forming fluids, and implications for polyamorphism in water. *Ind. & Eng. Chem. Res.* 37:3012-3020 (1998).
5. Roberts CJ, Debenedetti PG* Structure and dynamics in concentrated amorphous carbohydrate-water systems by molecular dynamics simulation. *J. Phys. Chem. B* 103:7308-7318 (1999).
6. Debenedetti PG*, Stillinger FH, Truskett TM, Roberts CJ. The equation of state of an energy landscape. *J. Phys. Chem. B* 103:7390-7397 (1999).
7. Roberts CJ, Stillinger FH, Debenedetti PG* Equation of state of the energy landscape of SPC/E water. *J. Phys. Chem. B* 103:10258-10265 (1999).
8. Roberts CJ*, Ji Q, Zhang L, Darrington RT. Dissolution behavior of porcine somatotropin with simultaneous gel-formation and lysine Schiff-base hydrolysis. *J. Controlled Release*, 77:107-116 (2001).
9. Waterman KC*, Adami RC, Alsante KM, Hong J, Landis MS, Lombardo F, Roberts CJ. Stabilization of pharmaceuticals to oxidative degradation. *Pharm. Dev. Tech.* 7:1-32 (2002).
10. Roberts CJ, Debenedetti PG* Engineering pharmaceutical stability with amorphous solids. *AIChE J.* 48:1140-1144 (2002).
11. Roberts CJ. Kinetics of irreversible protein aggregation: analysis of extended Lumry-Eyring models and implications for shelf life prediction *J. Phys. Chem. B* 107:1194-1207 (2003).
12. Roberts CJ*, Darrington RT, Whitley MB. Irreversible aggregation of recombinant bovine granulocyte-colony stimulating factor (bG-CSF) and implications for predicting protein shelf life. *J. Pharm. Sci.*, 92:1095-1111 (2003).
13. Roberts CJ. Improved quasi-chemical equation of state based on energy and density fluctuations in the small system grand canonical ensemble, *J. Phys. Chem. B* 108:19843-19851 (2004).
14. Shah PP, Roberts CJ* Molecular solvation in water-methanol and water-sorbitol mixtures: the roles of preferential hydration, hydrophobicity, and the equation of state, *J. Phys. Chem. B* 111:4467-4476 (2007).
15. Andrews JM, Roberts CJ* Non-native aggregation of α-chymotrypsinogen occurs through nucleation and growth with competing nucleus sizes and negative activation energies, *Biochemistry* 46:7558-7571 (2007).
16. Andrews JM, Roberts CJ* A Lumry-Eyring nucleated-polymerization model of protein aggregation kinetics: 1. Aggregation with pre-equilibrated unfolding, *J. Phys. Chem. B* 111:7897-7913 (2007).
17. Roberts CJ Nonnative protein aggregation kinetics. *Biotechnol. Bioeng.* 98:927-938 (2007).
18. Young TM, Roberts CJ* A quasichemical approach for protein-cluster free energies in dilute solution, *J. Chem. Phys.* 127:165101/1-10 (2007).
19. Weiss WF IV, Hodgdon TK, Kaler EW, Lenhoff AM, Roberts CJ* Nonnative protein polymers: structure, morphology, and relation to nucleation and growth, *Biophys. J.* 93:4392-4403 (2007).
20. Shah PP, Roberts CJ* Solvation in mixed-aqueous solvents from a thermodynamic cycle approach, *J. Phys. Chem. B* 112:1049-1052 (2008).
21. Andrews JM, Weiss WF IV, Roberts CJ* Nucleation, growth, and activation energies for seeded and unseeded aggregation of α-chymotrypsinogen A. *Biochemistry* 47:2397-2403 (2008).
22. Top A, Kiick KL*, Roberts CJ* Modulation of self-association and subsequent fibril formation in an alanine-rich helical polypeptide. *Biomacromolecules* 9:1595-1603 (2008).
