

# Yaping Liu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9175822/publications.pdf>

Version: 2024-02-01

30  
papers

15,448  
citations

331670

21  
h-index

552781

26  
g-index

40  
all docs

40  
docs citations

40  
times ranked

30565  
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
2	Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017, 550, 204-213.	27.8	3,500
3	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	27.8	1,252
4	Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , 2017, 550, 244-248.	27.8	764
5	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. <i>Nature Communications</i> , 2018, 9, 1825.	12.8	748
6	Regions of focal DNA hypermethylation and long-range hypomethylation in colorectal cancer coincide with nuclear lamina-associated domains. <i>Nature Genetics</i> , 2012, 44, 40-46.	21.4	588
7	Dynamic landscape and regulation of RNA editing in mammals. <i>Nature</i> , 2017, 550, 249-254.	27.8	495
8	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. <i>Nature Genetics</i> , 2018, 50, 956-967.	21.4	389
9	Genome-wide mapping of nucleosome positioning and DNA methylation within individual DNA molecules. <i>Genome Research</i> , 2012, 22, 2497-2506.	5.5	381
10	Bis-SNP: Combined DNA methylation and SNP calling for Bisulfite-seq data. <i>Genome Biology</i> , 2012, 13, R61.	9.6	230
11	The impact of rare variation on gene expression across tissues. <i>Nature</i> , 2017, 550, 239-243.	27.8	229
12	Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease. <i>Nature Genetics</i> , 2017, 49, 1664-1670.	21.4	179
13	Estimating the causal tissues for complex traits and diseases. <i>Nature Genetics</i> , 2017, 49, 1676-1683.	21.4	166
14	Joint profiling of DNA methylation and chromatin architecture in single cells. <i>Nature Methods</i> , 2019, 16, 991-993.	19.0	155
15	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. <i>Genome Research</i> , 2017, 27, 1843-1858.	5.5	139
16	Identification and characterization of novel amphioxus microRNAs by Solexa sequencing. <i>Genome Biology</i> , 2009, 10, R78.	9.6	136
17	Machine learning enables detection of early-stage colorectal cancer by whole-genome sequencing of plasma cell-free DNA. <i>BMC Cancer</i> , 2019, 19, 832.	2.6	110
18	The role of DNA methylation in directing the functional organization of the cancer epigenome. <i>Genome Research</i> , 2015, 25, 467-477.	5.5	90

#	ARTICLE	IF	CITATIONS
19	Identifying <i>cis</i> -mediators for <i>trans</i> -eQTLs across many human tissues using genomic mediation analysis. <i>Genome Research</i> , 2017, 27, 1859-1871.	5.5	72
20	HDMCP uncouples yeast mitochondrial respiration and alleviates steatosis in L02 and hepG2 cells by decreasing ATP and H2O2 levels: A novel mechanism for NAFLD. <i>Journal of Hepatology</i> , 2009, 50, 1019-1028.	3.7	40
21	Evidence of reduced recombination rate in human regulatory domains. <i>Genome Biology</i> , 2017, 18, 193.	8.8	38
22	At the dawn: cell-free DNA fragmentomics and gene regulation. <i>British Journal of Cancer</i> , 2022, 126, 379-390.	6.4	27
23	FinaleDB: a browser and database of cell-free DNA fragmentation patterns. <i>Bioinformatics</i> , 2021, 37, 2502-2503.	4.1	20
24	Cell identity bookmarking through heterogeneous chromatin landscape maintenance during the cell cycle. <i>Human Molecular Genetics</i> , 2017, 26, 4231-4243.	2.9	14
25	Oral administration of <i>Lactobacillus plantarum</i> 299v modulates gene expression in the ileum of pigs: prediction of crosstalk between intestinal immune cells and sub-mucosal adipocytes. <i>Genes and Nutrition</i> , 2015, 10, 10.	2.5	8
26	Abstract 5177: Spatial co-fragmentation pattern of cell-free DNA recapitulates in vivo chromatin organization and identifies tissue-of-origin. , 2019, , .		2
27	Su1658 " Machine Learning Enables Detection of Early-Stage Colorectal Cancer by Whole-Genome Sequencing of Plasma Cell-Free Dna. <i>Gastroenterology</i> , 2019, 156, S-600-S-601.	1.3	1
28	Abstract 5689: Identify tissue-of-origin in cancer cfDNA by whole genome sequencing. , 2017, , .		1
29	Exploring the cancer methylome. <i>BMC Proceedings</i> , 2012, 6, .	1.6	0
30	Abstract 4780: The effects of the global loss of DNA methylation on the functional organization of the epigenome. , 2014, , .		0