Yue Lu

List of Publications by Year in descending order

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		125106	111975
68	4,866 citations	35	67
papers	citations	h-index	g-index
70	70	70	11427
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Methyl-lysine readers PHF20 and PHF20L1 define two distinctÂgene expression–regulating NSL complexes. Journal of Biological Chemistry, 2022, 298, 101588.	1.6	1
2	Defining the mammalian coactivation of hepatic 12-h clock and lipid metabolism. Cell Reports, 2022, 38, 110491.	2.9	13
3	Usp22 Overexpression Leads to Aberrant Signal Transduction of Cancer-Related Pathways but Is Not Sufficient to Drive Tumor Formation in Mice. Cancers, 2021, 13, 4276.	1.7	4
4	CARM1 inhibition reduces histone acetyltransferase activity causing synthetic lethality in CREBBP/EP300-mutated lymphomas. Leukemia, 2020, 34, 3269-3285.	3.3	28
5	LRIG1 is a pleiotropic androgen receptor-regulated feedback tumor suppressor in prostate cancer. Nature Communications, 2019, 10, 5494.	5.8	13
6	Usp22 controls multiple signaling pathways that are essential for vasculature formation in the mouse placenta. Development (Cambridge), 2019 , 146 , .	1.2	30
7	GCN5 Regulates FGF Signaling and Activates Selective MYC Target Genes during Early Embryoid Body Differentiation. Stem Cell Reports, 2018, 10, 287-299.	2.3	27
8	Histone 2B-GFP Label-Retaining Prostate Luminal Cells Possess Progenitor Cell Properties and Are Intrinsically Resistant to Castration. Stem Cell Reports, 2018, 10, 228-242.	2.3	36
9	Digital Restriction Enzyme Analysis of Methylation (DREAM). Methods in Molecular Biology, 2018, 1708, 247-265.	0.4	11
10	Response to "XPA is primarily cytoplasmic but is transported into the nucleus upon UV damage― DNA Repair, 2018, 62, 30-31.	1.3	3
11	Linking prostate cancer cell AR heterogeneity to distinct castration and enzalutamide responses. Nature Communications, 2018, 9, 3600.	5.8	96
12	KDM6B overexpression activates innate immune signaling and impairs hematopoiesis in mice. Blood Advances, 2018, 2, 2491-2504.	2.5	29
13	CARM1 methylates MED12 to regulate its RNA-binding ability. Life Science Alliance, 2018, 1, e201800117.	1.3	43
14	MicroRNA-141 suppresses prostate cancer stem cells and metastasis by targeting a cohort of pro-metastasis genes. Nature Communications, 2017, 8, 14270.	5.8	187
15	Caloric restriction delays age-related methylation drift. Nature Communications, 2017, 8, 539.	5.8	204
16	Comprehensive analysis of gene expression patterns in Friedreich's ataxia fibroblasts by RNA sequencing reveals altered levels of protein synthesis factors and solute carriers. DMM Disease Models and Mechanisms, 2017, 10, 1353-1369.	1.2	38
17	Transcriptional consequences of XPA disruption in human cell lines. DNA Repair, 2017, 57, 76-90.	1.3	19
18	Downregulation of Human Endogenous Retrovirus Type K (HERV-K) Viral <i>env</i> RNA in Pancreatic Cancer Cells Decreases Cell Proliferation and Tumor Growth. Clinical Cancer Research, 2017, 23, 5892-5911.	3.2	88