23. Weiss WF IV, Young TM, Roberts CJ* Principles, approaches, and challenges for prediction of protein aggregation kinetics and shelf life *J. Pharm. Sci.*, 98:1246-1277 (2009).

24. Li Y, Weiss WF IV, Roberts CJ* Characterization of high molecular-weight nonnative aggregates and aggregation kinetics by size exclusion chromatography with inline multi-angle laser light scattering. *J. Pharm. Sci.* 98:3997-4016 (2009).
25. Spatara ML, Roberts CJ, Robinson AS* Kinetic folding studies of the P22 tailspike beta-helix domain reveal multiple unfolded states. *Biophys. Chem.* 141:214-221 (2009).
26. Li Y, Roberts CJ* A Lumry-Eyring nucleated-nolymerization (LENP) model of protein aggregation kinetics 2. Competing growth via condensation- and chain-polymerization. *J. Phys. Chem. B* 113:7020-7032 (2009).
27. Young TM, Roberts CJ* Structure and thermodynamics of colloidal protein cluster formation: comparison of square-well and simple dipolar models. *J. Chem. Phys.* 131:125104/1-9 (2009).
28. Li Y, Ogunnaike BA, Roberts CJ* Multi-variate approach to global protein aggregation behavior and kinetics: effects of pH, NaCl, and temperature for α-chymotrypsinogen A. *J. Pharm. Sci.* 99:645-662 (2010).
29. Sahin E, Grillo AO, Perkins MD, Roberts CJ* Comparative effects of pH and ionic strength on protein-protein interactions, unfolding, and aggregation for IgG1 antibodies, *J. Pharm. Sci.* 99:4830-4848 (2010).
30. Zhang A, Jordan JL, Ivanova MA, Weiss WF, Roberts CJ, Fernandez EJ* Molecular-level insights into thermally-induced α-chymotrypsinogen A amyloid aggregation mechanism and semi-flexible protofibril morphology. *Biochemistry* 49:10553-10564 (2010).
31. Sahin E, Jordan JL, Zhang A, Naranjo A, Costanzo JA, Weiss WF IV, Spatara ML, Robinson AS, Fernandez EJ*, Roberts CJ* Computational design and biophysical characterization of point mutations for gamma-D-crystallin illustrate a balance of conformational stability and intrinsic aggregation propensity. *Biochemistry* 50:628-639 (2011).
32. Brummitt RK, Nesta DP, Chang L, Chase SF, Laue TM, Roberts CJ* Non-native aggregation of an IgG1 antibody in acidic conditions: 1. Unfolding, colloidal interactions, and formation of amyloid-like high molecular weight aggregates. *J Pharm Sci* 100:2087-2103 (2011).
33. Brummitt RK, Nesta DP, Chang L, Kroetsch AM, Roberts CJ* Non-native aggregation of an IgG1 antibody in acidic conditions: 2. Nucleation-and-growth kinetics with competing growth mechanisms. *J Pharm Sci* 100:2104-2119 (2011).
34. Top A, Roberts CJ*, Kiick KL* Conformational and aggregation properties of a PEGylated alanine-rich polypeptide *Biomacromolecules* 12:2184–2192 (2011).
35. Blanco MA, Sahin E, Li Y, Roberts CJ* Reexamining Protein-Protein and Protein-Solvent Interactions from Kirkwood-Buff Analysis of Light Scattering in Multi-Component Solutions. *J Chem Phys* 134:225103/1-12 (2011).
36. Brummitt, RK, Nesta DP, Roberts, CJ* Predicting accelerated and low-temperature aggregation rates for monoclonal antibody formulations. *J Pharm Sci* 100:4234-4243 (2011).
37. Roberts CJ*, Das TK, Sahin E. Predicting Aggregation Rates for Therapeutic Proteins: Approaches and Challenges. *Int J Pharm* 418:318-333 (2011).
