Aiwu Zhou

List of Publications by Year
in descending order

65 papers	2,732 citations	186265 28 h-index	182427 51 g-index
67 all docs	67 docs citations	67 times ranked	3770 citing authors

#	Article	IF	Citations
1	Structural basis of von Willebrand factor multimerization and tubular storage. Blood, 2022, 139, 3314-3324.	1.4	15
2	Structural mechanism of VWF Dâ€™D3 dimer formation. Cell Discovery, 2022, 8, 14.	6.7	5
3	TRPV1 SUMOylation suppresses itch by inhibiting TRPV1 interaction with H1 receptors. Cell Reports, 2022, 39, 110972.	6.4	5
4	Purification, crystallization, and X-ray diffraction analysis of myocyte enhancer factor 2D and DNA complex. Protein Expression and Purification, 2021, 179, 105788.	1.3	3
5	Angiotensinogen and the Modulation of Blood Pressure. Frontiers in Cardiovascular Medicine, 2021, 8, 645123.	2.4	11
6	Identification of HSP47 Binding Site on Native Collagen and Its Implications for the Development of HSP47 Inhibitors. Biomolecules, 2021, 11, 983.	4.0	9
7	Kynurenine derivative 3-HAA is an agonist ligand for transcription factor YY1. Journal of Hematology and Oncology, 2021, 14, 153.	17.0	7
8	Structure of the cytochrome <i>aa</i> _{<i>3</i>} -600 heme-copper menaquinol oxidase bound to inhibitor HQNO shows TM0 is part of the quinol binding site. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 872-876.	7.1	21
9	Identification of clinical molecular targets for childhood Burkitt lymphoma. Translational Oncology, 2020, 13, 100855.	3.7	8
10	Structure of CTLA-4 complexed with a pH-sensitive cancer immunotherapeutic antibody. Cell Discovery, 2020, 6, 79.	6.7	6
11	Heparin Blocks the Inhibition of Tissue Kallikrein 1 by Kallistatin through Electrostatic Repulsion. Biomolecules, 2020, 10, 828.	4.0	4
12	DUSP6 SUMOylation protects cells from oxidative damage via direct regulation of Drp1 dephosphorylation. Science Advances, 2020, 6, eaaz0361.	10.3	42
13	SUMOylation modulates the LIN28Aâ€•letâ€•7 signaling pathway in response to cellular stresses in cancer cells. Molecular Oncology, 2020, 14, 2288-2312.	4.6	9
14	SENP1-Sirt3 Signaling Controls Mitochondrial Protein Acetylation and Metabolism. Molecular Cell, 2019, 75, 823-834.e5.	9.7	119
15	A novel â€œmosaic-typeâ€•nanoparticle for selective drug release targeting hypoxic cancer cells. Nanoscale, 2019, 11, 2211-2222.	5.6	22
16	Characterization of PPIB interaction in the P3H1 ternary complex and implications for its pathological mutations. Cellular and Molecular Life Sciences, 2019, 76, 3899-3914.	5.4	9
17	Structural basis for enzymatic photocatalysis in chlorophyll biosynthesis. Nature, 2019, 574, 722-725.	27.8	88
18	Structural basis for the specificity of renin-mediated angiotensinogen cleavage. Journal of Biological Chemistry, 2019, 294, 2353-2364.	3.4	21

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19	Identification of a natural inhibitor of methionine adenosyltransferase 2A regulating one-carbon metabolism in keratinocytes. EBioMedicine, 2019, 39, 575-590.	6.1	19
20	Transcriptional Approach for Decoding the Mechanism of rpoC Compensatory Mutations for the Fitness Cost in Rifampicin-Resistant Mycobacterium tuberculosis. Frontiers in Microbiology, 2018, 9, 2895.	3.5	14
21	Structural basis of a novel PD-L1 nanobody for immune checkpoint blockade. Cell Discovery, 2017, 3, 17004.	6.7	147
22	Insights into Hunter syndrome from the structure of iduronate-2-sulfatase. Nature Communications, 2017, 8, 15786.	12.8	68
23	Structural basis of a novel heterodimeric Fc for bispecific antibody production. Oncotarget, 2017, 8, 51037-51049.	1.8	41
24	Structural basis of the therapeutic anti-PD-L1 antibody atezolizumab. Oncotarget, 2017, 8, 90215-90224.	1.8	68
25	Molecular Mechanism of Z Î±1-Antitrypsin Deficiency. Journal of Biological Chemistry, 2016, 291, 15674-15686.	3.4	30
26	Heparin Binds Lamprey Angiotensinogen and Promotes Thrombin Inhibition through a Template Mechanism. Journal of Biological Chemistry, 2016, 291, 24900-24911.	3.4	9
27	A redox mechanism underlying nucleolar stress sensing by nucleophosmin. Nature Communications, 2016, 7, 13599.	12.8	94
28	Sequential posttranslational modifications regulate PKC degradation. Molecular Biology of the Cell, 2016, 27, 410-420.	2.1	30
29	Thermodynamic and Kinetic Characterization of the Protein Z-dependent Protease Inhibitor (ZPI)-Protein Z Interaction Reveals an Unexpected Role for ZPI Lys-239. Journal of Biological Chemistry, 2015, 290, 9906-9918.	3.4	8
30	Crystallization and crystallographic studies of kallistatin. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1135-1138.	0.8	2
31	14-3-3Ï„ Promotes Surface Expression of Cav2.2 (Î±1B) Ca2+ Channels. Journal of Biological Chemistry, 2015, 290, 2689-2698.	3.4	8
32	Physical and Functional Links between Anion Exchanger-1 and Sodium Pump. Journal of the American Society of Nephrology: JASN, 2015, 26, 400-409.	6.1	11
33	Temperature-responsive release of thyroxine and its environmental adaptation in Australians. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20132747.	2.6	24
34	Crystal Structures of PI3KÎ± Complexed with PI103 and Its Derivatives: New Directions for Inhibitors Design. ACS Medicinal Chemistry Letters, 2014, 5, 138-142.	2.8	81
35	Towards Engineering Hormone-Binding Globulins as Drug Delivery Agents. PLoS ONE, 2014, 9, e113402.	2.5	13
36	How Changes in Affinity of Corticosteroid-binding Globulin Modulate Free Cortisol Concentration. Journal of Clinical Endocrinology and Metabolism, 2013, 98, 3315-3322.	3.6	68

