

# 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	Plasticity in structure and assembly of SARS-CoV-2 nucleocapsid protein. , 2022, 1, .		36
2	Global multi-method analysis of interaction parameters for reversibly self-associating macromolecules at high concentrations. Scientific Reports, 2021, 11, 5741.	3.3	7
3	A multi-laboratory benchmark study of isothermal titration calorimetry (ITC) using Ca <sup>2+</sup> and Mg <sup>2+</sup> binding to EDTA. European Biophysics Journal, 2021, 50, 429-451.	2.2	12
4	Energetic and structural features of SARS-CoV-2 N-protein co-assemblies with nucleic acids. IScience, 2021, 24, 102523.	4.1	34
5	Characterization of DNA-protein complexes by nanoparticle tracking analysis and their association with systemic lupus erythematosus. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	7
6	Competing stress-dependent oligomerization pathways regulate self-assembly of the periplasmic protease-chaperone DegP. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	11
7	Calibrating analytical ultracentrifuges. European Biophysics Journal, 2021, 50, 353-362.	2.2	4
8	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
9	Measuring aggregates, self-association, and weak interactions in concentrated therapeutic antibody solutions. MAbs, 2020, 12, 1810488.	5.2	14
10	Resuspending samples in analytical ultracentrifugation. Analytical Biochemistry, 2020, 604, 113771.	2.4	2
11	Quantitative Analysis of Protein Self-Association by Sedimentation Velocity. Current Protocols in Protein Science, 2020, 101, e109.	2.8	8
12	Ultrasml Gold Nanoparticles Coated with Zwitterionic Glutathione Monoethyl Ester: A Model Platform for the Incorporation of Functional Peptides. Journal of Physical Chemistry B, 2020, 124, 3892-3902.	2.6	12
13	Nucleic acid-induced dimerization of HIV-1 Gag protein. Journal of Biological Chemistry, 2019, 294, 16480-16493.	3.4	15
14	Efficient data acquisition with three-channel centerpieces in sedimentation velocity. Analytical Biochemistry, 2019, 586, 113414.	2.4	5
15	Measuring Ultra-Weak Protein Self-Association by Non-ideal Sedimentation Velocity. Journal of the American Chemical Society, 2019, 141, 2990-2996.	13.7	22
16	Enhanced Sample Handling for Analytical Ultracentrifugation with 3D-Printed Centerpieces. Analytical Chemistry, 2019, 91, 5866-5873.	6.5	16
17	Role of humoral immunity against hepatitis B virus core antigen in the pathogenesis of acute liver failure. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11369-E11378.	7.1	59
18	Cooperative assembly of a four-molecule signaling complex formed upon T cell antigen receptor activation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11914-E11923.	7.1	24

#	ARTICLE	IF	CITATIONS
19	Measuring macromolecular size distributions and interactions at high concentrations by sedimentation velocity. <i>Nature Communications</i> , 2018, 9, 4415.	12.8	48
20	A radial calibration window for analytical ultracentrifugation. <i>PLoS ONE</i> , 2018, 13, e0201529.	2.5	8
21	Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5. <i>ELife</i> , 2018, 7, .	6.0	73
22	Sedimentation of Reversibly Interacting Macromolecules with Changes in Fluorescence Quantum Yield. <i>Biophysical Journal</i> , 2017, 112, 1374-1382.	0.5	8
23	An allosteric site in the T-cell receptor C $\hat{1}$ <sup>2</sup> domain plays a critical signalling role. <i>Nature Communications</i> , 2017, 8, 15260.	12.8	64
24	Use of fluorescence-detected sedimentation velocity to study high-affinity protein interactions. <i>Nature Protocols</i> , 2017, 12, 1777-1791.	12.0	37
25	Preferential assembly of heteromeric kainate and AMPA receptor amino terminal domains. <i>ELife</i> , 2017, 6, .	6.0	25
26	Higher-order oligomerization promotes localization of <sc>SPOP</sc> to liquid nuclear speckles. <i>EMBO Journal</i> , 2016, 35, 1254-1275.	7.8	172
27	Integration and global analysis of isothermal titration calorimetry data for studying macromolecular interactions. <i>Nature Protocols</i> , 2016, 11, 882-894.	12.0	225
28	Variable Field Analytical Ultracentrifugation: II. Gravitational Sweep Sedimentation Velocity. <i>Biophysical Journal</i> , 2016, 110, 103-112.	0.5	25
29	3D-Printing for Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2016, 11, e0155201.	2.5	27
30	Monochromatic multicomponent fluorescence sedimentation velocity for the study of high-affinity protein interactions. <i>ELife</i> , 2016, 5, .	6.0	11
31	Mechanistic Implications of the Unique Structural Features of the Anti- $\sigma$ Domain of the <i>Pseudomonas</i> Sigma Regulator, <i>PupR</i> . <i>FASEB Journal</i> , 2016, 30, 1118.3.	0.5	0
32	A histogram approach to the quality of fit in sedimentation velocity analyses. <i>Analytical Biochemistry</i> , 2015, 483, 1-3.	2.4	14
33	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
34	Biocalorimetry. <i>Methods</i> , 2015, 76, 1-2.	3.8	9
35	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
36	Variable-Field Analytical Ultracentrifugation: I. Time-Optimized Sedimentation Equilibrium. <i>Biophysical Journal</i> , 2015, 109, 827-837.	0.5	12

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37	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
38	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
39	Solution properties of $\beta$ -crystallins: Hydration of fish and mammal $\beta$ -crystallins. <i>Protein Science</i> , 2014, 23, 88-99.	7.6	30
40	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
41	Analysis of Protein Interactions with Picomolar Binding Affinity by Fluorescence-Detected Sedimentation Velocity. <i>Analytical Chemistry</i> , 2014, 86, 3181-3187.	6.5	41
42	Improved measurement of the rotor temperature in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2014, 451, 69-75.	2.4	20
43	Measurement of the temperature of the resting rotor in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2014, 458, 37-39.	2.4	14
44	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
45	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
46	Recorded scan times can limit the accuracy of sedimentation coefficients in analytical ultracentrifugation. <i>Analytical Biochemistry</i> , 2013, 437, 104-108.	2.4	102
47	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
48	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
49	Tools for the Quantitative Analysis of Sedimentation Boundaries Detected by Fluorescence Optical Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2013, 8, e77245.	2.5	27
50	Analysis of high-affinity assembly for AMPA receptor amino-terminal domains. <i>Journal of General Physiology</i> , 2012, 139, 371-388.	1.9	45
51	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
52	High-Precision Isothermal Titration Calorimetry with Automated Peak-Shape Analysis. <i>Analytical Chemistry</i> , 2012, 84, 5066-5073.	6.5	440
53	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
54	The Molecular Refractive Function of Lens $\beta$ -Crystallins. <i>Journal of Molecular Biology</i> , 2011, 411, 680-699.	4.2	68

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55	The boundary structure in the analysis of reversibly interacting systems by sedimentation velocity. <i>Methods</i> , 2011, 54, 16-30.	3.8	35
56	On the Distribution of Protein Refractive Index Increments. <i>Biophysical Journal</i> , 2011, 100, 2309-2317.	0.5	410
57	Accounting for Solvent Signal Offsets in the Analysis of Interferometric Sedimentation Velocity Data. <i>Macromolecular Bioscience</i> , 2010, 10, 736-745.	4.1	26
58	Macromol. Biosci. 7/2010. <i>Macromolecular Bioscience</i> , 2010, 10, .	4.1	0
59	Basic Principles of Analytical Ultracentrifugation. , 0, , .		69