

# Xiaodong Cheng

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5730317/publications.pdf>

Version: 2024-02-01

131  
papers

15,763  
citations

28242

55  
h-index

17580

121  
g-index

171  
all docs

171  
docs citations

171  
times ranked

15525  
citing authors

#	ARTICLE	IF	CITATIONS
1	Repurposing epigenetic inhibitors to target the <i>Clostridioides difficile</i> -specific DNA adenine methyltransferase and sporulation regulator CamA. <i>Epigenetics</i> , 2022, 17, 970-981.	1.3	8
2	Structural characterization of dicyanopyridine containing DNMT1-selective, non-nucleoside inhibitors. <i>Structure</i> , 2022, 30, 793-802.e5.	1.6	11
3	Enzymatic characterization of mRNA cap adenosine-N6 methyltransferase PCIF1 activity on uncapped RNAs. <i>Journal of Biological Chemistry</i> , 2022, 298, 101751.	1.6	8
4	Differential ETS1 binding to T:G mismatches within a CpG dinucleotide contributes to C-to-T somatic mutation rate of the IDH2 hotspot at codon Arg140. <i>DNA Repair</i> , 2022, 113, 103306.	1.3	1
5	Enzymatic Characterization of In Vitro Activity of RNA Methyltransferase PCIF1 on DNA. <i>Biochemistry</i> , 2022, 61, 1005-1013.	1.2	6
6	A Role for N6-Methyladenine in DNA Damage Repair. <i>Trends in Biochemical Sciences</i> , 2021, 46, 175-183.	3.7	14
7	ZNF410 Uniquely Activates the NuRD Component CHD4 to Silence Fetal Hemoglobin Expression. <i>Molecular Cell</i> , 2021, 81, 239-254.e8.	4.5	48
8	Enzymatic characterization of three human RNA adenosine methyltransferases reveals diverse substrate affinities and reaction optima. <i>Journal of Biological Chemistry</i> , 2021, 296, 100270.	1.6	21
9	Preferential CEBP binding to T:G mismatches and increased C-to-T human somatic mutations. <i>Nucleic Acids Research</i> , 2021, 49, 5084-5094.	6.5	8
10	<i>Clostridioides difficile</i> specific DNA adenine methyltransferase CamA squeezes and flips adenine out of DNA helix. <i>Nature Communications</i> , 2021, 12, 3436.	5.8	16
11	Human MettL3-MettL14 RNA adenine methyltransferase complex is active on double-stranded DNA containing lesions. <i>Nucleic Acids Research</i> , 2021, 49, 11629-11642.	6.5	40
12	MBD5 and MBD6 couple DNA methylation to gene silencing through the J-domain protein SILENZIO. <i>Science</i> , 2021, 372, 1434-1439.	6.0	38
13	Chemoproteomic Study Uncovers HemK2/KMT9 As a New Target for NTMT1 Bisubstrate Inhibitors. <i>ACS Chemical Biology</i> , 2021, 16, 1234-1242.	1.6	6
14	Discovery of a first-in-class reversible DNMT1-selective inhibitor with improved tolerability and efficacy in acute myeloid leukemia. <i>Nature Cancer</i> , 2021, 2, 1002-1017.	5.7	99
15	Structural basis for human ZBTB7A action at the fetal globin promoter. <i>Cell Reports</i> , 2021, 36, 109759.	2.9	15
16	Discovery of a first-in-class reversible DNMT1-selective inhibitor with improved tolerability and efficacy in acute myeloid leukemia. <i>Nature Cancer</i> , 2021, 2, 1002-1017.	5.7	23
17	Detection of DNA Modifications by Sequence-Specific Transcription Factors. <i>Journal of Molecular Biology</i> , 2020, 432, 1661-1673.	2.0	15
18	Structure of HhaI endonuclease with cognate DNA at an atomic resolution of 1.0 Å... <i>Nucleic Acids Research</i> , 2020, 48, 1466-1478.	6.5	5

