

Jikui Song

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

71 papers	3,287 citations	28 h-index	56 g-index
72 ext. papers	4,115 ext. citations	13.3 avg, IF	5.27 L-index

#	Paper	IF	Citations
71	SARS-CoV-2 nucleocapsid protein targets a conserved surface groove of the NTF2-like domain of G3BP1.. <i>Journal of Molecular Biology</i> , 2022 , 167516	6.5	2
70	DNMT1 reads heterochromatic H4K20me3 to reinforce LINE-1 DNA methylation. <i>Nature Communications</i> , 2021 , 12, 2490	17.4	13
69	Two conserved oligomer interfaces of NSP7 and NSP8 underpin the dynamic assembly of SARS-CoV-2 RdRP. <i>Nucleic Acids Research</i> , 2021 , 49, 5956-5966	20.1	10
68	Substrate deformation regulates DRM2-mediated DNA methylation in plants. <i>Science Advances</i> , 2021 , 7,	14.3	2
67	Chemoproteomic Approach toward Probing the Interactomes of Perfluoroalkyl Substances. <i>Analytical Chemistry</i> , 2021 , 93, 9634-9639	7.8	2
66	YY1 interacts with guanine quadruplexes to regulate DNA looping and gene expression. <i>Nature Chemical Biology</i> , 2021 , 17, 161-168	11.7	22
65	UVR8 interacts with de novo DNA methyltransferase and suppresses DNA methylation in Arabidopsis. <i>Nature Plants</i> , 2021 , 7, 184-197	11.5	10
64	Structural basis for impairment of DNA methylation by the DNMT3A R882H mutation. <i>Nature Communications</i> , 2020 , 11, 2294	17.4	22
63	Inhibiting Matrix Metalloproteinase-2 Activation by Perturbing Protein-Protein Interactions Using a Cyclic Peptide. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 6979-6990	8.3	7
62	Comprehensive structure-function characterization of DNMT3B and DNMT3A reveals distinctive de novo DNA methylation mechanisms. <i>Nature Communications</i> , 2020 , 11, 3355	17.4	42
61	Dissect the DNMT3A- and DNMT3B-mediated DNA Co-methylation through a Covalent Complex Approach. <i>Journal of Molecular Biology</i> , 2020 , 432, 569-575	6.5	10
60	Direct readout of heterochromatic H3K9me3 regulates DNMT1-mediated maintenance DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 18439-18447	11.5	26
59	Structural basis for STAT2 suppression by flavivirus NS5. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 875-885	17.6	18
58	DNA sequence-dependent activity and base flipping mechanisms of DNMT1 regulate genome-wide DNA methylation. <i>Nature Communications</i> , 2020 , 11, 3723	17.4	25
57	BAHCC1 binds H3K27me3 via a conserved BAH module to mediate gene silencing and oncogenesis. <i>Nature Genetics</i> , 2020 , 52, 1384-1396	36.3	25
56	Complex DNA sequence readout mechanisms of the DNMT3B DNA methyltransferase. <i>Nucleic Acids Research</i> , 2020 , 48, 11495-11509	20.1	7
55	Structural basis for the ORC1-Cyclin A association. <i>Protein Science</i> , 2019 , 28, 1727-1733	6.3	4

