

# Yue Lu

## List of Publications by Year in descending order

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Version: 2024-02-01

68  
papers

4,866  
citations

109321

35  
h-index

98798

67  
g-index

70  
all docs

70  
docs citations

70  
times ranked

10420  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dnmt3a is essential for hematopoietic stem cell differentiation. <i>Nature Genetics</i> , 2012, 44, 23-31.	21.4	916
2	REL, encoding a member of the NF- $\kappa$ B family of transcription factors, is a newly defined risk locus for rheumatoid arthritis. <i>Nature Genetics</i> , 2009, 41, 820-823.	21.4	305
3	Caloric restriction delays age-related methylation drift. <i>Nature Communications</i> , 2017, 8, 539.	12.8	204
4	Arginine Methylation Facilitates the Recruitment of TOP3B to Chromatin to Prevent R Loop Accumulation. <i>Molecular Cell</i> , 2014, 53, 484-497.	9.7	199
5	MicroRNA-141 suppresses prostate cancer stem cells and metastasis by targeting a cohort of pro-metastasis genes. <i>Nature Communications</i> , 2017, 8, 14270.	12.8	187
6	TDRD3 Is an Effector Molecule for Arginine-Methylated Histone Marks. <i>Molecular Cell</i> , 2010, 40, 1016-1023.	9.7	185
7	Stem cell and neurogenic gene-expression profiles link prostate basal cells to aggressive prostate cancer. <i>Nature Communications</i> , 2016, 7, 10798.	12.8	166
8	Molecular mechanism by which the nucleoid occlusion factor, SlmA, keeps cytokinesis in check. <i>EMBO Journal</i> , 2011, 30, 154-164.	7.8	140
9	A Molecular Portrait of High-Grade Ductal Carcinoma <i>in Situ</i> . <i>Cancer Research</i> , 2015, 75, 3980-3990.	0.9	122
10	TET1 is a maintenance DNA demethylase that prevents methylation spreading in differentiated cells. <i>Nucleic Acids Research</i> , 2014, 42, 6956-6971.	14.5	108
11	ATXN7L3 and ENY2 Coordinate Activity of Multiple H2B Deubiquitinases Important for Cellular Proliferation and Tumor Growth. <i>Molecular Cell</i> , 2016, 62, 558-571.	9.7	106
12	Activation of HERV-K Env protein is essential for tumorigenesis and metastasis of breast cancer cells. <i>Oncotarget</i> , 2016, 7, 84093-84117.	1.8	106
13	Aberrant DNA Methylation Is Associated with Disease Progression, Resistance to Imatinib and Shortened Survival in Chronic Myelogenous Leukemia. <i>PLoS ONE</i> , 2011, 6, e22110.	2.5	97
14	Linking prostate cancer cell AR heterogeneity to distinct castration and enzalutamide responses. <i>Nature Communications</i> , 2018, 9, 3600.	12.8	96
15	Serum exosomal miR-4772-3p is a predictor of tumor recurrence in stage II and III colon cancer. <i>Oncotarget</i> , 2016, 7, 76250-76260.	1.8	93
16	Downregulation of Human Endogenous Retrovirus Type K (HERV-K) Viral <i>env</i> RNA in Pancreatic Cancer Cells Decreases Cell Proliferation and Tumor Growth. <i>Clinical Cancer Research</i> , 2017, 23, 5892-5911.	7.0	88
17	SOX9 Regulates Multiple Genes in Chondrocytes, Including Genes Encoding ECM Proteins, ECM Modification Enzymes, Receptors, and Transporters. <i>PLoS ONE</i> , 2014, 9, e107577.	2.5	86
18	<i>TET2</i> Mutations Affect Non-CpG Island DNA Methylation at Enhancers and Transcription Factor Binding Sites in Chronic Myelomonocytic Leukemia. <i>Cancer Research</i> , 2015, 75, 2833-2843.	0.9	80