#	ARTICLE	IF	CITATIONS
19	The inactive Dnmt3b3 isoform preferentially enhances Dnmt3b-mediated DNA methylation. <i>Genes and Development</i> , 2020, 34, 1546-1558.	2.7	44
20	Biochemical and structural basis for YTH domain of human YTHDC1 binding to methylated adenine in DNA. <i>Nucleic Acids Research</i> , 2020, 48, 10329-10341.	6.5	26
21	KRAB domain of ZFP568 disrupts TRIM28-mediated abnormal interactions in cancer cells. <i>NAR Cancer</i> , 2020, 2, zcaa007.	1.6	4
22	Beta class amino methyltransferases from bacteria to humans: evolution and structural consequences. <i>Nucleic Acids Research</i> , 2020, 48, 10034-10044.	6.5	21
23	Characterization of SETD3 methyltransferase-mediated protein methionine methylation. <i>Journal of Biological Chemistry</i> , 2020, 295, 10901-10910.	1.6	14
24	An engineered variant of SETD3 methyltransferase alters target specificity from histidine to lysine methylation. <i>Journal of Biological Chemistry</i> , 2020, 295, 2582-2589.	1.6	15
25	The ZBTB24-CDCA7 axis regulates HELLS enrichment at centromeric satellite repeats to facilitate DNA methylation. <i>Protein and Cell</i> , 2020, 11, 214-218.	4.8	21
26	Structural basis for the target specificity of actin histidine methyltransferase SETD3. <i>Nature Communications</i> , 2019, 10, 3541.	5.8	27
27	The cell cycle-regulated DNA adenine methyltransferase CcrM opens a bubble at its DNA recognition site. <i>Nature Communications</i> , 2019, 10, 4600.	5.8	26
28	Human HemK2/KMT9/N6AMT1 is an active protein methyltransferase, but does not act on DNA in vitro, in the presence of Trm112. <i>Cell Discovery</i> , 2019, 5, 50.	3.1	27
29	Structural basis of specific DNA binding by the transcription factor ZBTB24. <i>Nucleic Acids Research</i> , 2019, 47, 8388-8398.	6.5	29
30	Structural basis for preferential binding of human TCF4 to DNA containing 5-carboxylcytosine. <i>Nucleic Acids Research</i> , 2019, 47, 8375-8387.	6.5	19
31	Discovery of a Novel Chemotype of Histone Lysine Methyltransferase EHMT1/2 (GLP/G9a) Inhibitors: Rational Design, Synthesis, Biological Evaluation, and Co-crystal Structure. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 2666-2689.	2.9	33
32	Human MettL3-MettL14 complex is a sequence-specific DNA adenine methyltransferase active on single-strand and unpaired DNA in vitro. <i>Cell Discovery</i> , 2019, 5, 63.	3.1	45
33	Structural basis for effects of CpA modifications on C/EBP $\beta$ binding of DNA. <i>Nucleic Acids Research</i> , 2019, 47, 1774-1785.	6.5	23
34	SETD3 is an actin histidine methyltransferase that prevents primary dystocia. <i>Nature</i> , 2019, 565, 372-376.	13.7	116
35	The non-specific adenine DNA methyltransferase M.EcoGII. <i>Nucleic Acids Research</i> , 2018, 46, 840-848.	6.5	41
36	Role for first zinc finger of WT1 in DNA sequence specificity: Denys-Drash syndrome-associated WT1 mutant in ZF1 enhances affinity for a subset of WT1 binding sites. <i>Nucleic Acids Research</i> , 2018, 46, 3864-3877.	6.5	20