54	Structure and regulation of ZCCHC4 in mA-methylation of 28S rRNA. <i>Nature Communications</i> , 2019 , 10, 5042	17.4	32
53	A DNA aptamer for binding and inhibition of DNA methyltransferase 1. <i>Nucleic Acids Research</i> , 2019 , 47, 11527-11537	20.1	8
52	Chemical Proteomic Profiling of Lysophosphatidic Acid-Binding Proteins. <i>Analytical Chemistry</i> , 2019 , 91, 15365-15369	7.8	3
51	METTL13 Methylation of eEF1A Increases Translational Output to Promote Tumorigenesis. <i>Cell</i> , 2019 , 176, 491-504.e21	56.2	56
50	Protein Interactions at Oxidized 5-Methylcytosine Bases. <i>Journal of Molecular Biology</i> , 2019 , 432, 1718-1738	17.5	8
49	Structural basis for DNMT3A-mediated de novo DNA methylation. <i>Nature</i> , 2018 , 554, 387-391	50.4	121
48	Structure and function of Zika virus NS5 protein: perspectives for drug design. <i>Cellular and Molecular Life Sciences</i> , 2018 , 75, 1723-1736	10.3	36
47	An Intramolecular Interaction of UHRF1 Reveals Dual Control for Its Histone Association. <i>Structure</i> , 2018 , 26, 304-311.e3	5.2	21
46	CARM1 suppresses serine synthesis by promoting PKM2 activity. <i>Journal of Biological Chemistry</i> , 2018 , 293, 15290-15303	5.4	11
45	Structure-Based Design of Novel EphA2 Agonistic Agents with Nanomolar Affinity in Vitro and in Cell. <i>ACS Chemical Biology</i> , 2018 , 13, 2633-2644	4.9	15
44	Suppression of Type I Interferon Signaling by NS5. <i>Viruses</i> , 2018 , 10,	6.2	23
43	Structural Basis of DNMT1 and DNMT3A-Mediated DNA Methylation. <i>Genes</i> , 2018 , 9,	4.2	41
42	The structure of Zika virus NS5 reveals a conserved domain conformation. <i>Nature Communications</i> , 2017 , 8, 14763	17.4	59
41	Mechanism of host substrate acetylation by a YopJ family effector. <i>Nature Plants</i> , 2017 , 3, 17115	11.5	32
40	Structure of a pathogen effector reveals the enzymatic mechanism of a novel acetyltransferase family. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 847-52	17.6	27
39	Endosidin2 targets conserved exocyst complex subunit EXO70 to inhibit exocytosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E41-50	11.5	88
38	Tet3 Reads 5-Carboxylcytosine through Its CXXC Domain and Is a Potential Guardian against Neurodegeneration. <i>Cell Reports</i> , 2016 , 14, 493-505	10.6	84
37	BS69/ZMYND11 C-Terminal Domains Bind and Inhibit EBNA2. <i>PLoS Pathogens</i> , 2016 , 12, e1005414	7.6	12

36	Are there specific readers of oxidized 5-methylcytosine bases?. <i>BioEssays</i> , 2016 , 38, 1038-47	4.1	28
35	Crystal Structure of Human DNA Methyltransferase 1. <i>Journal of Molecular Biology</i> , 2015 , 427, 2520-2531	6.5	74
34	An Allosteric Interaction Links USP7 to Deubiquitination and Chromatin Targeting of UHRF1. <i>Cell Reports</i> , 2015 , 12, 1400-6	10.6	55
33	Two serine residues in <i>Pseudomonas syringae</i> effector HopZ1a are required for acetyltransferase activity and association with the host co-factor. <i>New Phytologist</i> , 2015 , 208, 1157-68	9.8	34
32	A Meier-Gorlin syndrome mutation impairs the ORC1-nucleosome association. <i>ACS Chemical Biology</i> , 2015 , 10, 1176-80	4.9	7
31	Effects of Tet-induced oxidation products of 5-methylcytosine on Dnmt1- and DNMT3a-mediated cytosine methylation. <i>Molecular BioSystems</i> , 2014 , 10, 1749-52		42
30	Arsenite binds to the RING finger domains of RNF20-RNF40 histone E3 ubiquitin ligase and inhibits DNA double-strand break repair. <i>Journal of the American Chemical Society</i> , 2014 , 136, 12884-7	16.4	31
29	An H3K36 methylation-engaging Tudor motif of polycomb-like proteins mediates PRC2 complex targeting. <i>Molecular Cell</i> , 2013 , 49, 571-82	17.6	165
28	Bacterial effector activates jasmonate signaling by directly targeting JAZ transcriptional repressors. <i>PLoS Pathogens</i> , 2013 , 9, e1003715	7.6	150
27	The BAH domain of ORC1 links H4K20me2 to DNA replication licensing and Meier-Gorlin syndrome. <i>Nature</i> , 2012 , 484, 115-9	50.4	241
26	Structure-based mechanistic insights into DNMT1-mediated maintenance DNA methylation. <i>Science</i> , 2012 , 335, 709-12	33.3	234
25	Structure of DNMT1-DNA complex reveals a role for autoinhibition in maintenance DNA methylation. <i>Science</i> , 2011 , 331, 1036-40	33.3	312
24	Protein-RNA and protein-protein recognition by dual KH1/2 domains of the neuronal splicing factor Nova-1. <i>Structure</i> , 2011 , 19, 930-44	5.2	44
23	In vitro interaction of tubulin with the photoreceptor cGMP phosphodiesterase gamma-subunit. <i>Neuroscience Letters</i> , 2010 , 482, 225-9	3.3	
22	Cleavage of peptide bonds bearing ionizable amino acids at P(1) by serine proteases with hydrophobic S(1) pocket. <i>Biochemical and Biophysical Research Communications</i> , 2010 , 400, 507-10	3.4	3
21	Pro isomerization in MLL1 PHD3-bromo cassette connects H3K4me readout to Cyp33 and HDAC-mediated repression. <i>Cell</i> , 2010 , 141, 1183-94	56.2	145
20	Structural insights into RNA recognition by the alternate-splicing regulator CUG-binding protein 1. <i>Structure</i> , 2010 , 18, 1364-77	5.2	57
19	Structures of two <i>Arabidopsis thaliana</i> major latex proteins represent novel helix-grip folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 76, 237-43	4.2	52

