

# Kaixiang Cao

## List of Publications by Year in descending order

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Version: 2024-02-01

12  
papers

728  
citations

933447

10  
h-index

1281871

11  
g-index

12  
all docs

12  
docs citations

12  
times ranked

1383  
citing authors

#	ARTICLE	IF	CITATIONS
1	Histone H3K4 monomethylation catalyzed by Trr and mammalian COMPASS-like proteins at enhancers is dispensable for development and viability. <i>Nature Genetics</i> , 2017, 49, 1647-1653.	21.4	168
2	PAF1 regulation of promoter-proximal pause release via enhancer activation. <i>Science</i> , 2017, 357, 1294-1298.	12.6	95
3	Not All H3K4 Methylations Are Created Equal: Mll2/COMPASS Dependency in Primordial Germ Cell Specification. <i>Molecular Cell</i> , 2017, 65, 460-475.e6.	9.7	81
4	Uncoupling histone H3K4 trimethylation from developmental gene expression via an equilibrium of COMPASS, Polycomb and DNA methylation. <i>Nature Genetics</i> , 2020, 52, 615-625.	21.4	76
5	Histone H3K4 methylation-dependent and -independent functions of Set1A/COMPASS in embryonic stem cell self-renewal and differentiation. <i>Genes and Development</i> , 2017, 31, 1732-1737.	5.9	68
6	An Mll4/COMPASS-Lsd1 epigenetic axis governs enhancer function and pluripotency transition in embryonic stem cells. <i>Science Advances</i> , 2018, 4, eaap8747.	10.3	55
7	A cryptic Tudor domain links BRWD2/PHIP to COMPASS-mediated histone H3K4 methylation. <i>Genes and Development</i> , 2017, 31, 2003-2014.	5.9	54
8	SET1A/COMPASS and shadow enhancers in the regulation of homeotic gene expression. <i>Genes and Development</i> , 2017, 31, 787-801.	5.9	48
9	DOT1L-controlled cell-fate determination and transcription elongation are independent of H3K79 methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27365-27373.	7.1	43
10	Coordinated regulation of cellular identity-associated H3K4me3 breadth by the COMPASS family. <i>Science Advances</i> , 2020, 6, eaaz4764.	10.3	37
11	A synthetic lethality screen reveals ING5 as a genetic dependency of catalytically dead Set1A/COMPASS in mouse embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2118385119.	7.1	3
12	Genetic and Epigenetic Deregulation of Enhancers in Cancer. , 2018, , .		0