

# Xiaodong Zhang

## List of Publications by Year in descending order

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123  
papers

8,561  
citations

38660

50  
h-index

48187

88  
g-index

151  
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151  
docs citations

151  
times ranked

8657  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structures of Class I and Class II Transcription Complexes Reveal the Molecular Basis of RamA-Dependent Transcription Activation. <i>Advanced Science</i> , 2022, 9, e2103669.	5.6	13
2	GMT8 aptamer conjugated PEGylated Ag@Au core-shell nanoparticles as a novel radiosensitizer for targeted radiotherapy of glioma. <i>Colloids and Surfaces B: Biointerfaces</i> , 2022, 211, 112330.	2.5	13
3	Mechanism of auto-inhibition and activation of Mec1ATR checkpoint kinase. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 50-61.	3.6	17
4	Rad51 filament dynamics and its antagonistic modulators. <i>Seminars in Cell and Developmental Biology</i> , 2021, 113, 3-13.	2.3	11
5	Roles of ATM and ATR in DNA double strand breaks and replication stress. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 161, 27-38.	1.4	14
6	p97 and p47 function in membrane tethering in cooperation with FTCD during mitotic Golgi reassembly. <i>EMBO Journal</i> , 2021, 40, e105853.	3.5	13
7	Roles of ATM and ATR in DNA double strand breaks and replication stress. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 163, 109-119.	1.4	14
8	The renaissance in biophysics and molecular biology enabled by the interface of DNA repair and replication with cancer. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 163, 1-4.	1.4	0
9	One-stop preoperative assessment of renal vessels for living donors with 3.0 T non-contrast-enhanced magnetic resonance angiography: compared with computerized tomography angiography and surgical results. <i>British Journal of Radiology</i> , 2021, 94, 20210589.	1.0	1
10	Crystal structure of the catalytic D2 domain of the AAA+ ATPase p97 reveals a putative helical split-washer-type mechanism for substrate unfolding. <i>FEBS Letters</i> , 2020, 594, 933-943.	1.3	6
11	Structures and regulations of ATM and ATR, master kinases in genome integrity. <i>Current Opinion in Structural Biology</i> , 2020, 61, 98-105.	2.6	31
12	Cryo-EM Structure of Nucleotide-Bound Tel1ATR Unravels the Molecular Basis of Inhibition and Structural Rationale for Disease-Associated Mutations. <i>Structure</i> , 2020, 28, 96-104.e3.	1.6	28
13	Structural basis of homologous recombination. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 3-18.	2.4	88
14	Editorial overview: Macromolecular assemblies. <i>Current Opinion in Structural Biology</i> , 2020, 61, vi-viii.	2.6	0
15	Bacterial Enhancer Binding Proteins' AAA+ Proteins in Transcription Activation. <i>Biomolecules</i> , 2020, 10, 351.	1.8	27
16	Structural basis of transcription inhibition by the DNA mimic protein Ocr of bacteriophage T7. <i>ELife</i> , 2020, 9, .	2.8	8
17	RNA Polymerase Reaches 60: Transcription Initiation, Elongation, Termination, and Regulation in Prokaryotes. <i>Journal of Molecular Biology</i> , 2019, 431, 3945-3946.	2.0	3
18	Isomerization of BRCA1-BARD1 promotes replication fork protection. <i>Nature</i> , 2019, 571, 521-527.	13.7	88