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19	Developing a Novel Two-Dimensional Culture System to Enrich Human Prostate Luminal Progenitors that Can Function as a Cell of Origin for Prostate Cancer. Stem Cells Translational Medicine, 2017, 6, 748-760.	1.6	19
20	Analysis of DNA polymerase $\hat{1}\frac{1}{2}$ function in meiotic recombination, immunoglobulin class-switching, and DNA damage tolerance. PLoS Genetics, 2017, 13, e1006818.	1.5	12
21	RNA sequencing analyses reveal novel differentially expressed genes and pathways in pancreatic cancer. Oncotarget, 2017, 8, 42537-42547.	0.8	46
22	DMBA induced mouse mammary tumors display high incidence of activating <i>Pik3caH1047</i> and loss of function <i>Pten</i> mutations. Oncotarget, 2016, 7, 64289-64299.	0.8	51
23	PHF20 Readers Link Methylation of Histone H3K4 and p53 with H4K16 Acetylation. Cell Reports, 2016, 17, 1158-1170.	2.9	44
24	Deep RNA-Seq analysis reveals unexpected features of human prostate basal epithelial cells. Genomics Data, 2016, 7, 318-320.	1.3	0
25	Histone H3K4 methylation regulates deactivation of the spindle assembly checkpoint through direct binding of Mad2. Genes and Development, 2016, 30, 1187-1197.	2.7	21
26	Defining a Population of Stem-like Human Prostate Cancer Cells That Can Generate and Propagate Castration-Resistant Prostate Cancer. Clinical Cancer Research, 2016, 22, 4505-4516.	3.2	78
27	ATXN7L3 and ENY2 Coordinate Activity of Multiple H2B Deubiquitinases Important for Cellular Proliferation and Tumor Growth. Molecular Cell, 2016, 62, 558-571.	4.5	106
28	NANOG reprograms prostate cancer cells to castration resistance via dynamically repressing and engaging the AR/FOXA1 signaling axis. Cell Discovery, 2016, 2, 16041.	3.1	41
29	Stem cell and neurogenic gene-expression profiles link prostate basal cells to aggressive prostate cancer. Nature Communications, 2016, 7, 10798.	5.8	166
30	DNA Methylation Signature Reveals Cell Ontogeny of Renal Cell Carcinomas. Clinical Cancer Research, 2016, 22, 6236-6246.	3.2	47
31	Maternal Setdb1 Is Required for Meiotic Progression and Preimplantation Development in Mouse. PLoS Genetics, 2016, 12, e1005970.	1.5	75
32	Activation of HERV-K Env protein is essential for tumorigenesis and metastasis of breast cancer cells. Oncotarget, 2016, 7, 84093-84117.	0.8	106
33	Serum exosomal miR-4772-3p is a predictor of tumor recurrence in stage II and III colon cancer. Oncotarget, 2016, 7, 76250-76260.	0.8	93
34	Tyrosine kinase inhibitors induce mesenchymal stem cell–mediated resistance in BCR-ABL+ acute lymphoblastic leukemia. Blood, 2015, 125, 2968-2973.	0.6	29
35	<i>TET2</i> Mutations Affect Non-CpG Island DNA Methylation at Enhancers and Transcription Factor–Binding Sites in Chronic Myelomonocytic Leukemia. Cancer Research, 2015, 75, 2833-2843.	0.4	80
36	LSD1 is essential for oocyte meiotic progression by regulating CDC25B expression in mice. Nature Communications, 2015, 6, 10116.	5.8	38

