Christopher J Roberts

List of Publications by Year
in descending order

88 papers	5,020 citations	81900 39 h-index	95266 68 g-index
103 all docs	103 docs citations	103 times ranked	3203 citing authors

#	Article	IF	Citations
1	Therapeutic protein aggregation: mechanisms, design, and control. Trends in Biotechnology, 2014, 32, 372-380.	9.3	339
2	Nonâ€native protein aggregation kinetics. Biotechnology and Bioengineering, 2007, 98, 927-938.	3.3	292
3	Principles, approaches, and challenges for predicting protein aggregation rates and shelf life. Journal of Pharmaceutical Sciences, 2009, 98, 1246-1277.	3.3	257
4	Protein aggregation and its impact on product quality. Current Opinion in Biotechnology, 2014, 30, 211-217.	6.6	220
5	Protein aggregation, particle formation, characterization & rheology. Current Opinion in Colloid and Interface Science, 2014, 19, 438-449.	7.4	213
6	A Lumryâ^'Eyring Nucleated Polymerization Model of Protein Aggregation Kinetics:â€‰ 1. Aggregation with Pre-Equilibrated Unfolding. Journal of Physical Chemistry B, 2007, 111, 7897-7913.	2.6	205
7	Comparative Effects of pH and Ionic Strength on Proteinâ€"Protein Interactions, Unfolding, and Aggregation for IgG1 Antibodies. Journal of Pharmaceutical Sciences, 2010, 99, 4830-4848.	3.3	188
8	Protein aggregation â€" Mechanisms, detection, and control. International Journal of Pharmaceutics, 2018, 550, 251-268.	5.2	164
9	Kinetics of Irreversible Protein Aggregation:â€‰ Analysis of Extended Lumryâ^'Eyring Models and Implications for Predicting Protein Shelf Life. Journal of Physical Chemistry B, 2003, 107, 1194-1207.	2.6	148
10	Predicting solution aggregation rates for therapeutic proteins: Approaches and challenges. International Journal of Pharmaceutics, 2011, 418, 318-333.	5.2	128
11	Lumryâ^'Eyring Nucleated-Polymerization Model of Protein Aggregation Kinetics. 2. Competing Growth via Condensation and Chain Polymerization. Journal of Physical Chemistry B, 2009, 113, 7020-7032.	2.6	120
12	Non-Arrhenius Protein Aggregation. AAPS Journal, 2013, 15, 840-851.	4.4	116
13	Nonnative Aggregation of an IgG1 Antibody in Acidic Conditions: Part 1. Unfolding, Colloidal Interactions, and Formation of High-Molecular-Weight Aggregates. Journal of Pharmaceutical Sciences, 2011, 100, 2087-2103.	3.3	103
14	Size-Exclusion Chromatography with Multi-angle Light Scattering for Elucidating Protein Aggregation Mechanisms. Methods in Molecular Biology, 2012, 899, 403-423.	0.9	94
15	Characterization of High-Molecular-Weight Nonnative Aggregates and Aggregation Kinetics by Size Exclusion Chromatography With Inline Multi-Angle Laser Light Scattering. Journal of Pharmaceutical Sciences, 2009, 98, 3997-4016.	3.3	90
16	Reexamining proteinâ€"protein and proteinâ€"solvent interactions from Kirkwood-Buff analysis of light scattering in multi-component solutions. Journal of Chemical Physics, 2011, 134, 225103.	3.0	86
17	Multi-variate approach to global protein aggregation behavior and kinetics: Effects of pH, NaCl, and temperature for Î±-chymotrypsinogen A. Journal of Pharmaceutical Sciences, 2010, 99, 645-662.	3.3	85
18	Irreversible aggregation of recombinant bovine granulocyte-colony stimulating factor (bG-CSF) and implications for predicting protein shelf life. Journal of Pharmaceutical Sciences, 2003, 92, 1095-1111.	3.3	80

