Kaifu Chen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7664443/publications.pdf

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56	4,479	186254	155644
papers	citations	28 h-index	55 g-index

58	58	58	8550
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Methylation-dependent and -independent roles of EZH2 synergize in CDCA8 activation in prostate cancer. Oncogene, 2022, 41, 1610-1621.	5.9	6
2	MACMIC Reveals A Dual Role of CTCF in Epigenetic Regulation of Cell Identity Genes. Genomics, Proteomics and Bioinformatics, 2021, 19, 140-153.	6.9	4
3	A PRC2-independent function for EZH2 in regulating rRNA 2â€²-O methylation and IRES-dependent translation. Nature Cell Biology, 2021, 23, 341-354.	10.3	54
4	Fli1 ⁺ cells transcriptional analysis reveals an Lmo2â€“Prdm16 axis in angiogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	9
5	Reprogramming of bivalent chromatin states in NRAS mutant melanoma suggests PRC2 inhibition as a therapeutic strategy. Cell Reports, 2021, 36, 109410.	6.4	17
6	BMI1 is directly regulated by androgen receptor to promote castration-resistance in prostate cancer. Oncogene, 2020, 39, 17-29.	5.9	22
7	Antihistamine Drug Ebastine Inhibits Cancer Growth by Targeting Polycomb Group Protein EZH2. Molecular Cancer Therapeutics, 2020, 19, 2023-2033.	4.1	15
8	Reservoir of Fibroblasts Promotes Recovery From Limb Ischemia. Circulation, 2020, 142, 1647-1662.	1.6	33
9	Broad genic repression domains signify enhanced silencing of oncogenes. Nature Communications, 2020, 11, 5560.	12.8	10
10	Machine learning uncovers cell identity regulator by histone code. Nature Communications, 2020, 11, 2696.	12.8	25
11	MIF as a biomarker and therapeutic target for overcoming resistance to proteasome inhibitors in human myeloma. Blood, 2020, 136, 2557-2573.	1.4	33
12	TADsplimer reveals splits and mergers of topologically associating domains for epigenetic regulation of transcription. Genome Biology, 2020, 21, 84.	8.8	6
13	Role of Endothelial and Mesenchymal Cell Transitions in Heart Failure and Recovery Thereafter. Frontiers in Genetics, 2020, 11, 609262.	2.3	5
14	Beclin 2 negatively regulates innate immune signaling and tumor development. Journal of Clinical Investigation, 2020, 130, 5349-5369.	8.2	16
15	Nuclear S -Nitrosylation Defines an Optimal Zone for Inducing Pluripotency. Circulation, 2019, 140, 1081-1099.	1.6	17
16	Genetic Determinants of Allograft Hypertrophy- A Human Myocardial Biopsy Study. Journal of Cardiac Failure, 2019, 25, S110.	1.7	0
17	AIBP-mediated cholesterol efflux instructs hematopoietic stem and progenitor cell fate. Science, 2019, 363, 1085-1088.	12.6	90
18	Polycomb group proteins EZH2 and EED directly regulate androgen receptor in advanced prostate cancer. International Journal of Cancer, 2019, 145, 415-426.	5.1	51

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19	Roles of the HOXA10 gene during castrate-resistant prostate cancer progression. Endocrine-Related Cancer, 2019, 26, 279-292.	3.1	8
20	BMI1 regulates androgen receptor in prostate cancer independently of the polycomb repressive complex 1. Nature Communications, 2018, 9, 500.	12.8	65
21	TBX20 Regulates Angiogenesis Through the Prokineticin 2â€“Prokineticin Receptor 1 Pathway. Circulation, 2018, 138, 913-928.	1.6	31
22	PAF-Myc-Controlled Cell Stemness Is Required for Intestinal Regeneration and Tumorigenesis. Developmental Cell, 2018, 44, 582-596.e4.	7.0	22
23	Dna2 nuclease deficiency results in large and complex DNA insertions at chromosomal breaks. Nature, 2018, 564, 287-290.	27.8	33
24	HP1Î³ Promotes Lung Adenocarcinoma by Downregulating the Transcription-Repressive Regulators NCOR2 and ZBTB7A. Cancer Research, 2018, 78, 3834-3848.	0.9	63
25	3â€² UTR shortening represses tumor-suppressor genes in trans by disrupting ceRNA crosstalk. Nature Genetics, 2018, 50, 783-789.	21.4	148
26	MLL4 Is Required to Maintain Broad H3K4me3 Peaks and Super-Enhancers at Tumor Suppressor Genes. Molecular Cell, 2018, 70, 825-841.e6.	9.7	123
27	Homeobox oncogene activation by pan-cancer DNA hypermethylation. Genome Biology, 2018, 19, 108.	8.8	94
28	RPA binds histone H3-H4 and functions in DNA replicationâ€“coupled nucleosome assembly. Science, 2017, 355, 415-420.	12.6	71
29	Developing Spindlin1 small-molecule inhibitors by using protein microarrays. Nature Chemical Biology, 2017, 13, 750-756.	8.0	47
30	Lmo2 (LIM-Domain-Only 2) Modulates Sphk1 (Sphingosine Kinase) and Promotes Endothelial Cell Migration. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 1860-1868.	2.4	21
31	Sparse conserved under-methylated CpGs are associated with high-order chromatin structure. Genome Biology, 2017, 18, 163.	8.8	16
32	ZMYND8 Reads the Dual Histone Mark H3K4me1-H3K14ac to Antagonize the Expression of Metastasis-Linked Genes. Molecular Cell, 2016, 63, 470-484.	9.7	112
33	A feedback loop comprising PRMT7 and miR-24-2 interplays with Oct4, Nanog, Klf4 and c-Myc to regulate stemness. Nucleic Acids Research, 2016, 44, 10603-10618.	14.5	56
34	Broad H3K4me3 as A Novel Epigenetic Signature for Normal Development and Disease. Genomics, Proteomics and Bioinformatics, 2016, 14, 262-264.	6.9	8
35	An essential role for UTX in resolution and activation of bivalent promoters. Nucleic Acids Research, 2016, 44, 3659-3674.	14.5	63
36	The Overlooked Fact: Fundamental Need for Spike-In Control for Virtually All Genome-Wide Analyses. Molecular and Cellular Biology, 2016, 36, 662-667.	2.3	153

