

# Chao Xu

## List of Publications by Year in descending order

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78  
papers

5,048  
citations

117625  
34  
h-index

98798  
67  
g-index

82  
all docs

82  
docs citations

82  
times ranked

8229  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis for METTL6-mediated m <sup>3</sup> C RNA methylation. <i>Biochemical and Biophysical Research Communications</i> , 2022, 589, 159-164.	2.1	5
2	Molecular basis for cysteine oxidation by plant cysteine oxidases from <i>Arabidopsis thaliana</i> . <i>Journal of Structural Biology</i> , 2021, 213, 107663.	2.8	7
3	Crystal structure of the WD40 domain of human PLRG1. <i>Biochemical and Biophysical Research Communications</i> , 2021, 534, 474-477.	2.1	1
4	Molecular basis for arginine C-terminal degron recognition by Cul2FEM1 E3 ligase. <i>Nature Chemical Biology</i> , 2021, 17, 254-262.	8.0	33
5	Structural basis for RNA 3' end recognition by the PIWIL2 PAZ domain. <i>Biochemical and Biophysical Research Communications</i> , 2021, 553, 187-190.	2.1	0
6	Structural insights into SMCR8 C-degron recognition by FEM1B. <i>Biochemical and Biophysical Research Communications</i> , 2021, 557, 236-239.	2.1	9
7	Molecular basis for PICS-mediated piRNA biogenesis and cell division. <i>Nature Communications</i> , 2021, 12, 5595.	12.8	7
8	Dynamic crotonylation of EB1 by TIP60 ensures accurate spindle positioning in mitosis. <i>Nature Chemical Biology</i> , 2021, 17, 1314-1323.	8.0	29
9	Structural basis for the recognition of RFX7 by ANKRA2 and RFXANK. <i>Biochemical and Biophysical Research Communications</i> , 2020, 523, 263-266.	2.1	3
10	Crystal structure of TbEsa1 presumed Tudor domain from <i>Trypanosoma brucei</i> . <i>Journal of Structural Biology</i> , 2020, 209, 107406.	2.8	5
11	LOTUS domain is a novel class of G-rich and G-quadruplex RNA binding domain. <i>Nucleic Acids Research</i> , 2020, 48, 9262-9272.	14.5	21
12	Ameliorating Effects of Transcutaneous Electrical Acustimulation Combined With Deep Breathing Training on Refractory Gastroesophageal Reflux Disease Mediated via the Autonomic Pathway. <i>Neuromodulation</i> , 2019, 22, 751-757.	0.8	14
13	Functional Proteomics Identifies a PICS Complex Required for piRNA Maturation and Chromosome Segregation. <i>Cell Reports</i> , 2019, 27, 3561-3572.e3.	6.4	28
14	Molecular basis of vasohibins-mediated detyrosination and its impact on spindle function and mitosis. <i>Cell Research</i> , 2019, 29, 533-547.	12.0	56
15	PRC2 recruitment and H3K27me <sub>3</sub> deposition at <i>FLC</i> require FCA binding of <i>COOLAIR</i> . <i>Science Advances</i> , 2019, 5, eaau7246.	10.3	106
16	A telomerase subunit homolog La protein from <i>Trypanosoma brucei</i> plays an essential role in ribosomal biogenesis. <i>FEBS Journal</i> , 2019, 286, 3129-3147.	4.7	8
17	Structural insight into the unique dsDNA binding topology of the human ORC2 wing helix domain. <i>FEBS Journal</i> , 2019, 286, 2726-2736.	4.7	2
18	Solution structure of TbTFIIS2-2 PWWP domain from <i>Trypanosoma brucei</i> and its binding to H4K17me <sub>3</sub> and H3K32me <sub>3</sub> . <i>Biochemical Journal</i> , 2019, 476, 421-431.	3.7	6