38. Top A, Zhong S, Yan C, Roberts CJ*, Pochan DJ*, Kiick KL* Controlling assembly of helical polypeptides via PEGylation strategies. *Soft Matter* 7:9758-9766 (2011).
39. Sahin E, Weiss WF IV, Kroetsch AM, King KR, Kessler RK, Das TK, Roberts CJ* Non-native aggregation and pH-temperature phase behavior of aggregates for an IgG2 antibody *J Pharm Sci* 101:1678–1687 (2012).
40. Siderius DW*, Krekelberg WP, Roberts CJ, Shen VK. Osmotic virial coefficients for model protein and colloidal solutions: Importance of ensemble constraints. *J Chem Phys,* 136(17) 175102/1-9 (2012).
41. Brummitt RK, Andrews JM, Jordan JL, Fernandez EJ, Roberts CJ* Thermodynamics of amyloid dissociation provide insights into aggregate stability regimes *Biophys Chem,* 168-169: 10-18 (2012).
42. Kroetsch AM, Sahin E, Wang H-Y, Krizman S, Roberts CJ* Relating particle formation to salt- and pH-dependent phase separation of non-native aggregates of alpha-chymotrypsinogen A. *J Pharm Sci,* 101:3651-3660 (2012).
43. Sahin E, Roberts CJ* Size-Exclusion Chromatography with Multi-Angle Light Scattering (SEC-MALS) for Elucidating Protein Aggregation Mechanisms. *Methods Mol Biol* 899:403-423 (2012).
44. Grünberger A, Lai P-K, Blanco MA, Roberts CJ* Coarse-grained modeling of protein second osmotic virial coefficients: sterics and non-specific attractions. *J Phys Chem B*, 117:763-770 (2013).
45. Kim N, Remmele RL, Liu D, Razinkov V, Fernandez EJ, Roberts CJ* Aggregation of Anti-Streptavidin Immunoglobulin Gamma-1 Mediated by Fab Unfolding and Competing Growth Pathways. *Biophys Chem,* 172:26-36 (2013).
46. Wang W*, Roberts CJ* Non-Arrhenius Protein Aggregation. *AAPS J*, (online only) doi: 10.1208/s12248-013-9485-3 (2013).
47. Roberts CJ*, Nesta DP, Kim N. Effects of temperature and osmolytes on parallel degradation routes for an IgG1 antibody. *J Pharm Sci* 102:3556-3566 (2013).

48. Murphy RM*, Roberts CJ. Protein misfolding and aggregation research: some thoughts on improving quality and utility. *Biotechnol Prog* 29:1109-1115 (2013).
49. Maurer RW, Hunter AK, Wang X, Wang WK, Robinson AS*, Roberts CJ* Folding and aggregation of a multi-domain engineered immunotoxin. *Biochem Eng J.* 81:8-14 (2013).
50. Blanco MA, Sahin E, Robinson AS, Roberts CJ* Coarse-grained model of protein-protein interactions, B_{22}, and protein cluster formation. *J Phys Chem B* 117: 16013-16028 (2013).
51. Weiss WF IV, Zhang A, Jordan JL, Ivanova MA, Sahin E, Fernandez EJ, Roberts CJ* Reduction of the C191-C220 disulfide of α-chymotrypsinogen A accelerates amyloid formation via reduced nucleation barriers. *Biophys Chem* 185:79-87 (2014).
52. Maurer RW, Hunter AK, Robinson AS*, Roberts CJ* Aggregates of α-chymotrypsinogen anneal to access more stable aggregate states. *Biotechnol Bioeng* 111: 782-791 (2014).
53. Wu H, Kroe-Barrett R, Singh S, Robinson AS, Roberts CJ* Competing aggregation pathways for monoclonal antibodies. *FEBS Letters* 588: 936-941(2014).
54. Costanzo JA, O'Brien CJ, Tiller K, Tamargo E, Robinson AS, Roberts CJ*, Fernandez EJ* Computational Design to Control Protein Aggregation Rates Through Conformational Stability. *Protein Engineering Design & Selection* 27: 157-167 (2014).
