

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
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82
all docs

82
docs citations

82
times ranked

8229
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Structure and function of WD40 domain proteins. <i>Protein and Cell</i> , 2011, 2, 202-214.	11.0	494
3	YTH Domain: A Family of N6-methyladenosine (m6A) Readers. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 99-107.	6.9	277
4	Structural Basis for the Discriminative Recognition of N6-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
5	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
6	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
7	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
8	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
9	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
10	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
11	Structural and Histone Binding Ability Characterizations of Human PWWP Domains. <i>PLoS ONE</i> , 2011, 6, e18919.	2.5	137
12	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
13	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
14	Solution Structure of Human Brg1 Bromodomain and Its Specific Binding to Acetylated Histone Tails. <i>Biochemistry</i> , 2007, 46, 2100-2110.	2.5	106
15	PRC2 recruitment and H3K27me3 deposition at <i>FLC</i> require FCA binding of <i>COOLAIR</i> . <i>Science Advances</i> , 2019, 5, eaau7246.	10.3	106
16	A Radioactivity-Based Assay for Screening Human m6A-RNA Methyltransferase, METTL3-METTL14 Complex, and Demethylase ALKBH5. <i>Journal of Biomolecular Screening</i> , 2016, 21, 290-297.	2.6	95
17	Pup, a prokaryotic ubiquitin-like protein, is an intrinsically disordered protein. <i>Biochemical Journal</i> , 2009, 422, 207-215.	3.7	88
18	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

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19	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
20	Chemical basis for the recognition of trimethyllysine by epigenetic reader proteins. <i>Nature Communications</i> , 2015, 6, 8911.	12.8	72
21	Structural basis for the recognition and cleavage of histone H3 by cathepsin L. <i>Nature Communications</i> , 2011, 2, 197.	12.8	64
22	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
23	Structural insights into Gemin5-guided selection of pre-snRNAs for snRNP assembly. <i>Genes and Development</i> , 2016, 30, 2376-2390.	5.9	60
24	DNA Sequence Recognition of Human CXXC Domains and Their Structural Determinants. <i>Structure</i> , 2018, 26, 85-95.e3.	3.3	60
25	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
26	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
27	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
28	Crystal Structure of the Human SUV39H1 Chromodomain and Its Recognition of Histone H3K9me2/3. <i>PLoS ONE</i> , 2012, 7, e52977.	2.5	53
29	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
30	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
31	Epigenetic targets and drug discovery. , 2014, 143, 275-294.		43
32	Sequence-Specific Recognition of a PxLPxl/L Motif by an Ankyrin Repeat Tumbler Lock. <i>Science Signaling</i> , 2012, 5, ra39.	3.6	42
33	Structural insights into SETD3-mediated histidine methylation on Î ² -actin. <i>ELife</i> , 2019, 8, .	6.0	42
34	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
35	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
36	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

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37	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
38	Molecular basis for arginine C-terminal degron recognition by Cul2FEM1 E3 ligase. Nature Chemical Biology, 2021, 17, 254-262.	8.0	33
39	Crystal structures of the coil 2B fragment and the globular tail domain of human lamin B1. FEBS Letters, 2012, 586, 314-318.	2.8	32
40	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. Journal of Molecular Biology, 2008, 381, 361-372.	4.2	29
41	Dynamic crotonylation of EB1 by TIP60 ensures accurate spindle positioning in mitosis. Nature Chemical Biology, 2021, 17, 1314-1323.	8.0	29
42	Functional Proteomics Identifies a PICS Complex Required for piRNA Maturation and Chromosome Segregation. Cell Reports, 2019, 27, 3561-3572.e3.	6.4	28
43	A Hamiltonian Replica Exchange Approach and Its Application to the Study of Side-Chain Type and Neighbor Effects on Peptide Backbone Conformations. Journal of Chemical Theory and Computation, 2008, 4, 1348-1359.	5.3	26
44	A Large Intrinsically Disordered Region in SKIP and Its Disorder-Order Transition Induced by PPIL1 Binding Revealed by NMR. Journal of Biological Chemistry, 2010, 285, 4951-4963.	3.4	26
45	Structure and function of dioxygenases in histone demethylation and DNA/RNA demethylation. IUCr, 2014, 1, 540-549.	2.2	26
46	PHF13 is a molecular reader and transcriptional co-regulator of H3K4me2/3. Elife, 2016, 5, .	6.0	22
47	Recognition of hyperacetylated N-terminus of H2AZ by TbBDF2 from <i>Trypanosoma brucei</i> . Biochemical Journal, 2017, 474, 3817-3830.	3.7	22
48	LOTUS domain is a novel class of G-rich and G-quadruplex RNA binding domain. Nucleic Acids Research, 2020, 48, 9262-9272.	14.5	21
49	NMR structure and regulated expression in APL cell of human SH3BGRL3. FEBS Letters, 2005, 579, 2788-2794.	2.8	20
50	Crystal structure of the Cys2His2-type zinc finger domain of human DPF2. Biochemical and Biophysical Research Communications, 2011, 413, 58-61.	2.1	20
51	Crystal structure of human nuclear pore complex component NUP43. FEBS Letters, 2015, 589, 3247-3253.	2.8	18
52	Solution structure of the Taf14 YEATS domain and its roles in cell growth of <i>Saccharomyces cerevisiae</i> . Biochemical Journal, 2011, 436, 83-90.	3.7	17
53	Ankyrin Repeats of ANKRA2 Recognize a PxLPxL Motif on the 3M Syndrome Protein CCDC8. Structure, 2015, 23, 700-712.	3.3	17
54	Composition, recruitment and regulation of the PRC2 complex. Nucleus, 2011, 2, 277-282.	2.2	14

