

# Sheng Li

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6961790/publications.pdf>

Version: 2024-02-01

35  
papers

4,085  
citations

279798

23  
h-index

345221

36  
g-index

38  
all docs

38  
docs citations

38  
times ranked

8684  
citing authors

#	ARTICLE	IF	CITATIONS
1	methylKit: a comprehensive R package for the analysis of genome-wide DNA methylation profiles. <i>Genome Biology</i> , 2012, 13, R87.	9.6	1,541
2	Distinct evolution and dynamics of epigenetic and genetic heterogeneity in acute myeloid leukemia. <i>Nature Medicine</i> , 2016, 22, 792-799.	30.7	322
3	The Pivotal Regulatory Landscape of RNA Modifications. <i>Annual Review of Genomics and Human Genetics</i> , 2014, 15, 127-150.	6.2	284
4	Multi-platform assessment of transcriptome profiling using RNA-seq in the ABRF next-generation sequencing study. <i>Nature Biotechnology</i> , 2014, 32, 915-925.	17.5	217
5	Detecting and correcting systematic variation in large-scale RNA sequencing data. <i>Nature Biotechnology</i> , 2014, 32, 888-895.	17.5	174
6	A benchmark for RNA-seq quantification pipelines. <i>Genome Biology</i> , 2016, 17, 74.	8.8	160
7	Genetic and epigenetic heterogeneity in acute myeloid leukemia. <i>Current Opinion in Genetics and Development</i> , 2016, 36, 100-106.	3.3	130
8	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. <i>Nature Communications</i> , 2014, 5, 5125.	12.8	122
9	TET2 Deficiency Causes Germinal Center Hyperplasia, Impairs Plasma Cell Differentiation, and Promotes B-cell Lymphomagenesis. <i>Cancer Discovery</i> , 2018, 8, 1632-1653.	9.4	120
10	Lung mesenchymal cells elicit lipid storage in neutrophils that fuel breast cancer lung metastasis. <i>Nature Immunology</i> , 2020, 21, 1444-1455.	14.5	109
11	An optimized algorithm for detecting and annotating regional differential methylation. <i>BMC Bioinformatics</i> , 2013, 14, S10.	2.6	105
12	Loss of CHD1 Promotes Heterogeneous Mechanisms of Resistance to AR-Targeted Therapy via Chromatin Dysregulation. <i>Cancer Cell</i> , 2020, 37, 584-598.e11.	16.8	96
13	DNA methylation-calling tools for Oxford Nanopore sequencing: a survey and human epigenome-wide evaluation. <i>Genome Biology</i> , 2021, 22, 295.	8.8	87
14	CRISPR artificial splicing factors. <i>Nature Communications</i> , 2020, 11, 2973.	12.8	70
15	Dynamic evolution of clonal epialleles revealed by methclone. <i>Genome Biology</i> , 2014, 15, 472.	8.8	67
16	CUP-AI-Dx: A tool for inferring cancer tissue of origin and molecular subtype using RNA gene-expression data and artificial intelligence. <i>EBioMedicine</i> , 2020, 61, 103030.	6.1	67
17	Jak1 Integrates Cytokine Sensing to Regulate Hematopoietic Stem Cell Function and Stress Hematopoiesis. <i>Cell Stem Cell</i> , 2017, 21, 489-501.e7.	11.1	58
18	Molecular Biology and Evolution of Cancer: From Discovery to Action. <i>Molecular Biology and Evolution</i> , 2020, 37, 320-326.	8.9	43

#	ARTICLE	IF	CITATIONS
19	Enhanced CRISPR-based DNA demethylation by Casilio-ME-mediated RNA-guided coupling of methylcytosine oxidation and DNA repair pathways. <i>Nature Communications</i> , 2019, 10, 4296.	12.8	41
20	Graph embedding and unsupervised learning predict genomic sub-compartments from HiC chromatin interaction data. <i>Nature Communications</i> , 2020, 11, 1173.	12.8	40
21	The serine hydroxymethyltransferase-2 (SHMT2) initiates lymphoma development through epigenetic tumor suppressor silencing. <i>Nature Cancer</i> , 2020, 1, 653-664.	13.2	35
22	Genetic and epigenetic heterogeneity and the impact on cancer relapse. <i>Experimental Hematology</i> , 2017, 54, 26-30.	0.4	31
23	TET2 deficiency reprograms the germinal center B cell epigenome and silences genes linked to lymphomagenesis. <i>Science Advances</i> , 2020, 6, eaay5872.	10.3	29
24	Extracellular vesicles in DLBCL provide abundant clues to aberrant transcriptional programming and genomic alterations. <i>Blood</i> , 2018, 132, e13-e23.	1.4	23
25	Somatic Mutations Drive Specific, but Reversible, Epigenetic Heterogeneity States in AML. <i>Cancer Discovery</i> , 2020, 10, 1934-1949.	9.4	23
26	ChIA-PIPE: A fully automated pipeline for comprehensive ChIA-PET data analysis and visualization. <i>Science Advances</i> , 2020, 6, eaay2078.	10.3	22
27	Clinical Genomics: Challenges and Opportunities. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 2016, 26, 97-113.	0.9	12
28	HBA-DEALS: accurate and simultaneous identification of differential expression and splicing using hierarchical Bayesian analysis. <i>Genome Biology</i> , 2020, 21, 171.	8.8	7
29	epihet for intra-tumoral epigenetic heterogeneity analysis and visualization. <i>Scientific Reports</i> , 2021, 11, 376.	3.3	6
30	DNA methylation-calling tools for Oxford Nanopore sequencing: a survey and human epigenome-wide evaluation. <i>Genome Biology</i> , 2021, 22, 295.	8.8	6
31	JAK1 As a Convergent Regulator of Hematopoietic Stem Cell Function and Stress Hematopoiesis. <i>Blood</i> , 2016, 128, 722-722.	1.4	3
32	Divergent Dynamics of Epigenetic and Genetic Heterogeneity in Relapsed Acute Myeloid Leukemia. <i>Blood</i> , 2015, 126, 306-306.	1.4	2
33	EPIG-09GENETIC AND EPIGENETIC TUMOR EVOLUTION IN GLIOMATOSIS CEREBRI. <i>Neuro-Oncology</i> , 2015, 17, v88.1-v88.	1.2	1
34	Epigenetic Deregulation In Relapsed Acute Myeloid Leukemia. <i>Blood</i> , 2013, 122, 2499-2499.	1.4	1
35	Relapse-specific mutations in cytosolic 5â€™-nucleotidase II in childhood acute lymphoblastic leukemia.. <i>Journal of Clinical Oncology</i> , 2012, 30, 9507-9507.	1.6	0