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19	Aggregation of anti-streptavidin immunoglobulin gammaâ€1 involves Fab unfolding and competing growth pathways mediated by pH and salt concentration. Biophysical Chemistry, 2013, 172, 26-36.	2.8	76
20	Proteinâ€“Protein Interactions in Dilute to Concentrated Solutions: Î±-Chymotrypsinogen in Acidic Conditions. Journal of Physical Chemistry B, 2014, 118, 5817-5831.	2.6	76
21	Coarse-Grained Antibody Models for â€œWeakâ€•Proteinâ€“Protein Interactions from Low to High Concentrations. Journal of Physical Chemistry B, 2016, 120, 6592-6605.	2.6	75
22	Nonnative Aggregation of an IgG1 Antibody in Acidic Conditions, Part 2: Nucleation and Growth Kinetics with Competing Growth Mechanisms. Journal of Pharmaceutical Sciences, 2011, 100, 2104-2119.	3.3	74
23	Non-Native Aggregation of Î±-Chymotrypsinogen Occurs through Nucleation and Growth with Competing Nucleus Sizes and Negative Activation Energies. Biochemistry, 2007, 46, 7558-7571.	2.5	68
24	Relating Proteinâ€“Protein Interactions and Aggregation Rates From Low to High Concentrations. Journal of Pharmaceutical Sciences, 2016, 105, 1086-1096.	3.3	68
25	Predicting accelerated aggregation rates for monoclonal antibody formulations, and challenges for low-temperature predictions. Journal of Pharmaceutical Sciences, 2011, 100, 4234-4243.	3.3	66
26	Competing aggregation pathways for monoclonal antibodies. FEBS Letters, 2014, 588, 936-941.	2.8	64
27	Specific-Ion Effects on the Aggregation Mechanisms and Proteinâ€“Protein Interactions for Anti-streptavidin Immunoglobulin Gamma-1. Journal of Physical Chemistry B, 2015, 119, 5793-5804.	2.6	62
28	Nonnative Protein Polymers: Structure, Morphology, and Relation to Nucleation and Growth. Biophysical Journal, 2007, 93, 4392-4403.	0.5	60
29	How Well Do Low- and High-Concentration Protein Interactions Predict Solution Viscosities of Monoclonal Antibodies?. Journal of Pharmaceutical Sciences, 2019, 108, 142-154.	3.3	58
30	Aggregation and pHâ€“Temperature Phase Behavior for Aggregates of an IgG2 Antibody. Journal of Pharmaceutical Sciences, 2012, 101, 1678-1687.	3.3	54
31	Coarse-Grained Modeling of Protein Second Osmotic Virial Coefficients: Sterics and Short-Ranged Attractions. Journal of Physical Chemistry B, 2013, 117, 763-770.	2.6	54
32	Driving Forces for Nonnative Protein Aggregation and Approaches to Predict Aggregation-Prone Regions. Annual Review of Chemical and Biomolecular Engineering, 2017, 8, 139-159.	6.8	52
33	IgG cooperativity â€“ Is there allostery? Implications for antibody functions and therapeutic antibody development. MAbs, 2017, 9, 1231-1252.	5.2	52
34	Role of Anisotropic Interactions for Proteins and Patchy Nanoparticles. Journal of Physical Chemistry B, 2014, 118, 12599-12611.	2.6	49
35	Protein Adsorption, Desorption, and Aggregation Mediated by Solid-Liquid Interfaces. Journal of Pharmaceutical Sciences, 2015, 104, 1946-1959.	3.3	45
36	Predicting Protein-Protein Interactions of Concentrated Antibody Solutions Using Dilute Solution Data and Coarse-Grained MolecularÂModels. Journal of Pharmaceutical Sciences, 2018, 107, 1269-1281.	3.3	45