55. Blanco MA, Martorana E, Manno M, Perevozchikova T, Roberts CJ* Protein-protein interactions in dilute to concentrated solutions: alpha-chymotrypsinogen at acidic pH. *J Phys Chem B* 118: 5817-5831 (2014).
56. Roberts CJ. Therapeutic protein aggregation: mechanisms, design, and control. *Trends Biotech*. 32: 372-380 (2014).
57. Roberts CJ. Protein Aggregation and Its Impact on Product Quality. *Curr Opin Biotech* 30:211-217 (2014).
58. Roberts CJ,* Blanco MA. Role of anisotropic interactions for proteins and patchy nanoparticles. *J Phys Chem B* 118:12599-12611 (2014).
59. Amin S,* Barnett GV, Pathak J,* Roberts CJ, Sarangapani PS. Protein aggregation, particle formation, characterization, and rheology. *Curr Opin Coll Int Sci* 19:439-449 (2014).
60. Paik B, Blanco MA, Roberts CJ,* Jia X, Kiick KL* Aggregation of poly(acrylic acid)-containing elastin copolymers. *Soft Matter* 11:1839-1850 (2015).
61. Barnett GV, Razinkov V, Kerwin BA, Laue TM, Woodka A, Butler PD, Perevozchikova T, Roberts CJ* Specific ion effects on the aggregation mechanisms and protein-protein interactions for anti-streptavidin immunoglobulin gamma 1. *J Phys Chem B* 119:5793-5804 (2015).
62. Perevozchikova T, Nanda H, Nesta DP, Roberts CJ* Protein adsorption, desorption, and aggregation mediated by solid-liquid interfaces. *J Pharm Sci* 104:1946-1959 (2015).
63. Barnett GV, Qi W, Amin S, Lewis EN, Roberts CJ* Aggregate structure, morphology and the effect of aggregation mechanisms on viscosity at elevated protein concentrations. *Biophys Chem* 207:21-29 (2015).
64. Wu H, Truncali K, Ritchie J, Kroe-Barrett R, Singh S, Robinson AS, Roberts CJ* Weak protein interactions and pH- and temperature-dependent aggregation of human Fc1. *mAbs* 7:1-12 (2015).
65. Barnett GV, Qi W, Amin S, Lewis EN, Razinkov V, Kerwin BA, Liu Y, Roberts CJ* Structural Changes and Aggregation Mechanisms for Anti-streptavidin IgG1 at Elevated Concentration. *J Phys Chem B* 119:15150-15163 (2015).
66. Barnett GV, Razinkov V, Kerwin BA, Hillsley A, Roberts CJ* Acetate and Citrate Specific-Ion-Effects on Temperature-Dependent Aggregation Rates of Anti-Streptavidin IgG1. *J Pharm Sci* 105:1066-1073 (2016).
67. Ghosh R, Calero-Rubio C, Saluja A, Roberts CJ* Relating protein-protein interactions and aggregation rates from low to high concentrations. *J Pharm Sci* 105:1086-1096 (2016).
68. Barnett GV, Razinkov V, Kerwin BA, Blake S, Qi W, Curtis RA, Roberts CJ* Osmolyte Effects on Monoclonal Antibody Stability and Concentration-Dependent Protein Interactions with Water and Common Osmolytes *J Phys Chem B* 120:3318-3330 (2016).
69. O'Brien CJ, Blanco MA, Robinson AS,* Roberts CJ* Modulating Non-Native Aggregation and Electrostatic Protein-Protein Interactions with Computationally Designed Single Point Mutations, *Protein Engineering Design & Selection* 29:231-243 (2016).
70. Calero-Rubio C, Saluja A, Roberts CJ* Coarse-grained antibody models for "weak" protein-protein interactions from low to high concentrations *J Phys Chem B* 120:6592-6605 (2016).