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19	Defining a Population of Stem-like Human Prostate Cancer Cells That Can Generate and Propagate Castration-Resistant Prostate Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 4505-4516.	7.0	78
20	Age-related epigenetic drift in the pathogenesis of MDS and AML. <i>Genome Research</i> , 2014, 24, 580-591.	5.5	76
21	Maternal Setdb1 Is Required for Meiotic Progression and Preimplantation Development in Mouse. <i>PLoS Genetics</i> , 2016, 12, e1005970.	3.5	75
22	Architecture of epigenetic reprogramming following Twist1-mediated epithelial-mesenchymal transition. <i>Genome Biology</i> , 2013, 14, R144.	9.6	74
23	SINE Retrotransposons Cause Epigenetic Reprogramming of Adjacent Gene Promoters. <i>Molecular Cancer Research</i> , 2012, 10, 1332-1342.	3.4	73
24	Mutations Affecting the Development of the Peripheral Nervous System in <i>Drosophila</i> : A Molecular Screen for Novel Proteins. <i>Genetics</i> , 2000, 156, 1691-1715.	2.9	68
25	Conserved DNA methylation patterns in healthy blood cells and extensive changes in leukemia measured by a new quantitative technique. <i>Epigenetics</i> , 2012, 7, 1368-1378.	2.7	66
26	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. <i>Human Molecular Genetics</i> , 2015, 24, ddv397.	2.9	54
27	Defects of Lipid Synthesis Are Linked to the Age-Dependent Demyelination Caused by Lamin B1 Overexpression. <i>Journal of Neuroscience</i> , 2015, 35, 12002-12017.	3.6	51
28	DMBA induced mouse mammary tumors display high incidence of activating <i>Pik3caH1047</i> and loss of function <i>Pten</i> mutations. <i>Oncotarget</i> , 2016, 7, 64289-64299.	1.8	51
29	DNA Methylation Signature Reveals Cell Ontogeny of Renal Cell Carcinomas. <i>Clinical Cancer Research</i> , 2016, 22, 6236-6246.	7.0	47
30	RNA sequencing analyses reveal novel differentially expressed genes and pathways in pancreatic cancer. <i>Oncotarget</i> , 2017, 8, 42537-42547.	1.8	46
31	PHF20 Readers Link Methylation of Histone H3K4 and p53 with H4K16 Acetylation. <i>Cell Reports</i> , 2016, 17, 1158-1170.	6.4	44
32	CARM1 methylates MED12 to regulate its RNA-binding ability. <i>Life Science Alliance</i> , 2018, 1, e201800117.	2.8	43
33	NANOG reprograms prostate cancer cells to castration resistance via dynamically repressing and engaging the AR/FOXA1 signaling axis. <i>Cell Discovery</i> , 2016, 2, 16041.	6.7	41
34	The epigenome of AML stem and progenitor cells. <i>Epigenetics</i> , 2013, 8, 92-104.	2.7	38
35	LSD1 is essential for oocyte meiotic progression by regulating CDC25B expression in mice. <i>Nature Communications</i> , 2015, 6, 10116.	12.8	38
36	Comprehensive analysis of gene expression patterns in Friedreich's ataxia fibroblasts by RNA sequencing reveals altered levels of protein synthesis factors and solute carriers. <i>DMM Disease Models and Mechanisms</i> , 2017, 10, 1353-1369.	2.4	38

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37	Histone 2B-GFP Label-Retaining Prostate Luminal Cells Possess Progenitor Cell Properties and Are Intrinsically Resistant to Castration. <i>Stem Cell Reports</i> , 2018, 10, 228-242.	4.8	36
38	Integrated genetic approaches identify the molecular mechanisms of Sox4 in early B-cell development: intricate roles for RAG1/2 and CK1 $\mu$ . <i>Blood</i> , 2014, 123, 4064-4076.	1.4	35
39	Stabilization of the promoter nucleosomes in nucleosome-free regions by the yeast Cyc8 $\alpha$ Tup1 corepressor. <i>Genome Research</i> , 2013, 23, 312-322.	5.5	33
40	Epigenetic synergy between decitabine and platinum derivatives. <i>Clinical Epigenetics</i> , 2015, 7, 97.	4.1	33
41	A Polynomial Time Solvable Formulation of Multiple Sequence Alignment. <i>Journal of Computational Biology</i> , 2006, 13, 309-319.	1.6	32
42	Gcn5 and PCAF negatively regulate interferon $\beta$ production through HAT $\alpha$ -independent inhibition of TBK1. <i>EMBO Reports</i> , 2014, 15, 1192-1201.	4.5	31
43	Usp22 controls multiple signaling pathways that are essential for vasculature formation in the mouse placenta. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	30
44	Tyrosine kinase inhibitors induce mesenchymal stem cell $\alpha$ -mediated resistance in BCR-ABL+ acute lymphoblastic leukemia. <i>Blood</i> , 2015, 125, 2968-2973.	1.4	29
45	KDM6B overexpression activates innate immune signaling and impairs hematopoiesis in mice. <i>Blood Advances</i> , 2018, 2, 2491-2504.	5.2	29
46	CARM1 inhibition reduces histone acetyltransferase activity causing synthetic lethality in CREBBP/EP300-mutated lymphomas. <i>Leukemia</i> , 2020, 34, 3269-3285.	7.2	28
47	GCN5 Regulates FGF Signaling and Activates Selective MYC Target Genes during Early Embryoid Body Differentiation. <i>Stem Cell Reports</i> , 2018, 10, 287-299.	4.8	27
48	The Sox4/Tcf7l1 axis promotes progression of BCR-ABL-positive acute lymphoblastic leukemia. <i>Haematologica</i> , 2014, 99, 1591-1598.	3.5	22
49	Histone H3K4 methylation regulates deactivation of the spindle assembly checkpoint through direct binding of Mad2. <i>Genes and Development</i> , 2016, 30, 1187-1197.	5.9	21
50	Transcriptional consequences of XPA disruption in human cell lines. <i>DNA Repair</i> , 2017, 57, 76-90.	2.8	19
51	Developing a Novel Two-Dimensional Culture System to Enrich Human Prostate Luminal Progenitors that Can Function as a Cell of Origin for Prostate Cancer. <i>Stem Cells Translational Medicine</i> , 2017, 6, 748-760.	3.3	19
52	Improving accuracy of multiple sequence alignment algorithms based on alignment of neighboring residues. <i>Nucleic Acids Research</i> , 2009, 37, 463-472.	14.5	18
53	Methylome sequencing for fibrolamellar hepatocellular carcinoma depicts distinctive features. <i>Epigenetics</i> , 2015, 10, 872-881.	2.7	17
54	The tumor promoting activity of the EP4 receptor for $\alpha$ prostaglandin E <sub>2</sub> in murine skin. <i>Molecular Oncology</i> , 2014, 8, 1626-1639.	4.6	16