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19	Structural insights into SETD3-mediated histidine methylation on $\beta$ -actin. <i>ELife</i> , 2019, 8, .	6.0	42
20	Structural basis for the recognition of kinesin family member 21A (KIF21A) by the ankyrin domains of KANK1 and KANK2 proteins. <i>Journal of Biological Chemistry</i> , 2018, 293, 557-566.	3.4	13
21	DNA Sequence Recognition of Human CXXC Domains and Their Structural Determinants. <i>Structure</i> , 2018, 26, 85-95.e3.	3.3	60
22	YTH Domain: A Family of N <sup>6</sup> -methyladenosine (m <sup>6</sup> A) Readers. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 99-107.	6.9	277
23	Structural basis for the ability of MBD domains to bind methyl-CG and TG sites in DNA. <i>Journal of Biological Chemistry</i> , 2018, 293, 7344-7354.	3.4	54
24	Solution structure of TbCentrin4 from <i>Trypanosoma brucei</i> and its interactions with Ca <sup>2+</sup> and other centrins. <i>Biochemical Journal</i> , 2018, 475, 3763-3778.	3.7	7
25	Crystal structure of an ENT domain from <i>Trypanosoma brucei</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 505, 755-760.	2.1	3
26	Recognition of hyperacetylated N-terminus of H2AZ by TbBDF2 from <i>Trypanosoma brucei</i> . <i>Biochemical Journal</i> , 2017, 474, 3817-3830.	3.7	22
27	First critical repressive H3K27me3 marks in embryonic stem cells identified using designed protein inhibitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10125-10130.	7.1	39
28	PHF13 is a molecular reader and transcriptional co-regulator of H3K4me2/3. <i>ELife</i> , 2016, 5, .	6.0	22
29	Structural insights into Gemin5-guided selection of pre-snRNAs for snRNP assembly. <i>Genes and Development</i> , 2016, 30, 2376-2390.	5.9	60
30	Theory and implementation of a very high throughput true random number generator in field programmable gate array. <i>Review of Scientific Instruments</i> , 2016, 87, 044704.	1.3	14
31	A novel RNA-binding mode of the YTH domain reveals the mechanism for recognition of determinant of selective removal by Mmi1. <i>Nucleic Acids Research</i> , 2016, 44, 969-982.	14.5	64
32	A Radioactivity-Based Assay for Screening Human m <sup>6</sup> A-RNA Methyltransferase, METTL3-METTL14 Complex, and Demethylase ALKBH5. <i>Journal of Biomolecular Screening</i> , 2016, 21, 290-297.	2.6	95
33	Methyllysine Recognition by the Royal Family Modules: Chromo, Tudor, MBT, Chromo Barrel, and PWWP Domains. , 2015, , 49-82.		3
34	Ankyrin Repeats of ANKRA2 Recognize a PxLPxL Motif on the 3M Syndrome Protein CCDC8. <i>Structure</i> , 2015, 23, 700-712.	3.3	17
35	Crystal structure of human nuclear pore complex component NUP43. <i>FEBS Letters</i> , 2015, 589, 3247-3253.	2.8	18
36	Structural Basis for the Discriminative Recognition of N <sup>6</sup> -Methyladenosine RNA by the Human YT521-B Homology Domain Family of Proteins. <i>Journal of Biological Chemistry</i> , 2015, 290, 24902-24913.	3.4	228

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37	Chemical basis for the recognition of trimethyllysine by epigenetic reader proteins. <i>Nature Communications</i> , 2015, 6, 8911.	12.8	72
38	RPRD1A and RPRD1B are human RNA polymerase II C-terminal domain scaffolds for Ser5 dephosphorylation. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 686-695.	8.2	72
39	Epigenetic targets and drug discovery. , 2014, 143, 275-294.		43
40	Structures of Human ALKBH5 Demethylase Reveal a Unique Binding Mode for Specific Single-stranded N6-Methyladenosine RNA Demethylation. <i>Journal of Biological Chemistry</i> , 2014, 289, 17299-17311.	3.4	138
41	Structural basis for selective binding of m6A RNA by the YTHDC1 YTH domain. <i>Nature Chemical Biology</i> , 2014, 10, 927-929.	8.0	552
42	A Chromatin-Dependent Role of the Fragile X Mental Retardation Protein FMRP in the DNA Damage Response. <i>Cell</i> , 2014, 157, 869-881.	28.9	151
43	Structure and function of dioxygenases in histone demethylation and DNA/RNA demethylation. <i>IUCr</i> , 2014, 1, 540-549.	2.2	26
44	Ionic strength-dependent conformations of a ubiquitin-like small archaeal modifier protein (SAMP1) from <i>Haloferax volcanii</i> . <i>Protein Science</i> , 2013, 22, 1174-1182.	7.6	5
45	Tudor domains of the PRC2 components PHF1 and PHF19 selectively bind to histone H3K36me3. <i>Biochemical and Biophysical Research Communications</i> , 2013, 430, 547-553.	2.1	50
46	Ionic strength-dependent conformations of a ubiquitin-like small archaeal modifier protein (SAMP2) from <i>Haloferax volcanii</i> . <i>Scientific Reports</i> , 2013, 3, 2136.	3.3	8
47	Sequence-Specific Recognition of a PxLPxL/L Motif by an Ankyrin Repeat Tumbler Lock. <i>Science Signaling</i> , 2012, 5, ra39.	3.6	42
48	Tet3 CXXC Domain and Dioxygenase Activity Cooperatively Regulate Key Genes for <i>Xenopus</i> Eye and Neural Development. <i>Cell</i> , 2012, 151, 1200-1213.	28.9	227
49	Crystal structures of the coil 2B fragment and the globular tail domain of human lamin B1. <i>FEBS Letters</i> , 2012, 586, 314-318.	2.8	32
50	Crystal Structure of the Human SUV39H1 Chromodomain and Its Recognition of Histone H3K9me2/3. <i>PLoS ONE</i> , 2012, 7, e52977.	2.5	53
51	Structural basis for the recognition and cleavage of histone H3 by cathepsin L. <i>Nature Communications</i> , 2011, 2, 197.	12.8	64
52	Solution structure of Rap1 BRCT domain from <i>Saccharomyces cerevisiae</i> reveals a novel fold. <i>Biochemical and Biophysical Research Communications</i> , 2011, 404, 1055-1059.	2.1	12
53	Crystal structure of the Cys2His2-type zinc finger domain of human DPF2. <i>Biochemical and Biophysical Research Communications</i> , 2011, 413, 58-61.	2.1	20
54	Solution structure of the Taf14 YEATS domain and its roles in cell growth of <i>Saccharomyces cerevisiae</i> . <i>Biochemical Journal</i> , 2011, 436, 83-90.	3.7	17