#	ARTICLE	IF	CITATIONS
37	DNA Conformation Induces Adaptable Binding by Tandem Zinc Finger Proteins. <i>Cell</i> , 2018, 173, 221-233.e12.	13.5	52
38	Insights into the Action of Inhibitor Enantiomers against Histone Lysine Demethylase 5A. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 3193-3208.	2.9	9
39	Structure-Based Engineering of Irreversible Inhibitors against Histone Lysine Demethylase KDM5A. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 10588-10601.	2.9	28
40	KDM5 histone demethylases repress immune response via suppression of STING. <i>PLoS Biology</i> , 2018, 16, e2006134.	2.6	106
41	Detecting and interpreting DNA methylation marks. <i>Current Opinion in Structural Biology</i> , 2018, 53, 88-99.	2.6	39
42	Sirtuin 2 mutations in human cancers impair its function in genome maintenance. <i>Journal of Biological Chemistry</i> , 2017, 292, 9919-9931.	1.6	29
43	MAX is an epigenetic sensor of 5-carboxylcytosine and is altered in multiple myeloma. <i>Nucleic Acids Research</i> , 2017, 45, 2396-2407.	6.5	69
44	Structural Basis for the Versatile and Methylation-Dependent Binding of CTCF to DNA. <i>Molecular Cell</i> , 2017, 66, 711-720.e3.	4.5	198
45	A placental growth factor is silenced in mouse embryos by the zinc finger protein ZFP568. <i>Science</i> , 2017, 356, 757-759.	6.0	52
46	The Role of N-lysine acetyltransferase 10 Protein in DNA Methylation and Genomic Imprinting. <i>Molecular Cell</i> , 2017, 68, 89-103.e7.	4.5	36
47	The Molecular Basis of Histone Demethylation. <i>Cancer Drug Discovery and Development</i> , 2017, , 151-219.	0.2	8
48	Structural basis of human PR/SET domain 9 (PRDM9) allele-specific recognition of its cognate DNA sequence. <i>Journal of Biological Chemistry</i> , 2017, 292, 15994-16002.	1.6	15
49	Effector CD8 T cells dedifferentiate into long-lived memory cells. <i>Nature</i> , 2017, 552, 404-409.	13.7	378
50	Methyl-dependent and spatial-specific DNA recognition by the orthologous transcription factors human AP-1 and Epstein-Barr virus Zta. <i>Nucleic Acids Research</i> , 2017, 45, 2503-2515.	6.5	38
51	Denys-Drash syndrome associated WT1 glutamine 369 mutants have altered sequence-preferences and altered responses to epigenetic modifications. <i>Nucleic Acids Research</i> , 2016, 44, gkw766.	6.5	18
52	Distinctive Klf4 mutants determine preference for DNA methylation status. <i>Nucleic Acids Research</i> , 2016, 44, gkw774.	6.5	19
53	Structural Basis for KDM5A Histone Lysine Demethylase Inhibition by Diverse Compounds. <i>Cell Chemical Biology</i> , 2016, 23, 769-781.	2.5	80
54	DNA Base Flipping: A General Mechanism for Writing, Reading, and Erasing DNA Modifications. <i>Advances in Experimental Medicine and Biology</i> , 2016, 945, 321-341.	0.8	37