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19	Mechanisms of $\sigma^{54}$ -Dependent Transcription Initiation and Regulation. <i>Journal of Molecular Biology</i> , 2019, 431, 3960-3974.	2.0	70
20	Structure and regulation of the human INO80 nucleosome complex. <i>Nature</i> , 2018, 556, 391-395.	13.7	148
21	Cryo-EM structures of the human INO80 chromatin-remodeling complex. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 37-44.	3.6	46
22	A structural and dynamic model for the assembly of Replication Protein A on single-stranded DNA. <i>Nature Communications</i> , 2018, 9, 5447.	5.8	110
23	Structures of Bacterial RNA Polymerase Complexes Reveal the Mechanism of DNA Loading and Transcription Initiation. <i>Molecular Cell</i> , 2018, 70, 1111-1120.e3.	4.5	46
24	Single-Particle Electron Microscopy Analysis of DNA Repair Complexes. <i>Methods in Enzymology</i> , 2017, 592, 159-186.	0.4	2
25	Structures of RNA Polymerase Closed and Intermediate Complexes Reveal Mechanisms of DNA Opening and Transcription Initiation. <i>Molecular Cell</i> , 2017, 67, 106-116.e4.	4.5	44
26	Crosstalk within a functional INO80 complex dimer regulates nucleosome sliding. <i>ELife</i> , 2017, 6, .	2.8	21
27	Transcription Regulation and Membrane Stress Management in Enterobacterial Pathogens. <i>Advances in Experimental Medicine and Biology</i> , 2016, 915, 207-230.	0.8	9
28	The bacterial enhancer-dependent RNA polymerase. <i>Biochemical Journal</i> , 2016, 473, 3741-3753.	1.7	40
29	The Dimeric Architecture of Checkpoint Kinases Mec1ATR and Tel1ATM Reveal a Common Structural Organization. <i>Journal of Biological Chemistry</i> , 2016, 291, 13436-13447.	1.6	35
30	A second DNA binding site in human BRCA2 promotes homologous recombination. <i>Nature Communications</i> , 2016, 7, 12813.	5.8	33
31	Mutations in RNA Polymerase Bridge Helix and Switch Regions Affect Active-Site Networks and Transcript-Assisted Hydrolysis. <i>Journal of Molecular Biology</i> , 2015, 427, 3516-3526.	2.0	6
32	The structural basis for enhancer-dependent assembly and activation of the AAA transcriptional activator NorR. <i>Molecular Microbiology</i> , 2015, 95, 17-30.	1.2	13
33	Structures of the RNA polymerase $\sigma^{54}$ reveal new and conserved regulatory strategies. <i>Science</i> , 2015, 349, 882-885.	6.0	77
34	Mutational analysis of dimeric linkers in peri- and cytoplasmic domains of histidine kinase DctB reveals their functional roles in signal transduction. <i>Open Biology</i> , 2014, 4, 140023.	1.5	10
35	Molecular basis of nucleotide-dependent substrate engagement and remodeling by an AAA+ activator. <i>Nucleic Acids Research</i> , 2014, 42, 9249-9261.	6.5	4
36	The p97-FAF1 Protein Complex Reveals a Common Mode of p97 Adaptor Binding. <i>Journal of Biological Chemistry</i> , 2014, 289, 12077-12084.	1.6	24

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37	Domain movements of the enhancer-dependent sigma factor drive DNA delivery into the RNA polymerase active site: insights from single molecule studies. <i>Nucleic Acids Research</i> , 2014, 42, 5177-5190.	6.5	24
38	Structure and mechanism of action of the BRCA2 breast cancer tumor suppressor. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 962-968.	3.6	95
39	Inter-ring rotations of AAA ATPase p97 revealed by electron cryomicroscopy. <i>Open Biology</i> , 2014, 4, 130142.	1.5	23
40	A fast multiparameter MRI approach for acute stroke assessment on a 3T clinical scanner: preliminary results in a non-human primate model with transient ischemic occlusion. <i>Quantitative Imaging in Medicine and Surgery</i> , 2014, 4, 112-22.	1.1	27
41	The Role of the N-Domain in the ATPase Activity of the Mammalian AAA ATPase p97/VCP. <i>Journal of Biological Chemistry</i> , 2012, 287, 8561-8570.	1.6	104
42	Interactions between the nucleosome histone core and Arp8 in the INO80 chromatin remodeling complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20883-20888.	3.3	47
43	Distinct conformations of the protein complex p97-Ufd1-Npl4 revealed by electron cryomicroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1098-1103.	3.3	41
44	DBL-1, a TGF- $\beta$ 2, is essential for <i>Caenorhabditis elegans</i> aversive olfactory learning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17081-17086.	3.3	53
45	Coupling AAA protein function to regulated gene expression. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2012, 1823, 108-116.	1.9	32
46	Regulation of p97 in the ubiquitin-proteasome system by the UBX protein-family. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2012, 1823, 125-129.	1.9	61
47	Transcriptional regulation by the dedicated nitric oxide sensor, NorR: a route towards NO detoxification. <i>Biochemical Society Transactions</i> , 2011, 39, 289-293.	1.6	36
48	Intramolecular signal transmission in a tetrameric repressor of the IclR family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15372-15377.	3.3	17
49	Activity Map of the Escherichia coli RNA Polymerase Bridge Helix. <i>Journal of Biological Chemistry</i> , 2011, 286, 14469-14479.	1.6	25
50	RNA polymerase and transcription elongation factor Spt4/5 complex structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 546-550.	3.3	139
51	Mechanisms for activating bacterial RNA polymerase. <i>FEMS Microbiology Reviews</i> , 2010, 34, 611-627.	3.9	66
52	From signal perception to signal transduction: ligand-induced dimeric switch of DctB sensory domain in solution. <i>Molecular Microbiology</i> , 2010, 75, 1484-1494.	1.2	19
53	Nitric oxide-responsive interdomain regulation targets the $\beta$ 54-interaction surface in the enhancer binding protein NorR. <i>Molecular Microbiology</i> , 2010, 77, 1278-1288.	1.2	20
54	Domain Cross-talk during Effector Binding to the Multidrug Binding TTGR Regulator. <i>Journal of Biological Chemistry</i> , 2010, 285, 21372-21381.	1.6	26