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37	MeCP2 binds to non-CG methylated DNA as neurons mature, influencing transcription and the timing of onset for Rett syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5509-5514.	7.1	256
38	Broad H3K4me3 is associated with increased transcription elongation and enhancer activity at tumor-suppressor genes. Nature Genetics, 2015, 47, 1149-1157.	21.4	276
39	A matter of access. Transcription, 2014, 5, e29355.	3.1	4
40	MACE: model based analysis of ChIP-exo. Nucleic Acids Research, 2014, 42, e156-e156.	14.5	84
41	Nucleosome loss leads to global transcriptional up-regulation and genomic instability during yeast aging. Genes and Development, 2014, 28, 396-408.	5.9	265
42	Transcriptional and genomic mayhem due to aging-induced nucleosome loss in budding yeast. Microbial Cell, 2014, 1, 133-136.	3.2	2
43	DANPOS: Dynamic analysis of nucleosome position and occupancy by sequencing. Genome Research, 2013, 23, 341-351.	5.5	331
44	Stabilization of the promoter nucleosomes in nucleosome-free regions by the yeast Cyc8â€“Tup1 corepressor. Genome Research, 2013, 23, 312-322.	5.5	33
45	Discovering Thiamine Transporters as Targets of Chloroquine Using a Novel Functional Genomics Strategy. PLoS Genetics, 2012, 8, e1003083.	3.5	22
46	Loss of the Methyl Lysine Effector Protein PHF20 Impacts the Expression of Genes Regulated by the Lysine Acetyltransferase MOF. Journal of Biological Chemistry, 2012, 287, 429-437.	3.4	30
47	Foxa2 and H2A.Z Mediate Nucleosome Depletion during Embryonic Stem Cell Differentiation. Cell, 2012, 151, 1608-1616.	28.9	181
48	SIRT7 links H3K18 deacetylation to maintenance of oncogenic transformation. Nature, 2012, 487, 114-118.	27.8	503
49	The Fun30 nucleosome remodeller promotes resection of DNA double-strand break ends. Nature, 2012, 489, 576-580.	27.8	219
50	NSD2 Links Dimethylation of Histone H3 at Lysine 36 to Oncogenic Programming. Molecular Cell, 2011, 44, 609-620.	9.7	356
51	An evolutionary analysis of trypanosomatid GP63 proteases. Parasitology Research, 2011, 109, 1075-1084.	1.6	23
52	Sampangine Inhibits Heme Biosynthesis in both Yeast and Human. Eukaryotic Cell, 2011, 10, 1536-1544.	3.4	23
53	A comprehensive analysis of protein phosphatases in rice and Arabidopsis. Plant Systematics and Evolution, 2010, 289, 111-126.	0.9	7
54	Sequence Signatures of Nucleosome Positioning in Caenorhabditis elegans. Genomics, Proteomics and Bioinformatics, 2010, 8, 92-102.	6.9	11

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55	The Complete Chloroplast Genome Sequence of Date Palm (Phoenix dactylifera L.). PLoS ONE, 2010, 5, e12762.	2.5	255
56	A novel DNA sequence periodicity decodes nucleosome positioning. Nucleic Acids Research, 2008, 36, 6228-6236.	14.5	33