#	ARTICLE	IF	CITATIONS
55	Lin28A Binds Active Promoters and Recruits Tet1 to Regulate Gene Expression. <i>Molecular Cell</i> , 2016, 61, 153-160.	4.5	74
56	Characterization of a Linked Jumonji Domain of the KDM5/JARID1 Family of Histone H3 Lysine 4 Demethylases. <i>Journal of Biological Chemistry</i> , 2016, 291, 2631-2646.	1.6	95
57	Structural basis for human PRDM9 action at recombination hot spots. <i>Genes and Development</i> , 2016, 30, 257-265.	2.7	46
58	Binding of 14-3-3 reader proteins to phosphorylated DNMT1 facilitates aberrant DNA methylation and gene expression. <i>Nucleic Acids Research</i> , 2016, 44, 1642-1656.	6.5	16
59	Structure of <i>Naegleria</i> Tet-like dioxygenase (NgTet1) in complexes with a reaction intermediate 5-hydroxymethylcytosine DNA. <i>Nucleic Acids Research</i> , 2015, 43, 10713-10721.	6.5	26
60	Biochemical characterization of a <i>Naegleria</i> TET-like oxygenase and its application in single molecule sequencing of 5-methylcytosine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4316-4321.	3.3	51
61	Structures of <i>Escherichia coli</i> DNA adenine methyltransferase (Dam) in complex with a non-GATC sequence: potential implications for methylation-independent transcriptional repression. <i>Nucleic Acids Research</i> , 2015, 43, 4296-4308.	6.5	11
62	Structural and Functional Consequences of Circular Permutation on the Active Site of Old Yellow Enzyme. <i>ACS Catalysis</i> , 2015, 5, 892-899.	5.5	19
63	The Mechanisms of Generation, Recognition, and Erasure of DNA 5-Methylcytosine and Thymine Oxidations. <i>Journal of Biological Chemistry</i> , 2015, 290, 20723-20733.	1.6	35
64	Structure and mutagenesis of the DNA modification-dependent restriction endonuclease AspBHI. <i>Scientific Reports</i> , 2015, 4, 4246.	1.6	14
65	Properly Substituted Analogues of BIX-01294 Lose Inhibition of G9a Histone Methyltransferase and Gain Selective Anti-DNA Methyltransferase 3A Activity. <i>PLoS ONE</i> , 2014, 9, e96941.	1.1	35
66	Wilms tumor protein recognizes 5-carboxylcytosine within a specific DNA sequence. <i>Genes and Development</i> , 2014, 28, 2304-2313.	2.7	111
67	Modification-dependent restriction endonuclease, MspJl, flips 5-methylcytosine out of the DNA helix. <i>Nucleic Acids Research</i> , 2014, 42, 12092-12101.	6.5	22
68	Structure of 5-hydroxymethylcytosine-specific restriction enzyme, AbaSI, in complex with DNA. <i>Nucleic Acids Research</i> , 2014, 42, 7947-7959.	6.5	27
69	Structural basis for Klf4 recognition of methylated DNA. <i>Nucleic Acids Research</i> , 2014, 42, 4859-4867.	6.5	81
70	Structure of a <i>Naegleria</i> Tet-like dioxygenase in complex with 5-methylcytosine DNA. <i>Nature</i> , 2014, 506, 391-395.	13.7	113
71	Ectopic DNMT3L Triggers Assembly of a Repressive Complex for Retroviral Silencing in Somatic Cells. <i>Journal of Virology</i> , 2014, 88, 10680-10695.	1.5	26
72	The Carboxy-Terminal Domain of ROS1 Is Essential for 5-Methylcytosine DNA Glycosylase Activity. <i>Journal of Molecular Biology</i> , 2014, 426, 3703-3712.	2.0	18

#	ARTICLE	IF	CITATIONS
73	Selective Non-nucleoside Inhibitors of Human DNA Methyltransferases Active in Cancer Including in Cancer Stem Cells. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 701-713.	2.9	111
74	Structural and Functional Coordination of DNA and Histone Methylation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a018747-a018747.	2.3	88
75	Fragile X syndrome due to a missense mutation. <i>European Journal of Human Genetics</i> , 2014, 22, 1185-1189.	1.4	73
76	Selective Excision of 5-Carboxylcytosine by a Thymine DNA Glycosylase Mutant. <i>Journal of Molecular Biology</i> , 2013, 425, 971-976.	2.0	28
77	Activity and crystal structure of human thymine DNA glycosylase mutant N140A with 5-carboxylcytosine DNA at low pH. <i>DNA Repair</i> , 2013, 12, 535-540.	1.3	28
78	DNA Recognition of 5-Carboxylcytosine by a Zfp57 Mutant at an Atomic Resolution of 0.97 Å... <i>Biochemistry</i> , 2013, 52, 9310-9317.	1.2	19
79	A common mode of recognition for methylated CpG. <i>Trends in Biochemical Sciences</i> , 2013, 38, 177-183.	3.7	89
80	An atomic model of Zfp57 recognition of CpG methylation within a specific DNA sequence. <i>Genes and Development</i> , 2012, 26, 2374-2379.	2.7	112
81	Structure and cleavage activity of the tetrameric MspII DNA modification-dependent restriction endonuclease. <i>Nucleic Acids Research</i> , 2012, 40, 9763-9773.	6.5	38
82	Recognition and potential mechanisms for replication and erasure of cytosine hydroxymethylation. <i>Nucleic Acids Research</i> , 2012, 40, 4841-4849.	6.5	400
83	Excision of thymine and 5-hydroxymethyluracil by the MBD4 DNA glycosylase domain: structural basis and implications for active DNA demethylation. <i>Nucleic Acids Research</i> , 2012, 40, 8276-8284.	6.5	88
84	Excision of 5-hydroxymethyluracil and 5-carboxylcytosine by the thymine DNA glycosylase domain: its structural basis and implications for active DNA demethylation. <i>Nucleic Acids Research</i> , 2012, 40, 10203-10214.	6.5	134
85	Introduction of Epiphanies in Epigenetics. <i>Progress in Molecular Biology and Translational Science</i> , 2011, 101, 1-21.	0.9	18
86	Lysine methylation of the NF- $\kappa$ B subunit RelA by SETD6 couples activity of the histone methyltransferase GLP at chromatin to tonic repression of NF- $\kappa$ B signaling. <i>Nature Immunology</i> , 2011, 12, 29-36.	7.0	230
87	Defective heart development in hypomorphic LSD1 mice. <i>Cell Research</i> , 2011, , .	5.7	2
88	Structural basis of SETD6-mediated regulation of the NF- $\kappa$ B network via methyl-lysine signaling. <i>Nucleic Acids Research</i> , 2011, 39, 6380-6389.	6.5	61
89	Coordinated Chromatin Control: Structural and Functional Linkage of DNA and Histone Methylation. <i>Biochemistry</i> , 2010, 49, 2999-3008.	1.2	199
90	Adding a Lysine Mimic in the Design of Potent Inhibitors of Histone Lysine Methyltransferases. <i>Journal of Molecular Biology</i> , 2010, 400, 1-7.	2.0	108

