

Huaying Zhao

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

3,270
citations

218677

26
h-index

168389

53
g-index

82
all docs

82
docs citations

82
times ranked

4557
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Precision Isothermal Titration Calorimetry with Automated Peak-Shape Analysis. <i>Analytical Chemistry</i> , 2012, 84, 5066-5073.	6.5	440
2	On the Distribution of Protein Refractive Index Increments. <i>Biophysical Journal</i> , 2011, 100, 2309-2317.	0.5	410
3	SEDPHAT – A platform for global ITC analysis and global multi-method analysis of molecular interactions. <i>Methods</i> , 2015, 76, 137-148.	3.8	264
4	Integration and global analysis of isothermal titration calorimetry data for studying macromolecular interactions. <i>Nature Protocols</i> , 2016, 11, 882-894.	12.0	225
5	Higher-order oligomerization promotes localization of <sc>SPOP</sc> to liquid nuclear speckles. <i>EMBO Journal</i> , 2016, 35, 1254-1275.	7.8	172
6	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
7	Combining biophysical methods for the analysis of protein complex stoichiometry and affinity in <i>SEDPHAT</i>. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 3-14.	2.5	139
8	Recorded scan times can limit the accuracy of sedimentation coefficients in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2013, 437, 104-108.	2.4	102
9	Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5. <i>ELife</i> , 2018, 7, .	6.0	73
10	A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2015, 10, e0126420.	2.5	71
11	Basic Principles of Analytical Ultracentrifugation. , 0, , .		69
12	The Molecular Refractive Function of Lens $\hat{3}$ -Crystallins. <i>Journal of Molecular Biology</i> , 2011, 411, 680-699.	4.2	68
13	An allosteric site in the T-cell receptor C $\hat{2}$ domain plays a critical signalling role. <i>Nature Communications</i> , 2017, 8, 15260.	12.8	64
14	Improving the thermal, radial, and temporal accuracy of the analytical ultracentrifuge through external references. <i>Analytical Biochemistry</i> , 2013, 440, 81-95.	2.4	60
15	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.	7.1	59
16	A comparison of binding surfaces for SPR biosensing using an antibody-antigen system and affinity distribution analysis. <i>Methods</i> , 2013, 59, 328-335.	3.8	52
17	Global Multi-Method Analysis of Affinities and Cooperativity in Complex Systems of Macromolecular Interactions. <i>Analytical Chemistry</i> , 2012, 84, 9513-9519.	6.5	48
18	Measuring macromolecular size distributions and interactions at high concentrations by sedimentation velocity. <i>Nature Communications</i> , 2018, 9, 4415.	12.8	48

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19	Analysis of high-affinity assembly for AMPA receptor amino-terminal domains. <i>Journal of General Physiology</i> , 2012, 139, 371-388.	1.9	45
20	Analysis of Protein Interactions with Picomolar Binding Affinity by Fluorescence-Detected Sedimentation Velocity. <i>Analytical Chemistry</i> , 2014, 86, 3181-3187.	6.5	41
21	Use of fluorescence-detected sedimentation velocity to study high-affinity protein interactions. <i>Nature Protocols</i> , 2017, 12, 1777-1791.	12.0	37
22	Plasticity in structure and assembly of SARS-CoV-2 nucleocapsid protein. , 2022, 1, .		36
23	The boundary structure in the analysis of reversibly interacting systems by sedimentation velocity. <i>Methods</i> , 2011, 54, 16-30.	3.8	35
24	Energetic and structural features of SARS-CoV-2 N-protein co-assemblies with nucleic acids. <i>IScience</i> , 2021, 24, 102523.	4.1	34
25	The role of macromolecular crowding in the evolution of lens crystallins with high molecular refractive index. <i>Physical Biology</i> , 2011, 8, 046004.	1.8	31
26	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.	2.5	31
27	Solution properties of fish and mammal crystallins: Hydration of fish and mammal crystallins. <i>Protein Science</i> , 2014, 23, 88-99.	7.6	30
28	Tools for the Quantitative Analysis of Sedimentation Boundaries Detected by Fluorescence Optical Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2013, 8, e77245.	2.5	27
29	3D-Printing for Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2016, 11, e0155201.	2.5	27
30	Accounting for Solvent Signal Offsets in the Analysis of Interferometric Sedimentation Velocity Data. <i>Macromolecular Bioscience</i> , 2010, 10, 736-745.	4.1	26
31	Variable Field Analytical Ultracentrifugation: II. Gravitational Sweep Sedimentation Velocity. <i>Biophysical Journal</i> , 2016, 110, 103-112.	0.5	25
32	Preferential assembly of heteromeric kainate and AMPA receptor amino terminal domains. <i>ELife</i> , 2017, 6, .	6.0	25
33	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.	7.1	24
34	Measuring Ultra-Weak Protein Self-Association by Non-ideal Sedimentation Velocity. <i>Journal of the American Chemical Society</i> , 2019, 141, 2990-2996.	18.7	22
35	Improved measurement of the rotor temperature in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2014, 451, 69-75.	2.4	20
36	Enhanced Sample Handling for Analytical Ultracentrifugation with 3D-Printed Centerpieces. <i>Analytical Chemistry</i> , 2019, 91, 5866-5873.	6.5	16