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55	Structure and function of WD40 domain proteins. <i>Protein and Cell</i> , 2011, 2, 202-214.	11.0	494
56	Composition, recruitment and regulation of the PRC2 complex. <i>Nucleus</i> , 2011, 2, 277-282.	2.2	14
57	The structural basis for selective binding of non-methylated CpG islands by the CFP1 CXXC domain. <i>Nature Communications</i> , 2011, 2, 227.	12.8	111
58	Structural and Histone Binding Ability Characterizations of Human PWWP Domains. <i>PLoS ONE</i> , 2011, 6, e18919.	2.5	137
59	Sgf29 binds histone H3K4me2/3 and is required for SAGA complex recruitment and histone H3 acetylation. <i>EMBO Journal</i> , 2011, 30, 2829-2842.	7.8	218
60	Structural Basis for Specific Binding of Human MPP8 Chromodomain to Histone H3 Methylated at Lysine 9. <i>PLoS ONE</i> , 2011, 6, e25104.	2.5	41
61	Structural Studies of the Tandem Tudor Domains of Fragile X Mental Retardation Related Proteins FXR1 and FXR2. <i>PLoS ONE</i> , 2010, 5, e13559.	2.5	51
62	Binding of different histone marks differentially regulates the activity and specificity of polycomb repressive complex 2 (PRC2). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19266-19271.	7.1	202
63	A Large Intrinsically Disordered Region in SKIP and Its Disorder-Order Transition Induced by PP1L1 Binding Revealed by NMR. <i>Journal of Biological Chemistry</i> , 2010, 285, 4951-4963.	3.4	26
64	Structural basis for recognition of arginine methylated Piwi proteins by the extended Tudor domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 18398-18403.	7.1	132
65	Pup, a prokaryotic ubiquitin-like protein, is an intrinsically disordered protein. <i>Biochemical Journal</i> , 2009, 422, 207-215.	3.7	88
66	Mouse Piwi interactome identifies binding mechanism of Tdrkh Tudor domain to arginine methylated Miwi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20336-20341.	7.1	159
67	Solution structure of Urm1 from <i>Trypanosoma brucei</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 781-785.	2.6	9
68	Solution structure of SUMO from <i>Trypanosoma brucei</i> and its interaction with Ubc9. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 266-269.	2.6	40
69	Structural Basis for the Recognition of Methylated Histone H3K36 by the Eaf3 Subunit of Histone Deacetylase Complex Rpd3S. <i>Structure</i> , 2008, 16, 1740-1750.	3.3	84
70	Structure of a Second BRCT Domain Identified in the Nijmegen Breakage Syndrome Protein Nbs1 and its Function in an MDC1-Dependent Localization of Nbs1 to DNA Damage Sites. <i>Journal of Molecular Biology</i> , 2008, 381, 361-372.	4.2	29
71	A Hamiltonian Replica Exchange Approach and Its Application to the Study of Side-Chain Type and Neighbor Effects on Peptide Backbone Conformations. <i>Journal of Chemical Theory and Computation</i> , 2008, 4, 1348-1359.	5.3	26
72	Solution structure of BRD7 bromodomain and its interaction with acetylated peptides from histone H3 and H4. <i>Biochemical and Biophysical Research Communications</i> , 2007, 358, 435-441.	2.1	54

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73	Solution Structure of Human Brg1 Bromodomain and Its Specific Binding to Acetylated Histone Tails,. Biochemistry, 2007, 46, 2100-2110.	2.5	106
74	2P060 Solution Structure of the Bromodomain of Brd2 and Its Interaction with Acetylated Peptide from Histone H4 and CtBP(29. Protein structure and dynamics (II),Poster Session,Abstract,Meeting) Tj ETQq0 0 0 r9B /Overlock 10 Tf 5	0.0	0
75	Solution Structure of Human Peptidyl Prolyl Isomerase-like Protein 1 and Insights into Its Interaction with SKIP*. Journal of Biological Chemistry, 2006, 281, 15900-15908.	3.4	35
76	Letter to the Editor: Backbone and side chain assignments of human Peptidylprolyl Isomerase Like 1 (hPPIL1). Journal of Biomolecular NMR, 2005, 31, 179-180.	2.8	2
77	NMR structure and regulated expression in APL cell of human SH3BGRL3. FEBS Letters, 2005, 579, 2788-2794.	2.8	20
78	DNA Sequence Recognition of Human CXXC Domains and Their Structural Determinants. SSRN Electronic Journal, 0, , .	0.4	0