71. Calero-Rubio C, Paik BA, Jia X, Kiick KL*, Roberts CJ* Predicting unfolding thermodynamics and stable intermediates for alanine-rich helical peptides with the aid of coarse-grained molecular simulation. *Biophys Chem* 217:8-19 (2016).
72. Barnett GV, Drenski MC, Razinkov V, Reed WF*, Roberts CJ* Protein aggregation mechanisms and kinetics from combined monomer depletion rates and continuous scattering *Analytical Biochem* 511:80-91 (2016).

73. Barnett GV, Razinkov V, Kerwin BA, Blake S, Qi W, Curtis RA, Roberts CJ* Reply to Comment on Osmolyte Effects on Monoclonal Antibody Stability and Concentration-Dependent Protein Interactions with Water and Common Osmolytes. *J Phys Chem B* 120:11333-11334 (2016).
74. Bain DL, Brenowitz M, Roberts CJ. Commentary on higher education and next-generation researchers: Biophysical characterization, higher-order structure, and industrial/academic opportunities. *J Pharm Sci*. 105:3483-3486 (2016).
75. Meric UG, Robinson AS*, Roberts CJ* Driving forces for non-native protein aggregation and approaches for predicting aggregation-prone regions. *Ann Rev Chem Biomol Eng* 8 (2017), DOI: 10.1146/annurev-chembioeng-060816-101404
76. Mazzer A, Nanda T, Butler P, Roberts CJ, Clifton L, Bracewell DG* Neutron reflectivity measurement of protein A -- antibody complex at the solid-liquid interface. *J Chromatography A*, 1499:118-131 (2017).
77. Rosa MF, Roberts CJ, Rodriguez MA* Connecting High-Temperature and Low-Temperature Protein Stability and Aggregation, *PLOS One* (online only) DOI: 10/1371/journal.pone.0176748 (2017)
78. Woldeyes MA,** Calero-Rubio C,** Furst EM*, Roberts CJ* Predicting protein interactions in concentrated globular protein solutions using colloidal models *J Phys Chem B* 121:4756-4767 (2017).
79. Calero-Rubio C, Strab C, Barnett GV, Roberts CJ* Protein partial molar volumes in multi-component solutions from the perspective of inverse Kirkwood-Buff theory. *J Phys Chem B* 121:5897-5907 (2017).
80. Yang D, Kroe-Barrett R, Singh S, Roberts CJ, Laue TM* IgG cooperativity – is there allostery? Implications in therapeutic antibody development. *mAbs* 9:1231-1252 (2017).
81. Calero-Rubio C, Saluja A, Ghosh R, Roberts CJ* Predicting high-concentration monoclonal antibody interactions with dilute solution data and coarse-grained molecular simulations. *J Pharm Sci* 107:1269-1281 (2018).
82. O'Brien CJ**, Calero-Rubio C**, Razinkov V, Robinson AS, Roberts CJ* Biophysical characterization and molecular simulation of electrostatically driven self-association of an anti-fluorescein single-chain antibody. *Protein Sci* 27:1275-1285 (2018).
83. Yang D, Correia JJ, Stafford WF, Roberts CJ, Singh S, Hayes D, Kroe-Barrett R, Nixon A, Laue TM* Weak IgG self- and hetero-association characterized by fluorescence analytical ultracentrifugation. *Protein Sci* 27: 1334-1348 (2018).
84. Gomes D, Kalman RK, Pagels R, Rodrigues MA, Roberts CJ* Parallel Chromatography and In Situ Scattering to Interrogate Competing Protein Aggregation Pathways. *Protein Sci* 27:1325-1333 (2018).
85. Wang W*, Roberts CJ Protein Aggregation – Mechanisms, Detection, and Control. *Int J Pharm Sci* 550:251-268 (2018).
86. Woldeyes MA, Lam LJ, Leiske D, Galush W, Roberts CJ*, Furst EM* Viscosities and protein interactions of bispecific antibodies and their monospecific mixtures. *Mol Pharm* 15:4745-4755 (2018).