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37	Nucleic acid-induced dimerization of HIV-1 Gag protein. <i>Journal of Biological Chemistry</i> , 2019, 294, 16480-16493.	3.4	15
38	Measurement of the temperature of the resting rotor in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2014, 458, 37-39.	2.4	14
39	A histogram approach to the quality of fit in sedimentation velocity analyses. <i>Analytical Biochemistry</i> , 2015, 483, 1-3.	2.4	14
40	Measuring aggregates, self-association, and weak interactions in concentrated therapeutic antibody solutions. <i>MABs</i> , 2020, 12, 1810488.	5.2	14
41	Variable-Field Analytical Ultracentrifugation: I. Time-Optimized Sedimentation Equilibrium. <i>Biophysical Journal</i> , 2015, 109, 827-837.	0.5	12
42	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.	2.6	12
43	A multi-laboratory benchmark study of isothermal titration calorimetry (ITC) using Ca ²⁺ and Mg ²⁺ binding to EDTA. <i>European Biophysics Journal</i> , 2021, 50, 429-451.	2.2	12
44	Accounting for Photophysical Processes and Specific Signal Intensity Changes in Fluorescence-Detected Sedimentation Velocity. <i>Analytical Chemistry</i> , 2014, 86, 9286-9292.	6.5	11
45	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, .	7.1	11
46	Monochromatic multicomponent fluorescence sedimentation velocity for the study of high-affinity protein interactions. <i>ELife</i> , 2016, 5, .	6.0	11
47	Biocalorimetry. <i>Methods</i> , 2015, 76, 1-2.	3.8	9
48	Sedimentation of Reversibly Interacting Macromolecules with Changes in Fluorescence Quantum Yield. <i>Biophysical Journal</i> , 2017, 112, 1374-1382.	0.5	8
49	A radial calibration window for analytical ultracentrifugation. <i>PLoS ONE</i> , 2018, 13, e0201529.	2.5	8
50	Quantitative Analysis of Protein Self-Association by Sedimentation Velocity. <i>Current Protocols in Protein Science</i> , 2020, 101, e109.	2.8	8
51	Global multi-method analysis of interaction parameters for reversibly self-associating macromolecules at high concentrations. <i>Scientific Reports</i> , 2021, 11, 5741.	3.3	7
52	Characterization of DNA-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, .	7.1	7
53	Mechanistic Implications of the Unique Structural Features and Dimerization of the Cytoplasmic Domain of the <i>Pseudomonas</i> Sigma Regulator, PupR. <i>Biochemistry</i> , 2015, 54, 5867-5877.	2.5	6
54	Efficient data acquisition with three-channel centerpieces in sedimentation velocity. <i>Analytical Biochemistry</i> , 2019, 586, 113414.	2.4	5

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55	Distinct disease features in chimpanzees infected with a precore HBV mutant associated with acute liver failure in humans. PLoS Pathogens, 2020, 16, e1008793.	4.7	4
56	Calibrating analytical ultracentrifuges. European Biophysics Journal, 2021, 50, 353-362.	2.2	4
57	Resuspending samples in analytical ultracentrifugation. Analytical Biochemistry, 2020, 604, 113771.	2.4	2
58	Macromol. Biosci. 7/2010. Macromolecular Bioscience, 2010, 10, .	4.1	0
59	Mechanistic Implications of the Unique Structural Features of the Anti- σ Domain of the Pseudomonas Sigma Regulator, PupR. FASEB Journal, 2016, 30, 1118.3.	0.5	0