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55	Crystal structure of TtgV in complex with its DNA operator reveals a general model for cooperative DNA binding of tetrameric gene regulators. <i>Genes and Development</i> , 2010, 24, 2556-2565.	2.7	33
56	Essential roles of three enhancer sites in $\lambda$ P <sub>54</sub> -dependent transcription by the nitric oxide sensing regulatory protein NorR. <i>Nucleic Acids Research</i> , 2010, 38, 1182-1194.	6.5	37
57	Foot-and-Mouth Disease Virus 2C Is a Hexameric AAA+ Protein with a Coordinated ATP Hydrolysis Mechanism. <i>Journal of Biological Chemistry</i> , 2010, 285, 24347-24359.	1.6	57
58	Crystal structure of MexZ, a key repressor responsible for antibiotic resistance in <i>Pseudomonas aeruginosa</i> . <i>Journal of Structural Biology</i> , 2010, 172, 305-310.	1.3	34
59	Structural and functional implications of phosphorylation and acetylation in the regulation of the AAA+ protein p97 This paper is one of a selection of papers published in this special issue entitled 8th International Conference on AAA Proteins and has undergone the Journal's usual peer review process. <i>Biochemistry and Cell Biology</i> , 2010, 88, 41-48.	0.9	35
60	TtgV Represses Two Different Promoters by Recognizing Different Sequences. <i>Journal of Bacteriology</i> , 2009, 191, 1901-1909.	1.0	19
61	IHF-binding sites inhibit DNA loop formation and transcription initiation. <i>Nucleic Acids Research</i> , 2009, 37, 3878-3886.	6.5	27
62	Structure-based mechanism of lipoteichoic acid synthesis by <i>Staphylococcus aureus</i> LtaS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1584-1589.	3.3	93
63	Functional roles of the pre- $\epsilon$ sensor I insertion sequence in an AAA+ bacterial enhancer binding protein. <i>Molecular Microbiology</i> , 2009, 73, 519-533.	1.2	13
64	Automated Assignment in Selectively Methyl-Labeled Proteins. <i>Journal of the American Chemical Society</i> , 2009, 131, 9480-9481.	6.6	30
65	Neural-Immune Communication in <i>Caenorhabditis elegans</i> . <i>Cell Host and Microbe</i> , 2009, 5, 425-429.	5.1	33
66	Coupling $\lambda$ F Factor Conformation to RNA Polymerase Reorganisation for DNA Melting. <i>Journal of Molecular Biology</i> , 2009, 387, 306-319.	2.0	15
67	PhhR Binds to Target Sequences at Different Distances with Respect to RNA Polymerase in Order to Activate Transcription. <i>Journal of Molecular Biology</i> , 2009, 394, 576-586.	2.0	16
68	The 'glutamate switch' provides a link between ATPase activity and ligand binding in AAA+ proteins. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1223-1227.	3.6	105
69	<i>Modus operandi</i> of the bacterial RNA polymerase containing the $\lambda$ P <sub>54</sub> promoter-specificity factor. <i>Molecular Microbiology</i> , 2008, 68, 538-546.	1.2	118
70	Trapping of a Transcription Complex Using a New Nucleotide Analogue: AMP Aluminium Fluoride. <i>Journal of Molecular Biology</i> , 2008, 375, 1206-1211.	2.0	16
71	Mechanism of Homotropic Control to Coordinate Hydrolysis in a Hexameric AAA+ Ring ATPase. <i>Journal of Molecular Biology</i> , 2008, 381, 1-12.	2.0	13
72	Organization of an Activator-Bound RNA Polymerase Holoenzyme. <i>Molecular Cell</i> , 2008, 32, 337-346.	4.5	66

