Jian Xu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8133132/publications.pdf

Version: 2024-02-01

58	6,227	172457	168389
papers	citations	29 h-index	53 g-index

70	70	70	9092
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	MAnorm2 for quantitatively comparing groups of ChIP-seq samples. Genome Research, 2021, 31, 131-145.	5.5	36
2	Guanosine triphosphate links MYC-dependent metabolic and ribosome programs in small-cell lung cancer. Journal of Clinical Investigation, 2021, 131, .	8.2	33
3	Silencing of LINE-1 retrotransposons is a selective dependency of myeloid leukemia. Nature Genetics, 2021, 53, 672-682.	21.4	47
4	SIRT1 regulates sphingolipid metabolism and neural differentiation of mouse embryonic stem cells through c-Myc-SMPDL3B. ELife, 2021, 10, .	6.0	22
5	A unified model of human hemoglobin switching through single-cell genome editing. Nature Communications, 2021, 12, 4991.	12.8	22
6	Inner nuclear protein Matrin-3 coordinates cell differentiation by stabilizing chromatin architecture. Nature Communications, 2021, 12, 6241.	12.8	25
7	Convergence of oncogenic cooperation at single-cell and single-gene levels drives leukemic transformation. Nature Communications, 2021, 12, 6323.	12.8	10
8	Mixed Phenotype Acute Leukemia, B/Myeloid (Bilineal and Biphenotypic), With t(2;22)(q35;q12);EWSR1-FEV. Journal of Pediatric Hematology/Oncology, 2021, 43, e388-e394.	0.6	5
9	Therapy Response and Outcome Explained by Leukemia Cell of Origin. Cancer Discovery, 2020, 10, 1445-1447.	9.4	1
10	Lactate Dehydrogenase A Governs Cardiac Hypertrophic Growth in Response to Hemodynamic Stress. Cell Reports, 2020, 32, 108087.	6.4	43
11	Discovering How Heme Controls Genome Function Through Heme-omics. Cell Reports, 2020, 31, 107832.	6.4	21
12	Model-based analysis of chromatin interactions from dCas9-Based CAPTURE-3C-seq. PLoS ONE, 2020, 15, e0236666.	2.5	1
13	Enhancer dependence of cell-typeâ€“specific gene expression increases with developmental age. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21450-21458.	7.1	32
14	Multiplexed capture of spatial configuration and temporal dynamics of locus-specific 3D chromatin by biotinylated dCas9. Genome Biology, 2020, 21, 59.	8.8	27
15	Interrogation of enhancer function by enhancer-targeting CRISPR epigenetic editing. Nature Communications, 2020, 11, 485.	12.8	139
16	Noncoding Variants Connect Enhancer Dysregulation with Nuclear Receptor Signaling in Hematopoietic Malignancies. Cancer Discovery, 2020, 10, 724-745.	9.4	25
17	Elucidating Mechanisms of Acquired Resistance to IDH Inhibition By Saturation Variant Screening of Base-Edited Leukemia Cells. Blood, 2020, 136, 3-3.	1.4	0
18	MAP: model-based analysis of proteomic data to detect proteins with significant abundance changes. Cell Discovery, 2019, 5, 40.	6.7	11

#	Article	IF	Citations
19	Loss of EZH2 Reprograms BCAA Metabolism to Drive Leukemic Transformation. Cancer Discovery, 2019, 9, 1228-1247.	9.4	107
20	Installation of a cancer promoting WNT/SIX1 signaling axis by the oncofusion protein MLL-AF9. EBioMedicine, 2019, 39, 145-158.	6.1	13
21	Dissecting super-enhancer hierarchy based on chromatin interactions. Nature Communications, 2018, 9, 943.	12.8	179
22	Regulation of embryonic haematopoietic multipotency by EZH1. Nature, 2018, 553, 506-510.	27.8	70
23	Direct Promoter Repression by BCL11A Controls the Fetal to Adult Hemoglobin Switch. Cell, 2018, 173, 430-442.e17.	28.9	328
24	Quantitative integration of epigenomic variation and transcription factor binding using MAmotif toolkit identifies an important role of IRF2 as transcription activator at gene promoters. Cell Discovery, 2018, 4, 38.	6.7	17
25	GATA/Heme Multi-omics Reveals a Trace Metal-Dependent Cellular Differentiation Mechanism. Developmental Cell, 2018, 46, 581-594.e4.	7.0	31
26	CAPTURE: In Situ Analysis of Chromatin Composition of Endogenous Genomic Loci by Biotinylated dCas9. Current Protocols in Molecular Biology, 2018, 123, e64.	2.9	14
27	Regulation of mitochondrial biogenesis in erythropoiesis by mTORC1-mediated proteinÂtranslation. Nature Cell Biology, 2017, 19, 626-638.	10.3	126
28	The mitochondrial respiratory chain is essential for haematopoietic stem cell function. Nature Cell Biology, 2017, 19, 614-625.	10.3	244
29	CPS1 maintains pyrimidine pools and DNA synthesis in KRAS/LKB1-mutant lung cancer cells. Nature, 2017, 546, 168-172.	27.8	222
30	In Situ Capture of Chromatin Interactions by Biotinylated dCas9. Cell, 2017, 170, 1028-1043.e19.	28.9	236
31	In Situ Capture of the Molecular Composition of Erythroid Transcriptional Enhancers. Blood, 2017, 130, SCI-17-SCI-17.	1.4	0
32	Bcl11a Deficiency Leads to Hematopoietic Stem Cell Defects with an Aging-like Phenotype. Cell Reports, 2016, 16, 3181-3194.	6.4	85
33	Genetic inactivation of calpain-1 attenuates pain sensitivity in a humanized mouse model of sickle cell disease. Haematologica, 2016, 101, e397-e400.	3.5	14
34	Transcription factors LRF and BCL11A independently repress expression of fetal hemoglobin. Science, 2016, 351, 285-289.	12.6	260
35	Suppression of the SWI/SNF Component Arid1a Promotes Mammalian Regeneration. Cell Stem Cell, 2016, 18, 456-466.	11.1	112
36	Dynamic Control of Enhancer Repertoires Drives Lineage and Stage-Specific Transcription during Hematopoiesis. Developmental Cell, 2016, 36, 9-23.	7.0	204