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55	Theory and implementation of a very high throughput true random number generator in field programmable gate array. Review of Scientific Instruments, 2016, 87, 044704.	1.3	14
56	Ameliorating Effects of Transcutaneous Electrical Acustimulation Combined With Deep Breathing Training on Refractory Gastroesophageal Reflux Disease Mediated via the Autonomic Pathway. Neuromodulation, 2019, 22, 751-757.	0.8	14
57	Structural basis for the recognition of kinesin family member 21A (KIF21A) by the ankyrin domains of KANK1 and KANK2 proteins. Journal of Biological Chemistry, 2018, 293, 557-566.	3.4	13
58	Solution structure of Rap1 BRCT domain from <i>Saccharomyces cerevisiae</i> reveals a novel fold. Biochemical and Biophysical Research Communications, 2011, 404, 1055-1059.	2.1	12
59	Solution structure of Urm1 from <i>Trypanosoma brucei</i> . Proteins: Structure, Function and Bioinformatics, 2009, 75, 781-785.	2.6	9
60	Structural insights into SMCR8 C-degron recognition by FEM1B. Biochemical and Biophysical Research Communications, 2021, 557, 236-239.	2.1	9
61	Ionic strength-dependent conformations of a ubiquitin-like small archaeal modifier protein (SAMP2) from <i>Haloferax volcanii</i> . Scientific Reports, 2013, 3, 2136.	3.3	8
62	A telomerase subunit homolog La protein from <i>Trypanosoma brucei</i> plays an essential role in ribosomal biogenesis. FEBS Journal, 2019, 286, 3129-3147.	4.7	8
63	Solution structure of TbCentrin4 from <i>Trypanosoma brucei</i> and its interactions with Ca ²⁺ and other centrins. Biochemical Journal, 2018, 475, 3763-3778.	3.7	7
64	Molecular basis for cysteine oxidation by plant cysteine oxidases from <i>Arabidopsis thaliana</i> . Journal of Structural Biology, 2021, 213, 107663.	2.8	7
65	Molecular basis for PICS-mediated piRNA biogenesis and cell division. Nature Communications, 2021, 12, 5595.	12.8	7
66	Solution structure of TbTFIIS2-2 PWWP domain from <i>Trypanosoma brucei</i> and its binding to H4K17me3 and H3K32me3. Biochemical Journal, 2019, 476, 421-431.	3.7	6
67	Ionic strength-dependent conformations of a ubiquitin-like small archaeal modifier protein (SAMP1) from <i>Haloferax volcanii</i> . Protein Science, 2013, 22, 1174-1182.	7.6	5
68	Crystal structure of TbEsa1 presumed Tudor domain from <i>Trypanosoma brucei</i> . Journal of Structural Biology, 2020, 209, 107406.	2.8	5
69	Structural basis for METTL6-mediated m ³ C RNA methylation. Biochemical and Biophysical Research Communications, 2022, 589, 159-164.	2.1	5
70	Methyllysine Recognition by the Royal Family Modules: Chromo, Tudor, MBT, Chromo Barrel, and PWWP Domains. , 2015, , 49-82.		3
71	Crystal structure of an ENT domain from <i>Trypanosoma brucei</i> . Biochemical and Biophysical Research Communications, 2018, 505, 755-760.	2.1	3
72	Structural basis for the recognition of RFX7 by ANKRA2 and RFXANK. Biochemical and Biophysical Research Communications, 2020, 523, 263-266.	2.1	3

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73	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
74	Structural insight into the unique dsDNA binding topology of the human ORC2 wing helix domain. FEBS Journal, 2019, 286, 2726-2736.	4.7	2
75	Crystal structure of the WD40 domain of human PLRG1. Biochemical and Biophysical Research Communications, 2021, 534, 474-477.	2.1	1
76	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 rgt /Overlock 10 Tf 5	0.0	0
77	Structural basis for RNA 3'-end recognition by the PIWIL2 PAZ domain. Biochemical and Biophysical Research Communications, 2021, 553, 187-190.	2.1	0
78	DNA Sequence Recognition of Human CXXC Domains and Their Structural Determinants. SSRN Electronic Journal, 0, , .	0.4	0