18	Haematopoietic malignancies caused by dysregulation of a chromatin-binding PHD finger. <i>Nature</i> , 2009 , 459, 847-51	50.4	330
17	Intrinsically disordered gamma-subunit of cGMP phosphodiesterase encodes functionally relevant transient secondary and tertiary structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 1505-10	11.5	82
16	Structural basis for RNA recognition by a type II poly(A)-binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 15317-22	11.5	17
15	Structural basis for the catalytic mechanism of mammalian 25-kDa thiamine triphosphatase. <i>Journal of Biological Chemistry</i> , 2008 , 283, 10939-48	5.4	18
14	Solution structure of human sorting nexin 22. <i>Protein Science</i> , 2007 , 16, 807-14	6.3	13
13	Structures of proteins of biomedical interest from the Center for Eukaryotic Structural Genomics. <i>Journal of Structural and Functional Genomics</i> , 2007 , 8, 73-84		9
12	Small-scale, semi-automated purification of eukaryotic proteins for structure determination. <i>Journal of Structural and Functional Genomics</i> , 2007 , 8, 153-66		27
11	Cautionary tail: the presence of an N-terminal tag on dynein light-chain Roadblock/LC7 affects its interaction with a functional partner. <i>Protein and Peptide Letters</i> , 2007 , 14, 265-8	1.9	14
10	Three-dimensional structure determined for a subunit of human tRNA splicing endonuclease (Sen15) reveals a novel dimeric fold. <i>Journal of Molecular Biology</i> , 2007 , 366, 155-64	6.5	13
9	Rieske protein from <i>Thermus thermophilus</i> : 15N NMR titration study demonstrates the role of iron-ligated histidines in the pH dependence of the reduction potential. <i>Journal of the American Chemical Society</i> , 2006 , 128, 10672-3	16.4	34
8	Solution structure of isoform 1 of Roadblock/LC7, a light chain in the dynein complex. <i>Journal of Molecular Biology</i> , 2005 , 354, 1043-51	6.5	24
7	Probing the sweet determinants of brazzein: wild-type brazzein and a tasteless variant, brazzein-ins(R18a-I18b), exhibit different pH-dependent NMR chemical shifts. <i>Biochemical and Biophysical Research Communications</i> , 2005 , 335, 256-63	3.4	5
6	Solution structure of At3g04780.1-des15, an <i>Arabidopsis thaliana</i> ortholog of the C-terminal domain of human thioredoxin-like protein. <i>Protein Science</i> , 2005 , 14, 1059-63	6.3	10
5	Comparison of cell-based and cell-free protocols for producing target proteins from the <i>Arabidopsis thaliana</i> genome for structural studies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 59, 633-43	4.2	52
4	X-ray structure of <i>Arabidopsis</i> At1g77680, 12-oxophytodienoate reductase isoform 1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 206-8	4.2	7
3	Hypothetical protein At2g24940.1 from <i>Arabidopsis thaliana</i> has a cytochrome b5 like fold. <i>Journal of Biomolecular NMR</i> , 2004 , 30, 215-8	3	12
2	Solution structure of a calmodulin-like calcium-binding domain from <i>Arabidopsis thaliana</i> . <i>Journal of Biomolecular NMR</i> , 2004 , 30, 451-6	3	8
1	NMR chemical shift mapping of the binding site of a protein proteinase inhibitor: changes in the (1)H, (13)C and (15)N NMR chemical shifts of turkey ovomucoid third domain upon binding to bovine chymotrypsin A(alpha). <i>Journal of Molecular Recognition</i> , 2001 , 14, 166-71	2.6	14