#	Article	IF	Citations
37	Developmental Control of Polycomb Subunit Composition by GATA Factors Mediates a Switch to Non-Canonical Functions. Molecular Cell, 2015, 57, 304-316.	9.7	119
38	Role of the clathrin adaptor PICALM in normal hematopoiesis and polycythemia vera pathophysiology. Haematologica, 2015, 100, 439-451.	3.5	35
39	PRC2 Is Required to Maintain Expression of the Maternal Gtl2-Rian-Mirg Locus by Preventing De Novo DNA Methylation in Mouse Embryonic Stem Cells. Cell Reports, 2015, 12, 1456-1470.	6.4	64
40	Polycomb Repressive Complex 2 Regulates Normal Hematopoietic Stem Cell Function in a Developmental-Stage-Specific Manner. Cell Stem Cell, 2014, 14, 68-80.	11.1	275
41	Inflammatory signaling regulates embryonic hematopoietic stem and progenitor cell production. Genes and Development, 2014, 28, 2597-2612.	5.9	214
42	An SCF-FBXW7 Ubiquitin Ligase Mediated Feedback Loop Facilitates GATA Factor Switching and Reinforces Commitment to Terminal Erythroid Maturation. Blood, 2014, 124, 245-245.	1.4	0
43	Inflammatory Signaling Regulates Embryonic Hematopoietic Stem and Lymphoid Progenitor Cell Formation. Blood, 2014, 124, 2902-2902.	1.4	0
44	An Erythroid Enhancer of BCL11A Subject to Genetic Variation Determines Fetal Hemoglobin Level. Science, 2013, 342, 253-257.	12.6	518
45	Corepressor-dependent silencing of fetal hemoglobin expression by BCL11A. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6518-6523.	7.1	189
46	Identification Of BCL11A Structure-Function Domains For Fetal Hemoglobin Silencing. Blood, 2013, 122, 435-435.	1.4	3
47	Designing an Enhancer Landscape. Cell, 2012, 151, 929-931.	28.9	13
48	Combinatorial Assembly of Developmental Stage-Specific Enhancers Controls Gene Expression Programs during Human Erythropoiesis. Developmental Cell, 2012, 23, 796-811.	7.0	183
49	Inability to Express HOXA Cluster and BCL11A Genes Compromises Self-Renewal and Multipotency of hESC-Derived Hematopoietic Cells. Blood, 2012, 120, 1190-1190.	1.4	1
50	Hematopoietic SIN Lentiviral Micro RNA-Mediated Silencing of BCL11A: Pre-Clinical Evidence for a Sickle Cell Disease Gene-Therapy Trial. Blood, 2012, 120, 753-753.	1.4	1
51	Correction of Sickle Cell Disease in Adult Mice by Interference with Fetal Hemoglobin Silencing. Science, 2011, 334, 993-996.	12.6	281
52	A Functional Element Necessary for Fetal Hemoglobin Silencing. New England Journal of Medicine, 2011, 365, 807-814.	27.0	161
53	The erythroid/myeloid lineage fate paradigm takes a new player. EMBO Journal, 2011, 30, 983-985.	7.8	1
54	Correction of Murine Sickle Cell Disease Through Interference with Fetal Hemoglobin Silencing. Blood, 2011, 118, 351-351.	1.4	1

#	Article	IF	Citations
55	Transcriptional silencing of Î³-globin by BCL11A involves long-range interactions and cooperation with SOX6. Genes and Development, 2010, 24, 783-798.	5.9	304
56	Role of the KruÌˆppel-Type Zinc Finger Transcription Factor ZBP-89 In Human Globin Gene Regulation and Erythroid Development. Blood, 2010, 116, 2067-2067.	1.4	0
57	Developmental and species-divergent globin switching are driven by BCL11A. Nature, 2009, 460, 1093-1097.	27.8	339
58	Human Fetal Hemoglobin Expression Is Regulated by the Developmental Stage-Specific Repressor BCL11A. Science, 2008, 322, 1839-1842.	12.6	759