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37	Structural basis for catalytic activation of protein Zâ€“dependent protease inhibitor (ZPI) by protein Z. Blood, 2012, 120, 1726-1733.	1.4	19
38	Solving Serpin Crystal Structures. Methods in Enzymology, 2011, 501, 49-61.	1.0	5
39	Serpins as Hormone Carriers. Methods in Enzymology, 2011, 501, 89-103.	1.0	7
40	Allosteric Modulation of Hormone Release from Thyroxine and Corticosteroid-binding Globulins. Journal of Biological Chemistry, 2011, 286, 16163-16173.	3.4	45
41	Glyceraldehyde 3-phosphate dehydrogenase is required for band 3 (anion exchanger 1) membrane residency in the mammalian kidney. American Journal of Physiology - Renal Physiology, 2011, 300, F157-F166.	2.7	25
42	A redox switch in angiotensinogen modulates angiotensin release. Nature, 2010, 468, 108-111.	27.8	191
43	Temperature-Responsive Release of Cortisol from Its Binding Globulin: A Protein Thermocouple. Journal of Clinical Endocrinology and Metabolism, 2010, 95, 4689-4695.	3.6	98
44	Angiotensinogen adjusts its shape to complex with renin and modulate blood pressure. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s30-s30.	0.3	0
45	Probing Conformational Motion of Serpin by Time-Resolved and Single Molecule Fluorescence. Biophysical Journal, 2009, 96, 377a.	0.5	0
46	Probing nanosecond motions of plasminogen activator inhibitor-1 by time-resolved fluorescence anisotropy. Molecular BioSystems, 2009, 5, 1025.	2.9	12
47	Crystal structure of protein Zâ€“dependent inhibitor complex shows how protein Z functions as a cofactor in the membrane inhibition of factor X. Blood, 2009, 114, 3662-3667.	1.4	44
48	Crystal structures of two human vitronectin, urokinase and urokinase receptor complexes. Nature Structural and Molecular Biology, 2008, 15, 422-423.	8.2	103
49	Serpins show structural basis for oligomer toxicity and amyloid ubiquity. FEBS Letters, 2008, 582, 2537-2541.	2.8	21
50	Dimers Initiate and Propagate Serine Protease Inhibitor Polymerisation. Journal of Molecular Biology, 2008, 375, 36-42.	4.2	32
51	The S-to-R Transition of Corticosteroid-Binding Globulin and the Mechanism of Hormone Release. Journal of Molecular Biology, 2008, 380, 244-251.	4.2	64
52	Redirection of the reaction between activated protein C and a serpin to the substrate pathway. Thrombosis Research, 2008, 122, 397-404.	1.7	13
53	Human H+ATPase a4 subunit mutations causing renal tubular acidosis reveal a role for interaction with phosphofructokinase-1. American Journal of Physiology - Renal Physiology, 2008, 295, F950-F958.	2.7	54
54	Modulation of Serpin Reaction through Stabilization of Transient Intermediate by Ligands Bound to Î±-Helix F. Journal of Biological Chemistry, 2007, 282, 26306-26315.	3.4	16

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55	Functional structure of the somatomedin B domain of vitronectin. Protein Science, 2007, 16, 1502-1508.	7.6	22
56	Structural mechanism for the carriage and release of thyroxine in the blood. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13321-13326.	7.1	105
57	How Small Peptides Block and Reverse Serpin Polymerisation. Journal of Molecular Biology, 2004, 342, 931-941.	4.2	82
58	How vitronectin binds PAI-1 to modulate fibrinolysis and cell migration. Nature Structural and Molecular Biology, 2003, 10, 541-544.	8.2	217
59	The a-Subunit of the V-type H+-ATPase Interacts with Phosphofructokinase-1 in Humans. Journal of Biological Chemistry, 2003, 278, 20013-20018.	3.4	106
60	Serpin Polymerization Is Prevented by a Hydrogen Bond Network That Is Centered on His-334 and Stabilized by Glycerol. Journal of Biological Chemistry, 2003, 278, 15116-15122.	3.4	62
61	Targeting a Surface Cavity of Î±1-Antitrypsin to Prevent Conformational Disease. Clinical Science, 2003, 104, 57P-57P.	0.0	0
62	Polymerization of Plasminogen Activator Inhibitor-1. Journal of Biological Chemistry, 2001, 276, 9115-9122.	3.4	52
63	The Serpin Inhibitory Mechanism Is Critically Dependent on the Length of the Reactive Center Loop. Journal of Biological Chemistry, 2001, 276, 27541-27547.	3.4	121
64	Formation of the Antithrombin Heterodimer In Vivo and the Onset of Thrombosis. Blood, 1999, 94, 3388-3396.	1.4	76
65	High-level expression of active human plasminogen activator inhibitor type 1 (PAI-1) in E. coli. IUBMB Life, 1996, 39, 235-242.	3.4	1