#	ARTICLE	IF	CITATIONS
91	Structural basis for G9a-like protein lysine methyltransferase inhibition by BIX-01294. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 312-317.	3.6	272
92	Analysis of the Substrate Specificity of the Dim-5 Histone Lysine Methyltransferase Using Peptide Arrays. <i>Chemistry and Biology</i> , 2008, 15, 5-11.	6.2	68
93	Protein lysine methyltransferase G9a acts on non-histone targets. <i>Nature Chemical Biology</i> , 2008, 4, 344-346.	3.9	309
94	Mammalian DNA Methyltransferases: A Structural Perspective. <i>Structure</i> , 2008, 16, 341-350.	1.6	349
95	The SRA domain of UHRF1 flips 5-methylcytosine out of the DNA helix. <i>Nature</i> , 2008, 455, 826-829.	13.7	389
96	Epigenetic link between DNA methylation and histone modifications. <i>FASEB Journal</i> , 2008, 22, 778.1.	0.2	1
97	DNMT3L connects unmethylated lysine 4 of histone H3 to de novo methylation of DNA. <i>Nature</i> , 2007, 448, 714-717.	13.7	1,369
98	Recognition of unmethylated histone H3 lysine 4 links BHC80 to LSD1-mediated gene repression. <i>Nature</i> , 2007, 448, 718-722.	13.7	386
99	Structure of Dnmt3a bound to Dnmt3L suggests a model for de novo DNA methylation. <i>Nature</i> , 2007, 449, 248-251.	13.7	717
100	Structural dynamics of protein lysine methylation and demethylation. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2007, 618, 102-115.	0.4	61
101	Structure and Substrate Recognition of the Escherichia coli DNA Adenine Methyltransferase. <i>Journal of Molecular Biology</i> , 2006, 358, 559-570.	2.0	115
102	DNA nicking by HinP1I endonuclease: bending, base flipping and minor groove expansion. <i>Nucleic Acids Research</i> , 2006, 34, 939-948.	6.5	44
103	Structural and Sequence Motifs of Protein (Histone) Methylation Enzymes. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2005, 34, 267-294.	18.3	305
104	In Vitro and in Vivo Analyses of a Phe/Tyr Switch Controlling Product Specificity of Histone Lysine Methyltransferases. <i>Journal of Biological Chemistry</i> , 2005, 280, 5563-5570.	1.6	166
105	Structure of HinP1I endonuclease reveals a striking similarity to the monomeric restriction enzyme MspI. <i>Nucleic Acids Research</i> , 2005, 33, 1892-1901.	6.5	31
106	Transition from Nonspecific to Specific DNA Interactions along the Substrate-Recognition Pathway of Dam Methyltransferase. <i>Cell</i> , 2005, 121, 349-361.	13.5	90
107	The SET-domain protein superfamily: protein lysine methyltransferases. <i>Genome Biology</i> , 2005, 6, 227.	13.9	661
108	Structure of the Conserved Core of the Yeast Dot1p, a Nucleosomal Histone H3 Lysine 79 Methyltransferase. <i>Journal of Biological Chemistry</i> , 2004, 279, 43296-43306.	1.6	111