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37	A Molecular Portrait of High-Grade Ductal Carcinoma <i>In Situ</i> . Cancer Research, 2015, 75, 3980-3990.	0.4	122
38	Epigenetic synergy between decitabine and platinum derivatives. Clinical Epigenetics, 2015, 7, 97.	1.8	33
39	Expanded GAA repeats impede transcription elongation through the <i>FXN </i> gene and induce transcriptional silencing that is restricted to the <i>FXN </i> locus. Human Molecular Genetics, 2015, 24, ddv397.	1.4	54
40	Defects of Lipid Synthesis Are Linked to the Age-Dependent Demyelination Caused by Lamin B1 Overexpression. Journal of Neuroscience, 2015, 35, 12002-12017.	1.7	51
41	Methylome sequencing for fibrolamellar hepatocellular carcinoma depicts distinctive features. Epigenetics, 2015, 10, 872-881.	1.3	17
42	SOX9 Regulates Multiple Genes in Chondrocytes, Including Genes Encoding ECM Proteins, ECM Modification Enzymes, Receptors, and Transporters. PLoS ONE, 2014, 9, e107577.	1.1	86
43	The Sox4/Tcf7l1 axis promotes progression of BCR-ABL-positive acute lymphoblastic leukemia. Haematologica, 2014, 99, 1591-1598.	1.7	22
44	TET1 is a maintenance DNA demethylase that prevents methylation spreading in differentiated cells. Nucleic Acids Research, 2014, 42, 6956-6971.	6.5	108
45	Arginine Methylation Facilitates the Recruitment of TOP3B to Chromatin to Prevent R Loop Accumulation. Molecular Cell, 2014, 53, 484-497.	4.5	199
46	Age-related epigenetic drift in the pathogenesis of MDS and AML. Genome Research, 2014, 24, 580-591.	2.4	76
47	The tumor promoting activity of the EP4 receptor forÂprostaglandin E ₂ in murine skin. Molecular Oncology, 2014, 8, 1626-1639.	2.1	16
48	Gcn5 and <scp>PCAF</scp> negatively regulate interferonâ€Î² production through <scp>HAT</scp> â€independent inhibition of <scp>TBK</scp> 1. EMBO Reports, 2014, 15, 1192-1201.	2.0	31
49	Integrated genetic approaches identify the molecular mechanisms of Sox4 in early B-cell development: intricate roles for RAG1/2 and CK1 $\hat{l}\mu$. Blood, 2014, 123, 4064-4076.	0.6	35
50	The epigenome of AML stem and progenitor cells. Epigenetics, 2013, 8, 92-104.	1.3	38
51	Identification of the NF-κB activating protein-like locus as a risk locus for rheumatoid arthritis. Annals of the Rheumatic Diseases, 2013, 72, 1249-1254.	0.5	6
52	Stabilization of the promoter nucleosomes in nucleosome-free regions by the yeast Cyc8–Tup1 corepressor. Genome Research, 2013, 23, 312-322.	2.4	33
53	Access to the Nucleus and Functional Association with c-Myc Is Required for the Full Oncogenic Potential of Î"EGFR/EGFRvIII. Journal of Biological Chemistry, 2013, 288, 3428-3438.	1.6	12
54	Architecture of epigenetic reprogramming following Twist1-mediated epithelial-mesenchymal transition. Genome Biology, 2013, 14, R144.	13.9	74

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55	Conserved DNA methylation patterns in healthy blood cells and extensive changes in leukemia measured by a new quantitative technique. Epigenetics, 2012, 7, 1368-1378.	1.3	66
56	SINE Retrotransposons Cause Epigenetic Reprogramming of Adjacent Gene Promoters. Molecular Cancer Research, 2012, 10, 1332-1342.	1.5	73
57	dsPIG: a tool to predict imprinted genes from the deep sequencing of whole transcriptomes. BMC Bioinformatics, 2012, 13, 271.	1.2	12
58	Dnmt3a is essential for hematopoietic stem cell differentiation. Nature Genetics, 2012, 44, 23-31.	9.4	916
59	Aberrant DNA Methylation Is Associated with Disease Progression, Resistance to Imatinib and Shortened Survival in Chronic Myelogenous Leukemia. PLoS ONE, 2011, 6, e22110.	1.1	97
60	Molecular mechanism by which the nucleoid occlusion factor, SlmA, keeps cytokinesis in check. EMBO Journal, 2011, 30, 154-164.	3.5	140
61	TDRD3 Is an Effector Molecule for Arginine-Methylated Histone Marks. Molecular Cell, 2010, 40, 1016-1023.	4.5	185
62	Analysis of epigenetic modifications by next generation sequencing., 2009, 2009, 6730.		3
63	Improving accuracy of multiple sequence alignment algorithms based on alignment of neighboring residues. Nucleic Acids Research, 2009, 37, 463-472.	6.5	18
64	REL, encoding a member of the NF-κB family of transcription factors, is a newly defined risk locus for rheumatoid arthritis. Nature Genetics, 2009, 41, 820-823.	9.4	305
65	Digital Restriction Enzyme Analysis of Methylation (DREAM) by Next Generation Sequencing Yields High Resolution Maps of DNA Methylation Blood, 2009, 114, 567-567.	0.6	2
66	Multiple Sequence Alignment Based on Profile Alignment of Intermediate Sequences. Journal of Computational Biology, 2008, 15, 767-777.	0.8	11
67	A Polynomial Time Solvable Formulation of Multiple Sequence Alignment. Journal of Computational Biology, 2006, 13, 309-319.	0.8	32
68	Mutations Affecting the Development of the Peripheral Nervous System in Drosophila: A Molecular Screen for Novel Proteins. Genetics, 2000, 156, 1691-1715.	1.2	68