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55	LRIG1 is a pleiotropic androgen receptor-regulated feedback tumor suppressor in prostate cancer. <i>Nature Communications</i> , 2019, 10, 5494.	12.8	13
56	Defining the mammalian coactivation of hepatic 12-h clock and lipid metabolism. <i>Cell Reports</i> , 2022, 38, 110491.	6.4	13
57	dsPIC: a tool to predict imprinted genes from the deep sequencing of whole transcriptomes. <i>BMC Bioinformatics</i> , 2012, 13, 271.	2.6	12
58	Access to the Nucleus and Functional Association with c-Myc Is Required for the Full Oncogenic Potential of $\beta$ EGFR/EGFRvIII. <i>Journal of Biological Chemistry</i> , 2013, 288, 3428-3438.	3.4	12
59	Analysis of DNA polymerase $\beta$ function in meiotic recombination, immunoglobulin class-switching, and DNA damage tolerance. <i>PLoS Genetics</i> , 2017, 13, e1006818.	3.5	12
60	Multiple Sequence Alignment Based on Profile Alignment of Intermediate Sequences. <i>Journal of Computational Biology</i> , 2008, 15, 767-777.	1.6	11
61	Digital Restriction Enzyme Analysis of Methylation (DREAM). <i>Methods in Molecular Biology</i> , 2018, 1708, 247-265.	0.9	11
62	Identification of the NF- $\kappa$ B activating protein-like locus as a risk locus for rheumatoid arthritis. <i>Annals of the Rheumatic Diseases</i> , 2013, 72, 1249-1254.	0.9	6
63	Usp22 Overexpression Leads to Aberrant Signal Transduction of Cancer-Related Pathways but Is Not Sufficient to Drive Tumor Formation in Mice. <i>Cancers</i> , 2021, 13, 4276.	3.7	4
64	Analysis of epigenetic modifications by next generation sequencing. , 2009, 2009, 6730.		3
65	Response to $\alpha$ -XPA is primarily cytoplasmic but is transported into the nucleus upon UV damage $\beta$ ; DNA Repair, 2018, 62, 30-31.	2.8	3
66	Digital Restriction Enzyme Analysis of Methylation (DREAM) by Next Generation Sequencing Yields High Resolution Maps of DNA Methylation.. <i>Blood</i> , 2009, 114, 567-567.	1.4	2
67	Methyl-lysine readers PHF20 and PHF20L1 define two distinct $\beta$ gene expression $\beta$ “regulating NSL complexes. <i>Journal of Biological Chemistry</i> , 2022, 298, 101588.	3.4	1
68	Deep RNA-Seq analysis reveals unexpected features of human prostate basal epithelial cells. <i>Genomics Data</i> , 2016, 7, 318-320.	1.3	0