#	ARTICLE	IF	CITATIONS
109	Many paths to methyltransfer: a chronicle of convergence. Trends in Biochemical Sciences, 2003, 28, 329-335.	3.7	766
110	Structure of the Predominant Protein Arginine Methyltransferase PRMT1 and Analysis of Its Binding to Substrate Peptides. Structure, 2003, 11, 509-520.	1.6	317
111	Structure of the bacteriophage T4 DNA adenine methyltransferase. Nature Structural and Molecular Biology, 2003, 10, 849-855.	3.6	42
112	Structural Basis for the Product Specificity of Histone Lysine Methyltransferases. Molecular Cell, 2003, 12, 177-185.	4.5	307
113	Mismatch Repair in Methylated DNA. Journal of Biological Chemistry, 2003, 278, 5285-5291.	1.6	68
114	Structure of the Neurospora SET Domain Protein DIM-5, a Histone H3 Lysine Methyltransferase. Cell, 2002, 111, 117-127.	13.5	247
115	Cytosines Do It, Thymines Do It, Even Pseudouridines Do It—Base Flipping by an Enzyme that Acts on RNA. Structure, 2002, 10, 127-129.	1.6	11
116	The PWWP domain of mammalian DNA methyltransferase Dnmt3b defines a new family of DNA-binding folds. Nature Structural Biology, 2002, 9, 217-24.	9.7	168
117	A Taq attack displaces bases. , 2001, 8, 101-103.		10
118	Crystal structure of the conserved core of protein arginine methyltransferase PRMT3. EMBO Journal, 2000, 19, 3509-3519.	3.5	279
119	PvuII endonuclease contains two calcium ions in active sites <sup>1</sup> Edited by A. R. Fersht. Journal of Molecular Biology, 2000, 300, 1049-1056.	2.0	78
120	Mechanism of inhibition of DNA (cytosine C5)-methyltransferases by oligodeoxyribonucleotides containing 5,6-dihydro-5-azacytosine 1 Edited by R. Huber. Journal of Molecular Biology, 1999, 285, 2021-2034.	2.0	71
121	STRUCTURE AND EVOLUTION OF ADOMET-DEPENDENT METHYLTRANSFERASES. , 1999, , 1-38.		57
122	Structures of HhaI methyltransferase complexed with substrates containing mismatches at the target base. Nature Structural Biology, 1998, 5, 872-877.	9.7	102
123	BASE FLIPPING. Annual Review of Biochemistry, 1998, 67, 181-198.	5.0	327
124	Mechanistic link between DNA methyltransferases and DNA repair enzymes by base flipping. , 1997, 44, 139-151.		14
125	DNA modification by methyltransferases. Current Opinion in Structural Biology, 1995, 5, 4-10.	2.6	120
126	Universal Catalytic Domain Structure of AdoMet-dependent Methyltransferases. Journal of Molecular Biology, 1995, 247, 16-20.	2.0	246



#	ARTICLE	IF	CITATIONS
127	Structure-guided Analysis Reveals Nine Sequence Motifs Conserved among DNA Amino-methyl-transferases, and Suggests a Catalytic Mechanism for these Enzymes. Journal of Molecular Biology, 1995, 253, 618-632.	2.0	457
128	Hhal methyltransferase flips its target base out of the DNA helix. Cell, 1994, 76, 357-369.	13.5	988
129	The DNA (cytosine-5) methyltransferases. Nucleic Acids Research, 1994, 22, 1-10.	6.5	444
130	Crystal structure of the Hhal DNA methyltransferase complexed with S-adenosyl-l-methionine. Cell, 1993, 74, 299-307.	13.5	391
131	Restriction-Modification Systems. , 0, , 177-225.		17