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37	Coarse-Grained Model for Colloidal Protein Interactions, B₂₂, and Protein Cluster Formation. Journal of Physical Chemistry B, 2013, 117, 16013-16028.	2.6	44
38	Nucleation, Growth, and Activation Energies for Seeded and Unseeded Aggregation of Î±-Chymotrypsinogen A. Biochemistry, 2008, 47, 2397-2403.	2.5	43
39	Computational Design and Biophysical Characterization of Aggregation-Resistant Point Mutations for Î³D Crystallin Illustrate a Balance of Conformational Stability and Intrinsic Aggregation Propensity. Biochemistry, 2011, 50, 628-639.	2.5	43
40	Predicting Protein Interactions of Concentrated Globular Protein Solutions Using Colloidal Models. Journal of Physical Chemistry B, 2017, 121, 4756-4767.	2.6	40
41	Connecting high-temperature and low-temperature protein stability and aggregation. PLoS ONE, 2017, 12, e0176748.	2.5	39
42	Osmolyte Effects on Monoclonal Antibody Stability and Concentration-Dependent Protein Interactions with Water and Common Osmolytes. Journal of Physical Chemistry B, 2016, 120, 3318-3330.	2.6	37
43	Aggregate structure, morphology and the effect of aggregation mechanisms on viscosity at elevated protein concentrations. Biophysical Chemistry, 2015, 207, 21-29.	2.8	34
44	Weak protein interactions and pH- and temperature-dependent aggregation of human Fc1. MAbs, 2015, 7, 1072-1083.	5.2	32
45	Acetate- and Citrate-Specific Ion Effects on Unfolding and Temperature-Dependent Aggregation Rates of Anti-Streptavidin IgG1. Journal of Pharmaceutical Sciences, 2016, 105, 1066-1073.	3.3	31
46	Conformational and Aggregation Properties of a PEGylated Alanine-Rich Polypeptide. Biomacromolecules, 2011, 12, 2184-2192.	5.4	27
47	Weak IgG selfâ€•and heteroâ€association characterized by fluorescence analytical ultracentrifugation. Protein Science, 2018, 27, 1334-1348.	7.6	27
48	Electrostatically Mediated Protein-Protein Interactions for Monoclonal Antibodies: A Combined Experimental and Coarse-Grained Molecular Modeling Approach. Journal of Pharmaceutical Sciences, 2019, 108, 120-132.	3.3	27
49	Effects of Temperature and Osmolytes on Competing Degradation Routes for an IgG1 Antibody. Journal of Pharmaceutical Sciences, 2013, 102, 3556-3566.	3.3	25
50	Conformational stability as a design target to control protein aggregation. Protein Engineering, Design and Selection, 2014, 27, 157-167.	2.1	23
51	Identifying protein aggregation mechanisms and quantifying aggregation rates from combined monomer depletion and continuousÂscattering. Analytical Biochemistry, 2016, 511, 80-91.	2.4	23
52	Structural Changes and Aggregation Mechanisms for Anti-Streptavidin IgG1 at Elevated Concentration. Journal of Physical Chemistry B, 2015, 119, 15150-15163.	2.6	22
53	Protein misfolding and aggregation research: Some thoughts on improving quality and utility. Biotechnology Progress, 2013, 29, 1109-1115.	2.6	20
54	Modulation of Self-Association and Subsequent Fibril Formation in an Alanine-Rich Helical Polypeptide. Biomacromolecules, 2008, 9, 1595-1603.	5.4	18

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55	Modulating non-native aggregation and electrostatic proteinâ€“protein interactions with computationally designed single-point mutations. Protein Engineering, Design and Selection, 2016, 29, 231-243.	2.1	18
56	Predicting High-Concentration Interactions of Monoclonal Antibody Solutions: Comparison of Theoretical Approaches for Strongly Attractive Versus Repulsive Conditions. Journal of Physical Chemistry B, 2019, 123, 5709-5720.	2.6	18
57	Freezing of Aqueous Solutions and Chemical Stability of Amorphous Pharmaceuticals: Water Clusters Hypothesis. Journal of Pharmaceutical Sciences, 2019, 108, 36-49.	3.3	18
58	Molecular Level Insights into Thermally Induced Î±-Chymotrypsinogen A Amyloid Aggregation Mechanism and Semiflexible Protofibril Morphology. Biochemistry, 2010, 49, 10553-10564.	2.5	17
59	Temperature Dependence of Protein Solution Viscosity and Proteinâ€“Protein Interactions: Insights into the Origins of High-Viscosity Protein Solutions. Molecular Pharmaceutics, 2020, 17, 4473-4482.	4.6	17
60	Relating particle formation to saltâ€•and pHâ€dependent phase separation of nonâ€native aggregates of alphaâ€chymotrypsinogen a. Journal of Pharmaceutical Sciences, 2012, 101, 3651-3660.	3.3	16
61	Kinetics and Competing Mechanisms of Antibody Aggregation via Bulk- and Surface-Mediated Pathways. Journal of Pharmaceutical Sciences, 2020, 109, 1449-1459.	3.3	16
62	Nonnative Protein Aggregation. , 2006, , 17-46.		15
63	Thermodynamics of amyloid dissociation provide insights into aggregate stability regimes. Biophysical Chemistry, 2012, 168-169, 10-18.	2.8	14
64	Toward a Suite of Coarse-Grained Models for Molecular Simulation of Monoclonal Antibodies and Therapeutic Proteins. Journal of Physical Chemistry B, 2021, 125, 3574-3588.	2.6	14
65	Electrostatically Driven Proteinâ€“Protein Interactions: Quantitative Prediction of Second Osmotic Virial Coefficients to Aid Antibody Design. Journal of Physical Chemistry Letters, 2022, 13, 1366-1372.	4.6	14
66	Structure and thermodynamics of colloidal protein cluster formation: Comparison of square-well and simple dipolar models. Journal of Chemical Physics, 2009, 131, 125104.	3.0	13
67	Neutron reflectivity measurement of protein Aâ€“antibody complex at the solid-liquid interface. Journal of Chromatography A, 2017, 1499, 118-131.	3.7	13
68	Osmotic virial coefficients for model protein and colloidal solutions: Importance of ensemble constraints in the analysis of light scattering data. Journal of Chemical Physics, 2012, 136, 175102.	3.0	12
69	Predicting unfolding thermodynamics and stable intermediates for alanine-rich helical peptides with the aid of coarse-grained molecular simulation. Biophysical Chemistry, 2016, 217, 8-19.	2.8	12
70	Viscosities and Protein Interactions of Bispecific Antibodies and Their Monospecific Mixtures. Molecular Pharmaceutics, 2018, 15, 4745-4755.	4.6	12
71	A Rapid, Small-Volume Approach to Evaluate Protein Aggregation at Air-Water Interfaces. Journal of Pharmaceutical Sciences, 2021, 110, 1083-1092.	3.3	12
72	Biophysical characterization and molecular simulation of electrostatically driven selfâ€association of a singleâ€chain antibody. Protein Science, 2018, 27, 1275-1285.	7.6	11

