

# Chun-Xiao Song

## List of Publications by Year in descending order

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48  
papers

9,949  
citations

109137

35  
h-index

205818

48  
g-index

50  
all docs

50  
docs citations

50  
times ranked

10465  
citing authors

#	ARTICLE	IF	CITATIONS
1	Subtraction-free and bisulfite-free specific sequencing of 5-methylcytosine and its oxidized derivatives at base resolution. <i>Nature Communications</i> , 2021, 12, 618.	5.8	45
2	Endonuclease enrichment TAPS for cost-effective genome-wide base-resolution DNA methylation detection. <i>Nucleic Acids Research</i> , 2021, 49, e76-e76.	6.5	8
3	Cell-free DNA TAPS provides multimodal information for early cancer detection. <i>Science Advances</i> , 2021, 7, eabh0534.	4.7	41
4	Accurate targeted long-read DNA methylation and hydroxymethylation sequencing with TAPS. <i>Genome Biology</i> , 2020, 21, 54.	3.8	57
5	Mapping the epigenetic modifications of DNA and RNA. <i>Protein and Cell</i> , 2020, 11, 792-808.	4.8	174
6	Systematic allelic analysis defines the interplay of key pathways in X chromosome inactivation. <i>Nature Communications</i> , 2019, 10, 3129.	5.8	93
7	Bisulfite-free and base-resolution analysis of 5-methylcytidine and 5-hydroxymethylcytidine in RNA with peroxotungstate. <i>Chemical Communications</i> , 2019, 55, 2328-2331.	2.2	38
8	Bisulfite-free direct detection of 5-methylcytosine and 5-hydroxymethylcytosine at base resolution. <i>Nature Biotechnology</i> , 2019, 37, 424-429.	9.4	267
9	5-Carboxylcytosine is resistant towards phosphodiesterase I digestion: implications for epigenetic modification quantification by mass spectrometry. <i>RSC Advances</i> , 2019, 9, 29010-29014.	1.7	10
10	Glucose and glutamine availability regulate HepG2 transcriptional responses to low oxygen. <i>Wellcome Open Research</i> , 2018, 3, 126.	0.9	6
11	Quantitation and mapping of the epigenetic marker 5-hydroxymethylcytosine. <i>BioEssays</i> , 2017, 39, 1700010.	1.2	9
12	5-Hydroxymethylcytosine signatures in cell-free DNA provide information about tumor types and stages. <i>Cell Research</i> , 2017, 27, 1231-1242.	5.7	200
13	Simultaneously Monitoring Immune Response and Microbial Infections during Pregnancy through Plasma cfRNA Sequencing. <i>Clinical Chemistry</i> , 2017, 63, 1695-1704.	1.5	55
14	Simultaneous single-molecule epigenetic imaging of DNA methylation and hydroxymethylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4338-4343.	3.3	54
15	Identification of MLL-fusion/MYC-miR-26a-TET1 signaling circuit in MLL-rearranged leukemia. <i>Cancer Letters</i> , 2016, 372, 157-165.	3.2	25
16	Base-resolution maps of 5-formylcytosine and 5-carboxylcytosine reveal genome-wide DNA demethylation dynamics. <i>Cell Research</i> , 2015, 25, 386-389.	5.7	77
17	Detection of mismatched 5-hydroxymethyluracil in DNA by selective chemical labeling. <i>Methods</i> , 2015, 72, 16-20.	1.9	14
18	Hydroxymethylation at Gene Regulatory Regions Directs Stem/Early Progenitor Cell Commitment during Erythropoiesis. <i>Cell Reports</i> , 2014, 6, 231-244.	2.9	93