87. Woldeyes MA, Battistoni C, Razinkov V, Furst EM*, Roberts CJ*. How well do electrostatic protein-protein interactions predict changes in viscosity of monoclonal antibody solutions? *J Pharm Sci* 108:142-154 (2019).
88. Shalaev EY, Soper A, Zeitler JA, Ohtake S, Roberts CJ, Pikal MJ, Wu K, Boldyreva E. Freezing of aqueous solutions and chemical stability of amorphous pharmaceuticals: water clusters hypothesis *J Pharm Sci* 108:36-49 (2019)
89. Ferreira GM, Calero-Rubio C, Remmele RL, Samra H, Roberts CJ* Electrostatically mediated protein-protein interactions for monoclonal antibodies: a combined experimental and coarse-grained molecular modeling approach. *J Pharm Sci* 108:120-132 (2019).
90. Amidon GE*, Anderson BD, Balthasar JP, Bergstrom C, Huang S-W, Kasting G, Kesisoglou F, Khinast J, Mager D, Roberts CJ, Yu L, Fifty-eight Years and Counting: High-Impact Publishing in Computational Pharmaceutical Sciences and Mechanism-based Modeling. *J Pharm Sci* 108:2-7 (2019).
91. Calero-Rubio C, Saluja A, Sahin E, Roberts CJ* Predicting high-concentration interactions of monoclonal antibody solutions: Comparison of theoretical approaches for strongly attractive vs. repulsive conditions. *J Phys Chem B* (2019) http://dx.doi.org/10.1021/acs.jpcb.9b03779
92. Woldeyes MA, Calero-Rubio C, Furst EM, Roberts CJ* Light scattering to quantify thermodynamic and hydrodynamic protein-protein interactions at high protein concentrations. *Methods Mol Biol* (in press).

Book Chapters

1. Roberts CJ. Non-native protein aggregation: pathways, kinetics, and shelf-fife prediction, in *Misbehaving Proteins: Protein (Mis)Folding, Aggregation, and Stability*, Murphy, R. M. & Tsai, A. M. Eds., Springer-Verlag: New York, NY 2006.

2. Roberts CJ. Irreversible protein aggregation: principles and rationale for common stabilization strategies, in Encyclopedia of Agricultural, Food, and Biological Engineering, Heldman, D., Ed., Taylor and Francis, 2006. (http://www.dekker.com/sdek/issues~db=enc~content=t713172957)
3. Li Y, Roberts CJ* Protein Aggregation Pathways, Kinetics, and Thermodynamics, in *Aggregation of Therapeutic Proteins*. Wang, W & Roberts, CJ, Eds., John Wiley & Sons: New York, NY 2010.
4. Roberts, CJ Nucleation, Aggregation, and Conformational Distortion, Ch. 5 in *Biophysical Methods for Biotherapeutics: Discovery and Development Applications*, Das, TK (Ed.), John Wiley & Sons, Hoboken, NJ, 2014.
5. S. Ewing, A. Hussain, G. Collins, C. Roberts, E. Shalaev. Low-Temperature Mobility of Water in Sugar Glasses: Insights from Thermally Stimulated Current Studies, in *Water Stress in Biological, Chemical, Pharmaceutical, and Food Systems*, G. F. Gutierrez-Lopez, L. Alamilla-Beltran, M. del Pilar Buera, J. Welti-Chanes, E. Parada-Arias, G. V. Barbosa-Canovas (Eds.), Springer, New York (2015).

Books

Aggregation of Therapeutic Proteins, Eds. W. Wang and C. J. Roberts, John Wiley & Sons: New York, NY (2010).

Patents

Device and method for determining reaction kinetics, C. J. Roberts, G. V. Barnett, V. I. Razinkov, B. A. Kerwin, US Patent 9,632,095 (2017)