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73	Analysis of Nucleotide Binding to P97 Reveals the Properties of a Tandem AAA Hexameric ATPase. <i>Journal of Biological Chemistry</i> , 2008, 283, 13745-13752.	1.6	72
74	Insights into adaptor binding to the AAA protein p97. <i>Biochemical Society Transactions</i> , 2008, 36, 62-67.	1.6	120
75	Dissecting the ATP hydrolysis pathway of bacterial enhancer-binding proteins. <i>Biochemical Society Transactions</i> , 2008, 36, 83-88.	1.6	25
76	Visualizing the organization and reorganization of transcription complexes for gene expression. <i>Biochemical Society Transactions</i> , 2008, 36, 776-779.	1.6	4
77	Detailed Structural Insights into the p97-Npl4-Ufd1 Interface. <i>Journal of Biological Chemistry</i> , 2007, 282, 21361-21369.	1.6	60
78	Sensor I Threonine of the AAA+ ATPase Transcriptional Activator PspF Is Involved in Coupling Nucleotide Triphosphate Hydrolysis to the Restructuring of $\sigma$ 54-RNA Polymerase. <i>Journal of Biological Chemistry</i> , 2007, 282, 9825-9833.	1.6	17
79	Structural insights into the p97-Ufd1-Npl4 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 467-472.	3.3	87
80	A New Labeling Method for Methyl Transverse Relaxation-Optimized Spectroscopy NMR Spectra of Alanine Residues. <i>Journal of the American Chemical Society</i> , 2007, 129, 15428-15429.	6.6	108
81	Crystal Structures of Multidrug Binding Protein TtgR in Complex with Antibiotics and Plant Antimicrobials. <i>Journal of Molecular Biology</i> , 2007, 369, 829-840.	2.0	116
82	Coupling nucleotide hydrolysis to transcription activation performance in a bacterial enhancer binding protein. <i>Molecular Microbiology</i> , 2007, 66, 583-595.	1.2	31
83	Bacterial enhancer-binding proteins: unlocking $\sigma$ 54-dependent gene transcription. <i>Current Opinion in Structural Biology</i> , 2007, 17, 110-116.	2.6	93
84	p37 Is a p97 Adaptor Required for Golgi and ER Biogenesis in Interphase and at the End of Mitosis. <i>Developmental Cell</i> , 2006, 11, 803-816.	3.1	95
85	Structural Basis of the Nucleotide Driven Conformational Changes in the AAA+ Domain of Transcription Activator PspF. <i>Journal of Molecular Biology</i> , 2006, 357, 481-492.	2.0	75
86	Structure of the Whole Cytosolic Region of ATP-Dependent Protease FtsH. <i>Molecular Cell</i> , 2006, 22, 575-585.	4.5	140
87	Structures and organisation of AAA+ enhancer binding proteins in transcriptional activation. <i>Journal of Structural Biology</i> , 2006, 156, 190-199.	1.3	100
88	Going through the motions: The ATPase cycle of p97. <i>Journal of Structural Biology</i> , 2006, 156, 12-28.	1.3	90
89	Protein-induced DNA bending clarifies the architectural organization of the $\sigma$ 54-dependent glnAp2 promoter. <i>Molecular Microbiology</i> , 2006, 59, 168-180.	1.2	39
90	Conformational changes in the AAA ATPase p97-p47 adaptor complex. <i>EMBO Journal</i> , 2006, 25, 1967-1976.	3.5	95