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19	5mC Oxidation by Tet2 Modulates Enhancer Activity and Timing of Transcriptome Reprogramming during Differentiation. <i>Molecular Cell</i> , 2014, 56, 286-297.	4.5	285
20	Mechanism and Function of Oxidative Reversal of DNA and RNA Methylation. <i>Annual Review of Biochemistry</i> , 2014, 83, 585-614.	5.0	289
21	Potential functional roles of DNA demethylation intermediates. <i>Trends in Biochemical Sciences</i> , 2013, 38, 480-484.	3.7	133
22	Tet-mediated covalent labelling of 5-methylcytosine for its genome-wide detection and sequencing. <i>Nature Communications</i> , 2013, 4, 1517.	5.8	48
23	Genome-wide Profiling of 5-Formylcytosine Reveals Its Roles in Epigenetic Priming. <i>Cell</i> , 2013, 153, 678-691.	13.5	502
24	Chemical Modification-Assisted Bisulfite Sequencing (CAB-Seq) for 5-Carboxylcytosine Detection in DNA. <i>Journal of the American Chemical Society</i> , 2013, 135, 9315-9317.	6.6	116
25	Subtelomeric hotspots of aberrant 5-hydroxymethylcytosine-mediated epigenetic modifications during reprogramming to pluripotency. <i>Nature Cell Biology</i> , 2013, 15, 700-711.	4.6	87
26	Spatiotemporal clustering of the epigenome reveals rules of dynamic gene regulation. <i>Genome Research</i> , 2013, 23, 352-364.	2.4	58
27	Understanding Variation in Transcription Factor Binding by Modeling Transcription Factor Genome-Epigenome Interactions. <i>PLoS Computational Biology</i> , 2013, 9, e1003367.	1.5	26
28	HMGA2/TET1/HOXA9 signaling pathway regulates breast cancer growth and metastasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9920-9925.	3.3	231
29	<i>TET1</i> plays an essential oncogenic role in <i>MLL</i> -rearranged leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11994-11999.	3.3	185
30	Tet-assisted bisulfite sequencing of 5-hydroxymethylcytosine. <i>Nature Protocols</i> , 2012, 7, 2159-2170.	5.5	236
31	Mapping recently identified nucleotide variants in the genome and transcriptome. <i>Nature Biotechnology</i> , 2012, 30, 1107-1116.	9.4	197
32	Heterologous expression and purification of <i>Arabidopsis thaliana</i> VIM1 protein: In vitro evidence for its inability to recognize hydroxymethylcytosine, a rare base in <i>Arabidopsis</i> DNA. <i>Protein Expression and Purification</i> , 2012, 83, 104-111.	0.6	32
33	Genome-wide DNA hydroxymethylation changes are associated with neurodevelopmental genes in the developing human cerebellum. <i>Human Molecular Genetics</i> , 2012, 21, 5500-5510.	1.4	157
34	Base-Resolution Analysis of 5-Hydroxymethylcytosine in the Mammalian Genome. <i>Cell</i> , 2012, 149, 1368-1380.	13.5	912
35	5-formylcytosine and 5-carboxylcytosine reduce the rate and substrate specificity of RNA polymerase II transcription. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 831-833.	3.6	204
36	Sensitive and specific single-molecule sequencing of 5-hydroxymethylcytosine. <i>Nature Methods</i> , 2012, 9, 75-77.	9.0	219

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37	5-Hydroxymethylcytosine (5-hmC) Specific Enrichment. <i>Bio-protocol</i> , 2012, 2, .	0.2	2
38	Tet-Mediated Formation of 5-Carboxylcytosine and Its Excision by TDG in Mammalian DNA. <i>Science</i> , 2011, 333, 1303-1307.	6.0	2,332
39	Syntheses of Two 5-Hydroxymethyl-2'-deoxycytidine Phosphoramidites with TBDMS as the 5-Hydroxymethyl Protecting Group and Their Incorporation into DNA. <i>Journal of Organic Chemistry</i> , 2011, 76, 4182-4188.	1.7	39
40	Bioorthogonal Labeling of 5-Hydroxymethylcytosine in Genomic DNA and Diazirine-Based DNA Photo-Cross-Linking Probes. <i>Accounts of Chemical Research</i> , 2011, 44, 709-717.	7.6	46
41	5-hmC-mediated epigenetic dynamics during postnatal neurodevelopment and aging. <i>Nature Neuroscience</i> , 2011, 14, 1607-1616.	7.1	746
42	Selective chemical labeling reveals the genome-wide distribution of 5-hydroxymethylcytosine. <i>Nature Biotechnology</i> , 2011, 29, 68-72.	9.4	955
43	Detection of 5-hydroxymethylcytosine in a combined glycosylation restriction analysis (CGRA) using restriction enzyme TaqI. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2011, 21, 5075-5077.	1.0	33
44	Targeting MgrA-Mediated Virulence Regulation in <i>Staphylococcus aureus</i> . <i>Chemistry and Biology</i> , 2011, 18, 1032-1041.	6.2	55
45	Detection of 5-Hydroxymethylcytosine in DNA by Transferring a Keto-Glucose by Using T4 Phage $\beta$ -Glucosyltransferase. <i>ChemBioChem</i> , 2011, 12, 1682-1685.	1.3	21
46	The hunt for 5-hydroxymethylcytosine: the sixth base. <i>Epigenomics</i> , 2011, 3, 521-523.	1.0	29
47	Integrating 5-Hydroxymethylcytosine into the Epigenomic Landscape of Human Embryonic Stem Cells. <i>PLoS Genetics</i> , 2011, 7, e1002154.	1.5	250
48	Intra/Intermolecular Direct Allylic Alkylation via Pd(II)-Catalyzed Allylic C-H Activation. <i>Journal of the American Chemical Society</i> , 2008, 130, 12901-12903.	6.6	256