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73	Identifying Key Residues That Drive Strong Electrostatic Attractions between Therapeutic Antibodies. Journal of Physical Chemistry B, 2019, 123, 10642-10653.	2.6	11
74	Aggregation of poly(acrylic acid)-containing elastin-mimetic copolymers. Soft Matter, 2015, 11, 1839-1850.	2.7	10
75	Comparison of Huggins Coefficients and Osmotic Second Virial Coefficients of Buffered Solutions of Monoclonal Antibodies. Polymers, 2021, 13, 601.	4.5	9
76	Protein Partial Molar Volumes in Multicomponent Solutions from the Perspective of Inverse Kirkwoodâ€“Buff Theory. Journal of Physical Chemistry B, 2017, 121, 5897-5907.	2.6	8
77	Parallel chromatography and in situ scattering to interrogate competing protein aggregation pathways. Protein Science, 2018, 27, 1325-1333.	7.6	7
78	In situ neutron scattering of antibody adsorption during protein A chromatography. Journal of Chromatography A, 2020, 1617, 460842.	3.7	6
79	High-Pressure, Low-Temperature Induced Unfolding and Aggregation of Monoclonal Antibodies: Role of the Fc and Fab Fragments. Journal of Physical Chemistry B, 2022, 126, 4431-4441.	2.6	6
80	In Situ Monitoring of Protein Unfolding/Structural States under Cold High-Pressure Stress. Molecular Pharmaceutics, 2021, 18, 4415-4427.	4.6	5
81	Aggregates of Î±â€chymotrypsinogen anneal to access more stable states. Biotechnology and Bioengineering, 2014, 111, 782-791.	3.3	4
82	An Opportunity for Industryâ€“Academia Partnership: Training the Next Generation of Industrial Researchers in Characterizing Higher Order Protein Structure. Journal of Pharmaceutical Sciences, 2016, 105, 3483-3486.	3.3	4
83	Reduction of the C191-C220 disulfide of Î±-chymotrypsinogen A reduces nucleation barriers for aggregation. Biophysical Chemistry, 2014, 185, 79-87.	2.8	3
84	Reply to â€œComment on â€˜Osmolyte Effects on Monoclonal Antibody Stability and Concentration-Dependent Protein Interactions with Water and Common Osmolytesâ€™â€. Journal of Physical Chemistry B, 2016, 120, 11333-11334.	2.6	2
85	Challenges for design of aggregation-resistant variants of granulocyte colony-stimulating factor. Biophysical Chemistry, 2021, 277, 106630.	2.8	1
86	Folding and aggregation of a multi-domain engineered immunotoxin. Biochemical Engineering Journal, 2013, 81, 8-14.	3.6	0
87	Light Scattering to Quantify Proteinâ€“Protein Interactions at High Protein Concentrations. Methods in Molecular Biology, 2019, 2039, 23-37.	0.9	0
88	Characterizing aggregate growth and morphology of alanine-rich polypeptides as a function of sequence chemistry and solution temperature from scattering, spectroscopy, and microscopy. Biophysical Chemistry, 2020, 267, 106481.	2.8	0