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91	Role of Transcription Factors in Motoneuron Differentiation of Adult Human Olfactory Neuroepithelial-Derived Progenitors. <i>Stem Cells</i> , 2006, 24, 434-442.	1.4	32
92	Induction of Oligodendrocytes From Adult Human Olfactory Epithelial-Derived Progenitors by Transcription Factors. <i>Stem Cells</i> , 2005, 23, 442-453.	1.4	35
93	Structural Insights into the Activity of Enhancer-Binding Proteins. <i>Science</i> , 2005, 307, 1972-1975.	6.0	153
94	Multifunctional Roles of the Conserved Arg Residues in the Second Region of Homology of p97/Valosin-containing Protein. <i>Journal of Biological Chemistry</i> , 2005, 280, 40515-40523.	1.6	44
95	The Multidrug Efflux Regulator TtgV Recognizes a Wide Range of Structurally Different Effectors in Solution and Complexed with Target DNA. <i>Journal of Biological Chemistry</i> , 2005, 280, 20887-20893.	1.6	68
96	The TetR Family of Transcriptional Repressors. <i>Microbiology and Molecular Biology Reviews</i> , 2005, 69, 326-356.	2.9	989
97	Mechanisms of ATPases - A Multi-Disciplinary Approach. <i>Current Protein and Peptide Science</i> , 2004, 5, 89-105.	0.7	36
98	TtgV Bound to a Complex Operator Site Represses Transcription of the Promoter for the Multidrug and Solvent Extrusion TtgGHI Pump. <i>Journal of Bacteriology</i> , 2004, 186, 2921-2927.	1.0	46
99	Structural basis of the interaction between the AAA ATPase p97/VCP and its adaptor protein p47. <i>EMBO Journal</i> , 2004, 23, 1030-1039.	3.5	172
100	Structure, dynamics and interactions of p47, a major adaptor of the AAA ATPase, p97. <i>EMBO Journal</i> , 2004, 23, 1463-1473.	3.5	65
101	Letter to the Editor: Complete Backbone Resonance Assignments of p47: The 41kDa Adaptor Protein of the AAA ATPase p97. <i>Journal of Biomolecular NMR</i> , 2004, 28, 309-310.	1.6	4
102	A link between sequence conservation and domain motion within the AAA+ family. <i>Journal of Structural Biology</i> , 2004, 146, 189-204.	1.3	21
103	ATP-dependent Transcriptional Activation by Bacterial PspF AAA+Protein. <i>Journal of Molecular Biology</i> , 2004, 338, 863-875.	2.0	65
104	sigma54-dependent transcription activator phage shock protein F of Escherichia coli: a fragmentation approach to identify sequences that contribute to self-association. <i>Biochemical Journal</i> , 2004, 378, 735-744.	1.7	3
105	The crystal structure of murine p97/VCP at 3.6Å.... <i>Journal of Structural Biology</i> , 2003, 144, 337-348.	1.3	166
106	Motions and Negative Cooperativity Between p97 Domains Revealed by Cryo-electron Microscopy and Quantised Elastic Deformational Model. <i>Journal of Molecular Biology</i> , 2003, 327, 619-629.	2.0	97
107	The ATP hydrolyzing transcription activator phage shock protein F of Escherichia coli: Identifying a surface that binds A54. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2278-2283.	3.3	86
108	The localization and phosphorylation of p47 are important for Golgi disassembly and assembly during the cell cycle. <i>Journal of Cell Biology</i> , 2003, 161, 1067-1079.	2.3	96

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109	VCIP135, a novel essential factor for p97/p47-mediated membrane fusion, is required for Golgi and ER assembly in vivo. <i>Journal of Cell Biology</i> , 2002, 159, 855-866.	2.3	188
110	Machinery of protein folding and unfolding. <i>Current Opinion in Structural Biology</i> , 2002, 12, 231-238.	2.6	48
111	Mechanochemical ATPases and transcriptional activation. <i>Molecular Microbiology</i> , 2002, 45, 895-903.	1.2	143
112	Solution structure and interaction surface of the C-terminal domain from p47: A major p97-cofactor involved in SNARE disassembly. <i>Journal of Molecular Biology</i> , 2001, 311, 255-263.	2.0	80
113	BRCT Domain Interactions in the Heterodimeric DNA Repair Protein XRCC1~DNA Ligase III. <i>Biochemistry</i> , 2001, 40, 5906-5913.	1.2	59
114	The BRCA1 C-terminal domain: structure and function. <i>Mutation Research DNA Repair</i> , 2000, 460, 319-332.	3.8	128
115	Structure of the AAA ATPase p97. <i>Molecular Cell</i> , 2000, 6, 1473-1484.	4.5	394
116	X-ray crystallographic determination of the structure of the influenza C virus haemagglutinin-esterase-fusion glycoprotein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 945-961.	2.5	11
117	Structure of an XRCC1 BRCT domain: a new protein-protein interaction module. <i>EMBO Journal</i> , 1998, 17, 6404-6411.	3.5	223
118	Structure of the haemagglutinin-esterase-fusion glycoprotein of influenza C virus. <i>Nature</i> , 1998, 396, 92-96.	13.7	218
119	Mapping and Measuring DNA to Protein Ratios in Mammalian Sperm Head by XANES Imaging. <i>Journal of Structural Biology</i> , 1996, 116, 335-344.	1.3	141
120	Biological microscopy and soft X-ray optics at Stony Brook. <i>Journal of Electron Spectroscopy and Related Phenomena</i> , 1996, 80, 337-341.	0.8	6
121	Soft x-ray microscopy with coherent x rays (invited). <i>Review of Scientific Instruments</i> , 1992, 63, 557-563.	0.6	48
122	Chemical contrast in X-ray microscopy and spatially resolved XANES spectroscopy of organic specimens. <i>Science</i> , 1992, 258, 972-975.	6.0	356
123	Diffraction-limited imaging in a scanning transmission x-ray microscope. <i>Optics Communications</i> , 1991, 86, 351-364.	1.0	241